ROME, SEPTEMBER 16 - 19, 2023
AUDITORIUM DELLA TECNICA

12TH

PROBIOTICS, PREBIOTICS & NEW FOODS

NUTRACEUTICALS, BOTANICALS & PHYTOCHEMICALS FOR NUTRITION & HUMAN, ANIMAL AND MICROBIOTA HEALTH

3RD SCIENCE & BUSINESS SYMPOSIUM

SCIENTIFIC ORGANIZERS

L. Capurso (Italy)

A. Gasbarrini (Italy)

A. Guarino (Italy) - Pediatric Day

L. Morelli (Italy)

INTERNATIONAL SCIENTIFIC COMMITTEE

G. Barbara (Italy)

R. Berni Canani (Italy) - Pediatric Day

P. Brigidi (Italy)

G. Clarke (Ireland)

W. M. de Vos (The Netherlands)

D. Del Rio (Italy)

A. Fasano (USA)

V. Fogliano (The Netherlands)

F. Guarner (Spain)

M. Koch (Italy)

P. Lavermicocca (Italy)

P. Malard (Switzerland)

R. Marabelli (France)

A. Ouwehand (Finland)

G. Paraskevakos (Canada)

R. Pecere (Belgium)

L. Putignani (Italy)

M. Rescigno (Italy)

N. Segata (Italy)

K. M. Tuohy (UK)

F. Visioli (Italy)

UNDER THE PATRONAGE

Consiglio Nazionale delle Ricerche

ipa INTERNATIONAL PROBIOTICS ASSOCIATION

ipa EUROPE INTERNATIONAL PROBIOTICS ASSOCIATION

WORLD GASTROENTEROLOGY ORGANISATION WGO

European Helicobacter & Microbiota Study Group

PAN AMERICAN CROHN'S AND COLITIS ORGANISATION

SIGE

Fondazione Aldo Torsoli

SINut Società Italiana di Nutraceutica

FIMMG Federazione Italiana Medici di Famiglia

Società Italiana di Scienze dell'Alimentazione SISA

Nfi NUTRITION FOUNDATION OF ITALY

MTCC Mediterranean

MTCC, Mediterranean Task Force for Cancer Control

UNDER THE PATRONAGE

AGGEI
Associazione Giovani Gastroenterologi ed Endoscopisti Italiani

AGUI
Associazione Ginecologi Universitari Italiani

AIMO
Associazione Italiana Medici Oculisti

SIGR
Società Italiana di GastroReumatologia

European Scientific League Probiotics

GLOBAL PREBIOTIC ASSOCIATION

BIOSTIME INSTITUTE NUTRITION & CARE

SISDCA
Società Italiana per lo studio dei Disturbi del Comportamento Alimentare
ANORESSIE BULIMIE OBESITÀ

PROBIOSTUDIO
ITALIAN ACADEMY FOR THE STUDY OF HUMAN MICROBIOTA

Programme at a Glance

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Scientific Programme

Saturday, September 16

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Sunday, September 17

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Aula Louis Pasteur 2 14
Aula Élie Metchnikoff 22

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PROGRAMME AT A GLANCE

AUDITORIUM	AULA PASTEUR	AULA METCHNIKOFF	AULA ARCHITETTURA	AULA PASTEUR 2
		PEDIATRIC DAY **08.30-10.00** MICROBIOME: PREGNANCY, BIRTH AND INFANCY **(SESSIONE ECM)**		
9.00-9.50 LECTURES **(SESSIONE ECM)**	**9.00-11.00** PROBIOTICS: TECHNOLOGICAL AND FUNCTIONAL ASPECTS **(SESSIONE ECM)**			**09.30 – 13.30** ORAL COMMUNICATIONS
9.50-10.20 VIS A VIS **(SESSIONE ECM)**		**10.00-11.00** LECTURE **(SESSIONE ECM)**	**10.00-17.30** B2B	
10.20 -11.45 PHYTOCHEMICALS AND HUMAN HEALTH: NEW FINDINGS **(SESSIONE ECM)**	**11.00-11.30** LECTURE **(SESSIONE NON ECM)**	**11.00-11.30** LECTURE **(SESSIONE ECM)**		
	11.30 – 12.30 SYMPOSIUM EHMSG AND ItPROM **(SESSIONE NON ECM)**	**11.30-13.00** INFANCY **(SESSIONE ECM)**		
11.45-12.45 AGGEI SESSION **(NO ECM)**	**12.30 – 13.30** EYE MICROBIOTA **(NO ECM)**			
12.45-13.30 GUT-SKIN AXIS **(NO ECM)**		**13.00 - 13.30** LECTURE **(SESSIONE ECM)**		
13.30-14.30 LUNCH				
14.30-14.40 WELCOME ADDRESSES **(NO ECM)**				
14.40-17.20 OPENING SESSION **(NO ECM)**		**15.30-17.00** NUTRITION AND DIET IMPLICATIONS **(SESSIONE ECM)**		
		17.00-18.30 PRESENT AND FUTURE FOR PREBIOTICS, PROBIOTICS, POSTBIOTICS USE IN PREGNANCY AND INFANCY **(SESSIONE ECM)**		
17.20-19.20 LECTURES **(NO ECM)**				
19.30 WELCOME COCKTAIL				

AUDITORIUM	AULA PASTEUR	AULA METCHNIKOFF	AULA ARCHITETTURA	AULA PASTEUR 2
8.30-10.00 NEXT GENERATION THERAUPETIC BACTERIA: STATE OF THE ART **(SESSIONE ECM)**	**8.30-10.00** MODELLING PROBIOTIC, PREBIOTIC & NEW FOOD FUNCTIONALITY WITHIN THE GUT USING ADVANCED IN VITRO MODELS **(SESSIONE ECM)**			
10.00-12.00 GUT MICROBIOTA AND IMMUNITY **(SESSIONE ECM)**	**10.00-12.00** POLYPHENOLS AND HEALTH **(SESSIONE ECM)**	**IPA DAY** **10.00-13.30** MORNING SESSION: WELCOME AND I NTRODUCTION FROM IPA DESK. THE BIOTICS SESSION TALKS.	**10.00 – 17.30** B2B	**10.00 – 12.30** ORAL COMMUNICATIONS
12.00-13.30 IBD MICROBIOTA AND PROBIOTICS **(SESSIONE ECM)**	**12.00-13.30** GUT MICROBIOME AND DIET IN MALNUTRITION **(SESSIONE ECM)**			
13.30-14.30 LUNCH				
14.30-16.00 MICROBIOTA AND ITS MODULATION IN IBS **(SESSIONE ECM)**	**14.30-15.30** GUT-BRAIN AXIS **(SESSIONE ECM)**	**14.30-15.15** AFTERNOON SESSION: PUBLIC STANDARDS FOR THE PROBIOTIC INDUSTRY		**14.30 – 17.00** ORAL COMMUNICATIONS
16.00-17.00 THE MICROBIOME AND BILIOPANCREATIC DISORDERS: EGG OR CHICKEN? **(SESSIONE ECM)**	**15.30-17.00** AUTISM AND GUT/ORAL MICROBIOME **(SESSIONE ECM)**	**15.15-17.15** IPA EUROPE SESSION		
17.00-18.20 MICROBIOTA AND CANCER **(SESSIONE ECM)**	**17.00-19.00** LECTURES **(SESSIONE ECM)**			
18.20-19.00 LECTURES **(SESSIONE ECM)**				

AUDITORIUM	AULA PASTEUR
8.30-10.00 HUMAN GUT MICROBIOTA AND INTERACTION WITH THE HOST **(SESSIONE ECM)**	**8.30-10.00** MEDITERRANEAN TASK FORCE FOR CANCER CONTROL (MTCC) **(SESSIONE ECM)**
10.00-11.30 GUT MICROBIOTA AND LIVER **(SESSIONE ECM)**	
11.30-12.30 PRESENT AND FUTURE OF FMT **(SESSIONE ECM)**	

SCIENTIFIC PROGRAMME

CORSO FIMMG

SESSIONE ECM

09.00 - 14.00	**CONOSCIAMO VERAMENTE I PROBIOTICI? E PERCHÉ DOVREMMO UTILIZZARLI?**
09.00 - 09.30	Introduzione: *L. Capurso (Roma), A. Chiriatti (Roma)*
09.30 - 10.00	Probiotici e medico di medicina generale *A. Chiriatti (Roma)*
10.00 - 10.30	Il microbiota intestinale *L. Capurso (Roma)*
10.30 - 11.00	I probiotici *M. Marignani (Roma)*
11.00 - 11.30	Probiotici nelle malattie infiammatorie croniche intestinali (IBD) *F. Scaldaferri (Roma)*
11.30 - 12.00	Probiotici nella sindrome dell'intestino irritabile (IBS) *L. R. Lopetuso (Roma)*
12.00 - 12.30	Probiotici e fegato *M. Marignani (Roma)*
12.30 - 13.00	EBM e probiotici *M. Koch (Roma)*
13.00 - 13.30	Discussione
13.30 - 14.00	Conclusioni *L. Capurso (Roma), A. Chiriatti (Roma)*

SESSIONE ECM

09.00 - 09.50 **LECTURES**
Chairs: M. Koch (Italy), F. Scaldaferri (Italy)

09.00 - 09.30 Prospective cohort studies to mechanistically link gut microbiome to disease pathogenesis: the future of personalized treatments and disease interception
A. Fasano (USA)

09.30 - 09.50 The "*Inumata* ": a young woman in the history of the gluten intolerance
G. Gasbarrini (Italy)

SESSIONE ECM

09.50 - 10.20 **VIS À VIS**
Personalized vs Evidence-Based Probiotic Medicine and Nutrition: the case of Probiotics
M. Koch (Italy), G. Grosso (Italy)

SESSIONE ECM

10.20 - 11.45 **PHYTOCHEMICALS AND HUMAN HEALTH: NEW FINDINGS**
Chairs: D. Del Rio (Italy), F. Visioli (Italy)

10.20 - 10.35 The emerging role of probiotics as sport supplements
E. Iglesias (Spain)

10.35 - 10.50 Glucosinolates and their manifold biological activities
P. Riso (Italy)

10.50 - 11.05 Sulfaceuticals as emerging modulators of human health
V. Calderone (Italy)

11.05 - 11.20 (Poly)phenols and personalized nutrition: the role of the gut microbiota
P. Mena (Italy)

11.20 - 11.35 Gut microbiome response to personalized nutrition: a population-scale study
N. Segata (Italy), F. Asnicar (Italy)

11.35 - 11.45 Discussion

SESSIONE ECM

11.45 - 12.45 **AGGEI (ASSOCIAZIONE GIOVANI GASTROENTEROLOGI ED ENDOSCOPISTI ITALIANI) SESSION**
Chairs: L.R. Lopetuso (Italy), V. Petito (Italy)

11.45 - 12.05 Intestinal permeability, inflammation and microbiota: where do we stand
A. Fasano (USA)

12.05 - 12.20 Inflammation and microbiota in extraintestinal diseases: the new challenge
P. Puca (Italy), I. Teani (Italy)

12.20 - 12.35 New frontiers of probiotics in gut barrier modulation
R. de Sire (Italy), P. Visaggi (Italy)

12.35 - 12.45 Discussants: *I. Marafini (Italy), D. Noviello (Italy), L.F. Pisani (Italy), F. Strati (Italy), P. Visaggi (Italy),*

SESSIONE NON ECM

12.45 - 13.30 **GUT-SKIN AXIS**
Chair: M. Picardo (Italy)

12.45 - 13.10 Antioxidant dietary fiber reduces atopic dermatitis by modulating gut microbiota
V. Fogliano (The Netherlands)

13.10 - 13.30 The effect of probiotics on skin wrinkles and skin dryness
A. Ouwehand (Finland)

13.30 - 14.30 **Lunch**

SESSIONE NON ECM

14.30 - 14.40 **WELCOME ADDRESSES**
L. Capurso (Italy),
L. Frulloni (Italy) President SIGE (Società italiana di Gastroenterologia)

SESSIONE NON ECM

14.40 - 17.20 **OPENING SESSION**
Chair: A. Gasbarrini (Italy)

14.40 - 14.50 Welcome from WGO
G. Macedo, (Portugal)
President WGO (World Gastroenterology Organization)

14.50 - 15.10 Holobiota and holobiome: a "whole" introduction to "Holo"
L. Morelli (Italy)

15.10 - 15.30 ONE HEALTH, a Global Approach
R. Marabelli (France)

15.30 - 15.50 Challenges and opportunities in defining sustainable healthy foods and diets: where are we?
I. Gandolfi (Italy)

15.50 - 16.25 Gut microbiome and health: mechanistic insights
W. M. de Vos (The Netherlands)

16.25 - 16.50 The microbiota modulation: probiotics, antibiotics or fecal microbiota transplantation?
A. Gasbarrini (Italy)

16.50 - 17.05 The…all biotic revolution: what is next and what do all these terms really mean?
G. Paraskevakos (Canada)

17.05 - 17.20 Probiotics in Europe - How to strengthen the use of probiotics and support health
R. Pecere (Belgium)

SESSIONE NON ECM

17.20 - 19.20 **LECTURES**
Chairs: L. Capurso (Italy), L. Morelli (Italy)

17.20 - 17.40 Gut metabolomics in cardio-vascular diseases
G. Stefanini (Italy)

17.40 - 18.00 *In vitro* assessment of probiotic attributes as a useful prelude toward a personalized bacteriotherapy
E. Ghelardi (Italy)

18.00 - 18.30 Insights from recent studies on probiotics and gut microbiome
D. Obis (France)

18.30 - 19.00 From Michelangelo to Leonardo: translational challenges for *biotics in the microbiome era
G. Grompone (Sweden)

19.00 - 19.20 Face to face: Gut-Urogenital axis: a pathway to women's health
F. Franceschi (Italy), F. Vicariotto (Italy)

SESSIONE ECM

09.00 - 11.00 **PROBIOTICS: TECHNOLOGICAL AND FUNCTIONAL ASPECTS**
Chairs: C. Randazzo (Italy), R. Satokari (Finland)

09.00 - 09.20 Functional features of probiotics from the human niche
A. Pino (Italy)

09.20 - 09.40 Riboflavin (vit B2) production in Lactic Acid Bacteria
G. Spano (Italy)

09.40 - 10.00 *Odoribacter splanchnicus* interactions with the gut epithelium and formulation for potential therapeutic use
R. Satokari (Finland)

10.00 - 10.20 KILLING MIcrobes SOFTLY: balancing probiotics heat inactivation while preserving functionality
V. Taverniti (Italy)

10.20 - 10.40 Use of an advanced technology platform to investigate the impact of probiotics i n the GI tract
M. Marzorati (Belgium)

10.40 - 11.00 Discussion

SESSIONE NON ECM

11.00 - 11.30 **LECTURE**

11.00 - 11.30 Microbial biomarkers in metabolic syndrome
A. Gasbarrini (Italy)

11.30 - 12.30 SESSIONE NON ECM

EHMSG (EUROPEAN HELICOBACTER AND MICROBIOTA STUDY GROUP) AND ItPROM (ASSOCIAZIONE ITALIANA PER LA MEDICINA PROBIOTICA) SYMPOSIUM: WHAT'S NEWS ON GUT MICROBIOTA
Chairs: F. Franceschi (Italy), G. Gasbarrini (Italy)

11.30 - 11.50 Gastric Microbiota: cross talk among *H. pylori* and other microrganisms
E. Bessède (France)

11.50 - 12.10 Impact of the use of antibiotics on gut microbiota
F. Megraud, (France)

12.10 - 12.30 Probiotics to improve *H. Pylori* eradication
P. Malfertheiner, (Germany)

SESSIONE NON ECM

12.30 - 13.30 **EYE MICROBIOTA**
Chair: C. Tamburrelli (Italy)

12.30 - 12.50 Gut Microbioma and eye disease
P. Bonci (Italy)

12.50 - 13.10 Ocular Surface Microbiome in health and disease
D. Borroni (Italy)

13.10 - 13.30 Discussion

ORAL COMMUNICATION 09.30 - 13.30

Chairs: *M. Koch (Italy), F. Ferrario (Italy), P. Fracasso (Italy)*

GUT MICROBIOTA

OC.1 - 93 **PREDICTING EARLY RADIATION ENTEROPATHY FROM THE BASELINE BACTERIAL COMPOSITION OF THE INTESTINAL MICROBIOTA OF PROSTATE CANCER PATIENTS**

Jacopo Iacovacci [1] - Mara Serena Serafini [1] - Loris De Cecco [1] - Barbara Avuzzi [1] - Barbara Noris Chiorda [1] - Fabio Badenchini [1] - Tommaso Giandini [1] - Alessandro Cicchetti [1] - Nadia Zaffaroni [1] - Valentina Doldi [1] - Elisa Mancinelli [1] - Eliana Gioscio [1] - Andrea Devecchi [1] - Ester Orlandi [2] - Sergio Villa [1] - Michela Dispinzeri [1] - Luca Possenti [1] - Federica Palorini [1] - Miguel Reis Ferreira [3] - Riccardo Valdagni [1] - Tiziana Rancati [1]

Fondazione IRCCS Istituto Nazionale dei Tumori di Milano, -, Milan, Italy [1] - National Center for Oncological Hadrontherapy (CNAO), -, Pavia, Italy [2] - King's College London, London, United Kingdom [3]

OC.2 - 130 **INVESTIGATING THE MOLECULAR RELATIONSHIP BETWEEN BIFIDOBACTERIA AND HUMAN MILK HORMONE INSULIN**

Sonia Mirjam Rizzo [1] - Giulia Alessandri [1] - Gabriele Andrea Lugli [1] - Federico Fontana [1] - Chiara Tarracchini [1] - Leonardo Mancabelli [2] - Alice Viappiani [3] - Massimiliano G Bianchi [2] - Ovidio Bussolati [2] - Douwe van Sinderen [4] - Marco Ventura [1] - Francesca Turroni [1]

University of Parma, Department of Chemistry, Life Sciences and Environmental Sustainability, Parma, Italy [1] - University of Parma, Department of Medicine and Surgery, Parma, Italy [2] - GenProbio srl, Parma, Italy [3] - National University of Ireland, APC Microbiome Institute and School of Microbiology, Cork, Ireland [4]

OC.3 - 131 **EVALUATION OF THE PERSISTENCE OF BIFIDOBACTERIUM LONGUM SUBSP. LONGUM IN THE HUMAN GUT ACROSS THE ENTIRE LIFE SPAN AND ITS POTENTIAL ANTI-AGING ROLE AS NATURAL MODULATOR OF THE HOST INNATE IMMUNITY**

Giulia Longhi [1] - Gabriele Andrea Lugli [1] - Massimiliano Giovanni Bianchi [2] - Sonia Mirjam Rizzo [1] - Chiara Tarracchini [1] - Leonardo Mancabelli [2] - Laura Maria Vergna [1] - Giulia Alessandri [1] - Federico Fontana [1] - Giuseppe Taurino [2] - Martina Chiu [2] - Christian Milani [1] - Douwe van Sinderen [3] - Ovidio Bussolati [2] - Marco Ventura [1] - Francesca Turroni [1]

University of Parma, Department of Chemistry, Life Sciences, and Environmental Sustainability, Parma, Italy [1] - University of Parma, Department of Medicine and Surgery, Parma, Italy [2] - National University of Ireland, APC Microbiome Institute and School of Microbiology, Cork, Ireland [3]

OC.4 - 133 **EXPLORING THE INTERACTIONS BETWEEN NASOPHARYNGEAL AND GUT MICROBIOME IN THE MODULATION OF COVID-19 INFECTION: THE COVIDBIOME PROJECT**

Leonardo Mancabelli [1] - Giuseppe Taurino [1] - Andrea Ticinesi [2] - Tecla Ciociola [1] - Federica Vacondio [3] - Christian Milani [4] - Federico Fontana [4] - Gabriele Andrea Lugli [4] - Chiara Tarracchini [4] - Giulia Alessandri [4] - Alice Viappiani [5] - Massimiliano Bianchi [1] - Antonio Nouvenne [2] - Alfredo Antonio Chetta [1] - Francesca Turroni [4] - Tiziana Meschi [2] - Marco Mor [3] - Ovidio Bussolati [1] - Marco Ventura [4]

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OC.5 - 148

ROLE OF XENOSIALIZATION IN THE PATHOGENESIS OF COLITIS IN THE CANINE MODEL; POSSIBLE POSITIVE EFFECTS OF NEW PROBIOTIC BLENDS

Giacomo Rossi [1] - *Lucia Biagini* [1] - *Alessandra Gavazza* [1] - *Mateo Cerquetella* [1] - *Sara Mangiaterra* [1] - *Daniela Olivero* [2] - *Barbara Simionati* [3] - *Ilaria Patuzzi* [3] - *Fiorella Carnevali* [4]
University of Camerino, School of Biosciences and Veterinary Medicine, Camerino, Italy-[1] - BIESSEA - Laboratory of Veterinary analyses, Milano, Italy [2]- Eubiome Srl. University of Padova, Padova, Italy [3]- ENEA - Centro Ricerche Casaccia – Roma, Italy [4]

OC.6 - 167

A MECHANISTIC APPROACH TO HARNESS THE HYBRID TWO-COMPONENT SYSTEM OF THE HUMAN COLONIC BACTEROIDOTA AS BIOMARKERS FOR MANIPULATION OF HOST HEALTH

Isaac Cann [1] - *Ahmed Abdel-Hamid* [1] - *Janaina Cavalcante* [1] - *David Bianchi* [2] - *Gabriel Pereira* [1] - *Patrick Schimmel* [1] - *Weihao Ge* [2] - *Kingsley Boateng* [1] - *Rebecca Hess* [3] - *Misael Trigo* [2] - *Sophia Nelson* [3] - *Navya Jallepally* [4] - *Haley Brown* [5] - *Ka Lam Nguyen* [6] - *Manal Alhawsawi* [7] - *Francisco Vilaplana Domingo* [8] - *Wenyan Mei* [6] - *Nicole Koropatkin* [5] - *Christina Fliege* [2] - *Roderick Mackie* [1]
University of Illinois Urbana-Champaign, Carl R. Woese Institute for Genomic Biology, Urbana, United States [1] - University of Illinois Urbana-Champaign, National Center for Supercomputing Applications (NCSA), Urbana, United States [2]- University of Illinois Urbana-Champaign, School of Molecular and Cellular Biology, Urbana, United States [3]- University of Illinois Urbana-Champaign, Department of Animal Science, Urbana, United States [4]- University of Michigan Medical School, Department of Microbiology and Immunology, Ann Arbor, United States [5] - University of Illinois Urbana-Champaign, College of Veterinary Medicine, Urbana, United States [6] - University of Illinois Urbana-Champaign, Division of Nutritional Sciences, Urbana, United States [7] - KTH Royal Institute of Technology, Division of Glycoscience, Stockholm, Sweden [8]

OC.7 - 170

THE ROLE OF INTESTINAL BACTERIA RELEASING VITAMIN K2-MK7 IN THE PROCESS OF COLON CARCINOGENESIS

Magdalena Strus [1] - *Bogusław Baś* [2] - *Katarzyna Jedlińska* [2] - *Joanna Smajdor* [2] - *Aleksandra Polichт* [1] *Jagiellonian*
University Medical College, Department of Microbiology, Kraków, Poland [1] - AGH University of Science and Technology, Faculty of Materials Science and Ceramics; Department of Analytical Chemistry, Kraków, Poland [2]

OC.8 - 184

THE 16S RRNA GENE AMPLICON SEQUENCING ERROR: HOW FLUORESCENCE IN SITU HYBRIDISATION (FISH) REVEALS A MAJOR FLAW IN MICROBIOME ANALYSIS

Jiri Snaidr [1] - *Carolin Richly* [1] - *Claudia Beimfohr* [1]
Vermicon AG, Microbiology, Hallbergmoos, Germany [1]

OC.9 - 194

A PRECLINICAL STUDY TO EXPLORE THE IMPACT OF DIETARY GLYCOTOXINS ON GUT HOMEOSTASIS AND MICROBIOME COMPOSITION

Emanuela Tirelli [1] - *Mariachiara Pucci* [1] - *Gloria Bignotti* [2] - *Stefania Zini* [3] - *Linda Torri* [4] - *Marta Bardelli* [2] - *Moris Cadei* [3] - *Vincenzo Villanacci* [4] - *Simona Fiorentini* [2] - *Giulia Abate* [1] - *Daniela Uberti* [1]
University of Brescia, Department of Molecular and Translational Medicine, Brescia, Italy [1] - University of Brescia, Department of Molecular and Translational Medicine, Section of Microbiology, Brescia, Italy [2] - University of Brescia, Anatomic Pathology Unit, Brescia, Italy [3] - Spedali Civili di Brescia, Institute of Pathology, Brescia, Italy [4]

OC.10 - 83

PROBIOTICS FOR EARLY MICROBIOTA DEVELOPMENT (PEACE PROJECT)

Lise Sanchez [1] - *Alexis Mosca* [2] - *Philippe Langella* [3] - *Sylvie Binda* [1] - *Rebeca Martin Rosique* [3]
Lallemand Health Solutions, Research and development, Montreal, Canada [1] - *Assistance publique Hôpitaux de Paris (APHP), Hospital Robert Debré, Paris, France* [2] - *INRAE, MICALIS, Jouy-en-Josas, France* [3]

OC.11 - 110

INTERACTIONS BETWEEN INTESTINAL MICROBIOTA, MUCUS LAYER AND DIETARY FIBER: TOWARDS PREVENTIVE STRATEGIES TO MITIGATE VIRULENCE OF FOOD-BORNE PATHOGEN ENTEROTOXIGENIC ESCHERICHIA COLI

Lucie Etienne-Mesmin [1] - *Sauvaitre Thomas* [1] - *Van Landuyt Josefien* [2] - *Durif Claude* [1] - *Delbaere Karen* [2] - *Huile Ségolène* [3] - *Chaucheyras-Durand Frdrique* [4] - *Van Herreweghen Florence* [2] - *Van de Wiele Tom* [2] - *Blanquet-Diot Stéphanie* [1]
Université Clermont Auvergne, Umr 454 Medis, Clermont-Ferrand, France [1] - Ghent University, Faculty Of Bioscience Engineering, Center For Microbial Ecology And Technology (Cmet), Ghent, Belgium [2] - Hari&Co, Lyon, France [3] - Lallemand Sas, Blagnac, France [4]

OC.12 - 64

A NEW IN VITRO HUMAN COLON MODEL SIMULATING OBESITY-RELATED GUT MICROBIOTA DYSBIOSIS

Ophélie Uriot [1] - *Charlote Deschamps* [1] - *Morgane Brun* [1] - *Mélanie Pouget* [2] - *Lucie Etienne-Mesmin* [1] - *Monique Alric* [1] - *Cyril Chaudemanche* [3] - *Yves Boirie* [4] - ***Stéphanie Blanquet-Diot*** [1]
Umr 454 Medis, Universite Clermont Auvergne, Clermont-Ferrand, France [1] - Service De Nutrition Clinique, Chu Clermont-Fd : Site Gabriel-Montpied, Clermont-Ferrand, France [2] - General Mills France, -, Boulogne- Billancourt, France [3] - Umr 1019 Inrae, Unite De Nutrition Humaine, Chu Clermont-Fd : Site Gabriel-Montpied, Clermont-Ferrand, France [4]

OC.13 - 50 **EFFECTS OF PECTIN-ENRICHED SMOOTHIE CONSUMPTION ON GUT MICROBIOTA AND HEALTH PARAMETERS: A CROSSOVER STUDY**

Susan Pihelgas [(1)] - *Kristel Ehala-Aleksejev* [(1)] - *Rain Kuldjärv* [(2)] - *Ann Jõeleht* [(1)] - *Jekaterina Kazantseva* [(1)] - *Kaarel Adamberg* [(1)]
TFTAK, Metagenomics, Tallinn, Estonia [(1)] - TFTAK, Functional foods and beverages, Tallinn, Estonia [(2)]

OC.14 - 99 **EXERCISE AND GUT MICROBIOTA**

Sabrina Donati Zeppa [(1)] - *Vilberto Stocchi* [(2)]
Department of Biomolecular science, University of Urbino, Urbino, Italy [(1)] - Dipartimento di Scienze Umane e Promozione della Qualità della Vita, Università Telematica San Raffaele, Roma, Italy [(2)]

OC.15 - 34 **INSIGHT INTO THE ATHLETIC GUT MICROBIOTA: EXERCISE AS A DETERMINANT OF THE GUT MICROBIOTA COMPOSITION**

Silvia Barbaresi [(1)]
Ghent University, Movement and Sport Science, Ghent, Belgium [(1)]

ORAL COMMUNICATION
PROBIOTICS

OC.16 - 28 **EFFECT OF STANDARD AND PROBIOTIC YOGURT ON HYPERCHOLESTEROLEMIC RATS**

Amani Alrasheedi [1] - *Ghaida Obaid* [1]
King Abdulaziz University, Human Sciences and design, Jeddah, Saudi Arabia [1]

OC.17 - 47 **PHYSICHOCHEMICAL, ANTIOXIDANT, AND ANTIMICROBIAL ACTIVITIES OF A NANOENCAPSULATED SYNBIOTIC AS A TAILORED ANTIBIOTIC ALTERNATIVE FOR FOOD PRODUCING ANIMALS**

Nesrein M. Hashem [1] - *Nourhan S. Hosny* [2] - *Nagwa El-Desoky* [1] - *Yosra A. Soltan* [1] - *Mohamed G. Shehata* [3] - *Ahmed A. Elolimy* [4] - *Sobhy M.A. Sallam* [1] - *El-Sayed M. Abu-Tor* [1]
Animal and Fish Production Department, Faculty of Agriculture (El-Shatby), Alexandria University, Alexandria 21545, Egypt [1] - Livestock Research Department, Arid Lands Cultivation Research Institute, City of Scientific Research and Technological Applications (SRTA-City), Alexandria, Egypt [2] - Department of Food Technology, Arid Lands Cultivation Research Institute, City of Scientific Research and Technological Applications (SRTA-City), Alexandria, Egypt [3] - Animal Production Department, National Research Centre, Dokki, Giza 12622, Cairo, Egypt [4]

OC.18 - 124 **POTENTIAL EFFECT OF A PROBIOTIC MIX AGAINST SARS-COV-2 INFECTION**

Langella Philippe [1] - *Torres-Maravilla Edgar* [1] - *Wasniewski Marine* [2] - *Servat Alexandre* [2] - *Picard-Meyer Evelyne* [2] - *Saint-Criq Vinciane* [1] - *Aucouturier Anne* [1] - *Chain Florian* [1] - *Holowacz Sophie* [3] - *Boue Franck* [2] - *Waligora- Dupriet Anne-Judith* [4] - *Monchatre-Leroy Elodie* [2] - *Jacouton Elsa* [3]
INRAe, Micalis Institute, Jouy en Josas, France [1] - ANSES, LRFSN - Laboratoire de la rage et de la faune sauvage de Nancy, Malzéville, France [2] - PiLeJe, PiLeJe Laboratoire, Carré Suffren, 31–35 rue de la Fédération, 75015 Paris, France [3] - Université de Paris, INSERM, UMRS1139, 3PHM, F-75006, Paris, France [4]

OC.19 - 141 **THE ROLE OF A PROBIOTIC CONSORTIUM IN THE TREATMENT OF FATIGUE AND OTHER SYMPTOMS IN LONG COVID-19 SYNDROME: A RANDOMIZED, DOUBLE-BLIND, PLACEBO-CONTROLLED STUDY (DELONG#3)**

Federica Facciotti [1] - *Beatrice Marinoni* [2] - *Alessandro Rimondi* [2] - *Federico Botaro* [2] - *Clorinda Ciafardini* [3] - *Chiara Amoroso* [3] - *Martina Muià* [3] - *Bruna Caridi* [2] - *Daniele Noviello* [2] - *Alessandra Bandera* [4] - *Andrea Gori* [4] - *Marco Mantero* [5] - *Francesco Blasi* [5] - *Roberta Ferrucci* [6] - *Maurizio Vecchi* [3] - *Flavio Caprioli* [3]
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OC.20 - 119 **PROBIOTIC PROPERTIES OF LACTOBACILLUS FERMENTUM AND PEDIOCOCCUS PENTOSACEUS ENCAPSULATED WITH OR WITHOUT HYDROGEL CELLULOSE MICROFIBER FROM OIL PALM LEAVES**

Usman Usman [(1)] - *Yusmarini Yusuf* [(1)] - *Agrina Syahrul* [(2)] - *Emma Riftyan* [(1)] - *Faizan Muhammad* [(1)] - *Lula Mutia* [(1)] - Swiji Paluvi Lasari [(1)] - Chiara Aliya Ramadhana [(1)]
Universitas Riau, Agricultural Technology, Pekanbaru, Indonesia [(1)] - Universitas Riau, Nursing, Pekanbaru, Indonesia [(2)]

OC.21 - 159 **MOLECULAR DISSECTION OF THE MODE OF ACTION OF AKKERMANSIA MUCINIPHILA, A NEXT GEN BENEFICIAL MICROBE**

Anneleen Segers [(1)] - *Hanne L.P. Tytgat* [(1)] - *Willem M. de Vos* [(1)]
Wageningen University & Research, Laboratory of Microbiology, Wageningen, Netherlands [(1)]

OC.22 - 191 **EFFICACY OF ALIVE MULTISTRAIN PROBIOTIC CO-SUPPLEMENTATION WITH OMEGA-3 PUFA ON PANCREATIC BETA-CELL FUNCTION IN TYPE 2 DIABETES PATIENT**

Maryana Savytska [(1)] - *Dmytro Kyriienko* [(2)] - *Iuliia Komisarenko* [(3)] - *Tetyana Falalyeyeva* [(4)] - *Nazarii Kobyliak* [(3)]
Danylo Halytsky Lviv National Medical University, Normal Physiology Department, Lviv, Ukraine [(1)] - Kyiv City Clinical Endocrinology Center, Endocrinology Department, Kyiv, Ukraine [(2)] - Bogomolets National Medical University, Endocrinology Department, Kyiv, Ukraine [(3)] - Taras Shevchenko National University of Kyiv, Educational and Scientific Centre «Institute of Biology and Medicine», Kyiv, Ukraine [(4)]

OC.23 - 42 **PROTECTIVE EFFECT OF SYNBIOTIC MIX AGAINST INFLAMMATION: IN-VITRO AND IN-VIVO APPROACHES**

Anita Rawat [(1)] - *Mahendra Bishnoi* [(1)] - *Kanthi Kiran Kondepudi* [(1)]
National Agri-Food Biotechnology Institute, Food and Nutrition Biotechnology, Mohali, India [(1)]

OC.24 - 198 **THE EFFECT OF COMBINATION OF BUTYRIC ACID, BIFIDOBACTERIUM AND FRUCTOOLIGOSACCHARIDES IN A YOUNG PATIENT WITH RHOEMHELD SYNDROME A CASE PRESENTATION**

Vegim Zhaku [1], Sheqibe Beadini [1,2], Nexhbedin Beadini(3), Sevxhane Zhaku [4]
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OC.25 - 182 **AKKERMANSIA MUCINIPHILA ADMINISTRATION PROMOTES A HEALTHY AGING BY MODULATING THE GUT MICROBIOTA IN OLD FEMALE MICE**

Nuria Salazar [1] - Estefanía Diaz- Del Cerro [2] - Judith Félix-Escalera [2] - Silvia Arboleya [1] - Mónica de la Fuente [2] - Miguel Gueimonde [1]
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OC.26 - 180 **MANAGEMENT OF METABOLIC DISORDERS THROUGH SPECIFIC PROBIOTICS INTERVENTION**

Maria Magdalena Coman [1] - Maria Vitoria Micioni Di Bonaventura [2] - Carlo Cifani [2] - Francesco Sofi [3] - Amedeo Amedei [3] - Stefania Silvi [4] - Maria Cristina Verdenelli [1]
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OC.27 - 155 **EFFECT OF A MULTI STRAIN PROBIOTIC MIXTURE CONSUMPTION ON ANXIETY AND DEPRESSION SYMPTOMS INDUCED IN ADULT MICE BY POSTNATAL MATERNAL SEPARATION**

*Franccesca De Santa [1] - Georgios Strimpakos [1] - Nicole Marchetti [1] - Giorgio Gargari [2] - Alessio Torcinaro [1] - Stefania Arioli [2] - Diego Mora [2] - Carla Petrella [1] - **Stefano Farioli Vecchioli** [1]*
CNR, IBBC, Monterotondo Scalo (RM), Italy [1] - DEFENS, University of Milan, Milan, Italy [2]

OC.28 - 89 **THE ROLE OF PSYCHOBIOTIC CEREBIOME® IN MODULATING THE MICROBIOTA-GUT-BRAIN AXIS: A REVIEW OF PRECLINICAL AND CLINICAL DATA**

Ola Kassem [1]
Lallemand Health Solutions, Research & Development Department, Montreal, Canada [1]

OC.29 - 199 **EFFECT OF PROBIOTICS ON AUTONOMIC NERVOUS SYSTEM FUNCTION OF PATIENTS WITH MILD ALZHEIMER'S DISEASE**

*Stella Angeli [1] - Ioanna Kousiappa [2] - Stelios Georgiades [1] - Savvas Papacostas [1] - Andreas Koupparis [3] - Yiolanda Christou [4] - George Loucaides [5] - Stavros Bashiardes [6] - Andreas Hadjisavvas [7] - Mihalis Panagiotidis [7] - Aleksandar Jovanovic [1] - **Nicoleta Nicolaou** [1]*
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OC.30 - 181 **IN VITRO EVALUATION OF A NEW BLEND OF PROBIOTIC STRAINS AGAINST PATHOGENS INVOLVED IN ACNE DISORDER**

Lucia Occhigrossi [1] *- Maria Magdalena Coman [2] - Giulia Nannini [3] - Elena Niccolai [3] - Amedeo Amedei [3] - Stefania Silvi [1] - Maria Cristina Verdenelli [2]*
University of Camerino, School of Biosciences and Veterinary Medicine, Camerino, Italy [1] - Synbiotec Srl, R&D, Camerino, Italy [2] - University of Florence, Department of Experimental and Clinical Medicine, Florence, Italy [3]

OC.31 - 171 **COMPREHENSIVE PROFILING AND CHARACTERIZATION OF UNTARGETED EXTRA CELLULAR METABOLITES IN FERMENTATION PROCESSES: INSIGHTS AND ADVANCES IN ANALYSIS AND IDENTIFICATION**

Marianna Ciaccia [1] *- Giulia Mensa [2] - Monica Marzagalli [2] - Silvia Rapacioli [2] - Maurizio Bettiga [2] - Gennaro Agrimi [1] - Isabella Pisano [1]*
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OC.32 - 178 **CLINICAL EFFICACY OF PROBIOTICS IN ALLERGIC RHINITIS: PRELIMINARY RESULTS FROM A RANDOMIZED CONTROLLED TRIAL**

Lisa Lungaro [1] *- Francesca Manza [1] - Patrizia Malfa [2] - Anna Costanzini [1] - Guido Valentini [1] - Elisa Viciani [3] - Luisa Abate [4] - Fabio Caputo [1] - Giorgio Zoli [1] - Umberto Volta [5] - Giovanni Barbara [5] - Vincenzo Stanghellini [5] - Roberto De Giorgio [1] - Giacomo Caio [1]*
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PEDIATRIC DAY

THE GROWING CHILD AND THE EVOLVING GUT MICROBIOME: A WINDOW OF OPPORTUNITY TO IMPROVE HUMAN HEALTH AND PREVENT DISEASES

DEFINING BEST TRAJECTORIES FOR FUELING THE BENEFICIAL IMPACT OF GUT MICROBIOME ON CHILD HEALTH

SESSIONE ECM

08.30 - 10.00 **MICROBIOME: PREGNANCY, BIRTH AND INFANCY**
Chairs: A. Guarino (Italy), R. Berni Canani (Italy)

Pregnancy and neonatal age

08.30 - 08.50 The impact of maternal diet during pregnancy on the developing microbiome
O. Koren (Israel)

08.50 - 09.10 Impact of early life factors on microbiome development and later asthma risk
J. Stokholm (Denmark)

09.10 - 09.30 Oral microbiome in pregnancy and preterm delivery
F. Indrio (Italy)

09.30 - 09.50 Gut microbiome in preterm infants
S. Rautava (Finland)

09.50 - 10.00 Summary and conclusions

SESSIONE ECM

10.00 - 11.00 **LECTURES**
Chairs: F. Indrio (Italy), R. Shamir (Israel)

10.00 - 10.30 SARS-CoV 2 enterocyte interaction: the origin of the MIS-C
A. Guarino (Italy)

10.30 - 11.00 Biotics in infant or follow-on formulas, preterm formulas and cow milk allergy formulas
E. C. Dinleyici (Turkey)

SESSIONE ECM

11.00 - 11.30 **LECTURE**
Introduction: F. Vicariotto (Italy)

11.00 - 11.20 Probiotics supporting female life stages: reproduction, pregnancy and menopause
C. Montelius (Sweden)

11.20 - 11.30 Conclusions: *F. Vicariotto (Italy)*

SESSIONE ECM

11.30 - 13.00 **INFANCY**
Chair: R. Francavilla (Italy)

11.30 - 12.00 Microbiome and breastfeeding
C. Campoy (Spain)

12.00 - 12.30 Microbiome and growth
R. Shamir (Israel)

12.30 - 13.00 Summary and conclusions

SESSIONE ECM

13.00 - 13.30 **LECTURE**
Chair: A. Guarino (Italy)

13.00 - 13.30 Microbiota in undernourished children: a therapeutic opportunity?
A. Lo Vecchio (Italy)

13.30 - 14.30 **Lunch**

SESSIONE ECM

15.30 - 17.00 **NUTRITION AND DIET IMPLICATIONS**
Chair: R. Berni Canani (Italy)

15.30 - 15.50 Human milk oligosaccharide driven benefits for all life stages
J. Lane (Ireland)

15.50 - 16.10 Healthy diet and microbiome - a food system perspective
F. Fontaine (Italy)

16.10 - 16.30 Mimicking mother's milk: an effective strategy?
Y. Vandenplas (Belgium)

16.30 - 17.00 Summary and conclusions

SESSIONE ECM

17.00 - 18.30 **PRESENT AND FUTURE FOR PREBIOTICS, PROBIOTICS, POSTBIOTICS USE IN PREGNANCY AND INFANCY**
Chairs: A. Guarino (Italy), Y. Vandenplas (Belgium)

Acting on microbiome for diseases prevention and treatment

17.00 - 17.20 Prebiotics and synbiotics
R. Francavilla (Italy)

17.20 - 17.40 Probiotics
H. Szajewska (Poland)

17.40 - 18.00 Postbiotics
R. Berni Canani (Italy)

18.00 - 18.30 Summary and conclusions: *A. Guarino (Italy), R. Berni Canani (Italy)*

SESSIONE ECM

08.30 - 10.00 **NEXT GENERATION THERAPEUTIC BACTERIA: STATE OF THE ART**
Chair: W. M. de Vos (The Netherlands)

08.30 - 09.00 Potential uses of *Faecalibacterium prausnitzii* in human health
P. Langella (France)

09.00 - 09.30 Cardiometabolic benefits of *Anaerobacterium soehngenii (Eubacterium hallii)*
W. M. de Vos (The Netherlands)

09.30 - 10.00 *Dysosmobacter welbionis:* a novel candidate?
M. Van Hul (Belgium)

SESSIONE ECM

10.00 - 12.00 **GUT MICROBIOTA AND IMMUNITY**
Chair: G. Ippolito (Italy)

10.00 - 10.30 **Lecture:** *Bifidobacteria* a key microbial group of the human gut microbiota
M. Ventura (Italy)

10.30 - 10.50 **Workshop:** Modulation of the innate immune response by commensal microbiota

Introduction
M. Clementi (Italy)

10.50 - 11.10 The innate immune response to respiratory viruses
I. Zanoni (USA)

11.10 - 11.30 Priming of the antiviral immune response by the gut microbiota
N.O. Gekara (Sweden)

11.30 - 11.50 Modulation of the commensal microbiota as antiviral strategy: any possible clinical application
N. Mancini (Italy)

11.50 - 12.00 Discussion

SESSIONE ECM

12.00 - 13.30 **IBD MICROBIOTA AND PROBIOTICS**
Chairs: F. Scaldaferri (Italy), M. Vecchi (Italy)

12.00 - 12.15 Intestinal microbiota on inflammatory bowel disease
G. Veitia (Venezuela)

12.15 - 12.30 A specific microbiota signature is associated to various degree of ulcerative colitis
E. Savarino (Italy)

12.30 - 12.45 Bile salt hydrolase-competent probiotics in the management of IBD
A. Moschetta (Italy), R. Gadaleta (Italy)

12.45 - 13.00 FMT, microbiota and IBD: where do we stay and where do we go
F. Scaldaferri (Italy)

13.00 - 13.15 Probiotic in the treatment of IBD
M. Vecchi (Italy)

13.15 - 13.30 Discussion

13.30 - 14.30 **Lunch**

SESSIONE ECM

14.30 - 16.00 **MICROBIOTA AND ITS MODULATION IN IBS**
Chairs and introduction: G. Barbara (Italy), E. S. Corazziari (Italy)

14.30 - 14.50 Microbiota signatures
S. Guglielmetti (Italy)

14.50 - 15.10 Probiotics and prebiotics modulation
F. Guarner (Spain)

15.10 - 15.30 Microbial modulation of intestinal gas
F. Azpiroz (Spain)

15.30 - 15.50 Probiotics as "Living Drugs": Single Strain or Multi Strain combination?
C. Scarpignato (Italy)

15.50 - 16.00 Discussion

SESSIONE ECM

16.00 - 17.00 **THE MICROBIOME AND BILIOPANCREATIC DISORDERS: EGG OR CHICKEN?**
Chairs: S. Alfieri (Italy), G. Capurso (Italy)

16.00 - 16.20 Role of microbes in acute pancreatitis
C. Ammer-Herrmenau (Germany)

16.20 - 16.40 The microbioma in pancreatic adenocarcinoma
L. Archibugi (Italy)

16.40 - 17.00 The microbiome in biliopancreatic surgery
G. Gibiino (Italy)

SESSIONE ECM

17.00 - 18.20 **MICROBIOTA AND CANCER**
Chairs: P. Nisticò (Italy), M. Rescigno (Italy)

17.00 - 17.20 Cancer immunotherapy: achievements, pitfalls, and opportunities
M. Maio (Italy)

17.20 - 17.40 Sensitizing cancer cells to immune checkpoint inhibitors by microbiota metabolites
M. Rescigno (Italy)

17.40 - 18.00 *LGG* supernatant induces cell cycle arrest in cancer cell lines
M. Libra (Italy), D. Ricci (Italy)

18.00 - 18.20 Probiotic strain *Escherichia coli Nissle 1917* is genotoxic
J. P. Nougayrede (France)

SESSIONE ECM

18.20 - 19.00 **LECTURES**
Chair: A.M. Castellazzi (Italy)

18.20 - 18.40 Edible insects and food allergy
M. Miraglia del Giudice (Italy), C. Indolfi (Italy)

18.40 - 19.00 Probiotics in pet food: state of the art
A. Gramenzi (Italy)

SESSIONE ECM

08.30 - 10.00 **MODELLING PROBIOTIC, PREBIOTIC & NEW FOOD FUNCTIONALITY WITHIN THE GUT USING ADVANCED *IN VITRO* MODELS**
Chair: K.M. Tuohy (UK)

08.30 - 08.50 Modelling digestion and functional food mechanisms of effect along the GI tract
A. Mackie (UK)

08.50 - 09.10 Combined *ex vivo/in vitro* approaches to study the nutri-kinetics and health effects of dietary probiotics, prebiotics and polyphenols
C. Gill (UK)

09.10 - 09.30 A new high-throughput and scalable *in vitro* three stage continuous flow culture model for measuring gut microbiota diet and drug interactions
A. Buckley (UK)

09.30 - 09.50 Advanced models of host: microbe interactions along the gut-brain axis
R. M. Owens (UK)

09.50 - 10.00 Discussion

SESSIONE ECM

10.00 - 12.00 **POLYPHENOLS AND HEALTH**
Chairs: M. G. Ferruzzi (USA), P. Lavermicocca (Italy)

10.00 - 10.15 Phenolics in human milk and early diet
M. G. Ferruzzi (USA)

10.15 - 10.30 Phenolics and TMAO - Microbiota interactions for cardiovascular health
A. Neilson (USA)

10.30 - 10.45 Role of dietary polyphenols in the modulation of cardio-metabolic risk factors
R. Giacco (Italy)

10.45 - 11.00 Phenolics and carbohydrate interactions. Implications for digestion as well as gut microbiota
B.R. Hamaker (USA)

11.00 - 11.15 Impact of polyphenols on the metabolome - linkages between metabolites, biochemical and disease pathways
C. Kay (USA)

11.15 - 11.30 Prebiotic effects of dietary blueberries mediate the cardiovascular benefits
A.Velayutham (USA)

11.30 - 12.00 Closing remarks and discussion: *A. Cardinali (Italy)*

SESSIONE ECM

12.00 - 13.30 **GUT MICROBIOME AND DIET IN MALNUTRITION**
Chair: Y. Sanz (Spain)

12.00 - 12.15 Malnutrition: the big challenge
F. Fontaine (Italy)

12.15 - 12.30 Gut microbiome and diet in obesity prediction and management
Y. Sanz (Spain)

12.30 - 12.45 Impairment of gut microbial biotin metabolism and host biotin status in severe obesity
T. Le Roy (France)

12.45 - 13.00 Diet, microbiome and infections
S. Turroni (Italy)

13.00 - 13.15 How to produce nutritious foods for all: microbiomes & agriculture
R. Domenech Mata (Spain)

13.15 - 13.30 Discussion

13.30 - 14.30 **Lunch**

SESSIONE ECM

14.30 - 15.30 **GUT-BRAIN AXIS**
Chair: G. Clarke (Ireland)

14.30 - 14.45 Communication between enteric and central nervous systems through microbiota
P. Malard (Switzerland)

14.45 - 15.00 The gut microbiome and healthy aging
G. Clarke (Ireland)

15.00 - 15.15 Gut microbiome-brain axis in neurologic and/or psychiatric diseases
E. Merlo Pich (Italy)

15.15 - 15.30 The gut-brain axis and the role of microbiota in Parkinson's disease
F. Stocchi (Italy)

SESSIONE ECM

15.30 - 17.00 **AUTISM AND GUT/ORAL MICROBIOME**
Chairs: L. Putignani (Italy), S. Vicari (Italy)

15.30 - 15.45 Autism, new cutting edge therapeutic and research approaches
S. Vicari (Italy)

15.45 - 16.00 Oral and gut microbiome are the room for autism comorbidities modulation?
L. Putignani (Italy)

16.00 - 16.15 Clinic of autism microbiomics
L. Putignani (Italy), G. Valeri (Italy)

16.15 - 16.30 Gut microbiome ecological and functional profiles
P. Vernocchi (Italy)

16.30 - 16.45 Network-based data analyses for studying human diseases: autism spectrum disorders (ASDs)
F. Conte (Italy)

16.45 - 17.00 Conclusions: *M. Barberi (Italy), L. Putignani (Italy)*

SESSIONE ECM

17.00 - 19.00 **LECTURES**
Chairs: L. Capurso (Italy), M. Koch (Italy)

17.00 - 17.20 Xenobiotics-microbiota interactions
G. Clarke (Ireland)

17.20 - 17.40 Paolo Paoluzi Lecture: *Gut microbiota and probiotics in rheumatic diseases*
R. Pica (Italy)

17.40 - 18.00 Butyric Acid: an ancient controller of metabolism, inflammation and gut microbiota
A. Kiciak (Poland)

18.00 - 18.20 Gut microbiota and sarcopenia
F. Landi (Italy)

18.20 - 18.40 Gut microbiota and Covid-19, a space for probiotics?
F. Franceschi (Italy)

18.40 - 19.00 Oral microbiota
P. Simeone (Italy)

ORAL COMMUNICATION 10.00 - 12.30

Chair: *F. Scaldaferri (Italy)*

PROBIOTICS

OC.33 - 25 **DEVELOPMENT OF "PRECISION PROBIOTICS": STREPTOCOCCUS THERMOPHILUS AS A MODEL SYSTEM**

Diego Mora [1] - *Stefania Arioli* [1]
University of Milan, Department of Food Environmental and Nutritional Sciences (DeFENS), Milan, Italy [1]

OC.34 - 36 **DYNAMIC EFFECTS OF PROBIOTIC FORMULA ECOLOGIC®825 ON HUMAN SMALL INTESTINAL ILEOSTOMA MICROBIOTA: A NETWORK THEORY APPROACH**

Jack Jansma [1] - *Nicola Thome* [2] - *Markus Schwalbe* [1] - *Anastasia Chrysovalantou Chatziioannou* [1] - *Somayah El Sayed* [2] - *Gilles van Wezel* [2] - *Pieter van den Abbeele* [3] - *Saskia van Hemert* [4] - *Sahar El Aidy* [1]
University of Groningen, Host microbe interactions, Groningen, Netherlands [1] - University of Leiden, Department of Molecular Biotechnology, Leiden, Netherlands [2] - Cryptobiotix, Ghent, Belgium [3] - Winclove probiotics, Amsterdam, Netherlands [4]

OC.35 - 78 **EFFECT OF A MIX OF LACTICASEIBACILLUS CASEI LA205 AND LACTICASEIBACILLUS PARACASEI LA903 ON BEHAVIOUR, BIOCHEMICAL AND GUT MICROBIAL OUTCOMES OF MALE MICE FOLLOWING CHRONIC RESTRAINT STRESS**

Vivien Letenneur [1] - *Magali Monnoye* [1] - *Catherine Philippe* [1] - *Sophie Holowacz* [2] - *Sylvie Rabot* [1] - *Patricia Lepage* [1] - *Elsa Jacouton* [2] - ***Laurent Naudon*** [1]
INRAE, Micalis Institute, Jouy-en-Josas, France [1] - PiLeJe Laboratoire, Paris, France [2]

OC.36 - 82 **PANGENOME DATA MINING AND PHENOTYPIC EVALUATION OF WEISSELLA CIBARIA STRAINS FOR PROBIOTIC APPLICATIONS**

Alessandra Fontana [1] - *Vania Patrone* [1] - *Paolo Bellassi* [1] - *Maria Luisa Callegari* [1] - *Elisabeta Fanfoni* [1] - *Francois Bourdichon* [1] - *Dea Korcari* [2] - *Maria Grazia Fortina* [2] - *Lorenzo Morelli* [1]
Università Cattolica del Sacro Cuore, Department for Sustainable Food Process (DiSTAS), Piacenza and Cremona Campus, Italy [1] - Università degli Studi di Milano, Department of Food, Environmental and Nutritional Sciences (DeFENS), Milano, Italy [2]

OC.37 - 117 **ACHIEVING EFFICIENT VIABIILITY OF AKKERMANSIA MUCINIPHILA DURING AEROBIC STORAGE AND GASTROINTESTINAL PASSAGE THROUGH CALCIUM-ALGINATE ENCAPSULATION**

Daniela Machado [1] - *Mariana Fonseca* [1] - *Rita Vedor* [1] - *Joana Cristina Barbosa* [1] - *Ana Maria Gomes* [1]
Universidade Católica Portuguesa, CBQF – Centro de Biotecnologia e Química Fina – Laboratório Associado, Escola Superior de Biotecnologia, Porto, Portugal [1]

OC.38 - 151 **IN VITRO ASSESSMENT OF PROBIOTIC ATTRIBUTES AS USEFUL PRELUDE TOWARD PERSONALIZED BACTERIOTHERAPIES**

Dileta Mazzantini [1] - Marco Calvigioni [1] - Francesco Celandroni [1] - Antonella Lupetti [1] - Emilia Ghelardi [1]
University of Pisa, Department of Translational Research and New Technologies in Medicine and Surgery, Pisa, Italy [1]

OC.39 - 137 **BENEFICIAL EFFECTS OF ENRICHED POLYPHENOLS COLTURE OF LACTOBACILLI SPP. ON THE INTESTINAL CANDIDA ALBICANS GROWTH**

Silvia Rizzo [1] - Maura Di Vito [1] - Paola Matarelli [2] - Roberto Rosato [1] - Edoardo Napoli [3] - Maurizio Sanguinetti [1] - Francesca Bugli [1]
Università Cattolica del Sacro Cuore Roma, Dipartimento di Scienze Biotecnologiche di Base, Cliniche Intensivologiche e Perioperatorie, Rome, Italy [1] - Università di Bologna, Dipartimento di Scienze e Tecnologie Agro-Alimentari-DIST, Bologna, Italy [2] - Consiglio Nazionale delle Ricerche (CNR), Istituto di Chimica Biomolecolare, Catania, Italy (3)

OC.40 - 17 **ISOLATION, IDENTIFICATION AND RAW MATERIAL PRODUCTION OF FAECALI BACTERIUM PRAUSNITZII**

Irem Altuntas [1] - Hamideh Hammamchi [1] - Hatice Turan Pestel [1]
Pozitif R&D and Analysis Laboratory, R&D Department, İstanbul, Turkey [1]

OC.41 - 105 **WESTERN DIET-INDUCED OBESITY AND ASSOCIATED METABOLIC ALTERATIONS CAN BE PREVENTED BY PROBIOTIC LIMOSILACTOBACILLUS REUTERI DSM17938 ADMINISTRATION**

Arianna Mazzoli [1] - Angela Di Porzio [1] - Valentina Barrella [1] - Luisa Cigliano [1] - Gianluigi Mauriello [2] - Susanna Iossa [1]
University of Naples Federico II, Department of Biology, Naples, Italy [1] - University of Naples, Agricultural Science, Naples, Italy [2]

ORAL COMMUNICATION

PREBIOTICS POSTBIOTICS/PARABIOTICS

OC.42 - 30 **PREBIOTIC POTENTIAL OF HAWTHORN IN IN-VITRO AND IN-SITU SYSTEMS**

Merve Nur Tahran [1] - *Areeba Tariq* [1] - ***Sebnem Ozturkoglu-Budak*** [1]
Ankara University, Department of Dairy Technology, Ankara, Turkey [1]

OC.43 - 65 **BENEFICIAL EFFECTS OF A YEAST-EXTRACT PREBIOTIC IN A MOUSE MODEL OF ULCERATIVE COLITIS**

Samuele Sabbatini [1] - *Marco Gentili* [2] - *Eleonora Lusenti* [2] - *Emilia Nunzi* [3] - *Nathalie Ballet* [4] - *Simona Ronchetti* [2] - *Claudia Monari* [1]
University of Perugia, Department of Medicine and Surgery, Medical Microbiology Division, Perugia, Italy [1] - University of Perugia, Department of Medicine and Surgery, Pharmacology Division, Perugia, Italy [2] - University of Perugia, Department of Medicine and Surgery, Perugia, Italy [3] - Lesaffre International, Lesaffre Institute of Science & Technology, Marcq-en-Baroeul, France [4]

OC.44 - 74 **PARTIALLY-HYDROLYSED GUAR GUM IN THE TREATMENT OF IRRITABLE BOWEL SYNDROME: A SYSTEMATIC REVIEW OF HUMAN CLINICAL TRIALS**

Jason Hawrelak [1] - *Dawn Whiten* [1]
University of Tasmania, College of Health and Medicine, Hobart, Australia [1]

OC.45 - 129 **REGULATING GASTROINTESTINAL (G.I.) METABOLISM WITH PREBIOTICS TO SAFEGUARD THE MICROBIOTA FROM ANTIBIOTIC-INDUCED DISRUPTION**

Peter Belenky [1]
Brown University, Molecular microbiology and immunology, Providence, United States [1]

OC.46 - 53 **THE PREBIOTIC EFFECT OF MANNOOLIGOSACCHARIDES BROUGHT ABOUT BY ENZYMATIC HYDROLYSIS OF IVORY NUT LINEAR MANNAN**

Mihle Magengelele [1] - ***Samkelo Malgas*** [2] - *Bret Pletschke* [1]
Rhodes University, Biochemistry and Microbiology, Makhanda, South Africa [1] - University of Pretoria, Biochemistry, Genetics and Microbiology, Pretoria, South Africa (2)

OC.47 - 31 **A NEW INSIGHT: POSTBIOTICS AND PARAPROBIOTICS**

Aysegul Kirmizigul Peker [1] - *Ilkin Yucel Sengun* [1]
Ege University, Food Engineering, Izmir, Turkey [1]

OC.48 - 165 **POSTBIOTICS + STANDARD CHEMOTHERAPY AGAINST GASTRIC CANCER CELLS: FUTURE COMBINATION THERAPY?**

Radwa A. Eladwy [1] - *Dennis Chang* [1] - *Chun Guang Li* [1] - ***Deep Jyot i Bhuyan*** [1]
NICM Health Research Institute, Western Sydney University, Penrith, Australia [1]

OC.49 - 185 **EVALUATION OF THE CYTOTOXIC EFFECT ON COLORECTAL CANCER CELLS (CACO2 AND HT29) LINE OF PARAPROBIOTICS AND POSTBIOTICS OBTAINED FROM SOME POSSIBLE PROBIOTIC BACTERIA**

Gulcin Alp Avcı [1] - *Emre Avcı (2)*
Glhane Faculty of Dentistry, University of Health Sciences/ Department of Basic Medical Science, Ankara, Turkey
[1] - Gülhane Faculty of Pharmacy, University of Health Sciences/ Department of Biochemistry, Ankara, Turkey [2]

OC.50 - 193 **DETERMINATION OF THE ANTITUMOR EFFICACY OF PARAPROBIOTICS AND POSTBIOTICS ON THE CACO-2 CELL LINE AND THEIR ROLE IN IMMUNE RESPONSE**

Gulcin Alp Avcı [1] - *Ulku Irem Yılmaz* [2] - ***Emre Avcı*** [3]
Gülhane Faculty of Dentistry, University of Health Sciences/ Department of Basic Medical Science, Ankara, Turkey [1] - Vocation School of Health, University of Health Sciences/ Department of Pathology, Ankara, Turkey [2] - Gülhane Faculty of Pharmacy, University of Health Sciences/ Department of Biochemistry, Ankara, Turkey [3]

ORAL COMMUNICATION 14.30 - 17.30

Chairs: *M. Guarino (Italy), G. Spera (Italy)*

NUTRITION

OC.51 - 40 **MILLET POLYPHENOL EXTRACTS ALLEVIATES HIGH-FAT-HIGH-SUCROSE DIET INDUCED GUT DYSBIOSIS AND LIVER STEATOSIS IN MICE**

Ruchika Maurya [1] - *Mahendra Bishnoi* [1] - *Kanthi Kiran Kondepudi* [1]
National Agri-Food Biotechnology Institute, Food and Nutrition, Mohali, India [1]

OC.52 - 72 **SAUERKRAUT – A HEALTH PROMOTING MODULATOR OF THE MICROBIOME?**

Nelly Schropp [1] - *Virginie Stanislas* [1] - *Karin B. Michels* [1]
University Medical Center Freiburg, Institute for Prevention and Cancer Epidemiology, Freiburg, Germany [1]

OC.53 - 84 **GLUCOSE AND INSULIN RESPONSE TO KOMBUCHA TEA IN HUMANS: A RANDOMIZED TRIAL**

Julie Kapp [1] - *Quoc Bui* [2] - *Jill Kanaley* [3]
University of Missouri, College of Health Sciences, Columbia, United States [1] - Washington University School of Medicine, The Center for Biostatistics and Data Science, Saint Louis, United States [2] - University of Missouri, Nutrition & Exercise Physiology, Columbia, United States [3]

OC.54 - 81 **EVALUATION OF HONEY AND ITS ANTIMICROBIAL PROPERTIES IN COMBINATION WITH MEDITERRANEAN PREBIOTIC PRODUCTS**

Erjon Troja [1] - *Egnis Muça* [2] - *Ranela Ceci* [3] - *Eltion Dhamo* [2] - *Elena Muça* [2] - *Rozana Troja* [2]
University of Medicine, Faculty of Medicine, Department of Pharmacy, Tirana, Albania [1] - University of Tirana, Faculty of Natural Sciences, Department of Industrial Chemistry, Tirana, Albania [2] - National Agency of Drugs and Medical Devices, Regulatory Department, Tirana, Albania [3]

OC.55 - 22 **ALGERIAN HONEYS : NUTRITIONAL VALUES AND BIOLOGICAL PROPERTIES**

Ouchemoukh Salim [1] - *Amessis-Ouchemoukh Nadia* [1] - *Guenaoui Nawel* [1] - *Sadou Dyhia* [1] - *Ayad Rabha* [1] - *Zaidi Hicham* [1] - *Otmani Amar* [1]
University of Bejaia, Bejaia, Algeria [1]

OC.56 - 138 **CAROTENOIDS:PHYTOCHEMICALS TO COMBAT DOXORUBICIN-INDUCED CARDIOTOXICITY**

Bojana M. Andrejic Visnjic [1] - *Milana M. Bosanac* [1] - *Biljana R. Cvetkovic* [2] - *Alena M. Stupar* [2] - *Nikola B. Martic* [3]
Faculty of Medicine Novi Sad, University of Novi Sad/Department of Histology and Embryology, Novi Sad, Serbia [1] - Institute of food technology in Novi Sad, University of Novi Sad, Novi Sad, Serbia [2] - Faculty of Medicine Novi Sad, University of Novi Sad/Department of Pharmacology, Toxicology and Clinical Pharmacology, Novi Sad, Serbia [3]

OC.57 - 196 **THE NUTRITIONAL, PROBIOTIC AND HEALTH ROLE OF SHARR MOUNTAIN TEAS DURING EMBRYONIC DEVELOPMENT IN QUAIL AND CHICKEN EGGS**

*Nexhbedin Beadini[1], **Sheqibe Beadini**[2,3], Vegim Zhaku[2], Albulena Beadini[3], Avdi Nazifi[2], Adelina Elezi[4],Learta Asani[4],Albin Beadini[2]*
University of Tetova, Biology and Human Genetics, Tetovo, Macedonia, [1] Faculty of Medical Sciences, Department of Cell and molecular biology, University of Tetova, Republic of North Macedonia, [2] Faculty of Medical Sciences, Department of Physiology, University of Tetova, Republic of North Macedonia, [3] Faculty of Medical Sciences, Department of Biochemistry, University of Tetova, Republic of North Macedonia[4] Faculty of Medical Sciences, Department of Pathology, University of Tetova, Republic of North Macedonia [5]

OC.58 - 23 **BIOLOGICAL PROPERTIES OF EXTRACTS FROM THE MIXTURE OF HONEY AND BERRIES OF PISTACIA LENTISCUS.**

Amessis-Ouchemoukh Nadia [1] - Ouchemoukh Salim [1] - Ayad Rabha [1] - Otmani Amar [1] - Sadou Dyhia [1] - Guenaoui Nawel [1]
University of Bejaia, Bejaia, Algeria [1]

OC.59 - 49 **RESEARCH AND DEVELOPMENT OF CULTIVATION METHODS OF CANNABIS SATIVA L. TO MAXIMIZE THE YIELD OF NON-THC BIOACTIVE COMPOUNDS OF NUTRACEUTICAL, COSMECEUTICAL, AND PHARMACEUTICAL INTEREST**

*Fabio Ferrini [1] - Sabrina Donati Zeppa [1] - Vitoria Carrabs [1] - **Alessia Bartolacci** [1] - Piero Sestili [1]*
Dipartimento di Scienze Biomolecolari, Università degli Studi di Urbino Carlo Bò, Urbino, Italy[1]

OC.60 - 26 **THYMOQUINONE-INDUCED CELLULAR AND MITOCHONDRIAL HEALTH IN LIVER CANCER**

Consolato Sergi [1] - Reem Abdualmjid [2]
Children's Hospital of Eastern Ontario, University of Ottawa, LMP, Ottawa, Canada [1] - University of Alberta, LMP, Edmonton, Canada [2]

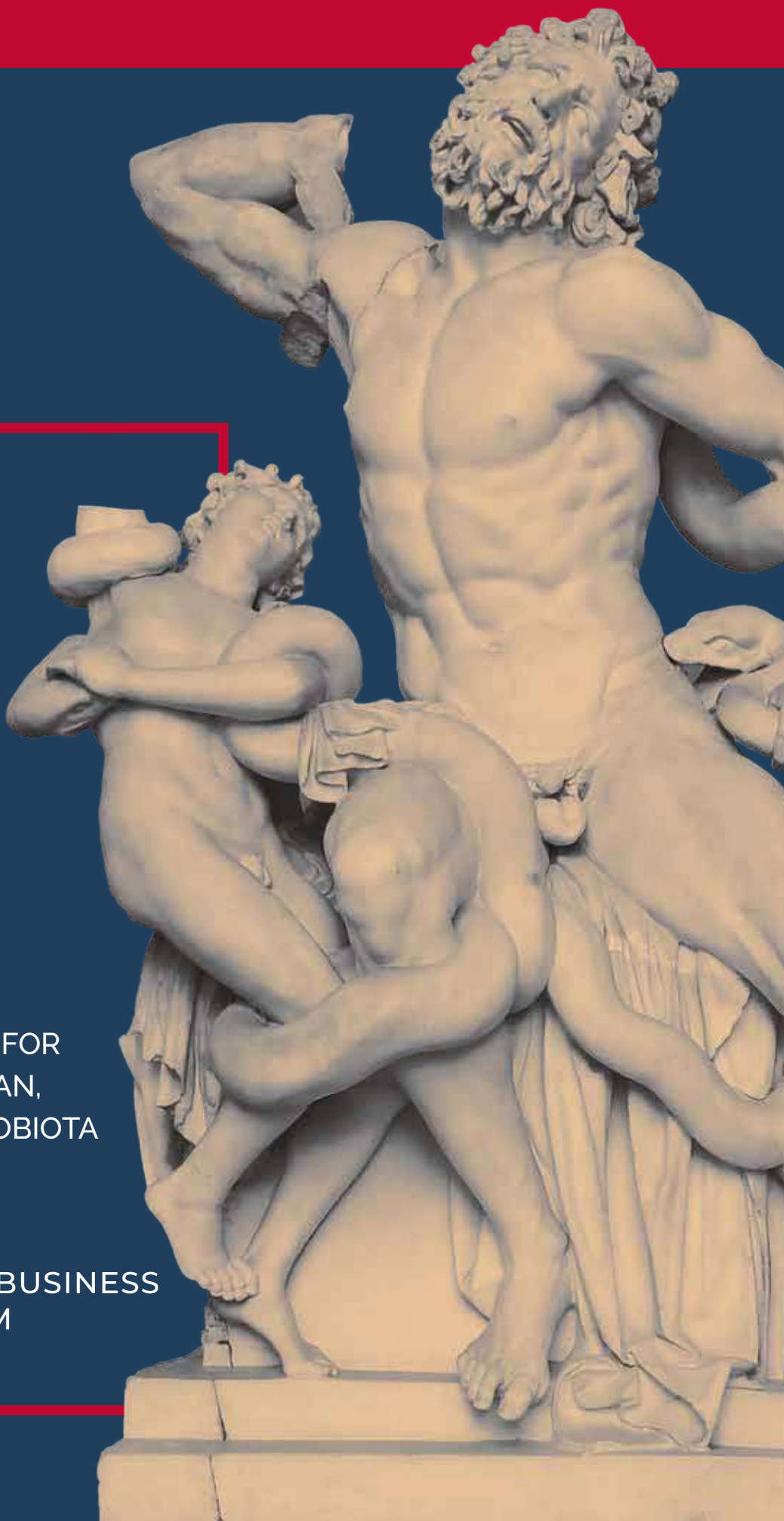
OC.61 - 27 **DYNAMIC REGULATION OF M6A IN PATIENTS WITH TYPE 2 DIABETES AND M6A BIOINFORMATICS REVIEW**

Fan Shen [1] - Consolato Sergi [2]
University of Alberta, LMP, Edmonton, Canada [1] - Children's Hospital of Eastern Ontario, University of Ottawa, LMP, Ottawa, Canada [2]

OC.62 - 38 **HOW DO DIET PATTERNS, SINGLE FOODS, PREBIOTICS AND PROBIOTICS IMPACT GUT MICROBIOTA?**

Giuseppe Merra [1] - Paola Gualtieri [1] - Laura Di Renzo [1] - Antonino De Lorenzo [1]
University of Tor Vergata, Department of Biomedicine and Prevention, Rome, Italy [1]

ROME
SEPTEMBER
2025



13TH

PROBIOTICS, PREBIOTICS & NEW FOODS

NUTRACEUTICALS, BOTANICALS & PHYTOCHEMICALS FOR NUTRITION & HUMAN, ANIMAL AND MICROBIOTA HEALTH

4TH SCIENCE & BUSINESS SYMPOSIUM

OC.63 - 97

AMBROSIA BAR: A FUNCTIONAL FOOD MODULATING THE MICROBIOTA-INFLAMMATION-BRAIN AXIS TO PREVENT UNDERNUTRITION IN HEART FAILURE.

Edda Russo [(1)] - *Maria Magdalena Coman* [(2)] - *Maria Cristina Verdenelli* [(2)] - *Marco Garcia Vaquero* [(3)] - *Giulia Nannini* [(1)] - *Simone Baldi* [(1)] - *Elena Niccolai* [(1)] - *Iain Brownlee* [(4)] - *Thomas Linger* [(5)] - *Gwendolyn Barceló-Coblijn* [(6)] - *Stefano Fumagalli* [(1)] - *Amedeo Amedei* [(1)]
University of Florence, Department of Experimental and Clinical Medicine, Florence, Italy [(1)] - SYNBIOTEC Srl., Camerino, Italy [(2)]- University College Dublin, Section of Food a nd Nutrition, School of Agriculture an d Food Science, Dublin, Ireland [(3)]- Northumbria University, Faculty of Health and Life Sciences, Newcastle upon Tyne, United Kingdom [(4)]- Genevention, GmbH, Gttingen, Germany [(5)] -Health Research Institute of the Balearic Islands, Lipids in Human Pathology, Institut d'Investigació Sanitària Illes Balears, Palma di Maiorca, Spain [(6)]

OC.64 - 128

ASSESSMENT OF AVOCADO (PERSEA AMERICANA MILL.) SEEDS AS A PROMINENT SOURCE OF NUTRIENTS, NUTRACEUTICAL COMPOUNDS AND NATURAL ANTIOXIDANTS FOR INDUSTRIAL FOOD APPLICATIONS

Muhammad Khalid Saeed [(1)] - *Naseem Zahra* [(1)] - *Asma Saeed* [(1)] - *Quratulain Syed* [(1)] - *Syed Hussain Imam Abidi* [(1)]
Food and Biotechnology Research Centre, PCSIR, Lahore, Pakistan [(1)]

OC.65 - 121

IMPACT OF QUINOA AND FOOD PROCESSING METHODS ON THE HUMAN GUT MICROBIOME THROUGH IN VITRO FERMENTATION

Franck Carbonero [(1)] - *Jagrani Minj* [(1)] - *Patrick Solverson* [(1)] - *Ahhria Kirkendall* [(2)] - *Devin Connolly* [(1)]
Washington State University, Elson Floyd College of Medicine, Department of Nutrition and Exercise Physiology, Spokane, United States [(1)] - Washington State University, School of Food Science, Pullman, United States [(2)]

OC.66 - 122

PROMOTING INNOVATION OF FERMENTED FOODS (PIMENTO) - COST ACTION CA20128

Antonio Del Casale [(1)] - *Juana Frias* [(2)] - *Zuzana Ciesarova* [(3)] - *Marta Laranjo* [(4)] - *Photis Papademas* [(5)] - *Effie Tsakalidou* [(6)] - *Guy Vergères* [(7)] - *Smilja Todorovic* [(8)] - *Marie Christine Champomier Vergès* [(9)] - *Vittorio Capozzi* [(10)] - *Christophe Chassard* [(11)]
MICROBION, Open Innovation Department, Verona, Italy [(1)] - Spanish National Research Council, Instituto de Ciencia y Tecnología de Alimentos y Nutrición (ICTAN-CSIC), Madrid, Spain [(2)]- National Agricultural and Food Centre, Food Research Institute, Bratislava, Slovakia (Slovak Republic) [(3)]- Universidade de Évora, Institute of Mediterranean Agricultural and Environmental Sciences, Évora, Portugal [(4)]- Cyprus University of Technology, Department of Agricultural Sciences, Biotechnology and Food Science, Limassol, Cyprus [(5)] - Agricultural University of Athens, Laboratory of Dairy Research, Athens, Greece [(6)] - Agroscope, Food Microbial Systems Research Division, Bern, Switzerland [(7)] - University of Belgrade, Institute for Biological Research "Sinisa Stankovic", Belgrade, Serbia [(8)] - INRAE, Micalis Institute, Paris, France [(9)] - National Research Council, Institute of Sciences of Food Production (ISPA-CNR), Foggia, Italy [(10)] - INRAE, VetAgro Sup, Université Clermont Auvergne, Clermont Auvergne, France [(11)]

IPA IN COLLABORATION WITH IPA EUROPE

AULA ÉLIE METCHNIKOFF - SEPTEMBER 18, 2023

IPA DAY Rome 10.00 am to 5.00 pm

IPA DAY - THE OLD, THE NEW AND THE FUTURE

As IPA turned 20 years old in the midst of the pandemic, we did not have time to celebrate this milestone. As we trying to make up for lost ground, IPA will once again collaborate with the congress in Rome, 12th Probiotics, Prebiotics, & New Foods.
This year's themes will have sessions covering important initiatives IPA has embarked on. These items are important to the probiotic industry and IPA has been working on for a few years now. Additionally, we will also have presentations looking at IPA's new expanded scope as the biotic revolution we are seeing is marching ahead. Finally, regulations being everyone's favorite topic during the IPA Europe session, we will also explore topics in the realm and how these are evolving.

Morning Session
Welcome and Introduction from IPA desk

The Biotics session talks:
Prebiotics: Koen Venema PhD, University Maastricht
Postbiotics: Simone Guglielmetti PhD, University of Milan
Next Gen Probiotics: Veera Kainulainen PhD, University of Helsinki
Synbiotics: Caroline Childs PhD, University of Southampton

Lunch:
1.30 - 2.30 pm

Afternoon Session:
2.30 - 3.15 pm

Public standards for the Probiotic industry
- Testing and IPA work with ISO realities - Adrianne Klijn PhD, Nestlé Institute of Food Safety and Analytical Sciences
- Manufacturing standards and IPA's work with ANSI

Afternoon Session:
IPA Europe session: 3.15 - 5.15 pm

Introduction by the IPA Europe President, Esben Laulund (Denmark)

Intervention of the Italian authorities, Dr. Valeria Di Giorgi (Italy), Head of office 4- Directorate General Hygiene, food safety and nutrition

The evolution of European demand of probiotics: Can the EC meet the challenges. IPA Europe will present the regulatory context in the European countries.

How to bridge the gap between science and industry: EUFIC, the European Food Information Council Debora Serra (Belgium), will illustrate some projects about nutrition and health, with focus on beneficial microorganisms and consumer's attitude and perception.

Opportunities by genome editing technologies for food cultures
Fabio Dal Bello (Italy), Scientific Director, Sacco System, Chair of the Regulatory Working Group, EFFCA

Probiotic and EC Regulation 2015/2283 on novel food: "How is a self-evaluation made to realise if a probiotic culture is a traditional species?", Svend Laulund (Denmark), Chr. Hansen

Closing and final remarks from the IPA President, Esben Laulund (Denmark).

Close of IPA Day.

SESSIONE ECM

08.30 - 10.00 **HUMAN GUT MICROBIOTA AND INTERACTION WITH THE HOST**
Chair: M. Ventura (Italy)

08.30 - 08.45 *Bifidobacteria* and the infant gut: how do they colonize and what do they do
D. Van Sinderen (Ireland)

08.45 - 09.00 Early life microbiomes and longer-term health outcomes
H. Browne (UK)

09.00 - 09.15 Modulation of the early life microbiome - lessons from controlled intervention trials
D. Haller (Germany)

09.15 - 09.30 Insight into the dialogue between beneficial gut bacteria and the host
A. Margolles (Spain)

09.30 - 09.45 *Bifidobacteria* and interaction with the human host
F. Turroni (Italy)

09.45 - 10.00 Discussion

SESSIONE ECM

10.00 - 11.30 **GUT MICROBIOTA AND LIVER**
Chairs: D. Alvaro (Italy), A. Benedetti (Italy), M. Koch (Italy)

10.00 - 10.20 Structure and function of the gut-liver axis
A. Moschetta (Italy)

10.20 - 10.40 Gut liver axis in NAFLD - NASH
L. Miele (Italy)

10.40 - 11.00 Microbial modulation of non-alcoholic fatty liver disease
A. Molinaro (Sweden)

11.00 - 11.30 Discussion

SESSIONE ECM

11.30 - 12.30 **PRESENT AND FUTURE OF FMT**
Chair: G. Ianiro (Italy)

11.30 - 11.50 FMT in clinical practice: state of the art and current issues
J. Keller (The Netherlands)

11.50 - 12.10 FMT: key determinants of success
G. Ianiro (Italy)

12.10 - 12.30 Beyond FMT: targeted modulation of gut microbiome
H. Bar-Yoseph (Israel)

SESSIONE ECM

08.30 - 10.00 **MEDITERRANEAN TASK FORCE FOR CANCER CONTROL (MTCC)**
Chair: P. G. Natali (Italy)

08.30 - 08.50 Green platforms for vaccine production
A. Venuti (Italy)

08.50 - 09.10 Antioxidants in cancer prevention and therapy
A. Saggioro (Italy)

09.10 - 09.30 Antioxidants as tools for preventing chemo-radiotherapy-induced mucositis
C. Pulito (Italy)

09.30 - 09.50 Tomato and olive phytocompounds as population remedy for environmental pollutants
M. Minacori (Italy)

09.50 - 10.00 Discussion

ORAL COMMUNICATION

GUT MICROBIOTA

OC.01_93 - PREDICTING EARLY RADIATION ENTEROPATHY FROM THE BASELINE BACTERIAL COMPOSITION OF THE INTESTINAL MICROBIOTA OF PROSTATE CANCER PATIENTS

Jacopo Iacovacci [(1)] - Mara Serena Serafini [(1)] - Loris De Cecco [(1)] - Barbara Avuzzi [(1)] - Barbara Noris Chiorda [(1)] - Fabio Badenchini [(1)] - Tommaso Giandini [(1)] - Alessandro Cicchetti [(1)] - Nadia Zaffaroni [(1)] - Valentina Doldi [(1)] - Elisa Mancinelli [(1)] - Eliana Gioscio [(1)] - Andrea Devecchi [(1)] - Ester Orlandi [(2)] - Sergio Villa [(1)] - Michela Dispinzeri [(1)] - Luca Possenti [(1)] - Federica Palorini [(1)] - Miguel Reis Ferreira [(3)] - Riccardo Valdagni [(1)] - Tiziana Rancati [(1)]
Fondazione Irccs Istituto Nazionale dei Tumori di Milano - Milan, Italy [(1)] - National Center for Oncological Hadrontherapy (CNAO) - Pavia, Italy [(2)] - King's College London - London, United Kingdom [(3)]

Objective:
To investigate the role of the intestinal microbiota in the development of radiotherapy-induced intestinal toxicity, the MicroLearner study collected faecal samples from 136 (discovery) and 79 (validation) consecutive prostate cancer patients before radiotherapy.

Methods:
We assessed intestinal toxicity weakly during radiotherapy using CTCAE. We used average grade>1.3 over time points to identify groups of patients (16 in discovery and 8 in validation) who suffered from acute toxicity. We characterized the microbiota using 16S rRNA amplicon sequencing and the Ion Reporter bioinformatics pipeline.

Results:
Hierarchical clustering of the core profiles revealed 8 clusters of patients in the discovery cohort displaying toxicity rates from 0 to 60%. The cluster with the highest rate (10 patients, 7% cohort, 38% toxicity population) was significantly enriched for toxicity (Fisher's exact test P<0.005). Based on selected high-risk microbiota compositional features (relative abundance of selected genera Faecalibacterium, Bacteroides, Parabacteroides, Alistipes, Prevotella, Phascolarctobaterium), we developed a decision-tree effectively predicting the toxicity risk of both in internal and external validation cohorts.

Conclusions:
Our results suggest that an altered ion homeostasis at the level of bacterial communities might predispose to radio-induced toxicity.
This study paves the way to the use of baseline faecal samples to improve pre-radiotherapy toxicity risk assessment and radiotherapy optimization.

OC.02_130 - INVESTIGATING THE MOLECULAR RELATIONSHIP BETWEEN BIFIDOBACTERIA AND HUMAN MILK HORMONE INSULIN

Sonia Mirjam Rizzo [(1)] - Giulia Alessandri [(1)] - Gabriele Andrea Lugli [(1)] - Federico Fontana [(1)] - Chiara Tarracchini [(1)] - Leonardo Mancabelli [(2)] - Alice Viappiani [(3)] - Massimiliano Giovanni Bianchi [(2)] - Ovidio Bussolati [(2)] - Douwe Van Sinderen [(4)] - Marco Ventura [(1)] - Francesca Turroni [(1)]
University of Parma, Department of Chemistry, Life Sciences and Environmental Sustainability, Parma, Italy [(1)] - University of Parma, Department of Medicine and Surgery, Parma, Italy [(2)] - Genprobio Srl, Parma, Italy [(3)] - National University of Ireland, Apc Microbiome Institute and School of Microbiology, Cork, Ireland [(4)]

Objective:
The early infant gut microbiota is nourished and shaped by the mother breast milk, a body fluid that underwent millennia of human evolution resulting in an optimal biological substrate composed of water, proteins, lipids, carbohydrates and hormones. An uninvestigated topic is the potential interactions between mother milk hormones and the infant gut microbial community. Insulin, which represents one of the most prevalent hormones in breast milk, is entangled in a metabolic disease that affects many pregnant women, i.e., gestational diabetes mellitus (GDM). In this study, we explored the molecular relationships between this hormone and Bifidobacterium bifidum taxon.

Methods:
An analysis of 3,620 publicly available metagenomic data sets were done to unveil if the newborns bifidobacterial community varies respecting to the different concentrations of insulin in breast milk of healthy and diabetic mothers. Then, we explored possible molecular interactions between insulin and infant bifidobacterial strains using 'omics' approaches.

Results:
The metagenomic analysis revealed a statistically significant higher relative abundance of B. bifidum (4.04%) in the infant fecal samples from healthy mothers compared to the GDM mothers (1.42%). Transcriptomic analyses highlighted that insulin seemed to induce a strain-specific molecular response. In addition, when the selected bifidobacterial species were grown together in a bioreactor mode, modulation of their relative abundances was observed in the presence of insulin respect to the control.

Conclusions:
Our results revealed that insulin modulates the bifidobacterial community by improving the persistence of the Bifidobacterium bifidum taxon in the infant gut environment compared to other typical infant-associated bifidobacterial species.

OC.03_131 - EVALUATION OF THE PERSISTENCE OF BIFIDOBACTERIUM LONGUM SUBSP. LONGUM IN THE HUMAN GUT ACROSS THE ENTIRE LIFE SPAN AND ITS POTENTIAL ANTI-AGING ROLE AS NATURAL MODULATOR OF THE HOST INNATE IMMUNITY

Giulia Longhi [(1)] - Gabriele Andrea Lugli [(1)] - Massimiliano Giovanni Bianchi [(2)] - Sonia Mirjam Rizzo [(1)] - Chiara Tarracchini [(1)] - Leonardo Mancabelli [(2)] - Laura Maria Vergna [(1)] - Giulia Alessandri [(1)] - Federico Fontana [(1)] - Giuseppe Taurino [(2)] - Martina Chiu [(2)] - Christian Milani [(1)] - Douwe Van Sinderen [(3)] - Ovidio Bussolati [(2)] - Marco Ventura [(1)] - Francesca Turroni [(1)]

University of Parma, Department of Chemistry, Life Sciences, and Environmental Sustainability, Parma, Italy [(1)] - University of Parma, Department of Medicine and Surgery, Parma, Italy [(2)] - National University of Ireland, Apc Microbiome Institute and School of Microbiology, Cork, Ireland [(3)]

Objective:
Aging is a physiological and immunologic degradation process of human health characterized by the progressive alteration of organs and their functions depending largely on lifestyle habits, the environment as well as genetic factors. Although the intestinal microbiota is not unharmed to perturbations that accompany aging and frailty of the elderly, it has been largely accepted that it is engaged in multiple interactions affecting the host health during the host's entire life span.

Methods:
In the current study, we performed an in silico investigation of the gut-associated bifidobacteria in healthy individuals from infants to centenarians followed by genome reconstruction and strain tracing to identify prototypes shared between human stages of life. Culturomics approach allowed the isolation of B. longum subsp. longum strains whose genomic content highly matched with the genotypes identified in elderly subjects and in vitro experiments were employed to molecularly assess their potential anti-aging and antioxidative activities.

Results:
Shotgun metagenomic analyses revealed that Bifidobacterium longum subsp. longum is one of the most common gut microbiota members throughout the entire life span as well as an important microbial biomarker correlated to longevity. Furthermore, B. longum subsp. longum strains isolated revealed a clear interaction with the immune system of the host with a reduction in the expression of inflammation-related cytokines encoding genes.

Conclusions:
Our study provides intriguing evidence for considering some candidates of B. longum subsp. longum strain as potential beneficial microbes in maintaining health and improving quality of life in the elderly population.

OC.04_133 - EXPLORING THE INTERACTIONS BETWEEN NASOPHARYNGEAL AND GUT MICROBIOME IN THE MODULATION OF COVID-19 INFECTION: THE COVIDBIOME PROJECT

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Objective:
this preliminary study investigated the possible correlation between nasopharyngeal microbiota and COVID-19 infection.

Methods:
we performed a shotgun metagenomics analysis to explore and compare the nasopharyngeal microbiota of hospitalized Italian patients with and without COVID-19 infection during the third and fourth pandemic waves. Additionally, lipidomic and deep-shotgun functional analyses of the fecal samples were performed to investigate the metabolic impact of the microbiome on the host's immune response.

Results:
the metagenomic analysis combined with specific correlation analyses suggested a positive association of several microbial species, such as Streptococcus parasanguinis and Prevotella melaninogenica, with the severity of COVID-19 infection. Furthermore, the comparison of the microbiota composition between the nasopharyngeal and their respective fecal samples highlighted an association between these different compartments represented by the sharing of several bacterial species. Additionally, lipidomic and deep-shotgun functional analyses of the fecal samples suggested a metabolic impact of the microbiome on the host's immune response, indicating the presence of key metabolic compounds in COVID-19 patients potentially related to the inflammatory state. Conversely, the patients without COVID-19 displayed enzymatic patterns that could positively impact disease severity and contribute to modulating COVID-19 infection.

Conclusions:
the analysis of the nasopharyngeal microbiota of hospitalized Italian patients with and without COVID-19 infection suggested a positive association of several microbial species with the severity of the disease and highlighted a sharing of several bacteria species with the respective fecal samples. Furthermore, the metabolic analyses suggested a possible impact of the microbiome on the host's immune response and the disease severity.

OC.05_148 - ROLE OF XENOSIALIZATION IN THE PATHOGENESIS OF COLITIS IN THE CANINE MODEL; POSSIBLE POSITIVE EFFECTS OF NEW PROBIOTIC BLENDS

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Objective:
Inflammatory bowel disease (IBD) is a heterogeneous state of chronic intestinal inflammation with no exact known cause. In dogs, IBD is expressed histologically with lymphoplasmacytic inflammation (LPL) of gastrointestinal tract. The study evaluates the possible correlation between microbiota, dietary absorption, enteric expression of N-glycolylneuraminic acid (Neu5Gc) (xenosialization) and intestinal inflammation (xenosialitis) in dogs with IBD. Neu5Gc is indeed synthesized from its N-acetyl precursor (Neu5Ac) by cytidine-5'-monophospho-N acetylneuraminic acid hydroxylase (CMAH), absent in humans, and polymorphic in dogs.

Methods:
105 dogs (divided by breed into 3 groups) with lymphoplasmacytic enterocolitis, compared with 10 healthy dogs (control). Neu5Gc in stools of healthy and enteropathic dogs (20 + 20) was evaluated by ELISA, before and after 30d of administration a probiotic mixture (FSG6822) rich in live bifidobacteria with sialic acid cross-feeding activity. Neu5GC was highlighted with specific antibody (Creative Diagnostic, DMABH-C003). The distribution of desializing bacteria was performed using two different sequencing techniques for different regions of the 16S rRNA gene on 127 + 167 dogs (healthy vs enteropathic).

Results:
Neu5Gc was associated with severe colitis ($p<0.005$), with no relationship to race. In enteropathic dogs there is a higher prevalence of Clostridiales and Bacteroidales ($p=0.0011$), without difference of Bifidobacteria.

Conclusions:
In dogs, the severity of colitis correlates with Neu5Gc and with an increase in Clostridiales and Bacteroidales. In the absence of an increase in desializing bifidobacteria this predisposes to xenosialitis. Actually, (FSG6822) probiotic mixture, shows good levels of reduction in fecal elimination of Neu5Gc, and could reduce xenosialization.

OC.06_167 - A MECHANISTIC APPROACH TO HARNESS THE HYBRID TWO-COMPONENT SYSTEM OF THE HUMAN COLONIC BACTEROIDOTA AS BIOMARKERS FOR MANIPULATION OF HOST HEALTH

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Objective:
The human colon is inhabited by trillions of microorganisms that impact host health. The majority of dietary polysaccharides flowing into the colon is fermented by the Bacillota and the Bacteroidota phyla. Thus, we hypothesized that by harnessing the polypeptide designated the Bacteroidota Hybrid Two Component System (HTCS), a regulator of nutrient metabolism, we will uncover biomarkers amenable to manipulation of the colonic microbiome.

Methods:
Amino acid sequences of the sensor modules in 2,348 HTCS were extracted for multiple sequence alignment and phylogenetic tree construction. To functionally annotate the tree, total RNA and culture supernatants of Bacteroides species, grown on different dietary polysaccharides, were subjected to RNAseq and metabolomic analysis, respectively. Isothermal titration calorimetry was then used to further confirm substrate specificities of the sensors and computational analyses employed to extract the metabolites associated with fermentation of each polysaccharide.

Results:
The sensor phylogenetic tree yielded 10 major clusters, with multiple sub-clusters. Transcriptional analysis (RNAseq), recombinant protein expression, and biophysical approaches (ITC) enabled identification of the clusters representing pectin, arabinan, and arabinoxylan sensors, while metabolomic analyses linked metabolism of dietary polysaccharides, especially complex arabinoxylans, to diverse compounds with antioxidant/anti-inflammatory, neurotransmitter, and antibacterial properties.

Conclusions:
The HTCS sensors constitute biomarkers in the colon for metabolism of different polysaccharides. These biomarkers, designated the Polysaccharide Sensing and Degradation Signature (PSDS), are proxies informing the capacity of an individual to metabolize different dietary polysaccharides. By linking the PSDS to metabolite production, rational manipulation of the colonic microbiome can be implemented through probiotics/prebiotics/synbiotics for health benefits.

OC.07_170 - THE ROLE OF INTESTINAL BACTERIA RELEASING VITAMIN K2-MK7 IN THE PROCESS OF COLON CARCINOGENESIS

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Objective:

Colorectal cancer is close corelated to the composition of the gut microbiome . Vitamin K2 is a compound of bacterial origin that plays a key role in the human body. The K2-MK7 homologue is detected in large amounts in soybeans fermented by Bacillus subtilis Natto. This strain is not a typical member of the microflora of the human digestive tract, and as a planktonic flora, temporarily inhabiting the intestinal epithelium.
We attempted to answer the question which species of bacteria living in the gastrointestinal tract are capable of producing vitamins from the K2 group, and we also analyzed the effect of various VK2 homologues on the stimulation of immune system cells to secrete pro- and anti-inflammatory cytokines .

Methods:

The bacterial strains used in this study were isolated from the healthy human gastrointestinal tract The total VK_2 content (sum of homologs) in all supernatants was determined by Differential Pulse Adsorptive Stripping Voltammetry. Morover we examined the effect of selected synthetic VK_2 on secretion of pro-inflammatory cytokines released by human Caco-2 intestinal epithelial cells.

Results:

Based of our research, 86 bacterial strains of intestinal origin were tested, from which the largest producers of VK_2 (Lactobacillus, Bifidobacterium, Bacillus) were selected.

Conclusions:

The bacterial production of VK_2 may depend not only on a specific genus but may even be a strain-dependent feature. The in vitro studies on the human colon adenocarcinoma Caco-2 cell line showed that all tested VK_2 homologs (especially long-chain) had a high potential to inhibit IL-8 secretion.

OC.08_184 - THE 16S RRNA GENE AMPLICON SEQUENCING ERROR: HOW FLUORESCENCE IN SITU HYBRIDISATION (FISH) REVEALS A MAJOR FLAW IN MICROBIOME ANALYSIS

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Objective:

Profiling of human microbial communities by 16S rRNA gene amplicon sequencing is a widely used tool. The differences in 16 rRNA patterns serve as important insights into the dynamics of microbial populations in the human gut. Moreover, these data are also used to quantify the analyzed samples, and conclusions are drawn about why populations are favored or inhibited in their growth.

Methods:

Fluorescence In Situ Hybridization (FISH) is a powerful tool for the analysis of microbial population patterns and dynamics. Microbial cells can be specifically detected by applying 16S rRNA-targeted fluorescence-labeled oligonucleotide probes directly at their site of action in the microbiome sample. The probes enter the cells and bind specifically to 16S rRNA targets in the ribosome. By binding several thousands of probes, live cells can specifically be identified and quantified using a conventional fluorescence microscope without the need for cultivation or amplification.

Results:

We analyzed human stool samples of male and female proband with 16S rRNA gene amplicon sequencing (indirect method) and FISH (direct method) and compared the results. While some microbial populations showed similar quantification results, there were major differences with other phylogenetic groups. The data retrieved from 16S rRNA gene amplicon analysis were prone to errors due to the abundance and accessibility of the cells.

Conclusions:

Our results challenge the reliability of 16S rRNA gene amplicon analyses as a tool for microbial diversity analysis and inevitably lead to the question of whether PCR-based analyses should be used for mapping the microbiome or other microbial biocenoses.

OC.09_194 - A PRECLINICAL STUDY TO EXPLORE THE IMPACT OF DIETARY GLYCOTOXINS ON GUT HOMEOSTASIS AND MICROBIOME COMPOSITION

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Objective:

Advanced glycation end products (AGEs), referred also as glycotoxins, represent a heterogeneous group of compounds, that are relatively unknown but potentially harmful components of diet. The effects of dietary AGEs, on intestinal homeostasis are limited explored. The aim of this study is to comprehensively evaluate the effects orally-administered methylglyoxal (MG), a highly reactive AGEs precursor, on gut homeostasis of aged mice. In particular, we investigated whether high MG intake could impact gut permeability, anti-microbial peptide production and microbiome composition, and ultimately leading to cognitive alteration.

Methods:

Twenty mice were gavage fed daily for 4 weeks with MG solution (100 mg/kg). Behavioural battery tests have been conducted and specific tissue and organs analysed and processed for immunohistochemical analysis. Proinflammatory cytokines, permeability markers, immunity mediators were evaluated by RT-PCR. Intestinal cryptidins have been isolated and tested for their antimicrobial activity by flow cytometry. 16S rRNA sequencing and bioinformatic analysis were performed to analyse the microbiome composition.

Results:

MG chronic treatment impacted on gut homeostasis, increasing the numbers of Paneth cells, altering the release of antibacterial peptides and changing microbiome composition. MG-mice showed also increased expression of proinflammatory cytokines and altered intestinal barrier. Interestingly, enhanced neuroinflammation at hippocampus level and behavioural defects was also observed in those MG treated mice.

Conclusions:

Our study demonstrated the involvement of dietary glycotoxins in gut dyshomeostasis, which, in turn, affects brain health. Although preliminary, these results suggest that AGEs/AGEs precursor compounds derived from the diet pose a real threat to the gut-brain axis.

OC.10_83 - PROBIOTICS FOR EARLY MICROBIOTA DEVELOPMENT (PEACE PROJECT)

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Objective:

The microbial colonisation of the newborn (primocolonisation) plays a fundamental role in human health. When this process is disrupted, an impairment of the function of the intestinal barrier can occur, with a predisposition to develop 'non-communicable' diseases. The aim of our study is to isolate and characterise novel beneficial bacteria (potential next-generation probiotics) to be used to counteract the disturbances associated with altered primocolonisation.

Methods:

Bacteria were isolated from the stools of 6 healthy babies. Strains belonging to species selected according to literature were submitted to a general microbiological characterisation. Safety properties were also assessed in-vitro by evaluating antibiotics resistance and DNase activity. Finally, to determine functionality features, immunomodulatory and intestinal barrier protective effects were assessed by co-culture experiments with eukaryotic cell lines.

Results:

From human fecal samples, 984 strains were isolated. Among them, 280 belonged to the researched species and 11 were selected (1 for each species and sample). Almost all bacteria selected reached the stationary phase at 24h. Overall, all bacteria were sensitive to 0,3% bile salts but not to acidic pH (from 3 to 6). Resistance to Gentamycin, Kanamycin, Streptomycin and Chloramphenicol has been observed in some strains but no presence of DNase was detected. Immunomodulatory and intestinal barrier effects were also strain specific.

Conclusions:

Based on the results, 4 promising strains were identified and are now characterized for in vitro human milk oligosaccharides degradation and cross feeding. At the end, one or two strains will be tested in models of altered primocolonisation.

OC.11_110 - INTERACTIONS BETWEEN INTESTINAL MICROBIOTA, MUCUS LAYER AND DIETARY FIBER: TOWARDS PREVENTIVE STRATEGIES TO MITIGATE VIRULENCE OF FOOD-BORNE PATHOGEN ENTEROTOXIGENIC ESCHERICHIA COLI

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Objective:

Dietary fibers exhibit well-known beneficial effects on human health, but their anti-infectious properties against enteric pathogens have been poorly investigated. Enterotoxigenic Escherichia coli (ETEC) is a major food-borne pathogen that causes acute traveler's diarrhea. Its virulence traits mainly rely on adhesion to epithelial surface, mucus degradation, and the secretion of two enterotoxins associated with intestinal inflammation. With the increasing burden of antibiotic resistance worldwide, there is an imperious need to develop novel alternative strategies to control ETEC infections. However, to date, studies specifically addressing how dietary fibers affect human ETEC strains are scarce.

Methods:

Using complementary in vitro approaches reproducing the human digestive conditions (including human gut microbiota) and host intestinal cells compartment, we aimed to investigate the inhibitory potential of two dietary fibers containing-products (a lentil extract and yeast cell walls) on various facets of human reference strain ETEC H10407's pathophysiology.

Results:

We showed that the lentil extract decreased toxin production in a dose-dependent manner, reduced pro-inflammatory IL-8 production, and modulated mucus-related genes induction in ETEC-infected mucus-secreting intestinal cells. We also reported that the yeast product reduced ETEC adhesion to mucin and Caco-2/HT29-MTX cells. Both fiber-containing products strengthened intestinal barrier function and modulated toxin-related gene expression. In a complex human gut microbial background, both products did not elicit a significant effect on ETEC colonization.

Conclusions:

These pioneering data demonstrate the promising role of dietary fibers in controlling different stages of the ETEC infection process and suggest important implications regarding how our immediate diet history may modify susceptibility to some enteric diseases.

OC.12_64 - A NEW IN VITRO HUMAN COLON MODEL SIMULATING OBESITY-RELATED GUT MICROBIOTA DYSBIOSIS

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Objective:

Obesity is a complex, multifactorial and highly prevalent disease, strongly associated with gut microbiota perturbations. For technical, regulatory, ethical and cost reasons, in vitro models simulating the human digestive tract are a relevant alternative to in vivo assays, provided they are fully validated against in vivo data in humans. To date, no relevant in vitro model reproducing the nutritional, physicochemical and microbial parameters of the obese human colon has been described.

Methods:

An intensive literature review was performed to adapt the Mucosal Artificial Colon (M-ARCOL) model to the specific colonic environment of obese patients (pH, retention time and ileal effluents composition). Stools from 9 donors (4 healthy and 5 obese) were used to inoculate two bioreactors ran in parallel, set-up to reproduce either healthy or obese parameters.

Results:

When applying obese parameters on healthy stool, significant shifts in microbiota activity and composition were observed, in accordance with in vivo data ($P<0.05$). Less methane but more short chain fatty acids and associated energy were produced. An increase in obesity-associated marker populations (Prevotellaceae, Veillonellaceae) and a decrease in healthy-associated marker populations (Archaea, Akkermanciaceae, Rikenellaceae and Christensenellaceae) were also observed in lumen and mucus-associated microbiota, together with a lower bacterial diversity. Interestingly, when applying healthy parameters on obese stools opposite trends were obtained demonstrating gut microbiota resilience.

Conclusions:

M-ARCOL model can represent a powerful platform as an alternative to in vivo animal assays in preclinical trials to perform mechanistic studies on obesity and evaluate pharmaceutical/nutritional strategies aiming to restore gut microbiota eubiosis.

OC.13_50 - EFFECTS OF PECTIN-ENRICHED SMOOTHIE CONSUMPTION ON GUT MICROBIOTA AND HEALTH PARAMETERS: A CROSSOVER STUDY

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Objective:
Consuming dietary fiber has a positive effect on human health. The aim of the present study was to evaluate the effect of a smoothie enriched with pectin and other soluble fibers on human gut microbiota and health parameters depending on the daily fiber intake during a short-term intervention study.

Methods:
DNA extraction from fecal samples, 16S rRNA sequencing using Illumina MiSeq platform, nutrition data collection with Nutridata dietary analysis program, statistical analysis with R version 4.2.1 (The R Foundation for Statistical Computing, Vienna, Austria) using public packages.

Results:
It was observed that the basal level of dietary fiber intake determined the changes in gut microbiota during smoothie consumption. Most of the up- or down-shifts (eg. Lachnospira, Colidextribacter and Bacteroides, or Dorea, Streptococcus and Holdemanella, respectively) were observed for low-fiber consumers (n=22) compared to that for high-fiber consumers (n=9). In both groups, pectin-enriched smoothie reduced the abundance of bacteria in the Ruminococcus torques group. As most of the changes in microbiota were recovered during the wash-out periods, we could suggest that short-term pectin-enriched smoothie consumption is not enough to make continuous changes in gut microbiota.

Conclusions:
We observed that baseline fiber intake determines the response of gut microbiota to smoothie consumption. Low-fiber consumers had more positive changes in their microbiota at the genus level after pectin-enriched smoothie intake. We could suggest that short-term pectin-enriched smoothie intake promotes the growth of fermentative gut bacteria and reduces the abundance of inflammation-related bacteria, but these effects are provisional.

OC.14_99 - EXERCISE AND GUT MICROBIOTA

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Objective:
The composition of the gut microbiota is crucial for health, and new evidence suggests that exercise-training programs can modify the composition and function of the gut microbiota. The impact of different types of exercise, such as resistance and aerobic training, on the human gut microbiome depends on metabolic pathways and fuel sources used. Aerobic activity increases cardiovascular adaptations, which raise peak oxygen consumption without changing strength significantly, whereas resistance exercise improves neurological responses that improve strength. This study aimed to investigate the efects of nine weeks of high-intensity interval exercise on gut microbiota composition in healthy young adults.

Methods:
The gut microbiota composition of seventeen healthy male college students was analysed before and after nine weeks of high-intensity interval cycling training by 16S rRNA amplicon sequencing. PERMANOVA for measures was used to test pre-post differences in the relative abundance of all taxonomic levels, and correlations between variations in microbial composition and physical and dietary features were also assessed.

Results:
Physical exercise induced changes in microbiota composition, at all taxonomic levels analysed, phyla, classes, orders, families, genera and species. Changes in the relative abundance of eighteen genera were correlated to changes of twenty environmental factors grouped in physical features, sport-related features, and dietary features. In particular, VO2max improvements were associated with increased Blautia and decreased Oscillospira abundance.

Conclusions:
Nine weeks of high-intensity exercise induced modifications in gut microbiota composition in healthy male college students, shifting the gut microbial population towards a healthier microbiome.

OC.15_34 - INSIGHT INTO THE ATHLETIC GUT MICROBIOTA: EXERCISE AS A DETERMINANT OF THE GUT MICROBIOTA COMPOSITION

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Objective:
The human gut microbiota is a consortium of 10^{14} microbial cells involved in metabolic, immunomodulatory, and physiological processes, altogether contributing to the systemic human health. Exercise elicits well-known effects on the energetic metabolism and immune system, but less is known on its influence on the gut microbiota, due to the diet-associated induced bias. Elite athletes offer remarkable physiology and unique metabolic characteristics (endurance-associated aerobic capacity, metabolic flexibility, cardiorespiratory adaptations) that consent exclusive insight into the gut microbiota research. The aim of this work is to collect recent studies on the effect of high-intensity and high-duration aerobic exercise on athletic gut microbiota.

Methods:
A comprehensive overview of what is already present in the literature was made following the guidelines of a systematic review (PRISMA), with exhaustive bibliographic search focusing on the studies published in the last 5 years. Confounding factors on gut microbiota modulation such as diet or medical treatment were limited according to the criteria fixed to categorize the studies.

Results:
Observational studies confirmed that athletes show higher faecal microbial diversity, increased production of short chain fatty acids (such as butyrate) and higher levels Akkermansia, Veillonella and Prevotella, compared to less active subjects. Limitation of these studies is the lack of causality since they only confirm associations between training status and microbiota populations.

Conclusions:
We believe that more intervention studies on athletic populations targeted to test their gut microbiota in response to a precise training stimulus are strongly recommended to better elucidate the bidirectional gut-muscle axis.

PROBIOTICS

OC.16_28 - EFFECT OF STANDARD AND PROBIOTIC YOGURT ON HYPERCHOLESTEROLEMIC RATS

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ABSTRACT

Objective:
To investigate the hypocholesterolemic effect of standard active yogurt and probiotic yogurt fermented with B. lactis/ animalis, L. acidophilus and L. gasseri in hypercholesterolemic rats.

Methods:
Twenty-four male Wister albino rats were distributed randomly into four equal groups. Control negative: normal diet, remaining groups were fed on high fat diet (HFD) for 8 weeks to induce hypercholesterolemia. Subsequently, the remaining rats were divided as follow: control positive, fed on HFD, standard group, fed on HFD with standard yogurt, and probiotic group, fed on HFD with probiotic yogurt for six weeks. Blood samples were collected for biochemical analysis and histological examination.

Results:
Significant reduction was observed in Total Cholesterol, Triglyceride and Low-Density Lipoprotein of standard and probiotic yogurt groups as compared to control positive. Also, the level of High Density Lipoprotein increased in standard and probiotic yogurt groups. Furthermore, significant reduction in liver enzymes AST and ALT and significant increase in antioxidants levels of Glutathione and Superoxide Dismutase were observed compared to control positive ($P < 0.01$). Histological examination of heart and liver tissues showed that standard and probiotic yogurt groups alleviated the histopathological degeneration compared to control positive and was more noticeable in probiotic yogurt group.

Conclusions:
Both standard and probiotic yogurt were effective to improve lipid profile parameters and antioxidants status in hypercholesterolemic rats. Probiotic yogurt was more beneficial at tissues level, which suggests the long-term effect of probiotics in the prevention of heart and liver diseases.

OC.17_47 - PHYSICHOCHEMICAL, ANTIOXIDANT, AND ANTIMICROBIAL ACTIVITIES OF A NANOENCAPSULATED SYNBIOTIC AS A TAILORED ANTIBIOTIC ALTERNATIVE FOR FOOD PRODUCING ANIMALS

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ABSTRACT:

A synbiotic composed of alginate nanoencapsulated prebiotic pomegranate peel phytogenics and multi-species probiotics (Lactococcus lactis, Lactobacillus plantarum, Lactobacillus paracasei, and Saccharomyces cerevisiae) has been developed as a potential eco-friendly alternative to antibiotics. The physicochemical properties of the encapsulated synbiotic were evaluated, and its gastric and storage tolerance, as well as its antioxidant and antimicrobial activity, were tested and compared to that of the non-encapsulated synbiotic (free synbiotic). The results showed that the prebiotic pomegranate peel ethanolic extract contained a total of seven phenolic compounds, with cinnamic being the most abundant (13.26 µl/mL). Sodium alginate-$CaCl_2$ nanocapsules were effective in encapsulating 84.06%±1.5 of the prebiotic's phenolic compounds and 98.85%±0.57 of the probiotics. The particle size of the alginate-$CaCl_2$ nanoencapsulated synbiotic was 544.5 nm, and the polydispersity index and zeta potential values were 0.593 and –12.3 mV, respectively. Thermogravimetric analysis showed that the alginate-$CaCl_2$ nanoencapsulated synbiotic had high thermal stability at high temperatures, with only 2.31% of its weight being lost within the temperature range of 70–100 °C. The count of viable probiotics in the nanoencapsulated synbiotic was significantly higher than that in the free synbiotic after exposure to gastric acidity and storage for six months at room temperature. The percent inhibition values of the nanoencapsulated synbiotic and ascorbic acid (as a standard antioxidant) were comparable and significantly greater than those of the free synbiotic. The half-maximal inhibitory concentration (IC50) of the nanoencapsulated synbiotic and ascorbic acid was significantly lower than that of the free synbiotic (3.96±0.42 µg/mL and 4.08±0.79µg/mL for nanoencapsulated synbiotic and ascorbic acid, respectively, vs. 65.75±2.14µg/mL for free synbiotic). The nanoencapsulated synbiotic showed the highest significant antimicrobial activity against Escherichia coli (ATCC 8739). Both the nanoencapsulated and free synbiotics showed antimicrobial activity against Staphylococcus aureus (ATCC 6538) similar to that of gentamicin, although the nanencapsulated synbiotic showed significantly higher inhibition activity compared to the free synbiotic. The nanoencapsulated synbiotic showed antimicrobial activity comparable to gentamicin against Pseudomonas aeruginosa (ATCC 90274), whereas the free synbiotic showed the least antimicrobial activity ($P<0.05$). Both synbiotics showed significantly higher antimicrobial activity against Salmonella typhi (ATCC 6539) than gentamicin. Both synbiotics showed antifungal activity against Aspergillus niger and Aspergillus flavus, with a stronger effect observed for the nanoencapsulated synbiotic. However, the activity of both synbiotics was significantly lower than that of fluconazole (an antifungal drug).

OC.18_124 - POTENTIAL EFFECT OF A PROBIOTIC MIX AGAINST SARS-COV-2 INFECTION

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Objective:

Studies reported a correlation between COVID-19 and intestinal microbiota dysbiosis which may explain abdominal pain and diarrhea symptoms in hospitalized patients[1]. Probiotic supplementation is an interesting strategy to help alleviate viral infection. In this study, the antiviral activity of a mix of Bifidobacterium longum LA101, Lactobacillus helveticus LA102, Lactococcus lactis LA103, and Streptococcus thermophilus LA104 was explored in an in vivo model of hamsters infected with SARS-CoV-2.

Methods:

Female golden Syrian hamsters (n=16) were fed with 10^9 CFU of the probiotic mix (PM) daily until necropsy. At day 7, hamsters were infected with SARS-CoV-2 by nasal instillation (10^4 $TCID_{50}$ units). Samples were collected 4 and 7 days post-infection (dpi) for analyses.

Results:

PM helped recover weight loss caused by viral infection, and significantly reduced viral load and titers in the lungs and upper respiratory tract (URT). At 4 dpi, viral load was reduced by ~2 logs ($p<0.05$) and completely abolished at 7 dpi ($p<0.05$) in URT. PM regulated the altered expression of Il-12p40 and Occludin genes in the small intestine, reduced Ifn-I at 4 dpi ($p<0.05$) in the colon and reduced the fecal proteolytic activity ($p<0.05$).

Conclusions:

Our work showed the potential of the PM in the alleviation of COVID-19 symptoms. Further analyses, such as gut microbiota analysis, are under investigation.

OC.19_141 - THE ROLE OF A PROBIOTIC CONSORTIUM IN THE TREATMENT OF FATIGUE AND OTHER SYMPTOMS IN LONG COVID-19 SYNDROME: A RANDOMIZED, DOUBLE-BLIND, PLACEBO-CONTROLLED STUDY (DELONG#3)

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Objective:

Long COVID is a chronic condition affecting individuals who recovered from acute COVID-19. It is characterized by a variety of symptoms, including fatigue, neurocognitive and sensory impairment, sleep disturbance, myalgia/arthralgia, and dysautonomia. Intestinal microbial dysbiosis has been reported and remains altered even after several months of recovery from acute SARS-CoV-2 infection. Restoration of microbiome normobiosis appears as a potential therapeutic approach for managing Long COVID symptoms.

Methods:

This ongoing research is a phase three, single-center, randomized, double-blind, placebo-controlled trial (NCT05874089) to evaluate the efficacy of a consortium of mixed probiotics at high concentration (VSL#3®, Actial Farmaceutica s.r.l), in reducing fatigue as well as in ameliorating different aspects of psychological patients' well-being.

Adult patients between the ages of 18 and 65, diagnosed with Long COVID according to diagnostic criteria, were recruited from the Long COVID Outpatient Clinic at Policlinico Hospital, Milan (Italy). Eligible patients with clinically significant fatigue, as determined by a Chalder Fatigue Scale score >4/11 and in whom other causes of fatigue were excluded, were randomized to receive either VSL#3® or placebo for a duration of 4 weeks, 2 anonymized sachets twice a day. Individuals with impaired cardio-pulmonary functions, active psychiatric conditions, and those currently using or who used in the past month antibiotics, or probiotics and who immunosuppressant/immunomodulatory drugs, opioids, antidepressants, were excluded.

The primary endpoint of the study was a reduction in fatigue as measured by the Chalder Fatigue Scale score after 4 weeks of VSL#3® treatment. Secondary outcomes included variations in scores of the Hospital Anxiety and Depression Scale (HADS), Short Form Health Survey (SF-36), Structured Assessment of Gastrointestinal Symptoms Scale (SAGIS), Symptoms Check List-90 (SCL-90) somatization dimension, Karnofsky Performance Status (KPS), and Visual Analogue Scale (VAS) after 4 weeks of treatment.

Results:

Between November 3, 2022, and May 9, 2023, a total of 279 Long COVID patients were assessed for eligibility, and 39 patients with relevant fatigue were included in the study. One patient was excluded after enrollment for scarce compliance. Of the participants, 20 were male (47.4%), with a mean baseline age of 54.2 years (±7.94). Among the included patients, 22 (57.9%) had been hospitalized during acute COVID-19, with an average hospital stay of 13.1 days (±16.75). All patients reported in addition to fatigue other Long-COVID symptoms.

A significant reduction of Chalder Fatigue Scale scores was observed in VSL#3® treated patients at t4 as compared with placebo ($p<0.0079$), which persisted at t8. Moreover, the SF-36 Fatigue/Energy score, the SF-36 physical functioning score and SAGIS score were also significantly reduced in the treatment group ($p<0.03$, $p<0.02$, $p<0.04$ respectively) (Table 1 and Figure e2, e3). No significant variations were observed in HADS, SCL-12, KPS and VAS scores after treatment in the two groups.

Conclusions:

Our results indicate that VSL#3® (Actial Farmaceutica) supplementation could be beneficial in reducing fatigue symptoms in patients with Long COVID. These results support the notion that targeting the gut microbiota with VSL#3® may have a positive impact on fatigue symptoms in patients with Long COVID, consistently with previous studies indicating a link between gut dysbiosis and fatigue

OC.20_119 - PROBIOTIC PROPERTIES OF LACTOBACILLUS FERMENTUM AND PEDIOCOCCUS PENTOSACEUS ENCAPSULATED WITH OR WITHOUT HYDROGEL CELLULOSE MICROFIBER FROM OIL PALM LEAVES

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Objective:

This study aimed at an in vitro characterization of the probiotic properties of Lactobacillus fermentum InaCC B1295 (LFB1295) and Pediococcus pentosaceus strain 2397 (PP2397) encapsulated with or without hydrogel cellulose microfiber (HCMF) from oil palm leaves (OPL).

Methods:

The experimental design used in this research was an in vitro study. The safety of LFB1295 and PP2397 encapsulated with or without HCMF from OPL was assessed, along with the probiotic qualities of auto-aggregation, co-aggregation, and hydrophobicity. Hemolytic activity, biogenic amines, cytolysin, gelatinase production, and antioxidant activities (hydroxyl radical-scavenging and DPPH radical-scavenging abilities) were also assessed.

Results:

The results showed that in vitro safety tests showed that PP2397 and LFB1295 cells encapsulated with or without HMCF did not have hemolytic activity and did not produce biogenic amines, cytolysin, and gelatinase. LFB1295 and PP2397, enclosed in HCMF from OPL, compared to free cells, showed higher antioxidant activity. Compared to free cells, LFB1295 and PP2397 encapsulated in HCMF from OPL showed higher antioxidant and auto-aggregation capabilities. LFB1295 free cells, however, exhibited the highest hydrophobicity score. Compared to free cells and cells enclosed in these two LABs, LFB1295 and PP2397 exhibited a higher rate of co-aggregation with the harmful bacteria Staphylococcus aureus and Escherichia coli.

Conclusions:

The present finding showed that CMFH-encapsulated LFB1295 was a safe probiotic ingredient with excellent antioxidant activity, autoaggregation, co-aggregation, and hydrophobicity.

OC.21_159 - MOLECULAR DISSECTION OF THE MODE OF ACTION OF AKKERMANSIA MUCINIPHILA, A NEXT GEN BENEFICIAL MICROBE

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Objective:

Administration of Akkermansia muciniphila Muc^T can counteract weight gain, intestinal barrier function disruptions, and metabolic disturbances in mice and man (Depommier et al., Nat Med 2019; Segers & de Vos, MRR 2023). Many of its health-promoting effects can be reproduced by the Type IV pilus-associated Amuc_1100 protein that has been shown to activate Toll-like receptor 2 (TLR2) and improve barrier function (Plovier et al., Nat Med 2017). Here, we provide further molecular insight in the host-signaling mechanisms of A. muciniphila.

Methods:

We used random mutagenesis to identify genes that were affected in mucus-binding since this is an expected first step in the host-signaling cascade, given the mucin-degrading capacity of A. muciniphila. Mutant libraries were screened for strains with significantly decreased mucin-binding, which were further characterized at physiological and genomic level.

Results:

Affected genes included genes encoding proteins involved in exopolysaccharide (EPS) synthesis and export, Sec translocation, and Type IV pilus production. Scanning electron microscopy revealed strains with reduced piliation. Furthermore, several strains, including strains with reduced piliation, showed a reduction in TLR2 activation capacity compared to wild type A. muciniphila.

Conclusions:

Taken together, these results suggest that mucin-binding requires specific secreted proteins, is related to EPS biosynthesis and that the presence of pili is essential. In addition, these results suggest that an intact pilus might be needed to optimally position the signaling molecule Amuc_1100. This allows us to generate a model of the mode of action of living and pasteurized A. muciniphila cells in promoting health.

OC.22_191 - EFFICACY OF ALIVE MULTISTRAIN PROBIOTIC CO-SUPPLEMENTATION WITH OMEGA-3 PUFA ON PANCREATIC BETA-CELL FUNCTION IN TYPE 2 DIABETES PATIENT

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Objective:
The current study assessed the efficacy of alive multistrain probiotic co-supplementation with omega-3 polyunsaturated fatty acids (PUFAs) vs. placebo on β-cell function in type 2 diabetes (T2D) patients.

Methods:
We conducted a secondary analysis of previously published RCT (NCT04201938, NCT03528707) with a total of 52 patients with T2D. The main inclusion criteria were the presence of beta-cell dysfunction (HOMA2-β<50%) and insulin therapy alone or in combination with oral anti-diabetic drugs. The primary outcome was the assessment of β-cell function as change C-peptide and HOMA-β (homeostasis model assessment-estimated β-cell function), which was calculated using HOMA2 calculator (Diabetes Trials Unit, University of Oxford). Secondary outcomes were the changes in glycemic control-related parameters, anthropomorphic variables and cytokines levels. ANCOVA was used to assess the difference between groups.

Results:
In the placebo group, all parameters change insignificantly after treatment. Supplementation with alive multiprobiotic and omega-3 PUFA was associated with a slightly insignificant improvement of β-cell function (HOMA-β increased from 42.2±15.4 to 62.21±33.98 (p=0.049), as compared to placebo. In the Probiotic-Omega group, a statistically significant decrease of body weight (93.61±12.23 vs 92.55±11.9; p=0.046), WC (98.25±10.61 vs 97.2±9.69; p=0.013) and TNF-α (38.77±7.73 vs 31.26±9.99; p=0.009) were recorded after eight weeks of treatment. The concentration of IL-1β, IL-6, IL-8, γand γ-INF didn't change statistically in the probiotic group.

Conclusions:
Co-supplementation of alive multistrain probiotic with omega-3 PUFA modestly improved β-cell function in patients with T2D.

OC.23_42 - PROTECTIVE EFFECT OF SYNBIOTIC MIX AGAINST INFLAMMATION: IN-VITRO AND IN-VIVO APPROACHES

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Objective:
Probiotics and prebiotics confer health benefits to the host. However, the underlying shifts in gut microbial communities, especially at the functional level, have not been detailed. In this study, the effect of synbiotic consisting of Bifidobacterium and Lactobacillus strains and IMOS on gut microbiota regulation and the alleviation of metabolic disorders has been investigated.

Methods:
The two Bifidobacterium and two Lactobacillus strains were evaluated for their compatibility through different approaches. Furthermore, in- vitro screening of probiotics in combination with isomaltooligosaccharides (IMOS) in preventing lipopolysaccharide (LPS)-induced inflammation in RAW 264.7 macrophages and human intestinal epithelial (Caco-2) cells was evaluated. In vivo studies have been performed in murine model of High fat high sucrose (HFHS) diet induced Metabolic syndrome to assess the preventive efficacy of the strains and the synbiotic in HFHS diet induced metabolic complications.

Results:
Results indicated that the bacterial strains were compatible with each other. In-vitro viability of RAW 264.7 and Caco-2 cells was not hampered also the blend of the strains reduced the LPS-induced nitric oxide and pro-inflammatory cytokine production. The combination of four strains curtailed the TNF-α and LPS-induced inflammation in the human intestinal epithelial cells as there was a reduction in IL-8 production. Oral administration of synbiotic mix show no sign of cellular or mucosal degeneration in treatment group whereas insulin, CRP level, body weight and inflammatory markers were increased in HFHS group which were prevented in intervention groups.

Conclusions:
These studies suggested that the synbiotic blend has the potential to alleviate metabolism associated diseases.

OC.24_198 - THE EFFECT OF COMBINATION OF BUTYRIC ACID, BIFIDOBACTERIUM AND FRUCTOOLIGOSACCHARIDES IN A YOUNG PATIENT WITH RHOEMHELD SYNDROME A CASE PRESENTATION

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Objective:

Roemheld syndrome, the condition involves issues in the stomach which can trigger palpitations, by stimulating heart muscles, while also activating the vagus nerve which can lower the heart rate.
Butyric acid is a short-chain fatty acid, it stimulates metabolism and their physiological maturation, maintaining the integrity and enhancing healing processes of the intestinal mucosa.
Bifidobacteria prevents intestinal colonization by hostile pathogenic bacteria and yeasts with which bifidobacteria compete for nutrients.
Fructooligosaccharides are complex carbohydrates, serving as food for live bacterial cultures.

Methods:

The patient, male 32 yo, presented at the University Clinic of Cardiology with palpitations, shortness of breath, epigastric discomfort and flatulence. Parameters: ECG a sinus rhythm with 105 bpm, blood pressure 112/78 mmHg. High sensitive troponin, d-dimers and complete blood count was done, all normal. Ultrasound of the heart revealed also normal. A 24 hours holter ecg was assigned.

Results:

After all cardiac examination were done, the patient was sent to gastroenterologist, who prescribed the aforementioned combination, a gastro-resistant tablet which was taken 2 times a day for two months, after that the maintenance dosage was 1 tablet a day. According to the subjective symptoms, patient reduced significantly palpitations. In the three holter ecg that patient carried out was seen a significant depression of the ectopic ventricular beats, which means that the combination therapy significantly impacted the symptoms which revealed from flatulence.

Conclusions:

Thus, our recommendation is to use this combination in people which is excluded any cardiac abnormality and when the definitive diagnosis is the Roemheld syndrome.

OC.25_182 - AKKERMANSIA MUCINIPHILA ADMINISTRATION PROMOTES A HEALTHY AGING BY MODULATING THE GUT MICROBIOTA IN OLD FEMALE MICE

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Objective:

We have previously shown that Akkermansia muciniphila ingestion induces beneficial changes in behavioral tests, immune functions, and on oxidative and inflammatory status in old mice, increasing their lifespan. The aim of the present study was to determine if A. muciniphila orally supplementation for 1 month in old female mice promoted changes in the gut microbiota composition and metabolic activity.

Methods:

Twenty old female ICR-CD1 mice (72 ± 4 weeks) were divided into two groups: one that received A. muciniphila CIP107961 strain (108 cfu/100 µl PBS) for 1 month (OA) and another group that received only PBS (OC). In addition, another group of ten adult mice (40 ± 4 weeks) was included to compare with the two previous groups (AC). In all experimental groups, the gut microbiota composition was analyzed by 16S rRNA gene sequencing and metabolic activity by quantifying fecal short-chain fatty acids (SCFA) and branched short chain fatty acids (BSCFA) using gas chromatography.

Results:

Akkermansia administration promoted changes in the microbial profile of OA group in comparison with OC and AC groups, highlighting the modulation of Actinomycetota phylum and Bifidobacterium genus. Major SCFA did not show significant changes between the three groups analyzed but BSCFA were significantly lower in the OA group compared to the OC group, showing similar levels to the AC group.

Conclusions:

Our results indicate that A. muciniphila CIP107961 strain supplementation for one month could be considered a good nutritional strategy to promote a healthy aging through gut microbiota modulation.

OC.26_180 - MANAGEMENT OF METABOLIC DISORDERS THROUGH SPECIFIC PROBIOTICS INTERVENTION

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Objective:

Obesity is the main precursor for metabolic diseases that can be targeted in developing various interventions; several physical, psychological, pharmaceutical and dietary approaches have been proposed for the management of obesity. Probiotic supplementation approach offers the possibility to shape the gut microbiota, enabling the development of innovative formulations able to improve intestinal wellbeing and consequently the related body weight modulation and energy metabolism.

Methods:

Fifty-nine overweight/obese subjects were randomly assigned to daily consume the probiotic Lactiplantibacillus plantarum IMC 510® or placebo for 3 months. Before and after the administration period, anthropometric and biochemical parameters, self-administered questionnaires, gut microbiota composition and some specific biomarkers were monitored for each subject.

Results:

Compared to placebo, probiotic supplementation determined a significant decrease in body weight, BMI, waist circumference, waist to height ratio and blood glucose, with a significant correlation between AdipoQ/Lep and the clinical parameters. Moreover, probiotic daily consumption produced significant decrease of the genera Hafnia-Obesumbacterium and Rombutsia and significant increase in beneficial gut bacterial groups, such as Lactobacilli and Bifidobacteria, also expanding the bacterial richness and diversity, maintaining low the Firmicutes/Bacteroidetes ratio. Conversely, placebo administration induced a decrease of Actinomycetaceae and an increase of Alloprevotella spp. along to increased levels of proinflammatory hexanoic and heptanoic acids.

Conclusions:

The results suggest that the probiotic strains IMC 510® beneficially modulate gut microbiota and improve the inflammatory status associated to metabolic disorders, restoring obesity-linked gut dysbiosis. Thanks to its effect on overweight/obese subjects, Lactiplantibacillus plantarum IMC 510® supplementation could represent a future and encouraging strategy for the obesity management.

OC.27_155 - EFFECT OF A MULTI STRAIN PROBIOTIC MIXTURE CONSUMPTION ON ANXIETY AND DEPRESSION SYMPTOMS INDUCED IN ADULT MICE BY POSTNATAL MATERNAL SEPARATION

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Objective:

Intestinal microbial composition not only affects the health of the gut, but also influences centrally mediated systems involved in mood, through the "gut-brain" axis, a bidirectional communication between gut microbiota and the brain.

Methods:

In this context, the modulation of intestinal microbiota and its metabolites through the administration of probiotics seems to represent a very promising approach in the treatment of the central nervous system alterations.

Early postnatal life is a critical period during which the brain undergoes profound and essential modulations in terms of maturation and plasticity. Maternal separation (MS), i.e. the disruption of the mother–pup interaction, represents a pivotal paradigm in the study of stress-related mood disorders, by inducing persistent changes in the immune system, inflammatory processes and emotional behavior in adult mammals.

Results:

We tested whether the prolonged consumption of a human consuming multi-strain probiotic formulation could reverse the impact of maternal separation in adult mice. Our data demonstrated that the treatment with probiotics was able to totally reverse the anxiety- and depressive-like behaviour, normalize the neuro-inflammatory state, by restoring the resting state of microglia, and finally induce a proneurogenic effect. Moreover, mice subjected to maternal separation showed a microbiota permissive to OttaBac® (OB) colonization which effects SCFAs production and specifically the butyrate level.

Conclusions:

Gut microbiota and its metabolites mediate the therapeutic action of the probiotic mix on MS-induced brain dysfunctions. Our findings extend the knowledge on the use of probiotics as a therapeutic tool not only in conditions of gastrointestinal dysfunction, but also in the presence of alterations of the emotional sphere.

OC.28_89 - THE ROLE OF PSYCHOBIOTIC CEREBIOME® IN MODULATING THE MICROBIOTA-GUT-BRAIN AXIS: A REVIEW OF PRECLINICAL AND CLINICAL DATA

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Objective:
The influence of microbiome dysbiosis on mental health has been well established. Modulating the Microbiome-Gut-Brain Axis (MGBA) offers a novel modality of alleviating neuropsychological disorder symptoms, a particularly pertinent approach given the continuously increasing prevalence of mental health conditions and the limitations of current treatments. Cerebiome®, a psychobiotic formulation, has demonstrated significant promise in this area, yet much remains to be uncovered. This review aims to highlight key data from preclinical and clinical studies and outline future research directions.

Methods:
A comprehensive review of both preclinical and clinical studies was conducted. Preclinical data involved assessment of Cerebiome® in animal models, examining its effects on depression- and anxiety- associated behavior, neuroinflammation, and intestinal inflammation and permeability. Clinical studies assess the role of Cerebiome® in mitigating psychological and physiological symptoms of stress, mood disorders, neurodegeneration, sleep, and perceived stress in subclinical and clinical populations.

Results:
Preclinical studies demonstrated the role of Cerebiome® in attenuating inflammation, maintaining blood-brain barrier, exerting anxiolytic activity, and modulating behavioral parameters of mood disorders. These finding were echoed in clinical studies which reported a significant role of Cerebiome® in enhancing psychological and physiological symptoms of stress, and mood disorders such as depression. Additionally, investigating potential MOA, particularly in the context of inflammageing and microglia activation, have been initiated.

Conclusions:
Cerebiome® presents promising potential as a psychobiotic intervention for stress and neuropsychological disorders. Further studies aimed at elucidating the precise MOA, expanding the horizon of clinical applications and target populations will enhance our understanding and inform future applications.

OC.29_199 - EFFECT OF PROBIOTICS ON AUTONOMIC NERVOUS SYSTEM FUNCTION OF PATIENTS WITH MILD ALZHEIMER'S DISEASE

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Objective:
The gut microbiome plays an integral part in neurodegeneration through its direct interaction with the central nervous system via the gut-brain axis and the autonomic nervous system (ANS) via the vagal nerve. The main objective of this work is to investigate whether administration of probiotics to patients with mild Alzheimer's Disease modifies ANS function in conjunction to changes in the MMSE score, compared to a patient group that receives placebo (no active probiotics).

Methods:
Patients with mild AD (MMSE: 19-23) who fulfil all eligibility criteria are enrolled on the study to take either probiotics or placebo (control) for 16 weeks. Data collection conducted at baseline and study completion (week 0 & 16) includes electrocardiogram (ECG) recorded during resting state (eyes open / closed). We analyse the ECG data of 4 patients (n_control=1) who have completed the study, out of the 14 active patients. We compare the ANS function via Poincaré plots (SD1 and SD2 measures) at baseline and study completion.

Results:
Our preliminary findings indicate changes to ANS activity that correspond to changes in MMSE scores but not study group allocation. One patient (n_study=1) displayed improvement in MMSE score and corresponding decrease in SD1/2 values. Three patients (n_control=1) displayed deterioration in MSSE score and corresponding increase in SD1/2 values.

Conclusions:
Changes in MMSE score appear to be associated to changes in ANS function, but considering that this was not uniformly observed in the study group, it is unclear whether this is related to the probiotic administration.

OC.30_181 - IN VITRO EVALUATION OF A NEW BLEND OF PROBIOTIC STRAINS AGAINST PATHOGENS INVOLVED IN ACNE DISORDER

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Objective:
The formulation of a new blend of probiotics to be used as innovative approach for Acne Vulgaris management, alongside conventional therapies, was designed. Several probiotic candidates were evaluated for their antimicrobial and anti-inflammatory proprieties against the main pathogens involved in the disorder's pathogenesis (Cutibacterium acnes, Streptococcus pyogenes, Staphylococcus epidermidis, Staphylococcus aureus) and for their ability to inhibit or dislocate the pathogens on keratinocytes.

Methods:
Antipathogenic assays were performed with several probiotic strains in order to spot the ones with the best antimicrobial activity. Three probiotic strains selected for their good antimicrobial activity were blended and tested in the competition assays. Pathogenic and probiotic strains were inoculated over HaCaT cells employing three mechanisms (inhibition, exclusion, displacement). The pathogen's adhesion was evaluated in each competition assay with the probiotic blend, compared to its adhesive capacity alone, by microbiological determination and microscopy observation. The inflammatory profiles were evaluated targeting selected pro/anti-inflammatory biomarkers.

Results:
The probiotic blend demonstrated a good adhesion ability to keratinocytes. The co-culture of the probiotic-blend with each pathogenic strain showed a significant reduction of pathogens adhesion on keratinocytes. The inflammatory profile showed a decreased level of proinflammatory cytokines and a significant increase of some anti-inflammatory cytokines, mainly through inhibition and exclusion mechanisms.

Conclusions:
The results suggest that the probiotic blend shows significant potentiality to inhibit the pathogens' adhesion and to modulate the inflammatory status in situ. In conclusion, the probiotic blend may be a good candidate for future skin formulations in managing acne.

OC.31_171 - COMPREHENSIVE PROFILING AND CHARACTERIZATION OF UNTARGETED EXTRACELLULAR METABOLITES IN FERMENTATION PROCESSES: INSIGHTS AND ADVANCES IN ANALYSIS AND IDENTIFICATION

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Objective:
Untargeted metabolomic analysis of extracellular metabolites is a powerful approach that focuses on comprehensively profiling in the extracellular space. In this study, we applied extracellular metabolomic analysis to investigate the metabolism of two probiotic microorganisms with health benefits that extend far beyond the digestive tract and the immune system.

Methods:
Analytical techniques employed in extracellular metabolomic analysis encompass various technologies, including mass spectrometry (MS), which enables the identification of metabolites present in the fermentation media, as well as the comparison of metabolic profiles under different experimental conditions. Multivariate statistical analysis techniques like principal component analysis (PCA) or partial least squares-discriminant analysis (PLS-DA), play a crucial role in uncovering metabolic signatures and understanding the dynamics of metabolic networks.

Results:
Different types of supernatants from fermentation processes, such as dairy-free, not dairy free media and media with no cells or pasteurized, were subjected to metabolite profiling, which contained a complex mixture of metabolites, including substrates, intermediates, and end-products. This profiling provided insights into the metabolic activity of the microorganisms. The integration of advanced software tools has facilitated the identification and the characterization of metabolites in different fermentation condition and microorganism strains.

Conclusions:
In conclusion, untargeted extracellular metabolomic analysis, combined with software tools, allowed the study of the metabolites consumed and produced during fermentation processes of probiotic microorganisms. Ongoing advancements in data analysis methods will further enhance the application of extracellular metabolomic analysis in fermentation research, leading to improved bioproduction and the advancement of sustainable manufacturing processes.

OC.32_178 - CLINICAL EFFICACY OF PROBIOTICS IN ALLERGIC RHINITIS: PRELIMINARY RESULTS FROM A RANDOMIZED CONTROLLED TRIAL

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Objective:

To evaluate the effects of a mixture of probiotic strains (L. acidophilus PBS066, L. rhamnosus LRH020, B. breve BB077, and B. longum subsp. longum BLG240) on symptoms and immune response in subjects with allergic rhinitis.

Methods:

This is a randomized, double-blind, placebo-controlled study on two parallel groups of subjects with allergic rhinitis. Group A (n=22) was treated with a placebo and Group B (n=19) with probiotics for eight weeks. The effects were evaluated at the beginning (T0), four (T1) and eight weeks (T2) of treatment, and after four weeks from the end of the treatment (T3). The immune response was assessed by inflammatory blood markers at T0, T2, and T3. Symptoms were evaluated by the Total Nasal Symptom Score (TNSS) and the Rhinitis questionnaire score Control Assessment Test (RCAT). The Quality of Life (QoL) was assessed by the Mini Rhinoconjunctivitis Quality of Life questionnaire at each time point. Fecal microbiome profiling variations were determined by 16S rRNA gene sequencing analysis (SA) at T0, T2, and T3.

Results:

Group B showed a statistically significant improvement in TNSS symptoms and MiniRQLQ at T3 vs. Group A, and intra-group differences between T0 and T3. At T2, Group B showed an increase of anti-inflammatory species (Dorea and Fusicatenibacter). Conversely, Group A showed an increase of pro-inflammatory species (Bilophila and Bacteroides) and Ruminococcus unassigned and Bacteroides at T3, likely associated with allergies.

Conclusions:

The probiotic mix appears to improve symptomatology, QoL and increases anti-inflammatory and anti-allergic bacterial species in subjects with allergic rhinitis.

OC.33_25 - DEVELOPMENT OF "PRECISION PROBIOTICS": STREPTOCOCCUS THERMOPHILUS AS A MODEL SYSTEM

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Objective:

The market offers plenty of food supplements marketed as probiotics and containing S. thermophilus biomasses. However, the use of the term "probiotic" for strains belonging to this species is still questioned. Recent advances in the physiology of S. thermophilus shed light to the possibility to design in a strain-dependent and/or strain-independent manner new food supplements enriched in specific and defined probiotic activities.

Methods:

Modulation of the cultural growth parameters, post-fermentation metabolic activation steps, use of the proper cryoprotectants will allow to design new category of probiotics called "precision probiotics".

Results:

Based on the above considerations, two example of "precision probiotics" will be shown. The first example represents the design of the new food supplement DIGEST based on S. thermophilus cells metabolically activated for the rapid consumption of lactose, as an alternative to the use of lactase by lactose intolerant subject. The second example will show how the modulation of the production process of S. thermophilus biomass can significantly affect the content of urease activity in fecal samples of healthy subjects, thus allowing the development of new products targeted to IBD patients.

Conclusions:

The increase in knowledge on the genetics, metabolism and more generally on the physiology of probiotics and new generation probiotics has led to the design and development of "precision probiotics" targeted to specific health problems. Based on the characteristics of this new category of probiotics, their design should be accompanied by the development of an adequate set of quality control criteria focusing on specific enzymatic activities, metabolic pathways and not limited only to the total live cell count.

OC.34_36 - DYNAMIC EFFECTS OF PROBIOTIC FORMULA ECOLOGIC®825 ON HUMAN SMALL INTESTINAL ILEOSTOMA MICROBIOTA: A NETWORK THEORY APPROACH

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Objective:

In this study, we investigated the effects of a probiotic formula (Ecologic®825) on the adult human small intestinal ileostoma microbiota.

Methods:

In this study, we employed a dynamic correlation-based metabolic network approach and multivariate analysis, incorporating experimental data obtained from proton-nuclear magnetic resonance (^{1}H-NMR), liquid chromatography-mass spectrometry (LC-MS), shallow shotgun sequencing and flow cytometry performed on ileostoma samples grown using ex vivo SIFR® technology to investigate the alterations caused by the supplementation of a 9-species probiotic formula.

Results:

The results showed that supplementation with the probiotic formula led to a reduction in the growth of pathobionts, such as Enterococcaceae and Enterobacteriaceae, and a decrease in ethanol production. These changes were associated with significant alterations in nutrient utilization and resistance to perturbations. These probiotic mediated alterations which coincided with an initial increase in lactate production and decrease in pH were followed by a sharp increase in the levels of butyrate and propionate. Moreover, the probiotic formula increased the production of multiple N-acyl amino acids in the stoma samples.

Conclusions:

The study demonstrates the utility of network theory in identifying novel microbiota-targeted therapies and improving existing ones. Overall, the findings provide insights into the dynamic molecular mechanisms underlying probiotic therapies, which can aid in the development of more effective treatments for a range of conditions.

OC.35_78 - EFFECT OF A MIX OF LACTICASEIBACILLUS CASEI LA205 AND LACTICASEIBACILLUS PARACASEI LA903 ON BEHAVIOUR, BIOCHEMICAL AND GUT MICROBIAL OUTCOMES OF MALE MICE FOLLOWING CHRONIC RESTRAINT STRESS

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Objective:

This study assessed the potential anxiolytic properties of a daily administered probiotic mix (LA205 and LA903) in mice undergoing chronic restraint stress (CRS) for 21 days.

Methods:

Four groups of male BALB/cByJrj mice were studied: non-stressed/solvent (NS-PBS), non-stressed/probiotics (NS-Probio), CRS/solvent (S-PBS), CRS/probiotics (S-Probio).

Results:

CRS resulted in a significantly lower body weight gain and an alteration of the coat state which were attenuated by the probiotic mix (PM). S-Probio mice spent more time in the open arms of the elevated plus maze test and in the central area during the open-field test than their NS counterpart, while no difference was seen in PBS mice.

Contrary to S-Probio mice, S-PBS mice exhibited a higher sera kynurenine/tryptophan ratio and a lower levels of serotonin than their NS counterpart. Corticosterone levels were significantly higher in the S-Probio group than in other groups. In the hippocampus, dopamine and serotonin transporter mRNA expression was lower in S-Probio than in S-PBS mice.

Gut microbiota 16S rRNA gene sequencing analysis indicated few differences in bacterial genera proportions with a lower relative abundance of Alistipes genus in S-Probio versus S-PBS. Analysis of the relative proportions of short-chain fatty acids in the caecal content showed that CRS was accompanied by a decrease in the proportion of acetate in S-PBS mice versus their NS counterpart, but not in PM groups.

Conclusions:

These data show that the PM could mitigate some of the consequences of the CRS potentially by influencing the composition of the gut microbiota.

OC.36_82 - PANGENOME DATA MINING AND PHENOTYPIC EVALUATION OF WEISSELLA CIBARIA STRAINS FOR PROBIOTIC APPLICATIONS

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Objective:
The aim of this study is a comprehensive analysis of the Weissella cibaria pangenome with a specific focus on the variome, which can include genetic traits responsible of probiotic or starter culture properties in certain strains belonging to this species. The selected genes can be exploited as biomarkers for a rapid screening of W. cibaria strains with probiotic potential.

Methods:
Comparative genomics analysis was performed on 111 strains of W. cibaria, including 12 newly sequenced strains, to evaluate the composition of the pangenome. Phenotypic tests were conducted on the new strains: adhesion to Caco2 cells, tolerance to bile salts and low pH, production of exopolysaccharides and antimicrobial compounds, which contribute to gastrointestinal tract colonization and resilience, to determine their potential for probiotic applications. Antibiotic susceptibility and decarboxylase activity were also performed to assess the safety for introduction in the food chain.

Results:
Comparative genomics and phylogenomics investigations allowed the identification of discriminant genetic traits, also considering the different isolation sources of W. cibaria. Among the newly isolated strains, a higher adhesion capability was observed compared to the reference probiotic strain Lacticaseibacillus rhamnosus GG. Additionally, some of these new W. cibaria strains demonstrated the production of antimicrobial compounds.

Conclusions:
This study provides evidence for different probiotic and starter traits among the investigated W. cibaria strains, both genotypically and phenotypically. The study also suggests the selection of specific genes to be used as biomarkers for rapid screening purposes.

OC.37_117 - ACHIEVING EFFICIENT VIABIILITY OF AKKERMANSIA MUCINIPHILA DURING AEROBIC STORAGE AND GASTROINTESTINAL PASSAGE THROUGH CALCIUM-ALGINATE ENCAPSULATION

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Objective:
Akkermansia muciniphila is considered a next generation probiotic that can be incorporated in new foods and pharmaceutical formulations. Effective delivery systems should be developed to ensure high probiotic viability and stability during manufacturing, product shelf-life and after consumption, namely, throughout digestion. Our work aimed to evaluate the effect of an extrusion method on A. muciniphila viability during 28-days refrigerated aerobic storage and when exposed to simulated gastrointestinal conditions.

Methods:
Upon cultivation, A. muciniphila was mixed in 2 %(w/v) sodium alginate and dripped into 4%(w/v) calcium chloride using extrusion. The calcium-alginate entrapped cells and free counterpart (control) were stored under refrigerated aerobic conditions (4 ºC) and their viability was assessed at 0, 7, 14, 21 and 28-days, enumerating colony-forming units (CFU) in appropriate media. Also, the survival of free and encapsulated A. muciniphila during gastrointestinal passage, at 1 and 28-days of storage, was assayed using Infogest digestion protocol.

Results:
Akkermansia muciniphila was encapsulated successfully in a calcium-alginate matrix via extrusion (encapsulation yield of 60%). Furthermore, encapsulated A. muciniphila exhibited a high stability in viability (loss < 0.2-log cycle) after 28-days of refrigerated aerobic storage, maintaining its viability around 8-log CFU/g. In contrast, free cell numbers decreased approximately 1-log cycle under similar storage conditions. At 28-days of storage, when exposed to digestion simulation, encapsulated bacteria reduced viable cell numbers around 1-log cycle, whereas free counterpart reported >2-log cycles reduction.

Conclusions:
Extrusion seems to be a promising strategy to safeguard A. muciniphila during refrigerated aerobic storage and gastrointestinal passage.

OC.38_151 - IN VITRO ASSESSMENT OF PROBIOTIC ATTRIBUTES AS USEFUL PRELUDE TOWARD PERSONALIZED BACTERIOTHERAPIES

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Objective:

Probiotics are frequently used without discrimination, but they possess different qualities and their effects on the host may profoundly differ. The in vitro assessment of probiotic attributes should be a key consideration, even before clinical studies are designed. This study aimed at evaluating several biological properties exhibited by strains found in commercial formulations, which appears critical for preselecting the most appropriate bacteriotherapy for each individual.

Methods:

Nine probiotic strains (Bacillus clausii, Bacillus coagulans, Bifidobacterium breve, Limosilactobacillus reuteri, Lacticaseibacillus rhamnosus, Saccharomyces boulardi) were isolated from commercial formulations and tested for their ability to tolerate simulated intestinal conditions, adhere to mucins, and produce beta-galactosidase, antioxidant enzymes, riboflavin, D-lactate, and short-chain fatty acids.

Results:

With the exception of B. breve, all microbes survived in simulated intestinal fluid. L. rhamnosus was the only one unable to adhere to mucins and differences in mucin adhesion were evidenced for L. reuteri and S. boulardii depending on oxygen levels. All microorganisms produced catalase and superoxide-dismutase, but only B. clausii, B. coagulans, B. breve, and L. reuteri synthesized beta-galactosidase. Riboflavin secretion was observed for Bacillus species and L. rhamnosus, while D-lactate production was limited to L. reuteri and L. rhamnosus. All microbes secreted acetic acid, with only B. clausii and S. boulardii additionally able to produce propionic and butyric acids.

Conclusions:

The analyzed probiotic strains showed distinct biological properties in vitro, thus potentially conferring different beneficial effects in vivo. Therefore, an in-depth characterization of strains contained in probiotic formulations could be a novel aspect to consider in the probiotic research and contribute to the spread of more targeted and personalized bacteriotherapy strategies to promote human health and manage diseases.

OC.39_137 - BENEFICIAL EFFECTS OF ENRICHED POLYPHENOLS COLTURE OF LACTOBACILLI SPP. ON THE INTESTINAL CANDIDA ALBICANS GROWTH

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Objective:

This study aimed to investigate the interfering effect of L. helveticus (LH) and L. rhamnosus (LR), stimulated by lyophilized residual water (ORAC9) obtained from the hydro-distillation of Origanum vulgare, in modulating intestinal C. albicans (CA) growth.

Methods:

Chemical analysis of ORCA9 was performed by HPLC-MS (high performance liquid chromatography-mass spectrometry). Growth kinetics and metabolic analysis of LH, LR and CA untreated and treated with ORAC9 were respectively conducted using Cytation 5 Cell Imaging Multi-Mode Reader and Biolog OmniLog Identification System. CA was co-cultured with Lactobacilli spp. stimulated by ORAC9 and relative CFU/mL were evaluated. Metabolomic and proteomic analysis were performed using mass spectrometry on Lactobacilli spp. secretome untreated and treated with ORAC9. ORAC9 toxicity was evaluated in vitro an in vivo on larvae models.

Results:

Rosmarinic acid (polyphenolic acid) was the main component of ORAC9 identified. Only Lactobacilli spp. growth and metabolic activity were stimulated by ORAC9 and in presence of Lactobacilli spp. and ORAC9 the growth of CA was significantly inhibited. Differences in metabolomic and proteomic profiles of Lactobacilli spp. untreated and treated with ORAC9 were highlighted. ORAC9 was not toxic at the concentration used in microbiological assay.

Conclusions:

ORAC9 enhances the action of Lactobacilli spp. against CA, stimulating their growth and metabolism. Restoring an intestinal eubiotic condition, they could contribute to control Candida spp. infections. Moreover, the increase of traditional antimycotic resistance supports the use of anti-Candida beneficial bacteria as candidiasis prophylaxis and therapy.

OC.40_17 - ISOLATION, IDENTIFICATION AND RAW MATERIAL PRODUCTION OF FAECALIBACTERIUM PRAUSNITZII

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Objective:
In recent years, the incidence of intestinal diseases worldwide has reached epidemic proportions. It seems that a critical factor in the etiology of intestinal-borne diseases is the intestinal microbiota. Initial reports comparing obese animals and humans with lean ones identified a different gut microbiota composition among them. This different composition may be due to the functional properties of the gut microbiota.
Faecalibacterium prausnitzii is a gut-colonizing bacterium isolated from human feces and showing probiotic properties. Studies show that these probiotics hold promise as a therapeutic target in microbiota-related diseases.

Methods:
It is planned to produce a quality and efficient probiotic product containing F. prausnitzii by testing its properties and safety with different tests. Isolation, identification and determination of probiotic properties (autoaggregation, adhesion etc.) of this bacterium with probiotic properties will be carried out within the scope of the study. In this study, it is aimed to microencapsulate the produced raw material. Thus, a usable probiotic form will be created.

Results:
Unlike the products on the market, a probiotic will be produced that can have a greater effect on changing the microbiota content. Thus, can be used for the prevention and treatment of many intestinal diseases.

Conclusions:
At the end of the study, a probiotic product containing F. prausnitzii as a new generation probiotic will be created for the first time in the world.

OC.41_105 - WESTERN DIET-INDUCED OBESITY AND ASSOCIATED METABOLIC ALTERATIONS CAN BE PREVENTED BY PROBIOTIC LIMOSILACTOBACILLUS REUTERI DSM17938 ADMINISTRATION

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Objective:
The "Western Diet" is one of the major culprits of obesity and metabolic syndrome, and gut microbiota is believed to play an important role in modulating its effects, paving the way for the use of probiotics as therapeutic approach. We therefore decided to evaluate the effect of L. reuteri DSM 17938, a probiotic bacterium whose possible efficacy in preventing WD-induced dysfunctions has not been explored yet, in adult rats.

Methods:
Male Wistar rats of 90 days were divided in 3 groups, fed a control diet (CD), a western diet alone (WD) or in combination with the administration of 10^8 CFU of L. reuteri (WD-R) for 8 weeks. Gut microbiota composition, whole body and ileum, colon and liver homeostasis were evaluated, with mitochondrial function in the liver.

Results:
We here demonstrate for the first time that L. reuteri DSM 17938 has a strong efficiency in preserving the integrity of the intestinal barrier, thus protecting the gut and the liver from the metabolic derangements elicited by the WD, and concomitantly exhibits a potential anti-obesity effect, partly inhibiting excess body lipid deposition typically induced by WD.

Conclusions:
L. reuteri DSM 17938 can be an effective probiotic in preventing the unhealthy consequences of the WD, opening to the formulation of new preparations able to improve gut-liver functions independently from the dietary habits.

PREBIOTICS POSTBIOTICS/PARABIOTICS

OC.42_30 - PREBIOTIC POTENTIAL OF HAWTHORN IN IN-VITRO AND IN-SITU SYSTEMS

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Objective:
The growth and fermentation profile of Bifidobacterium animalis subsp. lactis and Lactobacillus acidophilus were investigated in-vitro and in-situ in the yoghurts enriched with hawthorn.

Methods:
During the in-vitro studies, the growth medium were analysed in terms of pH, spectrophotometric cell density (OD600), probiotic bacterial counts, prebiotic activity score (PAS), organic acid content. As to in-situ experiments, the yogurt model produced by cow milk was evaluated for the functional properties of yoghurt including phenolic and antioxidant contents as well as the technological properties such as pH, titration acidity, dry matter content, sensory and texture.

Results:
Consequently, it was determined that the enrichment of probiotic yoghurt with hawthorn improved the survival of L. acidophilus and B. animalis subsp. lactis in in-vitro and in the yoghurt model. The count of probiotic bacteria and the acidity was determined higher in yoghurt with hawthorn during fermentation and 28 days of storage. It could be due to the hawthorn extract positively effect the in-vitro prebiotic activity. Antioxidant and phenolic contents also showed an increase in the yoghurt sample with howthorn. This increase was also determined during the storage period. However, the addition of howthorn had a negative impact on the firmness of yoghurts.

Conclusions:
The results of the current study show that hawthorn has positive effects on technological and functional properties of yoghurt as well as in the fermentation process and growth profile of probiotic bacteria and can be used as a potential prebiotic ingredient during symbiotic yoghurts.

OC.43_65 - BENEFICIAL EFFECTS OF A YEAST-EXTRACT PREBIOTIC IN A MOUSE MODEL OF ULCERATIVE COLITIS

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Objective:
Inflammatory bowel diseases are characterized by persistent inflammation and intestinal dysbiosis. Recently, intestinal overgrowth of Candida spp. has been reported, suggesting the involvement of commensal fungi in the etiopathogenesis of IBD. Given that prebiotics positively impact on gut dysbiosis, the objective of this study was to evaluate the potential beneficial effect of a yeast-extract prebiotic in a murine model of induced ulcerative colitis.

Methods:
Mice with dextran sodium sulphate-induced colitis were treated with prebiotic by gavage. Disease associated indices were recorded daily. Cytokines and epithelial barrier protein expression were evaluated by RT-PCR. Candida spp. intestinal burden was analysed by quantitative real-time PCR.

Results:
The administration of the prebiotic prolonged the survival of colitic mice and reduced the inflammatory burden resulting in a significant reduction of the disease score. These beneficial effects were associated with downregulation of Claudin-2, a tight junction protein whose up-regulation is involved in this disease and, interestingly, of the Candida spp. intestinal over-growth.

Conclusions:
The data obtained in this study provide evidence that a yeast-extract prebiotic has a protective effect on clinical, inflammatory and microbial parameters in a mouse model of IBD. These findings provide cellular and molecular bases for the use of yeast-extract prebiotics as potential functional foods in IBD to be associated to standard therapeutic protocols.

OC.44_74 - PARTIALLY-HYDROLYSED GUAR GUM IN THE TREATMENT OF IRRITABLE BOWEL SYNDROME: A SYSTEMATIC REVIEW OF HUMAN CLINICAL TRIALS

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Objective:
Irritable bowel syndrome (IBS) is considered a disorder of gut-brain interaction, characterised by abdominal pain that is associated with a change in bowel habit. It is one of the most common gastrointestinal disorders worldwide. Management has thus far proven challenging. Partially hydrolysed guar gum (PHGG) is a soluble fibre that demonstrates beneficial microbiota-modifying properties. Preliminary research has shown promising effects of PHGG in the treatment of a number of gastrointestinal conditions, including IBS. The aim of this review was to systematically evaluate the efficacy of PHGG in the treatment of IBS.

Methods:
A computer-based search of MEDLINE, EMBASE, and the Cochrane Library was conducted in June 2023. A hand-search of the bibliographies of relevant papers, previous reviews, and authors' personal libraries was also undertaken. Trials were included in the review if they were human clinical trials (of any design) investigating the effects of PHGG on IBS-related symptoms or quality of life. There were no language restrictions. Eligibility assessment and data extraction were performed by two independent researchers.

Results:
Nine trials were identified that met all eligibility criteria. Seven were open label trials and two were randomised, placebo-controlled trials. Heterogeniety in trial design and outcome measures precluded meta-analysis. All trials had results that were suggestive of the efficacy of PHGG.

Conclusions:
PHGG shows promise in the treatment of IBS. A number of different mechanisms of action have been suggested, including beneficial modulation of the gastrointestinal microbiota, normalisation of motility, and enhanced butyrate production. Large-scale, randomised controlled trials appear warranted.

OC.45_129 - REGULATING GASTROINTESTINAL (G.I.) METABOLISM WITH PREBIOTICS TO SAFEGUARD THE MICROBIOTA FROM ANTIBIOTIC-INDUCED DISRUPTION

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Objective:
Antibiotic exposure is associated with a risk of morbidity and mortality related to microbiome disruption. In vitro, data have established a clear connection between active bacterial metabolism and bacterial antibiotic toxicity. As the metabolic capabilities of the microbiome's bacteria are influenced by both diet and host metabolism, we propose that these factors also play a role in regulating antibiotic-induced disruptions within the microbiome.

Methods:
To gain further insight into the interplay between metabolism and microbiome susceptibility, we employed a comprehensive multi-omic approach that integrates whole microbiome metabolomics with shotgun metagenomics and metatranscriptomics, allowing us to investigate the effects of microbial metabolism on antibiotic susceptibility in mice, considering various dietary and metabolic conditions. Our investigations across a wide range of conditions consistently revealed that bacterial taxa exhibiting heightened metabolic activity were more vulnerable to antimicrobial agents than those with reduced metabolic capacity.

Results:
By utilizing metatranscriptomic RNA sequencing at a species-specific resolution, we discovered that the inclusion of prebiotic fibers or supplementation with polysaccharide prebiotics protected specific microbes, notably Bacteroides thetaiotaomicron, against the effects of amoxicillin. In parallel, our in vitro experiments demonstrated that prebiotic supplementation effectively shielded this bacterium from antibiotic susceptibility. Building upon these initial findings, we observed that reducing the redox potential of this microbe and others promoted microbial tolerance to beta-lactam antibiotics. By modifying the gastrointestinal (G.I.) environment in mice through prebiotic interventions or the use of small molecules to lower the redox potential, we were able to mitigate antibiotic-induced dysbiosis.

Conclusions:
Taken together, our findings strongly indicate that host metabolism plays a pivotal role in developing antibiotic-induced dysbiosis. Moreover, we propose that the modulation of microbial metabolism, mainly through redox adjustments, could serve as a promising therapeutic intervention to mitigate the complications arising from antibiotic usage.

OC.46_53 - THE PREBIOTIC EFFECT OF MANNOOLIGOSACCHARIDES BROUGHT ABOUT BY ENZYMATIC HYDROLYSIS OF IVORY NUT LINEAR MANNAN

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Objective:

Nutraceutical mannooligosaccharides (MOS) created by enzymatic hydrolysis of mannans, plant-derived hemicellulose, are attracting increased attention due to their useful bioactive properties such as prebiotic effects, pathogen inhibiting abilities, and antioxidant activity.

Methods:

We used the Aspergillus niger derived endo-mannanase, Man26A, to generate MOS from ivory nut derived linear mannan. Upon production, the MOS were subjected to simulated gastrointestinal and thermogravimetric analysis for cooking stability. Finally, the MOS were evaluated for their influence on the growth, biofilm formation and metabolic activity of selected beneficial bacteria; Streptococcus thermophilus and Bacillus subtilis.

Results:

Mannan hydrolysis produced MOS with a degree of polymerization (DP) of 2-4, at a 30% yield. A simulated gastrointestinal environment involving bile salts, α-amylase, trypsin and hydrochloric acid did not degrade MOS. Thermogravimetric analysis demonstrated that MOS withstand cooking, degrading at temperatures >150°C. The MOS significantly improved the growth of S. thermophilus and B. subtilis in 1×M9 minimal medium by ~3-fold compared to glucose as a carbon source. The MOS did not affect the auto-aggregation of the bacteria, while they improved biofilm formation ~3-fold. Additionally, short chain fatty acids were released in the culture media when MOS were used as a carbon source for the bacteria. Finally, MOS were shown to possibly upregulate mannan utilization genes in the bacteria.

Conclusions:

This study shed insights on the prebiotic potential of mannan-derived MOS and suggests that they may be potent additives for dietary foods.

OC.47_31 - A NEW INSIGHT: POSTBIOTICS AND PARAPROBIOTICS

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Objective:

The accepted definition defines probiotics as “live microorganisms that, when administered in adequate amounts, confer health benefits on the host”. The term “probiotic” refers to living cells, but it does not refer to metabolites or non-living cells. According to current knowledge, bacterial viability is not required to obtain the health effects of probiotics. In this context, novel probiotic-related concepts, such as postbiotics and paraprobiotics, have emerged to highlight health benefits beyond the inherent viability of probiotics. This review aims to provide an overview of the general aspects related to postbiotics and paraprobiotics.

Methods:

All articles related to the subject with the keywords “probiotic,” “postbiotic,” and “paraprobiotics” were searched in the Scopus and ScienceDirect databases.

Results:

Postbiotics and paraprobiotics have been used to refer to cell-free supernatants or non-viable microorganisms that may benefit the host by exhibiting bioactivities, respectively. Cell-free supernatants, exopolysaccharides, enzymes, short-chain fatty acids, and gut microbiota metabolites are the main examples of postbiotics. On the other hand, the cell envelope components, including peptidoglycan, teichoic acid, cell-wall polysaccharides, cell surface-associated proteins and proteinaceous filaments, and dead cells, are examples of paraprobiotics. They exhibit bioactivities such as anti-inflammatory, immunomodulatory, antioxidant, and antimicrobial properties. Compared to living microorganisms, postbiotics and paraprobiotics are more reliable and safer for use in food applications since their viability is not required during either large-scale production or daily intake, and they do not have antibiotic resistance genes.

Conclusions:

Consequently, they have great potential to develop functional products for the food industry.

OC.48_165 - POSTBIOTICS + STANDARD CHEMOTHERAPY AGAINST GASTRIC CANCER CELLS: FUTURE COMBINATION THERAPY?

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Objective:
Gastric cancer is the third leading cause of cancer-related deaths globally. We recently demonstrated that gut microbial metabolites (postbiotics), especially short-chain fatty acids (SCFAs), confer antiproliferative effects against gastric cancer cells. The aims of this study are to a) evaluate the interaction among the SCFAs and b) decipher their potential synergy with standard chemotherapy against the AGS gastric adenocarcinoma cells in vitro.

Methods:
The antiproliferative effects of three SCFAs- acetate (A), butyrate (B) and propionate (P) against the AGS cells was determined using the Alamar Blue assay. The potential synergy among these SCFAs and their interactions with standard chemotherapy- dexamethasone (D) and doxorubicin (Do) against the AGS cells were quantified using the combination index (CI) model. Furthermore, the molecular mechanisms of action of the SCFAs combinations with standard chemotherapy were elucidated using flow cytometry, reactive oxygen species (ROS) and anti-inflammatory analyses.

Results:
All three SCFAs and their combinations exhibited significant antiproliferative activity against the AGS cells. The SCFAs also displayed strong synergistic interactions with D and Do (CI values <1; Figure 1). The flow cytometry, anti-inflammatory and ROS analyses also revealed the potential molecular mechanisms of action of the SCFAs in combination with D and Do.

Conclusions:
The findings of this study underlined the interactions among the SCFAs against gastric adenocarcinoma cancer cells and their potential implementation as combination therapies with dexamethasone and doxorubicin in the future. Further in vivo studies are warranted to validate these findings.

OC.49_185 - EVALUATION OF THE CYTOTOXIC EFFECT ON COLORECTAL CANCER CELLS (CACO2 AND HT29) LINE OF PARAPROBIOTICS AND POSTBIOTICS OBTAINED FROM SOME POSSIBLE PROBIOTIC BACTERIA

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Objective:
Probiotic microorganisms are an important group of microorganisms that are in our intestines, which are called the second brain by scientists all over the world, and that enable the microbial flora to be kept in a healthy balance. With the effect of environmental factors, it becomes very difficult to keep this microbial flora in balance. For this reason, the importance of probiotics becomes even more remarkable. All societies unconsciously use probiotic products as an external supplement. However, the important thing is to benefit from using the right probiotic support at the right time. The same probiotic use is not suitable for everyone and for every situation. One of the most striking issues regarding probiotics in recent years is their effects on cancer cells. Some studies report the effects of probiotics on various cancer cells. However, there is not much data in the literature on how, through which pathway and through which mechanism probiotics are effective and their effects on healthy cells. Moreover, the shelf life of probiotics, the continuity of their viability and their use in immune suppressed patients are very limited.

Methods:
In our study, L.plantarum GA12 and L.reuteri obtained from our previous studies were used. In cytotoxicity studies, colorectal cancer cell lines (CaCO2, HT29) and healthy mouse fibroblast cell line (L929) were used as control group. Paraprobiotics were obtained by heat method. Postbiotics were obtained by precipitation of active cultures by centrifugation. All samples were lyophilized and stored. MTT method was used in cytotoxicity study. The certain concentrations (%5-50) used in cell applications. Cell counting and viability control were performed with the TC20™ automated cell counter device.

Results:
L.plantarum GA12 and L.reuteri strains showed a proliferative effect on L929 cells depending on the concentration (5-50%); It was determined that it showed cytotoxic effect on CaCO2 and HT29 cells due to increasing concentration. Postbiotics and paraprobiotics obtained from bacteria also showed similar effects, and it was observed that postbiotics had a better effect depending on the dose increase.

Conclusions:
In our studies, the healthy cell line L929 will be included as the control group, allowing the comparison of the effects on healthy and cancer cells. In addition, thanks to the data obtained in our study, the efficacy of new pharmabiotics was compared with living cells, and the basis for the elimination of limitations on shelf life, viability and their use in immune suppressed patients and the introduction of new commercial products.

OC.50_193 - DETERMINATION OF THE ANTITUMOR EFFICACY OF PARAPROBIOTICS AND POSTBIOTICS ON THE CACO-2 CELL LINE AND THEIR ROLE IN IMMUNE RESPONSE

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Objective:
Paraprobiotics and postbiotics are reported to exert a series of strain-specific health-promoting activities in the host, like probiotics, primarily in regulating intestinal health, developing immunomodulatory activity, and anti-inflammatory and anti-tumor properties. However, despite the available scientific evidence regarding these activities, their mechanisms of action and signaling pathways have not been fully elucidated. For this reason, in this study, it is aimed to obtain heat-inactivated paraprobiotics that can be used instead of probiotics and postbiotics released from probiotics and to reveal some of their properties (antitumor, antimicrobial and antioxidant activities) that can benefit human health.

Methods:
Lactobacillus reuteri and L. rhamnosus strains isolated in previous studies in our laboratory were used to obtain paraprobiotics and postbiotics. Human colon epithelial CaCO2 and healthy fibroblast (L929) cell lines were preferred for cell culture. In the production of paraprobiotics, bacteria were subjected to high temperature. Supernatants collected from active cultures were used to obtain postbiotics. All samples were lyophilized and dissolved in cell culture medium and passed through 0.22 µm filters. The 1,1-1,1-diphenyl-2-picrylhydrazil (DPPH) method was used to determine the antioxidant activity. Total antioxidant activities were determined by ELISA method. MTT method was used in cytotoxicity studies. In immunity studies, IL-10, IL-12, TNF-alpha and TAS parameters were evaluated by ELISA method.

Results:
In our study, it was determined that probiotics have a cytotoxic effect on cancer cells in parallel with the increasing concentration, and this effect is seen more in postbiotics. In addition, a decrease in TNF alpha and IL-12 levels in cancer cells, while an increase in IL10 and TAS levels were observed with this biotic applications.

Conclusions:
In our study, it is aimed to increase the usage areas of probiotics, which have been widely used all over the world in recent years and are stated to be beneficial for health. With the obtained paraprobiotics and postbiotics, the usage area of probiotics will be expanded, and more commercial application areas will be created.

NUTRITION

OC.51_40 - MILLET POLYPHENOL EXTRACTS ALLEVIATES HIGH-FAT-HIGH-SUCROSE DIET INDUCED GUT DYSBIOSIS AND LIVER STEATOSIS IN MICE

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Objective:
The health benefits of finger millet (FM) and kodo millet (KM) are numerous. Polyphenol rich extracts (PREs) from the millets have anti-oxidant and hypoglycaemic characteristics, according to several research. However, the protective roles of PREs from these millets in overcoming the metabolic syndrome caused by a high-fat, high-sucrose diet (HFHSD) remain unknown. It is critical to prevent or treat these multiple risk factors and stop their consequences using natural bioactive ingredients.

Methods:
The polyphenols from FM-PRE and KM-PRE were harnessed in this study to assess the impact of PREs in reducing palmitic acid-induced fat accumulation and inflammation in hepatocytes and intestinal epithelial cells, respectively. These parameters were also validated in HFHSD-induced obesity in C57BL/6 mice.

Results:
FM-PRE and KM-PRE supplementation protected against palmitic acid fat accumulation and had a protective impact on LPS-induced intestinal epithelial cells. Furthermore, millet PREs reduced HFHSD-related metabolic complications as weight gain, glucose homeostasis, gastrointestinal abnormalities, obesity, adipose tissue hypertrophy, hepatic steatosis, and systemic inflammation.

Conclusions:
According to the findings, FM-PRE and KM-PRE could be used as functional food ingredients or nutraceuticals to mitigate obesity and comorbidities

OC.52_72 - SAUERKRAUT – A HEALTH PROMOTING MODULATOR OF THE MICROBIOME?

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Objective:
Fermented foods have attracted scientific attention due to their health promoting potentials, which may be mediated by the intestinal microbiota. They are promising candidates for restoring or preserving immune homeostasis and metabolic health, but evidence from human intervention studies remains scarce. Sauerkraut is particularly rich in probiotic microorganisms but its health effects have been insufficiently studied. Therefore, we conducted a comprehensive human intervention study addressing the question whether and how regular consumption of sauerkraut influences the gut microbiota and associated factors.

Methods:
89 normal weight and overweight participants consumed 100g of each fresh and pasteurized sauerkraut per day for four weeks, respectively, concurrently avoiding other fermented foods. Each intervention phase was preceded by a washout period of four weeks length. Faecal samples collected during the trial are currently analysed: We perform shotgun metagenomic analysis to compare faecal bacterial composition before and after the intervention, and at a follow-up eight weeks later. Furthermore, we determine the influence on short chain fatty acids (SCFA's), serum inflammatory and oxidative stress markers, glucose regulation, and leaky gut markers.

Results:
Our results will help developing up-to-date dietary recommendations for the population. The differentiation between fresh sauerkraut, containing living microbes, and a heat-processed form of the dish contributes to a better understanding of the bioactive components of fermented foods in general.

Conclusions:
Regular consumption of sauerkraut for several weeks was well accepted and tolerated by the study participants. Sauerkraut is a food with a very high fermentation level and may contribute to a healthy microbiome.

OC.53_84 - GLUCOSE AND INSULIN RESPONSE TO KOMBUCHA TEA IN HUMANS: A RANDOMIZED TRIAL

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Objective:
Kombucha is a popular commercially available fermented tea beverage due to its perceived health benefits. Controlled human subjects studies are lacking; this is the first registered clinical trial in the U.S. or E.U. to report findings of kombucha's effect on glucose tolerance in humans. We examined kombucha's effect on glucose and insulin concentrations in response to an oral glucose challenge.

Methods:
27 overweight/obese subjects participated in a double-blinded counter-balanced placebo-controlled randomized trial. Subjects were healthy adults (30-65 years old, body mass index (27.8-48.8). Subjects completed four lab visits ≥ 2 weeks apart. Following an overnight fast, subjects consumed 8oz of one of the four study beverages as assigned by randomization: A) brewed kombucha, B) commercial kombucha, C) brewed tea, D) water. Thirty minutes later, subjects consumed 75 grams of glucose. Blood was sampled every 15 minutes for 3 hours. This study was prospectively registered in clinicaltrials.gov (NCT04051294).

Results:
Glucose and insulin concentrations significantly increased ($p<0.0001$) between Time -30 (fasting) and 0 (glucose ingestion) for A vs C, A vs D, B vs C, and B vs D. Peak values did not differ across drinks. No significant difference occurred for glucose total or net incremental area under the curve (AUC). However, insulin total AUC was greater for A vs D ($p=0.004$) and B vs D ($p=0.028$).

Conclusions:
When followed by an oral glucose load kombucha, either brewed or commercial, results in a greater insulin response compared to tea or water but had no impact on overall glucose concentrations.

OC.54_81 - EVALUATION OF HONEY AND ITS ANTIMICROBIAL PROPERTIES IN COMBINATION WITH MEDITERRANEAN PREBIOTIC PRODUCTS

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Objective:
The presented research work is part of a several-year study in the microbiological and physicochemical evaluation of traditional prebiotic products to ensure their safe use by Albanian consumers. The objective was to focus on local honey, obtained and used widely in different geographical areas of the country.

Methods:
The study aims to determine the microbiological profile of honey and its antimicrobial properties, combined with other functional and prebiotic foods. Microorganisms were collected to screen strains originating from the environment or food products. They were grown and consequently treated with honey and its combinations (cinnamon, lemon juice, and cranberry juice) by applying the Kirby Bauer test.

Results:
A significant reduction in the development of microorganisms, especially a change in morphological characteristics, a decrease in sporulation for spore-forming microorganisms, and a reduction in the reproduction process were observed.

Conclusions:
The microbiological profile of the honey was determined in detail. Selected samples and combinations effectively limited colonies' growth (genera Penicillium, Rhizopus, Saccharomyces, Rhodotorula, Aspergillus et al.) The observed results were optimistic regarding the benefits that honey and its combinations offer as an antimicrobial, prebiotic, and traditional product.

OC.55_22 - ALGERIAN HONEYS : NUTRITIONAL VALUES AND BIOLOGICAL PROPERTIES

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Objective:
Honey is a hive food rich in carbohydrates and water and the objectives were the determination of nutritional values and biological properties of Algerian honeys.

Methods:
Colorometric assays were used in this study. Algerian honeys were studied for their physicochemical parameters, nutritional values (moisture, brix, pH, electrical conductivity, and amounts of HMF, proteins, proline, total phenolic compounds and flavonoids) and some biological activities (antioxidant, antiinflammatory and enzymatic anti-browning). The antioxidant activities of the samples were estimated using different methods (ABTS, DPPH free radicals scavenging, reducing power, and chelating ferrous activity).

Results:
All honeys were acidic ($3.45 \leq pH \leq 4.65$). The color varied from mimosa yellow to dark brown. The specific rotation was levorotatory in most honey samples and the electrical conductivity, hydroxymethylfurfural, and proline values agreed with the international honey requirements. For antiinflammatory activity, the results showed that the inhibiting capacity of the denaturation of the BSA of the honeys analysed varied from 15 to 75 % with a maximum of activity at the concentration of 0,5 mg/ml. All honeys exhibited enzymatic anti-browning on different slices of fruits. In fact, the results showed that the controls had the greatest browning unit compared to the honeys studied and PPO and POD enzymes had the lowest enzyme activity.

Conclusions:
High significant correlations were found between the color of honey, its antioxidant content and its biological activities (antioxidant, anti-inflammatory and enzymatic anti-browning). The dark color of honey is a good indicator of the best biological properties therefore the best nutritional and therapeutic values.

OC.56_138 - CAROTENOIDS : PHYTOCHEMICALS TO COMBAT DOXORUBICIN-INDUCED CARDIOTOXICITY

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Methods:

In total, 60 animals were randomly divided into 6 groups. Animals were given saline (S), solvent (NADES – natural deep eutectic solvents, N, 1ml), carotenoids (C, 900 µg/kg), doxorubicin alone 4 doses (D, 2 mg/kg) or pretreated with solvent (ND) or carotenoids (CD). Tissue slides (stained with hematoxylin and eosin method) were microscopically analyzed for presence of myocardial damage, evaluated by doxorubicin damage score (DDS). As biochemical markers of DIC, creatinine kinase-MB (CK-MB), myocardial troponin (cTns) and brain natriuretic peptide (NT-proBNP) were tested, analyzed from blood.

Results:

Solvent and carotenoids don't alter myocardium properties, wich doesn't differ from the control group. Myocardium treated with doxorubicin shows high DDS and histological signs of tissue damage (disorganization of cardiomyocytes/myofilaments, presence of vacuoles, necrosis, hemorrhage, perinuclear changes). Carotenoids/DOX co-treatment lead to myocardial protection observed through statistically significant lower DDS. The histological findings were accompanied by statistically significant decrease of CK-MB, cTns and NT-proBNP in the CD group compared to D.

Conclusions:

Carotenoid and doxorubicin co-treatment has shown a cardioprotective role in terms of histological and biochemical changes. Further studies are needed to determine whether this effect is achieved only by reducing oxidative stress or by influencing the pathways of regulated cell death.

OC.57_196 - THE NUTRITIONAL, PROBIOTIC AND HEALTH ROLE OF SHARR MOUNTAIN TEAS DURING EMBRYONIC DEVELOPMENT IN QUAIL AND CHICKEN EGGS

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Objective:

The mountain massif of Sharr is characterized by a rich floristic biodiversity that has special nutritional, health, prebiotic and probiotic values and effects in preventive health.

Mountain tea is one of the most consumed medicinal plants worldwide they are preparations and widely used in various branches of both traditional, healthy and modern pharmacy.In the framework of teas with nutritional character and health benefits with prebiotic and probiotic effects, we can count species: mint (Mentha piperita), St. John's wort (Hypericum perforatum), sideritis (Sideritis scardica), chamomile (Matricaria camomila), thyme (Thymus serpyllium L).

Methods:

For the extraction of teas we used the Rota Buchi 480 and Soxhlet methods which made the extraction of teas in a liquid state as plant extract.

Results:

The results of research on experimental eggs treated with Menta piperita, Hypericum perforatum, Sideritis scardica, Matricaria camomila,Thymus serpillum L, which as a plant extract stimulated the ontogenetic stage of eggs chicken and sea bass.The nutritional effect of the mountain teas of Sharri is of special importance, both qualitatively and quantitatively, in the presence of organic and inorganic compounds in the prevention of many diseases.

Conclusions:

The effect of the extract of these teas has been studied on quail eggs Coturnix japonica, and on chicken eggs Gallus domestica, applying extract with a certain dose to quail and chicken eggs, at different stages of embryonic development during ontogenesis, will be claimed for an organic and healthy food which is like a trend of using qualitative and healthy food.

OC.58_23 - BIOLOGICAL PROPERTIES OF EXTRACTS FROM THE MIXTURE OF HONEY AND BERRIES OF PISTACIA LENTISCUS

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Objective:
The aim of the present study is to determine the antioxidant activity of the mixture of the extract of Pistacia lentiscus berries associated with honey at different concentrations (0.5; 2; 4; 8 and 12 %).

Methods:
Different apparatus are used to determine physico-chemical parameters. Also, the several methods of antioxidant activities are determined by colorometric assays.

Results:
According to the physico-chemical parameters (humidity, pH, electrical conductivity, color), the honey and the mixture analyzed are in conformity with the international standards. The protein content of the honey alone is 10.14 mg EBSA/100g and the H/BB and H/DP (honey / delipidated powder) mixtures vary from 13.77 to 143.96 and from 21.01 to 244.44 mg EBSA/100 g, respectively. The results of the antioxidant assay give a significant content of total phenolic compounds for the H/DP mixtures which varied from 131.66 to 1087.81 mg EAG/ 100g. The antioxidant activities (reducing power, FRAP, CUPRAC, CAT, DPPH, ABTS and Ferrozine tests) are also tested. The sample of honey alone analyzed exerts a weak antioxidant activity compared to the two mixtures made. The results for example of the DPPH and the CUPRAC tests vary from 35.84 to 95.16 % and from 63.74 to 988.86 mg E Trolox/100 g, respectively, for the H/DP mixtures.

Conclusions:
Honey is a product of the hive elaborated by the bees of the species APIS MELLIFERA. The honey and Pistacia compound constitutes an important source of antioxidants which intensifies very significantly the antioxidant activity of the blend.

OC.59_49 - RESEARCH AND DEVELOPMENT OF CULTIVATION METHODS OF CANNABIS SATIVA L. TO MAXIMIZE THE YIELD OF NON-THC BIOACTIVE COMPOUNDS OF NUTRACEUTICAL, COSMECEUTICAL, AND PHARMACEUTICAL INTEREST

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Objective:
For a long time, Cannabis sativa has been utilized as a source of food, fiber, medicine, and psychoactive properties. Recently, the nutraceutical potential of C. sativa has received increased attention, but C. sativa roots have been neglected. To address this, aeroponic (AP) and aeroponic-elicited cultures (AEP) were established and compared to soil-cultivated plant (SP).

Methods:
Ethanolic extract of Aeroponic Plant roots (APEX) has been prepared, and the content of the main roots' bioactive constituents was comparatively determined by Gas Chromatography-Mass Spectrometry (GC-MS).
Using cellular (cyto- and geno-protection in H_2O_2-treated cells) and acellular settings (DPPH and Fe^{2+} chelation effect), we evaluated APEX's antioxidant and anti-inflammatory properties and its major components. We also investigated its anti-inflammatory effect on LPS-stimulated Caco-2 cell line, measuring inflammatory-related gene and protein expression.

Results:
The AP and AEP methods were found to produce excessive plant growth, particularly in the roots, and an increase in the total content of bioactive molecules in the roots.
Our study identified and quantified valuable bioactives in extracts of C. sativa aeroponic roots (APEX), including beta-sitosterol (ST), friedelin (FR), epifriedelanol (EFR), stigmasterol, and campesterol.
The results showed that APEX and its main components exhibited significant antioxidant and anti-inflammatory activities, making them attractive as natural agents with technical and economic advantages of aeroponic cultivation.

Conclusions:
Overall, based on the results obtained, APEX's antioxidant and anti-inflammatory properties and its bioactive compounds could largely justify their industrial exploitation for developing pharmaceutical, nutraceutical, cosmeceutical, or food products according to desirable sustainability principles.

OC.60_26 - THYMOQUINONE-INDUCED CELLULAR AND MITOCHONDRIAL HEALTH IN LIVER CANCER

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Objective:
Thymoquinone (TQ) is a plant-based bioactive constituent, which has been re-discovered in the last few years. It is derived from the volatile oil of Nigella sativa, and is well known in the Middle East countries for a variable range of properties. TQ has been shown to harbor some anti-neoplastic activities, which can be useful for oncology. The present study aimed to investigate the mitochondria and cellular health in liver cancer.

Methods:
Hepatocellular carcinoma (HepG2) and cholangiocellular carcinoma (HuCCT1) cell lines were acquired. These are two of the most common primary tumors of the liver. All cell lines were treated with increasing concentrations of TQ for varying durations. The anti-proliferative effect of TQ was measured using the methoxyphenyl-2-(4-sulfophenyl)-2H-tetrazolium (MTS) assay. A systematic review of rodent animal models was also carried out.

Results:
We found dose- and time-dependent growth inhibition in both cell lines. Cell cycle, apoptosis, and assessment of mitochondria viability by morphology assessment and evaluation of the mitochondrial membrane potential were also corroborating a remarkable anti-neoplastic activity of this chemical compound.

Conclusions:
The present study confirms that TQ caused cell cycle arrest at different phases and induced apoptosis in both cell lines. Overall, our data seem to represent the most robust results in the current literature, emphasizing that TQ holds auspicious therapeutic potential as an anti-tumor agent for the treatment of liver cancer.

OC.61_27 - DYNAMIC REGULATION OF M6A IN PATIENTS WITH TYPE 2 DIABETES AND M6A BIOINFORMATICS REVIEW

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Objective:
The dysregulation of forkhead box O1 (FOXO1) contribute to abnormal glycol-lipidemia in Type 2 diabetes (T2D). Epigenetic changes in response to environmental stimuli are on focus in T2D, but RNA modifications are poorly investigated. N6-methyladenosine (m6A) is one of the most prevalent methylations in mRNA, particularly m6A methyltransferase complex, containing methyltransferaselike 3 (METTL3), methyltransferase-like 14 (METTL14), and fat mass obesity protein (FTO) genes. Our aim was to clarify whether glucose is involved in the dynamic regulation of m6A in T2D and review the m6A bioinformatics.

Methods:
Quantitative PCR and mass spectrometry were performed to determine the mRNA expression of target genes in 102 T2D patients and 107 controls and the m6A content. A review of the literature targeting the bioinformatics approaches was carried out.

Results:
In patients with T2D, the m6A content was decreased, and mRNA expression levels of several genes were increased. Interestingly, the m6A content was negatively associated with mRNA expression levels of METTL3, METTL14, and FTO. The review of the literature determined that a full panel bioinformatics approach should contain ingenuity pathway analysis (IPA), which was used to predict T2D-related differentially expressed genes (DEGs).

Conclusions:
In patients with T2D, high-glucose-enhanced FTO mRNA expression resulted in a decrease in m6A. The lower m6A content might be responsible for the upregulation of methyltransferases. Bioinformatic analysis showed that mMDEGs were enriched in T2D and insulin signaling pathways, where the insulin gene (INS), the type 2 membranal glycoprotein gene (MAFA), and hexokinase 2 (HK2) gene were also found.

OC.62_38 - HOW DO DIET PATTERNS, SINGLE FOODS, PREBIOTICS AND PROBIOTICS IMPACT GUT MICROBIOTA?

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Objective:
The human gastrointestinal tract hosts a complex and dynamic population of commensal bacterial species, which have coevolved with the host, generating a symbiotic relationship. Some compounds present in foods, such as polyols, prebiotic fibers or phenolic compounds, are poorly metabolized and absorbed by the host before the transformation guided by the colonic microbiota.

Methods:
By influencing gut microbiota, diet plays a fundamental role in understanding the beneficial effects of the gut microbiota on the host, including its long-term metabolism. The idea that probiotics can act not only by influencing the colonizing microbiota opens the door to a wider range of probiotic possibilities, encouraging innovation in the field. Furthermore, it has been shown both that some probiotics increase phagocytosis or the activity of natural killer cells. Current prebiotics are mainly based on carbohydrates, but other substances such as polyphenols and polyunsaturated fatty acids could exert prebiotic effects. A prebiotic substance has been defined as 'a substrate that is selectively used by host microorganisms that confer a health benefit', and so, can interact with the gut microbiota through competition for nutrients, antagonism, cross-feeding, and support of microbiota stability.

Results:
Influencing its composition in terms of richness and diversity, food components have a key impact on the intestinal microbiota. Eating habits can strongly influence the composition of the intestinal microbiota.

Conclusions:
A healthy intestinal microbiota is essential for maintaining general health, and diet is one of the major modulators of this fascinating world of microorganisms. This must give us one more reason to adopt a healthy lifestyle.

OC.63_97 - AMBROSIA BAR: A FUNCTIONAL FOOD MODULATING THE MICROBIOTA-INFLAMMATION-BRAIN AXIS TO PREVENT UNDERNUTRITION IN HEART FAILURE

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Objective:
The AMBROSIA project aims to develop a functional food to prevent undernutrition in Heart Failure (HF) and Atrial Fibrillation (AF) older patients: a new chocolate AMBROSIA bar (AB) with a mix of probiotic strains and a cocktail of micro/macronutrients (https://www.healthydietforhealthylife.eu/index.php/projects/research-area-supported-project/report/341?s=1).

Methods:
The efficacy of the AB is evaluated through a randomized clinical trial (RCT) with a Machine learning approach to identify predictive features related to treatment outcomes.

Results:
The AB has been designed and produced by SYNBIOTEC Srl (Italy), in collaboration with the University of Florence (Italy), and the Dublin University College (Ireland). Protein hydrolysates, Q10 enzyme and the probiotic blend SYNBIO® (patented RM2004A000166, EP1743042) were added to the chocolate bar.
The RCT is performed at the University of Florence where patients will be enrolled and the inflammatory and microbiome parameters will be evaluated. Lipid molecules will be analysed at the Health Research Institute of the Balearic Islands (Spain). Metabolites will be assessed at the Northumbria University (UK). All the obtained data will be analysed with a Machine learning approach by Genevention, GmbH (Germany). AMBROSIA project is a 3-year project, funded by ERAHDHL Call 2020-PREVNUT.

Conclusions:
The AMBROSIA project determines the efficacy of micronutrient supplementation in preventing undernutrition in older HF/AF patients. The results obtained on the modulation of the intestinal and systemic inflammatory tone will be used to design the FONZIE bar, to be administered in the post-operative management of patients with Crohn's disease and colorectal cancer.

OC.64_128 - ASSESSMENT OF AVOCADO (PERSEA AMERICANA MILL.) SEEDS AS A PROMINENT SOURCE OF NUTRIENTS, NUTRACEUTICAL COMPOUNDS AND NATURAL ANTIOXIDANTS FOR INDUSTRIAL FOOD APPLICATIONS

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Objective:
The avocado seed (Percea Americana Mill.) has significant levels of beneficial bioactive compounds and contain a variety of biological properties. The objectives of this study was to develop the avocado seed powder and assessed its phytochemicals, total polyphenols, flavonoids, antioxidant activity and nutritional facts.

Methods:
Avocado seed was developed by drying it at 50-60 ºC in hot air oven. Its nutritional facts and miniral composition were measure by standard AOAC methods where as phytochemicals was measured by ffollowing standard methods of Harborne and polyphenols was estimated by using Folin reagent while flavonoids was determined by NaNO2. Its antioxidant activity was determined by DPPH assay.

Results:
Its nutritional analysis showed that moisture (9.52±0.92 %), ash (2.38±0.05 %), fat (12.90±0.18 %), fiber (3.70±0.12 %), protein (7.30±1.08 %), carbohydrates (63.80±4.02 %), energy (398.70±6.48 Kcal/100g) while Na (1.2±0.03 mg/100g), K (3.95±0.05 mg/100g) and Ca (0.72±0.01 mg/100g. The aqueous extract's phytochemical screening revealed the presence of fatty acids, polyphenols, flavonoids, phytosterols, triterpenes, tannins, alkaloids and saponins. While anthraquinones and glycosides are absent. Total polyphenols of 52.60±1.03 mg/100g GAE and total flavonoids of 12.08±1.02 mg/100g QE were found in the water extract. The antioxidant activity (% Inhihibition) of its aqueous extract was found to be dose-dependent and ranged from 25.19±1.32–84.10±4.02 % at concentration 100–500 µg/ml.

Conclusions:
According to this study, avocado seed residue is a rich source of nutrients, bioactive substances and natural antioxidants that add value to organic waste and can be employed in a variety of industrial food applications.

OC.65_121 - IMPACT OF QUINOA AND FOOD PROCESSING METHODS ON THE HUMAN GUT MICROBIOME THROUGH IN VITRO FERMENTATION

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Objective:
Quinoa represents an excellent ingredient for novel nutritious foods, due to its status as a complete protein source. Little is known on the impact of food preparation methods on the nutritional properties of plant-based proteins. Here, we use in vitro gut microbiome impact as a proxy nutrition biomarker to explore the properties of quinoa in different presentations.

Methods:
A selected quinoa line was tested in raw, boiled, extruded and baked (cookies) forms. Dietary fiber and total polyphenols were profiled; and in vitro gut microbiome fermentation were conducted from 10 subjects' stool samples with five time-points. Gut microbiome profiles were obtained using Illumina sequencing and Mothur bioinformatic pipeline.

Results:
Extruding and boiling quinoa increased the total polyphenols significantly, whereas 100% quinoa flour cookies exhibit significantly lower total polyphenols, while consistently low dietary fiber levels were quantified in all products. Fecal fermentation trials with pre-digested quinoa substrates, derived from raw and processed samples, significantly increased the levels of probiotic genera, Lactobacillus and Bifidobacterium, with strong individuality in the intensity of the prebiotic effect. One subset was mainly characterized by the increase in Bifidobacterium, while the other subset responded with a succession of Bifidobacterium then Lactobacillus. None of the processing methods appeared to limit the prebiotic potential of quinoa.

Conclusions:
These preliminary findings indicate remarkable prebiotic properties of our quinoa line being maintained through a variety of popular cooking methods. Absolute quantitation of short-chain fatty acids and prebiotic genera are on-going to strengthen these conclusions.

OC.66_122 - PROMOTING INNOVATION OF FERMENTED FOODS (PIMENTO) - COST ACTION CA20128

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Objective:

The aim of the PIMENTO project is to foster innovation in Fermented Foods (FF) in order to maintain the Europe's leadership in this field.
The PIMENTO project is going to stimulate the networking and knowledge transfer within the research communities and the industries, as well as to stimulate the debate with policy makers and consumers associations.

Methods:

PIMENTO is organized in 5 Working Groups (WG):
WG1 - Build a multi-actor operational network, building a common vision and collective engagement to the objectives.
WG2 - Cartography of fermented foods in the diet of COST Countries, highlighting the variability shaped through centuries.
WG3 - Health benefits and risks of fermented foods to foster their integration in nutritional public health strategies.
WG4 - Federating scientists and Fermented Food producers to boost innovation for society to facilitate and foster sustainable innovation.
WG5 - Dissemination, training & events for the long-term impact of the COST Action.

Results:

WG2 is mapping FF in COST countries and is developing a questionnaire to investigate the frequency of consumption.
WG3 is analyzing scientific literature in order to make a meta-analysis of health benefits of FF and elaborate reports similar to those requested by EFSA in order to approve health claims.
WG4 is investigating bottlenecks of innovation in FF in order to elaborate a position paper addressed to the European Commission and national policy makers.

Conclusions:

The PIMENTO project is calling the research and the industry communities to collaborate in the ongoing work of the WG2, WG3 and WG4.

POSTERS

HUMANS AS HOLOBIONTS; ONE HEALTH

120 - THE IMMUNOMODULATORY ACTIVITY OF OPITUTAE BACTERIUM KCR 482 STRAIN ISOLATED FROM FAECES OF HEALTHY HUMAN

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Objective:
This study aims to characterize the immunomodulatory activity of Opitutae bacterium KCR 482 strain from phylum Verrucomicrobiota.

Methods:
Our study was conducted using Opitutae bacterium KCR 482 (GenBank accession number JARJBJ000000000.1). The immunological activity of conditioned medium (CM) from strain KCR 482 IL-8, CXCL10, IL-1β, TLR-4 and TLR-2 mRNA expression was investigated using HT-29 and THP-1 cells models with or without LPS induction. Cells were grown using standard protocol, induction was performed using E.coli O55:B5 LPS (100ng/ml). The cells were collected for qRT-PCR after 4 hours incubation.

Results:
A strain of obligately anaerobic, Gram-stain-negative polymorphic coccoid bacteria were isolated from healthy human faeces. Phylogenetic analysis based on 16S rRNA gene and whole-genome sequences revealed the strain to represent novel member of the phylum Verrucomicrobiota distantly related to the known genera. CM of Opitutae bacterium KCR 482 strain increased IL-8 gene expression by 50% (r=0.67, p=0.0005), CXCL-10 gene expression by 49% (r=0.39, p=0.0001), TLR-4 gene expression by 301% (r=0.50, p=0.0015) compared to LPS-induced control in the HT-29 cell model. However, CM of Opitutae bacterium KCR 482 strain decreased IL-8 gene expression by 74% (r=0.97, p=0.0004) and IL-1β gene expression by 90% (r=0.56, p=0.0002) compared to LPS-induced control in the THP-1 cell model. CM of Opitutae bacterium KCR 482 strain did not decrease expression levels of all studied genes after LPS induction.

Conclusions:
Our study showed that novel Opitutae bacterium KCR 482 has pro-inflammatory activity in the HT-29 cell model and anti-inflammatory activity in the THP-1 cell model.

GUT MICROBIOTA FOOD, DIET AND HEALTH

44 - ROLE OF DIETARY HABITS ON SYMPTOM CONTROL AND GUT MICROBIOTA COMPOSITION IN PATIENTS WITH IRRITABLE BOWEL SYNDROME WITH CONSTIPATION (IBS-C)

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Objective:
This pilot study aimed to investigate the interaction between the Mediterranean diet (MD), gastrointestinal (GI) symptoms and gut microbiota changes in IBS-C patients.

Methods:
17 IBS-C subjects underwent a 4-week targeted nutritional protocol, completing a food diary and the FAST questionnaire to assess IBS symptoms 2 weeks before (T0-14) and at the end of the nutritional intervention (T1). A faecal sample was collected during the same visits. The control group (17 healthy subjects) completed a food diary and a symptom questionnaire to exclude gastrointestinal complaints. The nutritional protocol was developed according to the macronutrient percentages and fiber amount recommended by 2014 LARN guidelines. The microbiota composition was assessed by rRNA-targeted metagenomics.

Results:
At T1, FAST questionnaire showed a significant reduction in pre-evacuation ($p<0.0016$) and total abdominal pain ($p<0.0012$). T1 food diaries of IBS patients, compared with those of controls, showed a decrease in protein ($p=0.0310$) and an increase in carbohydrates ($p=0.0126$) and dietary fiber ($p=0.0001$) intake. Regarding microbiota, a normalization of Firmicutes/Bacteroidetes ratio was observed in IBS patients, while at the family level, Ruminococcaceae, Lachnospiraceae, Clostridiales, Prevotellaceae decreased and Bacteroidaceae increased compared to the control group. After microbiota composition analysis, IBS patients were divided into OUT-LARN and IN-LARN for macronutrients according to diet adherence. The Firmicutes/Bacteroidetes ratio was higher in the OUT-LARN group than in the IN-LARN group.

Conclusions:
Results are promising and demonstrate the importance of an appropriate dietary pattern in managing IBS symptoms. Further investigations and a broadening of the sample are necessary to confirm these data.

70 - TRIBIOME: DEEPING THE KNOWLEDGE OF SOIL/PLANT/ ANIMAL/HUMAN MICROBIOME AND THEIR INTERACTION TO INFLUENCE THE HEALTH

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Objective:

The TRIBIOME project aims to deep the knowledge of soil/plant microbiome by developing technologies to influence their modulation in order to generate an upgrade quality food and positively influence the microbiomes of both animals and humans.

Methods:

Microorganisms have been isolated from soil and root samples at BBCH 51-57 of Triticum aestivum and T. durum coming from different climate, soil parameters and countries (Italy and Spain).
Samples were processed by adding peptone water and rotated at 160 rpm at RT for 2 hours. Serial dilutions were plated on LB agar plates. Different morphologies were isolated and evaluated for their Plant Growth Promoting (PGP) activities on specific media.

Results:

A pool of over 150 microorganisms has been isolated from soil and root samples of T. aestivum and T. durum coming from different climatic, cultivation zones and countries.
Several activities have been screened such as nitrogen fixation, phosphate mobilization, pigments, phytohormones and siderophores production, antioxidant, and free radical scavenging activities in order to select the most promising microorganisms.

Conclusions:

TRIBIOME aims to learn about the soil-plant microbiome.
Several microorganisms (<150), from different climate, soil parameters and countries, have been isolated and characterised for their Plant Growth Promoting (PGP) activities.
Further analysis of these microorganisms will narrow down to around 10 microorganisms which could be used in the field as wheat modulators.

87 - PRODUCTION OF Γ-AMINOBUTYRIC ACID BY AKKERMANSIA MUCINIPHILA AND CHARACTERIZATION OF ITS GLUTAMATE DECARBOXYLASE

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Objective:

Gut bacteria hold the potential to produce a broad range of metabolites that can modulate human functions. Besides the well-studied production of compounds such as short chain fatty acids (SCFAs), in recent years the neuroactive potential of human gut bacteria is increasingly being acknowledged. Here, we explore Akkermansia muciniphila's potential to produce γ-aminobutyric acid (GABA), the main inhibitory neurotransmitter of the central nervous system. A. muciniphila is predicted to encode the glutamate decarboxylase, the enzyme that catalyzes the conversion of glutamate to GABA, but has not yet been experimentally verified to produce GABA.

Methods:

A. muciniphila was grown in basal medium supplemented with either monosodium glutamate or glutamine. In batch cultures, samples were taken every 24 hours and SCFA and amino acid production and consumption was measured. To verify these findings, similar experiments were performed in bioreactor where, as opposed to the bath cultures, pH was controlled. Samples started at pH 5.8 and after stationary phase was reached, the pH was decreased every 24 hours to a final pH of 4.0. Amino acid and SCFA production were measured using HPLC-UV and GABA production was confirmed with HPLC-ESI-MSMS. Next to that, A. muciniphila's GAD protein was cloned and expressed in E. coli. After purification, protein assays were performed to determine the effect of pH on the enzymatic activity.

Results:

GABA production was observed when A. muciniphila was grown in low pH and in the presence of either glutamate or glutamine in the growth medium. We also demonstrate that A. muciniphila's GAD protein was active in pH levels between 6 and 4, with optimal activity at pH 5.

Conclusions:

A. muciniphila produces GABA as a response to acid stress (pH < 5.5) in the presence of either glutamate or glutamine in the growth medium.

98 - AZITHROMYCIN-SPECIFIC IMMEDIATE AND LONG-TERM CHANGES ON HUMAN GUT MICROBIOTA AND THE IMPACT OF FIBER AND PROBIOTIC SUPPLEMENTS: CASE STUDY

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Objective:

Consumption of antibiotics has a lethal effect not only on pathogenic microorganisms but also on beneficial human gut microbiota. The present case study evaluated the impact of 5-day-long oral azithromycin treatment on gut microbiota. Also, we estimated the effect of different dietary fiber supplements and probiotics (with species from Bifidobacterium and Lactobacillus genera) on gut microbiota following antibiotic intake.

Methods:

DNA extraction from fecal samples, 16S rRNA sequencing using Illumina MiSeq platform, nutrition data collection using Nutridata.

Results:

During the intervention study which was designed to test the long-term impact of four dietary fiber consumption interrupted by washout periods on gut microbiota, one participant required an azithromycin treatment for 5 days. We decided to continue the study and characterize azithromycin-specific immediate and long-term changes and the impact of fiber and probiotic supplements on human gut microbiota. We analyzed 30 fecal samples and observed dynamical fluctuations in bacteria consortia. Several species (Bifidobacterium adolescentis, Bacteroides ovatus) disappeared during antibiotic treatment and were not detected even 9 months after the treatment. The proportions of other bacteria (Alistipes obesi, Bacteroides massiliensis) increased post-azithromycin treatment. Furthermore, the ratio of Faecalibacterium prausnitzii decreased in response to antibiotics, but the abundance increased after pectin-enriched fiber consumption.

Conclusions:

Dietary fiber consumption during antibiotic treatment may have a beneficial effect on maintaining and restoring healthy gut bacterial community. However, consumed probiotics species were not detected. Some beneficial species disappeared and were not detected even 9 months after the antibiotic intake.

146 - IMPACT OF TYPE 3 RESISTANT STARCH ON HUMAN GUT MICROBIOTA AND IMMUNE CELLS USING COMPLEMENTARY IN VITRO APPROACHES

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Objective:

Resistant starches type 3 (RS3) are prebiotic insoluble fibers mainly found in cooked and cooled starchy food. RS3 can be provided by High Amylose Wheat (HAW) for which gut microbiota modulation has been documented but without being linked to immune responses so far. The aim of this study was to show the antioxydant potential of HAW RS3, compared with inulin, a soluble prebiotic fiber, as mediated by gut metabolites by using completary in vitro human colon model and isolated leukocytes.

Methods:

The ARtificial COLon was used to reproduce colonic physicochemical and microbial parameters of healthy human adults. Three bioreactors were run in parallel, one used as control and two daily supplemented with 15g/L of RS3 or inulin. Fermentations were performed in triplicate with stools from 3 healthy adult donors. Microbial activities were evaluated through gas and short chain fatty acid (SCFA) measurement. Bacterial composition was assessed by 16S Metabarcoding and qPCR analysis on targeted populations. Supernatants from ARCOL were incubated with leukocytes isolated from human blood to measure reactive oxygen species (ROS) by DHR123 fluorescent detection.

Results:

Supplementation with RS3 or inulin led to a significant increase in total SCFA and gas production, with donor-dependent effects on profiles. Both products also induced a rise in Ruminococcaceae levels. Fermentation supernatants decreased ROS production, but only in one donor.

Conclusions:

RS3, and inulin, induced donor-dependent beneficial modulation of microbiota function and composition, potentially associated with antioxidant effects. Metabarcoding analyses are ongoing to better link changes in gut microbiota and immune responses.

147 - SELECTION OF POTENTIALLY PROBIOTIC LACTIC ACID BACTERIA FROM AN ITALIAN TRADITIONAL RAW MILK CHEESE

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Objective:

The growing interest in fermented foods is mainly due to their contribution to a healthy gut microbiota, mediated by foodborne microorganisms with potential benefits. The aim of this study was the characterization of fermentative microbiota of pecorino di Picinisco, an Italian traditional PDO cheese obtained from ovine raw milk, and the evaluation of possible probiotic activities of selected strains.

Methods:

For lactic acid bacteria isolation, two selective media (MRS and LM17) and two growth temperatures (30 and 37 °C) were used. Strain selection and characterization at species level were performed by comparing Rep-PCR profiles and subsequent 16S rRNA sequencing. Adhesion to intestinal cells and antibiotic (ampicillin, erythromycin, tetracycline) susceptibility were evaluated.

Results:

From a total of fourty isolates, eleven strains were identified and three of them, representative of the different species found (Lactococcus lactis, Lactiplantibacillus plantarum and Latilactobacillus curvatus) were selected to test probiotic activities, by comparing them to the reference strain Lacticaseibacillus rhamnosus GG (LGG). Since adhesion to gut mucosa is one of the main selection criteria for probiotics, Caco-2 cells were used as an in vitro model of human intestinal epithelium to evaluate the adhesion capacity of the three strains, which resulted able to adhere to cells, at levels comparable to those of LGG. Concerning safety, all the strains were susceptible to ampicillin, erythromycin and tetracycline, supporting their possible food and pharma applications.

Conclusions:

These promising results lay the ground for further investigations, aimed at confirming the probiotic potential of the three strains examined in this study.

152 - GUAR GUM AS A MICROBIALLY DEGRADABLE COMPONENT FOR AN ORAL COLON DELIVERY SYSTEM BASED ON A COMBINATION STRATEGY: FORMULATION AND IN VITRO EVALUATION

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Objective:

Oral colon delivery is of utmost interest for probiotics. Many formulation approaches have been investigated, including exploitation of enteric soluble, swellable hydrophilic and microbially degradable polymers. However, colon targeting effectiveness is still an open issue. The present work investigated a novel double-coated delivery system for reliable colonic release based on a hybrid strategy leveraging intestinal pH, microbiota and transit time.

Methods:

This system comprised an immediate-release tablet core, an inner hydroxypropyl methylcellulose (HPMC) layer and an outer coating based on Eudragit® S and guar gum. Both layers were applied by spray-coating. The system was tested in 0.1 N HCl followed by phosphate buffer pH 7.4 and in simulated colonic fluid (SCF) containing fecal bacteria from an inflammatory bowel disease (IBD) patient.

Results:

Guar gum did not alter the barrier performance of the enteric film. The HPMC layer provided consistent lag phases, which were synergistically prolonged by the overlying Eudragit® S/guar gum coating. In SCF, prepared according to a purposely applied procedure, the system showed faster release than in the presence of beta-mannanase and in control culture medium.

Conclusions:

The proposed double-coated colon delivery system based on pH-, microbiota- and transit time appeared feasible, reliable and potentially effective in preventing early release in the small bowel and release failure.

183 - MOTHERS CONSUMING A FENNEL SEED INFUSION INCREASE BIFIDOBACTERIUM IN BREASTMILK AND MODULATE GUT MICROBIOTA IN COLIC BABIES

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Objective:

The objective of this study was to investigate the changes in breast milk and gut microbiota of infants with colic after ingestion of fennel infusion by their mothers.

Methods:

Ten mother-infant pairs recruited from local health centers on the island of Terceira (Azores, Portugal). The donors were healthy, breastfeeding women and their infants aged less than 5 months who were fed exclusively on breast milk, had colic and had not taken antibiotics in the last 6 months. The mothers were asked to drink 1L of fennel seed tea (20g fennel seeds) daily for one week. Samples of the mother's milk and the baby's stool were taken at the beginning (day 0) and at the end of the treatment (day 7). Identification of the bacterial community of the milk and stool samples was done by amplification and Illumina sequencing of the hypervariable V3-V4 region of the 16S rRNA gene. After denoising, taxonomic assignments for ASVs were determined using the SILVA database.

Results:

The results showed that the bacterial diversity and richness of the neonatal faecal microbiota increased after the intervention ($p<0.05$). In addition, OTUs of the genus Bifidobacterium increased in breast milk and in the baby's stool ($p<0.05$). Some mothers also reported a reduction in the duration of crying after the intervention.

Conclusions:

Despite the small sample size, the results suggest that consumption of fennel tea by the mothers caused a change in the breast milk and gut microbiota of the breastfed infants towards an increase in Bifidobacterium spp.

GUT MICROBIOTA AND DISEASES

1 - IMPACT OF CEFIXIME AND PROBIOTICS ON FUNCTIONAL ABDOMINAL BLOATING: A PILOT STUDY

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Objective:

Abdominal bloating is a prevalent condition affecting 30% of the population. The aim of the current study was to investigate the impact of cefixime and probiotics on the bloating sensation among patients with functional abdominal bloating (FAB).

Methods:

Of 763 patients with bloating 122 patients were diagnosed with FAB (Figure 1). Patients were, Group I treated by a combination of non-activated herbal charcoal and Silicone Dioxide with Dimethylpolysiloxane (conventional treatment group), group II treated by the same lines in group I in addition to cefixime 400 mg once daily for 6 days, and group III patients were treated by the same lines given to group I in addition to a probiotic formulation harboring the probiotic strain Lactobacillus helveticus candisis for 2 weeks. All patients were evaluated by history taking, clinical examination, lab assessment and relevant imaging and symptom questionnaire before and by the end of treatment.

Results:

The prevalence of FAB was 15.9% (122/763). Females predominate (58.1%). Patients treated with probiotics and cefixime reported significant improvement in the sense of bloating and the visible abdominal distension in comparison to conventional treatment (P 0.008 and 0.000 respectively). Abdominal pain, belching, bowel habits change, and nausea improved and were comparable among the three groups by the end of treatment. No adverse events related to the used medications.

Conclusions:

Cefixime and probiotics exert significant improvement in the subjective sensation of bloating and objective abdominal distension among patient with FAB in comparison to the conventional anti-flatulence therapy.

24 - INDIVIDUALIZED PROBIOTIC THERAPY FOR POST-COVID-19 PATIENTS: MONITORING EFFICACY USING MULTIPARAMETER ULTRASOUND MARKERS

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Objective:
The post-COVID condition or long COVID can result in prolonged symptoms that require personalized care and rehabilitation. Probiotics have shown promise as a therapy for post-COVID symptoms. Ultrasound can provide information on specific targets for affected organs in post-COVID patients. This study aimed to investigate the effectiveness of personalized probiotic therapy for post-COVID condition based on patients' phenotype, using multiparameter ultrasound markers.

Methods:
The study included 20 patients with COVID-19 and 20 healthy individuals as a control group. All patients underwent general clinical, lab tests, and radiology tests to develop a metabolic biomarker panel for stratification. Probiotic strains, including Lactobacillus and Bifidobacterium genus were administered selectively at a dose of 10^9 CFU per day for ten days. The protocol included diet, lifestyle correction, low/moderate-intensity physical exercises, and personalized probiotic therapy, and patients' lungs, gut, liver, and kidneys were monitored for 3-6 months.

Results:
A majority of patients with post-COVID condition experienced changes in the lungs, kidneys, liver, and gut. After personalized probiotic treatment, faster recovery was observed, and the changes detected on ultrasound improved faster compared to the control group. This included full restoration of the structure and functional parameters of the gut, metabolic markers, kidneys, lungs, and liver. The probiotic therapy showed promising results in alleviating the symptoms of post-COVID-19 conditions, especially for patients with comorbidities.

Conclusions:
Personalized delivery of probiotics may affect the outcomes for individual patients, and the use of ultrasound markers can be useful for developing safe and effective rehabilitation programs for post-COVID patients.

55 - THE EFFECT OF SINGLE-STRAIN PROBIOTIC LACTOBACILLI ON ATOPIC DERMATITIS IN CHILDREN

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Objective:
There is growing evidence that the infant gut and skin colonization have a role in the development of the immune system, which may be helpful in the prevention and treatment of atopic dermatitis. This systematic review focused on evaluating the effect of single-strain probiotic lactobacilli consumption on treating children's atopic dermatitis.

Methods:
Seventeen randomized placebo-controlled trials with the primary outcome of the Scoring Atopic Dermatitis (SCORAD) index were included in the systematic review. Clinical trials using single-strain lactobacilli were included. Due to different methods of reporting the SCORAD index, only 14 clinical trials with 1124 children were included in the meta-analysis (574 in the single-strain probiotic lactobacilli group and 550 in the placebo group).

Results:
Single-strain probiotic lactobacilli statistically significantly reduced the SCORAD index compared to the placebo in children with atopic dermatitis (mean difference [MD]: –4.50; 95% confidence interval [CI]: –7.50 to –1.49; Z = 2.93; p = 0.003; heterogeneity I2 = 90%). The subgroup meta-analysis showed that strains of Limosilactobacillus fermentum were significantly more effective than strains of Lactiplantibacillus plantarum, Lacticaseibacillus paracasei or Lacticaseibacillus rhamnosus. A longer treatment time and younger treatment age statistically significantly reduced symptoms of atopic dermatitis.

Conclusions:
Certain single-strain probiotic lactobacilli are more successful than others in reducing atopic dermatitis severity in children. Therefore, careful consideration to strain selection, treatment time and the age of the treated patients are important factors in enhancing the effectiveness of reducing atopic dermatitis in children when choosing probiotic single-strain lactobacilli.

80 - PROBIOTIC PROPERTIES OF LACTOCOCCUS LACTIS STRAINS ISOLATED FROM NATURAL WHEY STARTER CULTURES

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Objective:

Lactic acid bacteria (LAB) play an important role in animal and human health by different mechanisms; among them they exhibit antagonistic activity against pathogens. In previous studies we have already demonstrated the probiotic potential of eight Lactococcus lactis strains isolated from natural whey starter cultures. In this study we evaluated the adhesive potential and the ability to inhibit pathogens.

Methods:

The adhesive potential was evaluated via the auto and co-aggregation test. Antimicrobial activity of the LAB was determined by the agar well diffusion method against different tester pathogens. Competitive exclusion assays of S. thypimurium and E. coli strains were performed on Caco-2 and HT29-MTX cell lines with best performing L. lactis strains.

Results:

We reported that auto-aggregation of LAB strains was higher compared to the pathogens' one, however poor or no co-aggregation at all was observed between pathogens and LAB strains. Moreover, all the LAB strains were able to inhibit the growth of S. sonnei, while no antimicrobial activity was detected on the other tested pathogens. However, competitive exclusion assay revealed that four L. lactis strains were able to significantly reduce adhesion of enteric pathogens on gut epithelial cells.

Conclusions:

This study shows the probiotic potential of Lactococcus lactis strains, in terms of both pathogen exclusion and competition activity. Identification of new LAB probiotic strains from dairy products aims at the production of novel functional foods.

85 - MICROBIOTA IN ALLOGENEIC TRANSPLANTATION AND ACUTE GRAFT-VERSUS-HOST DISEASE

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Objective:

The aim of this study is to evaluate the intestinal microbiota in Brazilian patients undergoing allo-BMT that develops acute GvHD, correlating with clinical outcomes and systemic inflammatory markers.

Methods:

This is multicenter prospective cohort study that was approved by the Research Ethics Committee from Sao Paulo State University, and all patients signed the informed consent form. The sample size is estimated to be 388 patients in four years. Peripheral blood and stool samples were collected in the preconditioning, pre-allo-BMT, 30, 60, 90 and 180 days post-allo-BMT, and at GvHD diagnosis and relapse.

Results:

To date, fifty patients undergoing allo-BMT have been included, aged 13 to 65 (36.7 ± 13.6 years old). Forty percent were HLA-matched and 60% haploidentical. Allo-BMT indications were: Acute Myeloid Leukemia (31%), Acute Lymphoid Leukemia (25%), Severe Aplastic Anemia (14%), Myelodysplastic Syndrome (8%), Chronic Myeloid Leukemia (6%), Sickle Cell Disease (4%), non-Hodgkin's Lymphoma (4%), Hodgkin's Lymphoma (4%), Chronic Lymphocytic Leukemia and Myelofibrosis (2% each). Among patients with available clinical data until now, 33% (n=14/42) developed acute GvHD and 14% (n=7/50) of patients died.

Conclusions:

We expect to find differences in the gut microbiota composition and diversity in patients undergoing allo-BMT who develop aGvHD. In addition, we hope to find biomarkers of clinical response to allo-BMT, making it possible to develop pre- and post-transplantation monitoring strategies. Furthermore, we aim to propose interventions to modulate the microbiota, improving the response, morbi-mortality associated with allo-BMT.

95 - A MULTISTRAIN PROBIOTIC IN PATIENTS WITH IRRITABLE BOWEL SYNDROME WITH PREDOMINANT CONSTIPATION

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Objective:

To assess symptom outcome in patients with irritable bowel syndrome with predominant constipation (IBS-C) during supplementation with a multistrain probiotic.

Methods:

Adults with IBS-C (Rome IV criteria) presenting with moderate to severe IBS and abdominal pain ≥40 both according to the IBS-SSS questionnaire, were eligible for inclusion. Patients took one capsule of a combination of Bifidobacterium longum LA101, Lactobacillus helveticus LA102, Lactococcus lactis LA103, and Streptococcus thermophilus LA104 ($10x10^9$ CFU) per day for 84 days.

Results:

80 patients (86.3% female; 41.2±11.8 years) were included. Mean decrease in IBS-SSS score was significant ($p<0.0001$) compared to baseline on D28 (-167±88.6 points), D56 (-187.5±89.1) and D84 (-202.5±85.0). Clinically relevant results were: ≥95-point decrease in IBS-SSS score and ≥30% decrease in abdominal pain in 80-90% of patients at all three time points; significant increase in physical and mental state SF12 scores over time; improvement in stool frequency; fewer days with type 1-2 stools; ≥80% of patients reported a slight to marked improvement in their intestinal problems at all three time points; a majority of patients were satisfied to very satisfied with supplementation. Supplementation was well tolerated.

Conclusions:

Supplementation for one month with the probiotic in patients with IBS-C produced significant benefits, which were maintained an reinforced over the following two months.

96 - EFFECTS OF A 10-DAY SUPPLEMENTATION WITH A MIXTURE OF LACTOBACILLUS AND BIFIDOBACTERIUM IN PATIENTS WITH IRRITABLE BOWEL SYNDROME

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Objective:

To describe the evolution of symptoms in patients with irritable bowel syndrome (IBS) during supplementation with a multistrain probiotic and to analyse the gut microbiota.

Methods:

Adults with IBS according to Rome IV criteria, irrespective of subtype, were eligible for inclusion. Patients took two capsules containing 40x109 CFU/day of a combination of 8 strains for 10 days. Data and stools were collected on Days 0, 13 and 30.

Results:

186 patients (81.7% female; 47.6 ± 14.8 years) were included. A significant relief was observed on D13 and over one month. Clinically relevant results were: significant decreases in IBS-SSI score in the global population and IBS-C(onstipation), IBS-D(iarrhoea) and IBS-M(ixed) patients on D13 and D30 ($p<0.001$); ≥30% decrease in abdominal pain in 83% IBS-M, 68% IBS-D and 59% IBS-C patients on D30; ≥10% increase in GIQLI score in 75% IBS-M, 73% IBS-D and 66% IBS-C patients; decrease in type 1-2 stools in IBS C and type 6-7 in IBS-D; decrease in anxiety in the global, IBS-M and IBS-D populations; 77% of physicians reported an improvement of symptoms; 71% of patients were satisfied with supplementation. Microbiota analysis revealed significant increases in Shannon and Chao1 indices between D0 and D30 ($p<0.05$; unadjusted p values, Wilcoxon test). A slight increase in Lactobacillus gasseri was observed between D0 and D30 ($p=0.04$).

Conclusions:

A 10-day supplementation with the multistrain probiotic significantly improved IBS symptoms, which could be due to effects on the gut microbiota. A placebo-controlled study will be needed to confirm these results.

102 - THE EFFECT OF PULMONARY INFECTION WITH ASPERGILLUS FUMIGATUS ON LUNG AND GUT MICROBIOTA IN DARK AGOUTI AND ALBINO OXFORD RATS

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Objective:

The little data of the effect of pulmonary fungal infection on lung and gut microbiota exist, thus aim of our study was to examine the effect of Aspergillus fumigatus infection on bacterial homestasis in these organs in Dark Agouti (DA) and Albino Oxford (AO) rats known to develop different immune responce to the fungus.

Methods:

16S rRNA amplicon sequencing of the V3-V4 hypervariable region. Enzyme-linked immunosorbent assay for cytokine content (IL-10, IL-6, TNF, IL-1beta, IL-17 i IFN-gamma) in lung and gut homogenats, and plasma (IL-6, IL-17, TNF). Myeloperoxidase, catalase, glutathione S-transferase and content of reduced glutathione in lung homogenates.

Results:

No initial differences in lung bacterial microbiota between healthy DA and AO rats exists, but A. fumigatus infection resulted in increase in alpha diversity (without effect on bacterial composition) in both strains. Changes in relative abundance at genus and species level were expressed differently (increased in DA, decreased in AO). Dysbiosis in lung coincided with increase of IFN-gamma, IL-17 and MPO in both strains, and increase oxidative stress solely in DA. Gut inflammation was noted in both strains, while bacterial dysbiosis only in DA.

Conclusions:

Pulmonary fungal infection resulted in bacterial dysbiosis in lung (in both rat strains), and gut (solely in DA). Noted lung and gut inflammation in these two rat strains, coexisted with different effects on bacterial homeostasis, which could be due to different genetic background or bacterial composition prior infection.

108 - MICROBIOME PROFILE ALTERATION IN COLORECTAL CANCER PATIENTS' BIOPSY AND BLOOD PLASMA

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Objective:

Colorectal cancer (CRC) is one of the most common cancers in the world. More than 500 000 new cases of this disease are diagnosed every year. Therefore, it is necessary to search for new molecular biomarkers with easy applicability in clinical practice and high sensitivity and specificity. The aim of this study was to reveal microbiome profile of CRC patients using gut mucosa biopsy and blood and to find new potentian biomarcers for CRC diagnostic.

Methods:

In total, 313 individuals were included in this study, 108 of them were control individuals, 104 patients with CRC, and 101 patients with adenomatous polyps (AP). Biopsies were taken from damaged mucosa. From all biopsies DNA were extracted. V1–V2 region of bacterial 16S rRNA gene from all samples were amplified and sequenced on an Illumina MiSeq platform. To construct sample-similarity matrices abundances of taxonomic ranks in each sample type were used by applying Bray-Curtis algorithm. For significant differences between groups Permutational multivariate analysis of variance (PERMANOVA) and Mann-Whitney test followed by false-discovery rate test were used.

Results:

The global structures were significantly different between control, CRC, and AP groups both in biopsy and blood samples. Analysis revealed list of bacteria the number of which was significantly different between the groups. Tissues' microbiome was 20 times richer than blood microbiome. In CRC patients' samples bacterial richness and diversity decreased in tissue and increased in blood samples. Model of 8 bacterial DNA signatures in blood showed high sensitivity and specificity (AUC: 0.801).

Conclusions:

Based on tissue and blood microbial profile it was possible to distinguish heathy state from CRC or AP. Distinct bacterial DNA signatures in blood could presumably be used as biomarkers for CRC.

115 - IMPACT OF WESTERN DIET ON ENTEROHAEMORRHAGIC ESCHERICHIA COLI (EHEC) COLONISATION IN THE HUMAN IN VITRO MUCOSAL ARTIFICIAL COLON

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Objective:

Enterohemorrhagic Escherichia coli (EHEC) is a major food-borne pathogen causing human disease ranging from diarrhea to life-threatening complications. Relatively little data is available on interactions between EHEC and the human gut microbiota. Accumulating evidence demonstrates the involvement of Western diet in gut microbiota shifts that enhance susceptibility to enteric infection, but the effect of diet on EHEC pathogenesis remains unknown. Our research aimed to investigate the effects of healthy versus Western diet on gut microbiota composition and activities and EHEC colonisation in an in vitro human colon model M-ARCOL (Mucosal ARtificial COLon).

Methods:

M-ARCOL reproduces the main nutritional, physicochemical and microbial (luminal and mucus-associated microbiota) parameters of the colonic environment. Two bioreactors were inoculated with human fecal samples (n=4) and ran in parallel, one receiving a healthy diet, the other a Western diet and infected with EHEC strain EDL933. EHEC survival was determined by qPCR, gut microbiota composition was assessed by 16S metabarcoding and microbial activities were evaluated through gas and short chain fatty acid analysis

Results:

Diet, donor and EHEC infection impacted beta-diversity in luminal and mucosal samples. EHEC survival was dependant on both donor and diet in luminal samples. EHEC was more rapidly depleted with a healthy diet compared to a Western diet and eliminated sooner in some donors.

Conclusions:

EHEC was maintained in mucosal samples without elimination, suggesting a possible niche environment for colonisation and survival. The prolonged EHEC colonisation sustained by a Western diet in vitro could suggest an increased susceptibility to infection in humans.

116 - BENEFICIAL ROLES OF POSTBIOTICS IN CONTROLLING CHEMOTHERAPY-INDUCED INTESTINAL INJURY

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Objective:

Postbiotics are compounds released by microorganisms during their natural metabolic activities. Their beneficial effect is exerted by gastrointestinal immunomodulatory effects. It is known that alteration in intestinal barrier have been linked to several intestinal and systemic diseases. In fact, one of the most common morbidities in chemotherapy is intestinal mucositis. Therefore, we explored the function of the postbiotics in preventing chemotherapy-induced intestinal damage.

Methods:

Postbiotica s.r.l. has developed a novel PBTechâ postbiotic from Lactobacillus paracasei CNCM I-5220 strain. In vitro, LPS-stimulated cells were treated with postbiotic, while in vivo, mice were pretreated with postbiotic for 4 days followed by LPS stimulation.
To carry out intestinal mucositis experiment, mice were pretreated with postbiotic for 10 days, then mucositis was induced by administration of 5-FluoroUracile (5-FU) for following 4 days. Clinical signs and histological features were evaluated to understand the role of postbiotic in protecting against mucositis and preserving of intestinal barrier properties.

Results:

In vitro and in vivo, postbiotic exerted immunomodulatory effects by regulating LPS-dependent cytokine release. In mucositis experiment, mice showed an amelioration of clinical signs (weight loss, diarrhea and blood in faeces) and intestinal damage decrease upon postbiotic treatment. In addition, postbiotic was able to restore mucus reduction caused by 5-FU administration.

Conclusions:

In conclusion, postbiotic showed immunomodulatory effects both in vivo and in vitro. PBTech® postbiotic was able to preserve intestinal morphology in mouse model of chemotherapy-induced intestinal injury. Our results suggest that postbiotic supplementation could be further exploited in the management of therapy-dependent intestinal morbidities

127 - THE ROLE OF PROBIOTICS IN OUTPATIENTS WITH A VIRAL RESPIRATORY TRACT INFECTION: A MULTICENTER, RANDOMIZED, DOUBLE-BLIND, PLACEBO-CONTROLLED DIETARY STUDY

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Objective:
The objective of the study was to evaluate a role of probiotics in mild coronavirus disease-19.

Methods:
This was a randomized double-blind placebo-controlled multicenter study. Patients aged 18-65 years, positive antigen/PCR test received (Bifidobacterium (B.) lactis BI040, B. longum BL020, Lactobacillus (L) rhamnosus LR110, L. casei LC130, L. acidophilus LA120, 5 billion CFU total) or placebo 1 capsule a day for 28 days and self-reported symptoms using the Respiratory Illness Diary. After 3 months patients completed Post-COVID-19 Questionnaire (PCQ-19). On days 0-5 and 28-35, blood was sampled for IgG to nucleocapsid protein and receptor binding domain (RBD)/spike 1 (S1) protein. The primary outcome measure was a patient global symptom score, a sum of 12 symptoms scored 0-3 units, on 10 day of observation. The difference between groups was assessed using the Mann-Whitney U test.

Results:
We screened 203 age-matched patients, 70 were randomized and assessed for symptomatic response, 69 answered the PCQ-19, and 44 were assessed for antibody production. At day 10, the median global symptom score (interquartile range) was lower in the probiotic vs. placebo group (0.0 (0.0-2.0) vs. 2.0 (1.0-5.0), $P < 0.05$). The probiotic group showed a shorter duration of fatigue (28.0 (14.0-30.0) vs. 30.0 (30.0-60.0) days) and anxiety (10.5 (7.0-22.0) vs. 45.0 (42.0-56.0) days) as post-disease symptoms ($P < 0.05$) and greater increase of concentration of RBD/S1 IgG (225.9 vs. 105.6 units/mL, $P < 0.05$).

Conclusions:
Use of probiotics alleviates mild coronavirus disease-19 and post-disease symptoms, and improves humoral immune response to viral antigens.

160 - THE COMPARATIVE STUDY OF THE AKKERMANSIA MUCINIPHILA AND FAECALIBACTERIUM PRAUSNITZII INTERVENTION ON THE LIVER INJURY ATTENUATION BY TARGETING HEPCIDIN-FERROPORTIN AXIS IN MICE WITH CCL4INDUCED LIVER

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Objective:
Iron overload and accumulation in hepatocytes have been reported as common causes of liver fibrosis. On the other hand, gut microbiota can affect liver fibrosis by regulating iron metabolism through the hepcidin-FPN axis, which plays a key role in regulating iron flow. The aim of this study is to investigate the effect of A. muciniphila and F. prausnitzii, and their postbiotics (Cell-free Supernatant, CFS), on liver fibrosis induced by CCl4 in mice through the hepcidin-FPN axis in the colon and liver.

Methods:
CCl4-induced liver fibrosis mice were gavaged with A. muciniphila, F. prausnitzii, and their Cell-free Supernatant (CFS) for 4 weeks. Finally, liver and colon tissue were isolated from each mouse and subjected to histopathological analysis, immunohistochemical staining, and serum biochemical analysis. The expression of genes involved in the hepcidin-FPN axis was also analyzed using RT-qPCR.

Results:
Histological evaluation of the liver sections showed that interstitial connective tissue were reduced by F. prausnitzii and their CFS. Both bacteria and their postbiotics were also able to counteract the increase in serum levels of iron and liver enzymes caused by CCl4-induced liver fibrosis. Our results indicated that F. prausnitzii and their CFS upregulated the expression level (mRNA and protein) of HAMP and FPN and decreased the expression level of α-SMA compared to the liver fibrosis group.

Conclusions:
In conclusion, F. prausnitzii and their CFS have a high potential to ameliorate liver fibrosis through the hepcidin-FPN axis and could be promising for new therapeutic interventions to improve iron accumulation and liver fibrosis.

168 - CLINICAL ASSESSMENT OF THE EFFICACY OF A MULTI-STRAIN PROBIOTIC PRODUCT IN ASIAN SUBJECTS WITH ACNE

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Objective:

Acne prevalence in APAC region is around 88% where women, during adulthood, are more likely to suffer from skin discomfort than men, with a negative impact on quality of life and an increased risk of anxiety and depression. Previous trials demonstrated that L. plantarum PBS067, L. reuteri PBS072, and L. rhamnosus LRH020, contained in the probiotic formulation ProBeautyShield, are useful in supporting different skin conditions. The aim of this study is to evaluate the efficacy of this multi-strain probiotic complex in Asian subjects with acne.

Methods:

64 female adults were enrolled in a RDBCT to assess the multi-strain probiotic efficacy (3B CFU/day) in the improvement of skin appearance in Asian subjects with mild to moderate acne (score 1-3 according to IGA scale). Primary outcomes were related to an amelioration of skin hydration and evenness, as well as a reduction of skin sebum and in the numbers of acne lesions after 56 days of product administration and 14 days of follow-up. Instrumental assessment and dermatologist evaluation were carried out at each checkpoint.

Results:

Clinical results showed a 20% reduction of skin sebum in two months ($p<0.001$) and an improvement of 20% of skin hydration. The number of acne lesions reduced, touching a decrease of 31%. In addition, 90% of the subjects reported an improvement of skin complexion after two months of probiotic treatment.

Conclusions:

These results confirmed the use of ProBeautyShield in supporting skin health in the Asian population affected by acne.

179 - THE INFLUENCE OF CEMTIRESTAT ON INTESTINAL MICROBIOTA IN RAT MODELS OF DIABETES

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Objective:

A bacterial imbalance inside the gastrointestinal tract (dysbiosis) can be associated with metabolic disorders such as obesity, insulin resistance, diabetes and immunity dysfunction. The aim was to investigate the interactions between a novel aldose reductase inhibitor, cemtirestat (3-Mercapto-5H-1,2,4-Triazino[5,6-b]Indole-5-Acetic Acid) and the intestinal microbiota in rat models of diabetes.

Methods:

Intestinal microbiota was analysed using culture-dependent and culture-independent approaches. Fecal samples were collected and microflora were isolated and identified by 16S r RNA sequencing. Oxford Nanopore Technology sequencing using MinION device, a deeper microbial investigation of the intestinal microflora was provided. The contigs were subjected to analysis of the taxonomic classification by Kraken2 which was followed by computing the relative abundance of different species in the samples (alpha and beta-diversities).

Results:

Levels of bacteria varied considerably between samples in a range from 5.08 $\log_{10}$ CFU/g to 8.34 $\log_{10}$ CFU/g. Levels of lactobacilli were increased in diabetic rats treated with cemtirestat whereas level of clostridia were reduced. Culture-dependent identification indicated the presence of culturable bacteria Limosilactobacillus reuteri, Ligilactobacillus murinus, Enterococcus faecium, Enterococcus faecalis, Escherichia coli, Escherichia fergusonii, Weissella cibaria, Micrococcus luteus, Proteus mirabilis. Culture-independent approaches showed, that the most abundant microbes belonged to the top 5 genera, including Lactobacillus, Bacteroides, Prevotella Muribaculum and Ligilactobacillus

Conclusions:

By using a metagenomic approach, we have shown that cemtirestat didn't alter the diversity of the gut microbiome of diabetic rats to a great extent.

190 - MULTI-OMICS BIOCOMPUTATIONAL STATISTICAL APPROACHES IN GUT MICROBIOTA BIOMARKER DISCOVERY IN UC PATIENTS

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Objective:

In this study, we aimed to apply different statistical approaches to explore the gut bacterial and fungal ecosystems fused to metabolic profile in patients affected by ulcerative colitis (UC).

Methods:

16S rRNA and ITS2 region sequencing were performed to investigate bacterial and fungal metataxonomics, respectively, of faecal samples from UC patients and healthy subjects (CTRLs), under a study funded by the Italian Ministry of Health (GR-2016-02364891).

The sequences were analysed using the plugins of QIIME2 and volatile metabolites were measured by Gas Chromatography coupled by Mass Spectrometry by Solid-Phase Microextraction (GC–MS/SPME).

Multivariate partial least square-discriminant analysis (PLS-DA) was applied on each omic dataset, singularly, and the multivariate models based on integrated omic datasets, including Multi Block PLS-DA (MBPLS-DA), Multi Block Principal Component Analysis (MBPCA) and Common Dimension (ComDim) were applied on three omics datasets both on individual and fused matrixes.

Results:

The PLS-DA evidenced the presence of gut microbiota (GM) fingerprints specific of UC and CTRL cohorts. The MBPLS-DA, MBPCA and ComDim confirmed the presence of differentials omic profiles in UC and CTRLs, each characterized by a different distribution of bacteria, fungi and related metabolites.

Conclusions:

In conclusion, herein we propose three different biocomputational statistical approaches to reduce the high complexity of GM-related omic data. By our evidences these multi-omic approaches skilfully disentangle the complexity of omic datasets, deciphering GM patterns. Moreover, the PLS-DA approach represents a useful statistical tool in reducing the dimension of omic variables, still retaining as much information as possible from the original data.

192 - DYSBIOSIS INDEX AND GUT MICROBIOTA PROFILE IN INFLAMMATORY BOWEL DISEASES

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Objective:

Inflammatory bowel diseases (IBDs) are multifactorial chronic inflammatory intestinal diseases. Our main objective was to demonstrate the correlation between the gut microbiota profile and clinical characteristics of IBDs. Moreover, we defined bacterial biomarkers associated with intestinal dysbiosis degree.

Methods:

Faecal samples from 35 IBD paediatric patients were analysed by 16S rRNA metataxonomics. By a metagenomic method for in vitro diagnosis of gut dysbiosis, developed by our algorithm (patent N WO2017216820A1), we were able to assign a dysbiosis index in IBD patients compared to healthy subjects, matched for age and gender. Multivariate, univariate and Pearson's correlation analyses were applied on gut microbiota profile of patients stratified for clinical features and dysbiosis degree.

Results:

By statistical analyses applied to the metataxonomic profiles of patients stratified for gut disbiosys degree, we obtained the increase of Faecalibacterium, Lachnospiraceae, Lachnospiraceae Clostridium, Butyricicoccus in IBD with mild dysbiosis and of Enterobacteriaceae in IBD with high dysbiosis. Investigating the disease localisation biomarkers, we identified Fusobacterium and Veillonella in extensive colitis, Lachnospiraceae in proctitis, Oscillospira in pancolitis, Parabacteroides in ileo-colon and Ruminococcaceae in ileo. Moreover, WAL_1855D and Ruminococcaceae were increased in patients with active state disease. Furthermore, the Pearson's correlation test identified a positive correlation between Enterobacteriaceae, Fusobacterium Haemophilus, and WAL_1855D and dysbiosis index, while a negative correlation between Lachnospiraceae Clostridium, Bacteroides, Butyricicoccus, and Faecalibacterium and dysbiosis index.

Conclusions:

We defined bacterial biomarkers for dysbiosis severity, location and disease activity. The gut dysbiosis index combined to gut microbiota profiling could represent a new prognostic tool in IBD.

195 - SEARCHING FOR METAPROTEINS AS POSSIBLE POSTBIOTIC TARGETS IN COVID-19 PEADIATRIC DISEASE

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Objective:

Investigation of the gut microbiota (GM) may help elucidate the etiopathogenetic mechanisms of the disease, viral involvement in gut dysbiosis and discovery of new therapeutic strategies.

Methods:

Stools from 21 paediatric patients with COVID-19 were compared with 21 age- and gender-matched healthy subjects. Bacterial metaproteins were extracted, digested, identified and quantified by nanoLiquid Chromatography-Mass Spectrometry (nLC-MS). MetaLab-MAG was employed to perform label free quantification, taxonomic assignment by the lowest common ancestor (LCA) algorithm and functional annotation by COG and KEGG categories.

Results:

We identified a total of 1,932,126 peptide sequences corresponding to 1,182 species and 11,178 protein groups. COVID 19 was associated to a GM compositional dissimilarity respect to CTRLs both by functional profiles and LCA-derived taxonomy.

Conclusions:

To our knowledge, this study represents the first metaproteomic investigation of GM paediatric patients affected by COVID-19 to understand the functional roles of the gut microbial community in the disease onset trying to unveil new therapeutic targets.

208 - GUT-HEART AXIS MODULATION BY FMT IN A MOUSE MODEL OF MITOCHONDRIAL DAMAGE

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Objective:

Down-regulation of the key cardiac mitochondrial A-kinase anchoring protein 121 (AKAP 121) promotes pathological cardiac hypertrophy and heart failure (HF). Given the link between the gut microbiota and heart functionality, we firstly hypothesized that AKAP 121 levels could also influence gut microbiota (GM) composition and then that the established bacterial profile in AKAP 121 deficient mice could through the microbiota-heart axis affect heart functionality.

Methods:

Cardiac function, GM, intestinal barrier integrity and gut and systemic inflammation during aging in adult (6-month-old) and aged (24-month-old) Akap 1 wild type (Akap1+/+) and Akap1 heterozygous knockout mice (Akap1+/-) were studied by echocardiography, V3-V4 16S rDNA sequencing, mRNA analysis and serum ELISA assay, respectively. The impact of GM on cardiac functionality was explored by fecal microbiota transplantation (FMT) transferring GM from Akap1+/- donors mice to Akap1+/+ recipient mice; cardiac function, GM, permeability and inflammation upon FMT were evaluated.

Results:

Cardiac dysfunction in Akap1+/- mice is associated to a specific bacterial profile, impairment of colon permeability and increase of circulating pro-inflammatory cytokines. FMT from Akap1+/- mice to their wild-type counterpart induces decrease of fractional shortening (index of reduced cardiac function) and abnormal levels of markers of systemic inflammation and gut permeability.

Conclusions:

The aberrant GM profile induced by Akap1 partial deletion leads to abnormalities of gut homeostasis and contributes to cardiac dysfunction pathophysiology in Akap1+/- mice. These results may allow the identification of innovative effective fecal and tissue biomarkers and provide new insights for elucidating the metabolic process related to the microbiota-heart axis.

GUT MICROBIOTA AND METABOLISM & INTERACTION WITH FOOD

139 - PRODUCTION OF POSTBIOTIC METABOLITES FROM BISTORTA OFFICINALIS AND LYTHRUM SALICARIA IN HUMAN GUT MICROBIOTA EX VIVO CULTURES

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Objective:
Bistort rhizome (Bistorta officinalis) and Purple loosestrife herb (Lythrum salicaria) are plants widely present in Europe and Asia with potential health benefits properties due to the high tannin content. Bistort rhizome is particularly rich in condensed tannins and Purple loosestrife is a valuable source of ellagitannins. However, the low bioavailability of tannins casts doubt on their advantageous activity in vivo. This study aimed to evaluate metabolism of the Bistort rhizome and the Purple loosestrife extract constituents by human gut microbiota.

Methods:
Bistort rhizome and Purple loosestrife water extracts were incubated anaerobically with human fecal microbiota from three healthy donors. The composition of raw extract and the time-course production of postbiotic metabolites were determined using UPLC-DAD-MSn method.

Results:
After incubation of the Bistort rhizome extract with human gut microbiota 13 metabolites were detected, including flavan-3-ol derivatives. The most prevalent metabolite identified was 5-(3,4-dihydroxyphenyl)-gamma-valerolactone. The Purple loosestrife extract was found to be catabolized to 16 metabolites, mostly derivatives of ellagic acid. Among them, urolithin A was identified as the most dominant one.

Conclusions:
The Bistort rhizome, and the Purple loosestrife extracts are catabolized by human gut microbiota and are sources of bioactive postbiotic metabolites. According to the literature, the gamma-valerolactone and the urolithin A have anti-inflammatory activity that has been linked to therapeutic benefits in several conditions due to their high bioaviability. Therefore, the obtained data indicate that microbial metabolism of the Bistort rhizome, and the Purple loosestrife yields bioactive compounds that account for the systemic effects of raw tannin-rich plants.

157 - THE MUTUALISTIC RELATIONSHIP BETWEEN TORMENTILLAE TINCTURA AND HUMAN GUT MICROBIOTA IN POTENTIAL THERAPY OF LEAKY GUT SYNDROME

Aleksandra Kruk [(1)] - Dominik Popowski [(2)] - Jakub Patryk Piwowarski [(1)] - Sebastian Granica [(1)]
Medical University of Warsaw, Microbiota Lab, Department of Pharmaceutical Biology, Warsaw, Poland [(1)] *- Prof. Waclaw Dabrowski Institute of Agriculture and Food Biotechnology – State Research Institute, Department of Food Analysis, Warsaw, Poland* [(2)]

Objective:
Tormentillae tinctura (TT) obtained from roots of Potentilla erecta L. has been used for centuries to treat gastrointestinal tract ailments which etiologic is currently linked with the leaky gut syndrome (LGS). Its tannin-reach composition may have a beneficial effect on human gut microbiota (HGM) homeostasis. The research aimed to determine the mutualistic relationship between TT and HGM.

Methods:
TT metabolites were obtained by incubation of extract with human fecal slurries (samples obtained from 3 healthy donors). After incubation, samples were taken for the 16S rDNA sequencing, and the metabolite fractions were isolated. The composition of the obtained fractions (UHPLC-MSn), the differences in metabolic profiles, and their effect on intestinal barrier integrity (Caco-2 model, transepithelial electrical resistance measurement) were determined.

Results:
The UHPLC-MSn analysis showed the presence of selected non-metabolized TT components and new metabolites (TTM) in the samples. At the same time, TT impacted the HGM composition, as over a dozen taxa had significantly different abundance than in control incubations (LEfSe). The increase in alpha diversity indexes (vs. control) was also observed for the particular donor samples. TTMs were not cytotoxic to Caco-2 and stabilized cell monolayer integrity.

Conclusions:
TT components and TTM have beneficial effects on HGM biodiversity and intestinal barrier integrity. Due to these properties, TT could offer an opportunity for novel approaches to Leaky Gut Syndrome therapy.

207 - ISOLATION AND IDENTIFICATION OF INTESTINAL MICROBIOTA IN RESPONSE TO APPLE CIDER VINEGAR INTAKE IN WISTAR RATS USED AS A MODEL OF METABOLIC SYNDROME

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Higher School of Biological Sciences of Oran (ESSBO), Oran, Algeria [(1)] - Laboratory of Physiology of Nutrition and Food Security (LPNSA), Department of Nature and Life Sciences, University Oran 1 Ahmed Ben Bella, Oran, Algeria [(2)]

Objective:
This study focuses on the isolation and identification of intestinal microbiota (IM) in response to apple cider vinegar intake in Wistar rats with metabolic syndrome (MS) induced by a cafeteria-fructose diet (CFD).

Methods:
15 male Wistar rats (185 ± 10 g) were divided into 3 equal batches and fed for 5 months of experimentation either the standard laboratory diet (SD) or the cafeteria-fructose diet (CFD), supplemented or not with ACV (CFVD) at a rate of 3.5 ml/kg/day for 28 days by intragastric feeding. Throughout the experiment, body weight and blood glucose levels were monitored. At the end of experiment, the animals were sacrificed, and colic and fecal contents were freshly collected under sterile conditions for microbiological study. Bacterial strains were isolated and pre-identified by conventional phenotypic identification, then the study was followed by 16S RNA gene amplification of the bacterial isolate.

Results:
The results show that the CFD induces a highly significant ($p \leq 0.001$) increase in body weight, alterations in carbohydrate metabolism and an IM dysbiosis. In contrast, ACV intake leads to a significant decrease in body weight ($p \leq 0.001$), reduces fasting blood glucose and improves insulin sensitivity ($p \leq 0.01$). Moreover, ACV induced a significant decrease in Clostridium and Staphylococcus levels ($p \leq 0.001$), but the growth of Lactobacilli, total Coliforms and Enterococci was non-significant ($p>0.05$).

Conclusions:
ACV appears to have a hypoglycemic effect and may modulate IM by limiting the proliferation of pathogenic bacteria. ACV did not result in any significant improvement in beneficial bacteria, suggesting that the duration of supplementation was insufficient.

BEYOND THE MICROBIOTA: VIRUSES, FUNGS AND WORMS

67 - DEVELOPMENT OF BIOCONTROL TOOLS TO EXTEND THE SHELF LIFE AND IMPROVE THE QUALITY OF FRUITS

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Objective:
Fungal phytopathogens cause great harm during the storage of fruits, causing spoilage and producing mycotoxins. In most cases, strains of various Bacillus species are used as antagonist bacteria. Yeast-antagonists are promising tools for biocontrol due to their environmental friendliness and safety for humans. The purpose of this work was to compare the yeast Metschnikowia pulcherrima and strains of Bacillus subtilis in their ability to suppress the growth of phytopathogenic fungi.

Methods:
Antagonistic studies were performed by agar blocks as well as by co-cultivation to pathogenic fungi and bacilli on agar. 10 strains of yeast Metschnikowia pulcherrima, and 7 strains of bacteria Bacillus subtilis were isolated from apple fruits, and 8 strains of bacteria Bacillus subtilis were obtained from the collection of the Central Museum of the LLP "Republican Collection of Microorganisms". The strains were studied as antagonists of the phytopathogenic fungus Alternaria alternata, Acremonium alternatum, and Penicillium expansum.

Results:
All studied strains of yeast Metschnikowia pulcherrima showed rather high antagonistic activity. Of the 15 bacterial strains, only one Bacillus subtilis BS4 showed a high level of growth inhibition of Penicillium expansum and Acremonium alternatum, the remaining 14 strains showed low antagonistic activity.

Conclusions:
Our further work in the development of biocontrol tools will be associated only with strains of Metschnikowia pulcherrima. The Bacillus subtilis BS4 strain can be recommended in combination with yeast antagonists for the development of a complex biopreparation for processing apples.

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188 - A HOLISTIC VIEW OF THE GUT MICROBIOTA OF PEDIATRIC COVID-19 PATIENTS

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Objective:
Historically, the most studied microorganisms to inhabit the human body have been bacteria, with studies demonstrating their importance in human health and disease progression increasing year by year. However, those bacteria share an ecological niche with other microorganisms, such as fungi, viruses, phages and archaea which, thanks to developments in next generation sequencing technology, have also begun to attract attention from the scientific community. In fact, emerging evidence strongly suggests that each of these microbial kingdoms, both separately and together, also have an important role in infectious diseases. Here, we present a holistic, trans-kingdom profile of the gut microbiota (GM) of pediatric patients infected with SARS CoV-2.

Methods:
By performing shotgun metagenomics sequencing, we sequenced the entire GM of pediatric SARS-CoV2 patients and age-matched healthy controls. We mapped the bacteriome, mycome and virome of these patients, and we investigated the patterns of unclassified microorganisms present in our samples.

Results:
We identified the microorganisms most associated with SARS CoV-2 infection, and uncovered which trans-kingdom interactions are most relevant to COVID-19 progression. Furthermore, we described the functional profiles of these microorganisms in relation to infection.

Conclusions:
The holistic approach to GM studies can provide additional information with great clinical relevance, both as a predictor of disease severity, and as a potential target for modulation to control disease progression.

PROBIOTICS, PREBIOTICS AND POSTBIOTICS
PROBIOTICS

35 - DATA ON THE EFFECT OF BIFIDOBACTERIUM ANIMALIS SUBSP. LACTIS BB-12 AND LACTOBACILLUS PLANTARUM 299V® ON SOME BIOCHEMICAL PARAMETERS AND BODY MASS INDEX OF OBESE RABBITS FROM ITELV2006 LINE

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Obesity and metabolic syndrome have become a real public health problem in the world. Thus, the prevention of obesity and the promotion of a healthy and balanced diet are becoming of high priority. In this context, we aim by this study to evaluate the consequences of obesity on biochemical and morphometric parameters and to determine the effect of targeted probiotics on obese rabbits and their offspring. A first experiment used 40 rabbits of the ITELV2006 line that were divided into control and obese groups, and feeding them with a high-calorie, high-fat diet called "cafeteria" for 14 weeks to induce an experimental model of obesity and metabolic syndrome (MetS). Results revealed a significant increase in fasting blood glucose and OGTT ($p < 0.001$), as well as an altered lipid profile ($p < 0.001$) and an increase in body mass index (BMI) ($p < 0.01$), body weight ($p < 0.001$), and abdominal circumference ($p < 0.001$).
A second experiment involved 18 rabbits from the "Obese" group of the former experiment, dividing them into three subgroups of six rabbits each (control (TO), Bifidobacterium animalis subsp. lactis BB-12® (OB) and Lactobacillus plantarum 299v® (OL), for a trial of 30 days. The results demonstrated improvement in both groups that had the probiotics (OB and OL) compared to the control group in terms of a decrease in fasting blood glucose ($p < 0.001$), OGTT ($p < 0.05$), total cholesterol ($p < 0$, 001), triglycerides ($p < 0.01$) and LDL ($p < 0.001$). At the same time a significant increase in HDL ($p < 0.05$) and decrease in body weight ($p < 0.05$), abdominal circumference ($p < 0.05$) and BMI ($p < 0.05$) were recorded. in conclusion a relevant model of obesity and MetS induced by the introduction of the "Cafeteria" diet for 14 weeks, showed a change in biochemical and morphometric parameters, thus reproducing pre-obesity and metabolic syndrome in humans. In addition, treatment with two probiotics showed an improvement in certain parameters of induced obesity and MetS

41 - METABIOTICS PRODUCTION BY FERMENTING GLUTEN-FREE FLOURS AND OKARA WITH PROBIOTICS AND ADDED PARAPROBIOTICS

Mihaela Cotarlet [1] - Bogdan Păcularu-Burada [1] - Mihaela Aida Vasile [1] - Oana Viorela Nistor [1] - Leontina Grigore-Gurgu [1] - Nicoleta Stănciuc [1] - Gabriela Elena Bahrim [1]

Dunarea De Jos University, Faculty of Food Science and Engineering, Galati, Romania [1]

Objective:

This study's goal involved the achievement of metabiotics from fermented gluten-free flours and okara by using lactic acid bacteria probiotic strains.

Methods:

A fermentation medium based on chickpea, quinoa, and buckwheat flours and okara was inoculated with Lactiplantibacillus paraplantarum MIUG BL74 (the control – sample P1) and then, a paraprobiotic suspension of L. plantarum MIUG BL21 was added after (sample P2) /before fermentation (sample P3) and incubated at 37°C, 72 h. The paraprobiotic was ohmic (20 V/cm, 15 min) and thermic (at 75°C, 15 min) treated. The antioxidant activity was examined using DPPH and ABTS methods. For peptides (3, 10, and 30 kDa) antioxidant and anti-diabetic properties were examined. The short-chain fatty acids and polyphenols were investigated by HPLC assay.

Results:

A slightly antidiabetic effect was seen in peptides (30 KDa), extracted from samples P2 and P3. The peptides separated from sample P3 had a higher antioxidant potential (16.456% ± 2.063, DPPH method, 17.806% ± 0.285, ABTS method). Instead, fermented products highlighted a decreased DPPH/ABTS inhibition potential (11.39 ± 0.77% and respectively 7.62 ± 0.30%, for P3).

Lactic, propionic, isovaleric acids were identified in the gluten-free fermented metabiotic products. Syringic and ellagic acids, apigenin, caffeine, epigallocatechin, and quercetin derivative were quantified in the sample P3.

Conclusions:

The development of postbiotics using gluten-free flours with probiotic and paraprobiotic supplements is an encouraging challenge for food processing.

51 - THE COMBINED EFFECT OF PROBIOTICS AND PARAPROBIOTICS TO IMPROVE THE BIOACTIVE PROPERTIES OF FERMENTED BOVINE COLOSTRUM

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Objective:

The addition of the paraprobiotic obtained by ohmic heating and thermal treatments of Lactiplantibacillus plantarum MIUG BL21 probiotic strain's suspension, before or after the fermentation of bovine colostrum with the probiotic Lactiplantibacillus paraplantarum MIUG BL74 strain, was studied in order to improve the functional properties of the fermented products (FPs).

Methods:

The fermentation medium based on 8% bovine colostrum sterilized was prepared. Then, it was inoculated with 5%(v/v) fresh culture of MIUG BL74 probiotic. The paraprobiotics were added (10%v/v) before (FP-1) or after fermentation (FP-2). Control sample was without paraprobiotics (FP-C). After 72h of fermentation, titratable acidity (^{o}Th), antioxidant activity (inhibition ratio, %), antimicrobial activity (inhibition zone, mm) against Listeria monocytogenes Scott A, and Escherichia coli ATCC 25922 strains, and probiotic viability were evaluated as functional properties of the FPs.

Results:

The supplementation of the fermentation medium with paraprobiotics influenced the functional quality of the fermented product when the paraprobiotics were added after fermentation. Thus, the FP-2 showed titratable acidity of 65±0.20^{o}Th, DPPH scavenging ratios of 68.04±0.22%, respectively ABTS inhibition of 90.81±0.08%. The inhibition zones were 19.80±0.03 mm against L. monocytogenes, and 12.20±0.09 mm against E. coli. The probiotic count was 8.37 log CFU/mL.

Conclusions:

The results demonstrated that the fermentation medium's supplementation with 10% paraprobiotics after fermentation improved the postbiotic composition of the fermented product with a positive impact on the bioactive properties.

52 - PROBIOGENOMIC ANALYSIS OF LACTIPLANTIBACILLUS PLANTARUM BGPKM22 AS A POTENTIAL PROBIOTIC IN THE TREATMENT OF INTESTINAL INFECTION

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Objective:
Gastrointestinal infections are a major cause of morbidity and mortality worldwide, particularly in developing countries. Due to the ban on antibiotics in treatment for intestinal infections, alternatives like probiotics can be effective as well. The main objective of this research is to explore the beneficial and protective effects of Lactiplantibacillus plantarum BGPKM22 through research on antibacterial and probiotic properties.

Methods:
The probigenomic analysis of BGPKM22 includes genome sequencing and evaluation of bacteriocin production and probiotic properties The ability of BGPKM22 to upregulate the gene expression of tight junction proteins CLDN4, ZO-1, OCLN, and CDH1 is tested in co-incubation with HT29-MTX and Caco-2 cells using RT-PCR.

Results:
Lactiplantibacillus plantarum BGPKM22 was isolated from artisanal sour milk. The genome size is 3,356,812 bases with a GC content of 44.35%. The strain has potent antimicrobial activity against a broad range of pathogens. According to whole genome sequencing the highly antimicrobial capacity is related to the presence of three bacteriocin clusters: sactipeptide class, plantaricin E class, and lanthipeptide class IV as detected by the BAGEL 4 webserver. The BGPKM22 successfully survived transit through simulated gastrointestinal tract conditions. Also, co-incubation with HT29-MTX and Caco-2 cells significantly upregulates tight junction proteins gene expression.

Conclusions:
Since the strain has a beneficial effect on the intestinal barrier, production of bacteriocins, and probiotic properties, the L. plantarum BGPKM22 may be considered a suitable probiotic candidate used to treat intestinal infections.

54 - EFFECT OF ORAL BIFIDOBACTERIUM BREVE ON FACIAL SKIN: A RANDOMIZED DOUBLE-BLIND PLACEBO-CONTROLLED STUDY

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Objective:
The benefits of Bifidobacterium such as anti-inflammation and photoprotection are increasingly studied in both mice and humans, yet the full effects are still unknown. In this study, we aim to investigate the effect of oral B. breve M-16V on the facial skin in human.

Methods:
In a randomized double-blind placebo-controlled trial, adult women with no undergoing clinical treatment on face received Bifidobacterium breve M-16V ($1\acute{}10^{10}$ CFU) or placebo orally twice daily for 12 weeks. Facial skin condition was evaluated by dermatologist, Canfield VISIA® evolution and participants, at baseline, 4, 8 and 12 weeks. The primary outcome was the total VISIA® score at each check point. All the other skin parameters were also analysed.

Results:
The data of 120 participants (59 probiotic, 61 placebo) were collected. The mean total VISIA® score was tended small in probiotic group at week12 but did not show statistical difference (p=0.38). The count of brown spots decreased at week4 in probiotic group (p=0.011) while it worsened in placebo at week12 (p=0.001). The brown spot score decreased in probiotic group at week4 (p=0.001) and week8 (p=0.05). The subjective evaluation bowel movement improved in probiotic group at week12 (p=0.006). Adverse events were seen in 37.3%, and its frequency was not statistically different between the groups. No serious adverse events were reported during the trial.

Conclusions:
Oral intake of B. breve M-16V appears to benefit facial skin condition by improving brown spots and bowel movement.

56 - IN VITRO ANALYSIS OF THE BENEFICIAL EFFECT OF THE PROBIOTIC SOY MILK ON CACO-2 CELLS WITH INDUCED INFLAMMATION

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Objective:

Previous studies with Lactobacillus paraplantarum BGCG11 as a probiotic were in fermented milk product, but now we have analyzed the survival of this probiotic strain after simulated gastrointestinal tract (GIT) transition in soy milk and we have tested its ability to ameliorate the damage of induced inflammation in differentiated Caco-2 cells.

Methods:

Probiotic strain BGCG11was grown in soya milk for 16h at optimal growth temperature. This probiotic soy milk and its control, soy milk alone, was subjected to simulated passage through GIT. After this simulation differentiated human intestinal Caco-2 cells were used as a model for inflammation (with TNF-alpha and IL-beta, 10 ng/ml, for 2h). After induced inflammation, Caco-2 cells were treated with probiotic soy milk or with control soy milk for 4h. Total RNA was isolated from all treatments and relative gene expression for IL-8, TGF-beta, claudin, occludin and E-cadherin were analyzed by RT PCR.

Results:

BGCG11 survives the simulated GIT in soy milk, through gastric, duodenum and intestinal passage simulation. More than 23% of cells are recovering at the end of this passage. On Caco-2 cells after inflammation, probiotic soy milk showed a lowering effect on the level of IL-8 and a higher level of TGF-beta, while factors involved in the maintenance of the intestinal barrier kept similar level of relative gene expression as the damaged cells during inflammation.

Conclusions:

Probiotic soy milk is expressing beneficial effect on Caco-2 cells after induced inflammation and further experiments could help us reveal the mechanism(s) of its protective action.

57 - CONTINUOUS TREATMENT WITH LACTOBACILLUS PARAPLANTARUM BGCG11 - INFLUENCE ON ACTIVATION OF VARIOUS METABOLIC PROCESSES AND THE GUT MICROBIOTA COMPOSITION - THE IMPROVEMENT OF HEALTH OF DIABETIC RATS

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Objective:

Our previous studies showed that the probiotic treatment with Lactobacillus paraplantarum BGCG11 may have potential therapeutic benefits for managing diabetes and complications associated with hyperglycemia and damage of liver and kidneys. In this study, we profiled the gut microbiota composition in diabetic rats and identified several associations between bacterial taxa, and metabolic pathways during continuous administration of probiotic prior to and after the induction of diabetes.

Methods:

The albino Wistar rats were orally administered with BGCG11, starting one week before (P/D/P) the injection of streptozotocin, and continuing for four weeks afterward. DNA was extracted from fecal samples, and high-throughput 16S rDNA sequencing was performed. Comparisons of the microbial profiles were conducted using the linear discriminant analysis method.

Results:

During the moment of diabetes induction, 12 bacterial species and 30 bacterial genera were enriched in the P/D/P group. After four weeks of treatment with BGCG11, the enrichment pattern changed. Four bacterial species and 20 bacterial genera were enriched at the end of the treatment period. The results of our study indicate that at the end of the treatment, there was a significant increase in the abundance of taxa associated with enhanced insulin sensitivity, and the production of butyrate, isobutyrate, and isovalerate. Composition of the gut microbiota continued to evolve under the influence of the probiotic treatment.

Conclusions:

These findings suggest that the administration of L. paraplantarum BGCG11 led to positive changes in the gut microbiota composition, favoring the enrichment of bacterial taxa known for their beneficial effects on metabolic health.

61 - SEARCH FOR ACTION FACTORS IN LACTOBACILLI WITH PROBIOTIC PROPERTIES ISOLATED FROM TRADITIONAL KAZAKH FOOD

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Objective:

The relevance of the work is determined by the importance of searching for lactobacilli protein factors that perform adhesive and/or signal functions, by analogy with homologous proteins of pathogenic and commensal/probiotic bacteria and classified as functional factors. The goal is to study the molecular mechanisms of probiotic action implemented with the protein factors produced by probiotic lactobacilli, to solve the problems of creating new synbiotics and postbiotics from traditional Kazakh food products.

Methods:

Protein factors of probiotic action (action factors, AF) were isolated from lactobacilli that live in traditional Kazakh food products and have pronounced probiotic properties. AFs were fractionated from cell-free supernatants of four lactobacilli by saline extraction and column chromatography, then detected by Western blotting, and identified by enzymatic activity.

Results:

The AFs were found to perform adhesive functions like homologous proteins of probiotic bacteria. Three of the AF proteins, namely: ENO, GAPDH, and p66/DNA, are moonlighting proteins of adhesion to mammalian body components human plasminogen and porcine mucin, two proteins are muramidases P40 and P75, and all five proteins are classified as potential probiotic action factors.

Conclusions:

The practical significance of the results of this study lies in the possibility of their application in planning and carrying out activities in the field of ensuring food security in Kazakhstan. The prospects for further research lie in the need to find effective ways to isolate lactobacilli and their action factors from traditional food products to study the intestinal microflora and improve the quality of bacterial diagnosis of diseases of the gastrointestinal tract.

63 - ENGRAFTMENT AND MICROBIOTA INFLUENCES OF A WELL CHARACTERIZED MULTI-STRAIN NOT GASTRO-PROTECT PROBIOTIC IN HEALTHY VOLUNTEERS: A PRELIMINARY STUDY

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Objective:

Probiotics are commonly prescribed in clinical practice, although their use is only partially supported by current medical literature. We tested a well characterized commercial multi-strain probiotic mix (Prolife 10 Forte) (2 strains of Bifidobacteria, B. coagulans BC4 and 7 strains of Lactobacillus) to evaluate its metabolic pathways, the engraftment of its strains and its influence on faecal microbiota of healthy recipients.

Methods:

The multi-strain probiotic supplement was administered in not-gastro-protected blend (in vials) to 24 healthy volunteers divided by age (20-40, 41-59 and over 60years), at the dose of 1x1010 cfu/die for 20 days. Faecal samples were collected before administration (T0), after 21 days (T1) and 28 days from baseline (T2), analysed using Real Time-PCR and rRNA16S analysis. The same mix compound was analysed by metagenomic analysis (shot-gun sequencing) to determinate the potential metabolic pathways.

Results:

The multi-strain probiotic showed 324 potential metabolic pathways, including those associated with the enhancing of biosynthesis of deoxyribonucleotides, amminoacids, vitamins and SCFA. The RT-PCR showed a significant increase of all strains at T1 vs T0 and a relative increase of bifido-strains at T2 vs T0. The faecal microbiota analysis showed a persistence of probiotic-strains (Bifidus, Bacillus and Lactobacillus) in T1 vs T0 but also up toT2 in the older group and a SCFA producer (Cutibacterium acnes) as differentially abundant. A modulation of bacterial markers (A. muciniphila) of intestinal well-being was also observed.

Conclusions:

Prolife 10-Forte actively reaches the intestine by positively modulating the intestinal microbiota.

66 - EXPLORING HUMAN MILK OLIGOSACCHARIDE UTILISATION BY COMMERCIAL PROBIOTICS USING COMBINED GENOTYPE/ PHENOTYPE STRATEGIES

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Objective:

Human Milk Oligosaccharides (HMOs) are complex sugars found in breastmilk with proven health benefits for the developing infant. HMOs are resistant to gastrointestinal digestion and instead supply metabolic substrates necessary for beneficial bacteria in the intestinal tract. Several members of the infant associated Bifidobacterium genus have been shown to utilise HMOs as their sole carbon source, however, utilisation by other early colonizers is less explored. This study aimed to genotypically and phenotypically characterise the HMO utilisation of 23 clinically documented, commercial probiotic strains, including Bifidobacterium, Lactobacillus and Pediococcus strains, using a blend of 8 commercially available HMOs.

Methods:

Genome profiling was used to predict HMO utilisation capabilities by identifying glyco-genes including enzymes and transporters that may be involved in probiotic HMO utilisation. Phenotypic profiling included growth analyses, preferential HMO utilisation through the use of High pH Anion Exchange Chromatography with Pulsed Amperometric Detection and metabolomics analysis using High Pressure Liquid Chromatography with Refractive Index detection.

Results:

Our findings highlighted the growth of several commercial probiotic strains on the HMO blend with preferential utilisation and strain-specific superior growth observed for four infant-associated Bifidobacterium species. Individual HMO consumption revealed inter-species preferential utilisation of structures as well as strain-specific variation among members of the same species. HMO utilisation varied from >95% of available HMOs by B. bifidum and B. infantis strains, to <5% for several Lactobacillus species and the Pediococcus strain.

Conclusions:

This research gives insight into the complex relationship between HMOs and infant associated bacteria in the early stage of life.

68 - OBTAINING BIFIDOBACTERIUM ANIMALIS PARAPROBIOTIC THROUGH OHMIC-HEATING AND THE ASSESSMENT OF HEALTH BENEFITS

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Objective:

Paraprobiotics are recognized as inactivated form of probiotics, which different types of health promoting benefits (HPBs) have been reported for them. The aim of this study was the obtaining paraprobiotic from Bifidobacterium animalis Bb-12 (BB) with the highest HPB through ohmic heating (OH).

Methods:

Response surface methodology (RSM) was employed to optimize OH factors, including electric field, OH temperature, cell concentration, and OH time. The optimization was done based on properties of obtained BB paraprobiotics (BBP) including cell surface hydrophobicity (CSH), cell auto- and co-aggregation (CAA and CCA) by spectrophotometer, and membrane integrity (MI) by flow cytometery.

Results:

The linear model was more accurate for CCA and MI, and the quadratic model for other responses. The electric field had the most effect on the MI of BBP; however, for other responses this was for OH temperature. The surface characteristics (CSH, CAA, and CCA) of BBP obtained by OH were more than BB (control). The surface characteristics were increased as OH electric field and OH temperature increased. This could be attributed to thermal and electroporation effects of OH, which are considered as the main OH mechanisms and change the cell permeability by destruction of membrane structure and making pore in its structure. The changes in the membrane structure were confirmed by SEM analyses.

Conclusions:

The OH treatment including electric field of 8 V/cm, OH temperature of 88 °C, cell concentration of 8 log CFU/ml, and OH time of 3 min was considered as optimum OH condition to prepare BBP.

69 - PREBIOTICS AND SYNBIOTICS IN NILE TILAPIA FEED AND THEIR PROTECTION AGAINST STREPTOCOCCUS AGALACTIAE INFECTION

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Objective:

The use of probiotics, prebiotics and synbiotics provides protection against several bacterial pathogens. This study evaluated the potential probiotics (Limosilactobacillus fermentum SJRP43, Lactobacillus delbrueckii subsp. bulgaricus SJRP57 and Lacticaseibacillus casei SJRP145), combined with the prebiotic banana pseudosteam fiber (BPF) to promote protection of Nile tilapia (Oreochromis niloticus) against Streptococcus agalactiae infection.

Methods:

The experimental design consisted of four treatments: the control group (T1) received a basal diet without probiotics or prebiotics; the other treatment groups (T2, T3, and T4) received the basal diet supplemented with different active components. In T2, the prebiotic BPF was added (4.0 g/kg feed). In T3, the prebiotic BPF (4.0 g/kg feed) was combined with potential probiotics (L. fermentum SJRP43, L. delbrueckii subsp. bulgaricus SJRP57, and L. casei SJRP145, at dosages of $7.0x10^{10}$, $5.0x10^{7}$, and $6.4x10^{12}$ CFU/g feed, respectively). In T4, the prebiotic BPF (4.0 g/kg feed) was combined with commercial probiotics (Bacillus cereus var. toyoi and Bacillus subtilis, both at dosages of $4.0x10^{13}$ CFU/kg feed). The fishes were fed four times/day for 70 days. Subsequently, an experimental infection assay was conducted with S. agalactiae ($1,7x10^{4}$ CFU/g fish). The effect of the treatments was evaluated by the relative protection level (RPL).

Results:

T3 reduced the fish mortality when infected with S. agalactiae, as evidenced by a higher RPL of 46.00%, while T2 showed 6.00% RPL. However, T4 exhibited a higher mortality rate compared to T1.

Conclusions:

The inclusion of potential probiotic strains and prebiotic BPF in fish feed reduced the mortality caused by S. agalactiae.

73 - THIRD-PARTY CERTIFICATION: A TOOL TO ASSURE QUALITY AND IMPROVE CONSUMER TRUST IN PROBIOTICS

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Objective:

The quality of probiotic products is often debated. Several surveys on probiotic formulations present on worldwide market had shown that species identification as well as number of viable cells may not be exactly as shown on the labels. In order to increase end-user and professional confidence in probiotic quality, a process for a third-party certification of probiotic viability was developed.

Methods:

The certification scheme was created taking into account the European Accreditation Document EA 1/22 - "EA Procedure and Criteria for the Evaluation of Conformity Assessment Schemes by EA Accreditation Body Members".

Results:

The certification conformity is obtained when the product is in compliance with a technical scheme (DTP 118) promoted and approved by an accredited independent certification body. The requirements of the scheme are based on the Italian Guidelines on Probiotics and Prebiotics, rev. 2018 but with a more restrictive tolerance between the number of viable cells reported on the label and the values determined through analysis. Other necessary components of the scheme include: the availability of validated analytical methods, the organization of stability tests (accelerated and on-going), the audits by the certification body on quality system and all the critical aspects closely associated with the quality and viability of probiotics, the product testing by an accredited laboratory in order to verify the compliance with information reported on the labels.

Conclusions:

The third-party certification scheme here developed can be applied by the industry to manage the quality of probiotic formulations and enhance consumer and professional trust in probiotics.

75 - INTERSPECIES INTERACTION OF LACTIPLANTIBACILLUS PLANTARUM BGPKM22 STRAIN AND PRIMARY HUMAN BRONCHIAL EPITHELIAL CELLS STIMULATES THE SYNTHESIS OF EXOPOLYSACCHARIDE LAYER

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Objective:
The objective of this study was to investigate the effects of primary human bronchial epithelial cells (NHBE) on Lactiplanibacillus plantarum strain BGPKM22.

Methods:
Co-incubation experiments were conducted by co-culturing NHBE cells with Lactiplanibacillus plantarum strain BGPKM22. Subsequent analyses included differential gene expression (DEG) analysis, RT-PCR, and transmission electron microscopy (TEM).

Results:
Dual-RNA sequencing revealed 486 DEGs in L. plantarum strain BGPKM22 during co-incubation with NHBE cells. Among these DEGs, 265 genes were up-regulated while 221 genes were down-regulated. Notably, three glycosyl transferase genes associated with exopolysaccharide (EPS) biosynthesis were identified as up-regulated genes. RT-PCR confirmed these findings and validated two additional EPS biosynthesis genes, cps4A and cps4D. TEM imaging demonstrated the formation of a thicker EPS layer resulting from the interaction.

Conclusions:
While certain Lactobacillus spp. strains may naturally reside in the respiratory tract and contribute to respiratory health, L. plantarum is not known to be a lung commensal. The increased synthesis of EPS in response to environmental changes may reflect a stress response in this strain. Lactobacilli-produced EPS exhibits potential anti-inflammatory properties, suggesting its role in alleviating inflammation in specific conditions. Moreover, EPS facilitates the adherence of Lactobacillus spp. to epithelial cells, promoting the establishment of a healthy microbiota. Although co-incubation of NHBE and BGPKM22 may induce stress in the bacterial strain, the resulting effects of these strain on lung health could be beneficial. Further research is necessary to fully understand the immunomodulatory and therapeutic implications of this interaction in the context of respiratory health.

76 - EFFECT OF PARAPROBIOTIC L. PLANTARUM BGAN8 ON MITOCHONDRIAL FUNCTION IN HT-29 CELLS

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Objective:
The objective of this study was to investigate the impact of kanamycin treatment and UV inactivated bacteria on TMRE fluorescence staining and mitochondrial gene expression in HT-29 cells. The research builds upon a transcriptomic analysis indicating that UV-inactivated bacteria increase the expression of complex I mitochondrial genes.

Methods:
HT-29 cells were subjected to two treatments: kanamycin treatment (25 µg/ml) and exposure to UV inactivated L. plantarum BGAN8 (bacteria:eukaryotic cell ratio 100:1). The cells were stained with TMRE to assess mitochondrial membrane potential and fluorescence intensity. Additionally, real-time PCR was performed to evaluate the expression levels of mitochondrial genes.

Results:
Kanamycin treatment led to a significant decrease in TMRE fluorescence intensity, indicating a disruption in mitochondrial membrane potential. In contrast, treatment with UV inactivated bacteria reversed the effect of kanamycin, restoring TMRE fluorescence to levels like control cells. Moreover, the expression of mitochondrial genes was down-regulated following kanamycin treatment, while treatment with UV inactivated bacteria attenuated this down-regulation and brought the gene expression levels closer to those of control cells, consistent with the transcriptomic analysis.

Conclusions:
Our findings demonstrate that treatment with UV inactivated bacteria counteracted the negative effects of kanamycin on TMRE staining and mitochondrial gene expression in HT-29 cells, suggesting a potential protective role of our paraprobiotic on mitochondrial function. These results support the transcriptomic analysis indicating that UV-inactivated bacteria increase the expression of complex I mitochondrial genes. Understanding the interplay between antibiotic treatment, bacterial interactions, and mitochondrial health is critical for developing strategies to preserve mitochondrial function and cellular homeostasis.

91 - A NEW APPLICATION OF BIOTICS IN SKIN HEALTH: SKINBACTM BEAUTY

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Objective:

Recently, increasing evidence suggests the topical application of biotics as potential care product with considerable benefits for skin. Aim of this work was the evaluation of safety and efficacy, in vitro and in vivo, of Skinbac strains, to unravel their potential in skin health.

Methods:

Heat-treated probiotic strains L. plantarum SKINBAC™ SB01 and B. lactis SKINBAC™ SB05, namely Skinbac Beauty™, were evaluated on Normal Human Epidermal Keratinocytes (NHEK) by in vitro experiments. Safety was determined by MTT and LDH assays, efficacy was proved by studying: aquaporin3, claudin1 (CLND1) and occludin (OCLN) expression, Reactive Oxygen species (ROS) reduction, cytokines as Tumor Necrosis Factor-alpha (TNF-α), Interleukin6 (IL-6), Interleukin8 (IL-8) and Interleukin23 (IL-23) modulation, and pathogen inhibition. Additionally, Skinbac Beauty™, put as unique active ingredient in a face cream, was investigated in vivo by evaluating the following skin parameters: skin deep hydration, skin roughness, skin elasticity and skin density.

Results:

In vitro, Skinbac Beauty™ has resulted effective in increasing aquaporin3 expression (+22% vs untreated cells – $p<0.05$), in reducing ROS (-32% vs untreated cells – $p<0.05$), in increasing CLDN1 (+9% vs damaged cells – $p<0.05$) and OCLN (+5% vs damaged cells), in pathogen inhibition by reducing Staphilococcus aureus growth and biofilm, and in modulating cytokines as TNF-α, IL-6 and IL-8. In vivo, statistically significant improvements have been obtained in skin deep hydration, skin elasticity and skin density.

Conclusions:

Results demonstrate that Skinbac Beauty™ has different beneficial skin properties as important role in the maintenance of barrier regulation and integrity, and moisturizing, antioxidant and antipathogen effects suggesting their potential in skin health.

92 - STIMULATION OF PROBIOTIC BIFIDOBACTERIUM STRAINS BY HUMAN MILK OLIGOSACCHARIDES (HMOS) FOR THE DEVELOPMENT OF SYNBIOTIC FORMULAS

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Objective:

This work aims at assessing the ability of four probiotic strains, Bifidobacterium bifidum (DSM 33678) BB10, Bifidobacterium breve (DSM 16604) BR03, Bifidobacterium infantis (DSM 24687) BI02, Bifidobacterium longum (DSM 16603) BL03, to metabolize and grow on synthetic Human Milk Oligosaccharides (HMOs) (GlyCare™, DSM) to evaluate the feasibility in the development of a synbiotic finished formula.

Methods:

Strains were inoculated on de Man Rogosa Sharp supplemented with 2% (w/v) glucose or 2% (w/v) of each of the following HMOs: 2'-Fucosyllactose (2'-FL), 3'-O-Sialyllactose (3'-SL), 6'-O-Sialyllactose (6'-SL), Lacto-N-tetraose (LNT), Lacto-N-neotetraose (LnNT), 2'-Fucosyllactose/Difucosyllactose (2'-FL/DFL mix). The response of Bifidobacterium strains was studied in terms of a) metabolic activity by microcalorimetry (calScreener™, Symcel), b) growth by cytofluorimetric enumeration (Cytoflex, Beckman Coulter) and c) acidification kinetics (iCinac, AMS Alliance).

Results:

The strains metabolized HMOs with a species (strain) specific pattern. In particular, LNT and LNnT were efficiently assimilated by all the strains and specifically for BL03 and BB10 the growth was boosted over glucose. Furthermore, all the Bifidobacterium strains with exception of BB10 showed limited capability to grow on sialylated HMOs, while fucosylated HMOs were selectively utilized by BB10 and BI02. Noteworthy, results showed that not in all the conditions a higher metabolic activity was correlated with enhanced acidification and growth performances.

Conclusions:

This study discovers specific associations between HMOs and Bifidobacterium strains. This represents the first advancement in the development of innovative synbiotics and set the bases for further studies aimed at investigating beneficial effects derived from the administration of Bifidobacterium strains and HMOs.

106 - THE EFFICACY OF SINGLE-STRAIN PROBIOTIC FORMULATIONS CONTAINING BIFIDOBACTERIUM LACTIS BI040 OR BACILLUS COAGULANS BC300 IN ADULT PATIENTS WITH IRRITABLE BOWEL SYNDROME

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The Children's Memorial Health Institute, Department of Pathomorphology, Warsaw, Poland [(1)] - Medical University of Lublin, Department of Gastroenterology, Lublin, Poland [(2)] - Medical University of Lublin, Department of Health Promotion, Lublin, Poland [(3)]

Objective:

Probiotics offer a potential therapeutic approach for irritable bowel syndrome (IBS). The aim of this study was to assess the efficacy of the single-strain probiotic formulation in adult IBS patients, and to compare the effects of Bifidobacterium lactis NORDBIOTIC™ BI040 and Bacillus coagulans NORDBIOTIC™ BC300 in the three arms prospective randomized placebo controlled trial.

Methods:

The study included 123 IBS subjects diagnosed according to Rome IV criteria. The primary out-comes were changes in symptoms severity and clinical improvement assessed with the IBS Severity Scoring System (IBS-SSS) after 4, 8 and 12 weeks of intervention, and after 4 weeks of follow-up. Secondary outcomes included the assessment of individual IBS symptoms and the occurrence of adverse events [ClinicalTrial.gov NCT05064930].

Results:

During the 12-week intervention, IBS-SSS scores significantly decreased (p-values<0.001) in study groups, and at 16th week of follow-up a significant improvement in the total IBS-SSS score in comparison to the placebo group (20.5%) was found in 43.8% and 52.9% of the Bifidobacterium lactis (p=0.038, OR 3.0, [95%CI 1.1-8.6]) and in of the Bacillus coagulans (p=0.005, OR 4.6 [95%CI 1.5-12.2]) groups, respectively. Bifidobacterium lactis beneficially affected the intensity and frequency of pain, whereas Bacillus coagulans the dissatisfaction from the bowel. Both strains increased the percentage of patients with normal stool consistency after 6 weeks of intervention.

Conclusions:

A single strain supplementation was safe and efficient in IBS patients, but in a different range of effects. Bifidobacterium lactis BI040 reduced the sensation of pain, while Bacillus coagulans BC300 increased bowel satisfaction.

118 - EFFECTS OF PROBIOTIC B. SUBTILIS CU1 ON MUCOSAL AND PERIPHERAL IMMUNE SYSTEM

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Gnosis By Lesaffre, Research and Applications Department, Marcq-en-Baroeul, France [(1)] - NIZO, Department of Nutrition and Health, Ede, Netherlands [(2)]

Objective:

B. subtilis CU1 (BSCU1) has been shown effective in stimulating immune responses in elderly subjects. To further assess the effects of BSCU1 on mucosal and peripheral immune system, an innovative approach combining duodenum-intestine chip model integrating immune cells and an exploratory clinical trial were conducted.

Methods:

The impact of BSCU1 on cytokines secretion was evaluated in vitro using a Duodenum Intestine-Chip model combined with peripheral blood mononuclear cells (PBMCs). Furthermore, an exploratory clinical trial was conducted in 3 different age groups. A range of immune assays were rationally selected to assess the impact of probiotic supplementation on immune function, including basal serum cytokine levels and ex vivo cytokine levels in LPS-stimulated whole blood ; gene expression in PBMCs. The impact of probiotic supplementation on fecal microbiota composition was analysed using shotgun sequencing.

Results:

In vitro challenge with BSCU1 resulted in transient immune modulation as shown by significant increase of TNF-alpha, IL-1beta and IL-8.
BSCU1 treatment significantly reduced basal levels of most of measured serum cytokines (IL-10, TNF-alpha, MIP-1alpha, IL-8) in the elderly. Furthermore, BSCU1 intervention significantly increased ex vivo release of cytokines following LPS challenge (IL-1beta, IL-6, IFN-gamma, IL-12, TNF-alpha, MIP-1alpha, IL-8). Interestingly, probiotic intervention resulted in a significant enrichment in clusters of genes involved in phagocytosis pathway. Overall, gut microbiota composition was not affected.

Conclusions:

Combined approach of duodenum-intestine chip model and exploratory clinical trial displayed local and peripheral innate immunomodulation after BSCU1 intervention. Furthermore, gene expression analyses suggested a potential impact of BSCU1 intervention on phagocytic activity.

123 - A REAL-WORLD STUDY ASSESSING BACILLUS CLAUSII FOUR-STRAIN PROBIOTIC USAGE, TREATMENT OUTCOMES AND PATIENT SATISFACTION IN ITALIAN COMMUNITY PHARMACIES

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Objective:

To evaluate the usage of Bacillus clausii probiotic among self-medicating patients at Italian community pharmacies, their treatment habits, and perceived benefits.

Methods:

This multicentre, prospective, non-interventional study included two visits (screening [T0] and end of study [T1]). Patients who were already inclined to buy B. clausii were enrolled, instructed to complete a questionnaire (at T0 and T1) and were asked to return to the pharmacy when symptoms had subsided (T1) and within 30 days after T0. The primary objective was to evaluate the reasons for taking B. clausii. Secondary objectives assessed treatment duration, perceived effectiveness, quality-of-life (QoL), treatment satisfaction and safety outcomes.

Results:

Overall, 268 patients were enrolled: 99.6% of which were evaluated at T0, 97.4% at T1 while 97.8% that had ≥ 1 dose of B. clausii were assessed for safety. At T0, average age was 50.7 years and majority were females. In the 12 months before enrolment, all patients reported at least one gastrointestinal symptom, most commonly being diarrhea (58.8%), abdominal pain (23.2%), and bloating (16.1%). Over 90% perceived their symptoms to have improved or improved very much. QoL improved in every aspect measured. Roughly 90% were satisfied, very satisfied or extremely satisfied. No adverse events were reported.

Conclusions:

This is the first pharmacy-based study in Italy offering real-world insights on usage of probiotics like B. clausii among self-managing adult patients. Most patients adhered to the leaflet information. Diarrhea was the most common reason for using B. clausii probiotic, with high-level of perceived effectiveness and patient satisfaction.

126 - TITAN PROJECT: TRANSPARENCY SOLUTIONS FOR TRANSFORMING THE FOOD SYSTEM - FOCUS ON THE PILOT RELATED TO BENEFICIAL MICROBES

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Objective:

TITAN is an Horizon Europe project started in September 2022 which aims to develop tools to enhance transparency in the food and supplements supply chains, providing tools to authenticate and trace ingredients, foods, plant extracts and supplements. TITAN is composed of 27 partners, developing 15 "pilots" which are innovative solutions organized in 3 main chapters: Food Safety, Sustainability and Health (to know more https://titanproject.eu/). Pilots are based on innovative technologies such as DNA Next-Generation-Sequencing, Blockchain, Internet of Things and Artificial Intelligence applied to rapid analysis and trace foods in order to collect and make easily accessible all the relevant information about its origin, authenticity, quality and safety.
Among the pilots developed in TITAN, the ST4.1c is focusing on rapidly ensuring the presence and viability of the microbial species indicated in products label. Products categories for the validation of this pilot solution includes: probiotic food supplements, fermented foods and foods with added microbes (functional foods and bio-protection cultures).

Methods:

The analytical methods used for the ST4.1c pilot is the DNA Next Generation Sequencing with metabarcoding approach. The project will overcome the issues and limitations related with the low resolution provided by the standard molecular marker used for bacteria identification, the 16S rRNA gene. The working group is going to adapt the standard protocols designed and validated for the Oxford Nanopore sequencing device in order to amplify and sequence a new class of molecular markers, the HPME markers, known to be able to provide much more resolution among the bacteria species most used in probiotic products and fermented foods, namely those belonging to the Lactobacillales oeder e the Bifidobacteriun genus and the Bacillus genus.
The amplification and sequencing protocols under development are going to be coupled with a database of HMPE markers DNA sequences of all the relevant species and strains, providing together a tool to rapidly compare and match the DNA sequences retrieved from the samples.

Results:

The ST4.1c pilot of TITAN will provide to the probiotic e fermented foods supply chains a tool to rapidly asses the correct composition of multi-strain products including cultures bulks, finished products and foods where they are added. ST4.1c pilot of TITAN will allow to overcome the current issues related to the quality control of multi-strain products, the stability during shalef-life and the emerging need to incicate on product label the concentration of each strain in the formulation (not only the total one).

Conclusions:

The ST4.1c pilot of TITAN is calling industries to propose case studies of multi-strain products where current analytical methods fail in

determining the microbial composition and where the new solution can be tested and validated.
The TITAN project is calling all the experts in the filed to join the project Stakeholders Board in order to discuss the project milestones, provide their valuable advices and guide the development of the ST4.1c pilot toward a more transparent supply chain of microbes for probiotic food supplements, for fermented foods and for foods with added microbes. In order to propose them-self candidates are requested to apply at https://titanproject.eu/stakeholder-board/ or to contact the poster authors.

136 - THE BENEFICIAL EFFECT OF PROBIOTICS IN PREVENTING IRINOTECAN-INDUCED DIARRHEA IN COLORECTAL CANCER PATIENTS WITH COLOSTOMY: COMBINED ANALYSIS OF TWO PROBIOTICS TRIALS

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Objective:
The incidence of irinotecan-induced diarrhea varies between 60-90%. Probiotics (PRO) could decrease it due to a reduction of intestinal beta-d-glucuronidase activity. This study included a combined analysis of two clinical trials aimed to determine the effectiveness of the probiotic in the prophylaxis of irinotecan-induced diarrhea in metastatic colorectal cancer (CRC) patients.

Methods:
This combined analysis included 46 patients with CRC enrolled in the Probio-SK-003 (NCT01410955) and randomized 1:1 to probiotic formula colon Dophilus™ that contains 6 probiotic strains or placebo (PLA). The second study (Probio-SK-005, NCT02819960) included 233 patients with identical eligibility criteria as the previous trial, randomized 1:1 to PLA or probiotic formula Probio-Tec BG-Vcap-6.5, that contains 2 lyophilized probiotic strains Bifidobacterium, BB-12 (50%) and Lactobacillus rhamnosus GG, LGG (50%).

Results:
Totally 279 patients were randomized (PLA 142, PRO 137). Administration of probiotics compared to placebo was not associated with a statistically significant reduction of grade 3/4 diarrhea (PLA 12.7% vs. PRO 6.6%, p = 0.11), neither the overall incidence of diarrhea (PLA 48.6% vs. PRO 41.6%, p = 0.28) nor the incidence of enterocolitis (PLA 4.2% vs. 0.7%, p = 0.12). However, subgroup analysis revealed that patients with colostomy that

received a placebo had a significantly higher incidence of any diarrhea (PLA 51.2% vs. PRO 25.7%, p = 0.028) and grade 3/4 diarrhea (PLA 14.6% vs. PRO 0.0%, p = 0.03) compared to the probiotic arm.

Conclusions:
This combined analysis suggests that probiotics could be beneficial in preventing irinotecan-induced diarrhea in colorectal cancer patients with colostomy.

149 - EFFECT OF PROBIOTIC SUPPLEMENTATION ON T2D: SYSTEMATIC REVIEW AND META-ANALYSIS

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Bachir Nour University Center, Faculty of Sciences, Department of Biology, El-Bayadh, Algeria [(1)] - Djillali Liabes University, Faculty of Natural Science and Life, Department of Biology, Sidi-bel-abbes, Algeria [(2)]

Objective:
The aim of the study is to evaluate the effect of probiotic supplementation on T2D.

Methods:
Articles were searched in Science Direct, Springer-Link, Nature and ProQuest from 2020 to April 2023. Articles were screened for eligibility, data were extracted, risk of bias was assessed, and meta-analyses were performed. Data were pooled using the random-effects model and expressed as standardized mean difference (SMD) with 95% confidence interval (CI). Heterogeneity was assessed and quantified (I2).

Results:
Seven (7) randomized controlled trials were included out of 913. Fasting blood glucose (FBG) (n=504) and glycosylated hemoglobin (HbA1c) (n=504) were collected in 7 studies; lipid profile (n=368) was collected in 5 studies; body mass index (n=272) was collected in 3 studies; homeostasis Model of Assessment of Insulin Resistance Index (HOMA-IR) (n=386) was collected in 3 studies; 2-hour postprandial blood glucose (n=275) was collected in 2 studies. Probiotics can significantly reduce FBG (SMD-0.35 mmol/L, 95% CI [-0.53,-0.18], I^2= 0%, P < 0, 0001) and HbA1c (SMD -0.30mmol/L, 95% CI [-0.52,-0.099], I^2=29%, P=0.006). No significant reduction was observed for: HOMAIR, TG, TC, HDL, LDL, BMI, 2hrPPG.

Conclusions:
Probiotics may improve glycemic control in patients with T2D. The use of probiotic agents may become a new method of glucose management in T2D.

150 - NOVEL PROBIOTICS FORMULA CONTAINING HYDROXYECTOINE FOR PRESERVING THE VIABILITY AND ENHANCE THE BIOLOGICAL ACTIVITY OF PROBIOTICS ON ENTEROCYTE BASED IN VITRO MODEL

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Objective:

Dysbiosis is commonly detected in patients with inflammatory bowel disease (IBD), supporting the concept that a dysregulated immune reaction to bacterial antigens has a pathogenic role in the development of intestinal inflammation (Fusco et al., 2023). We have investigated the beneficial effects of a novel probiotic formulation obtained by combining three probiotic biomasses (Lactobacillus fermentum, Lactobacillus brevis and Bifidobacterium lactis) with hydroxyectoine (HOE), before liophylization. HOE is a compatible solute, produced in high yield by halophilic microorganisms, that showed bioactivity in cryopreservation, as anti-inflammatory compound (Bethlehem & van Echten-Deckert, 2021).

Methods:

Briefly the three probiotics strains were lyophilized after the addition of HOE solution, and their viability were assessed after lyophilization, storage up to 6 months and after the exposure to simulated gastrointestinal juices. The anti-inflammatory ability of this formula was also investigated using differentiated enterocytes. These were challenged with LPS to induce cell inflammation alone or in the presence of a mixture of the three probiotics formulated with HOE.

Results:

The result showed the ability of HOE in preserving the viability of probiotics during lyophilization, subsequent storage and during the exposure to simulated gastrointestinal fluids. Moreover, adding HOE to probiotics improved the beneficial effects of the bacterial therapy by reducing the protein expression of TLR-4 and NF-Kbeta, reducing the expression of pro-inflammatory mediators including IL-6, IL-1beta and TNF-alpha. Interestingly, this formula also counteracted the loss of Zonulin (ZO-1) which was reduced in the presence of the sole LPS.

Conclusions:

In summary, we have shown that a novel three probiotics strains combined with HOE exerts beneficial effects on preserving probiotic`s viability during production and simulated digestion. Also this formula showed their potentialities as nutraceuticals to alleviate intestinal inflammation and improve mucosal barrier function.

158 - PREBIOTICS, PROBIOTICS, AND POSTBIOTICS TO ADOLESCENTS IN METABOLIC SYNDROME

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Objective:

The prevalence of childhood and adolescent obesity has globally reached alarming dimensions and many adolescents affected by obesity already present one or more obesity-related comorbidities. In recent years, emerging evidence supporting the role of gut microbiota in the pathophysiology of metabolic diseases has been reported and the use of prebiotics, probiotics, and postbiotics as a strategy to manipulate gut microbiota has become popular. The aim of this review is to explore the relationship between gut microbiota and metabolic syndrome in adolescents and to discuss the potential use of prebiotics, probiotics and postbiotics for the prevention and treatment of this clinical picture in adolescence.

Methods:

this is a narrative review.

Results:

According to the most recent literature, prebiotics and probiotics have no clear effect on MetS parameters, while only one study has examined the role of postbiotics in alleviating metabolic complications in children with obesity.

Conclusions:

More extensive research is needed to support the conclusions drawn so far and to develop effective microbiome-based interventions that may help improving the quality of life of children and adolescents exposed to the increasing prevalence of MetS.

163 - LACTOBACILLI AS CANDIDATE - PROBIOTICS FOR AQUACULTURES

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Objective:
Today the aquacultures, as food production method, are one of the most promising to meet global food demands. Due to the specificity of the habitats, however, they are under high stress conditions, which leads to increased susceptibility to diseases. New biocontrol agents are being sought. Probiotics are among them. The aim of present study was to design and complete of panel of assays for selection of candidate-probiotic lactobacilli, with health benefits for fish farming.

Methods:
In vitro model, based on the sequential effect of different factors simulating aqua systems was designed and the viability and biofilm of several lactobacilli was monitored. The effects on the fish pathogens growth and biofilms, formed were estimated by agar diffusion and crystal violet methods, respectively.

Results:
In vitro assays allow to pre-select 8 active Lactobacillus strains. They possessed strain-specific broad spectrum of activity against dangerous fish pathogens from the genus Yersinia spp, Aeromonas, Shevanella, Chryseobacterium. Their postmetabolites, produced in variable food matrices, inhibit the replication of Koi herpesvirus VR-1592 (strain F-347). The virucidal effect against extracellular KHV virions is also marked in combination with specific cytotoxic effects on CCB cells. A Lactiplantibacillus plantarum strain was selected for their high survival in conditions simulating real freshwater habitats and was applied in vivo.

Conclusions:
The in vitro tests in model systems are necessary step for functionality characterization and safety of active lactobacilli, as a base for further in vivo assessment and implementation as aquaprobiotics.

166 - ANTI-TUBERCULOUS EFFECT OF THE PROBIOTIC PMC STRAIN IN THE EXTENSIVELY DRUG-RESISTANT PULMONARY TUBERCULOSIS MOUSE MODEL

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Objective:
Tuberculosis is one of the highly contagious diseases caused by Mycobacterium tuberculosis. To fight antibiotic-resistant tuberculosis, it is necessary to develop a new anti-tuberculosis therapeutics concept that can overcome existing drug limitations.

Methods:
Anti-tuberculosis activity was performed in a lethal and latent pulmonary tuberculosis mouse model infected with an extensively drug-resistant (XDR) strain. Microbiome and inflammatory profile analysis in the lung microenvironment in vitro were evaluated.

Results:
Here, we report the anti-tuberculosis effect of a PMC probiotic strain isolated from kimchi, a traditional Korean fermented food. Inhalation administration of probiotic strain to mice led to a 100% survival rate in a lethal XDR (extensively drug-resistant tuberculosis) pulmonary tuberculosis model and a reduction in intrapulmonary M. tuberculosis burden in a latent tuberculosis model. Metagenomics analysis of the extracted lung showed that this probiotic strain reduced Mycobacterium and restored the disrupted lung microflora.

Conclusions:
These results suggest that PMC strain could be developed as an alternative to the current drug regimen to solve the drug-resistant tuberculosis problem.

169 - SURVIVAL OF CANDIDATE - PROBIOTIC LATOBACILLI IN DYNAMIC MODEL OF GUT TRANSIT

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Objective:

To exert their beneficial effect, it is considered that at the time of consumption, the probiotics need a high viable count. In this regard, a dynamic model was developed to evaluate in vitro transit tolerance of Lactiplantibacillus plantarum isolated from Bulgarian traditional milk product – "katak". The aim was to achieve an in vitro simulation of transit through the gastrointestinal tract (GIT) of the strains and to assess their probiotic potential.

Methods:

In vitro model, based on the sequential effect of different factors of the GIT simulating upper and lower GIT was used. The activity of the L. plantarum were evaluated after a passage simulating the real pathway of transiting probiotic cultures. Viability was counted by classical microbiological methods on selective media MRS and Rogosa agar. The effects on the biofilms formed were estimated by crystal violet method.

Results:

A strain-specific survival and activity of each stage of the GIT model was shown for 12 pre-selected lactobacilli. At 180 min in gastric juice, a viable cell reduction of about 1 log was observed. Survival remained high (in the range of 80-93%) for all strains. Significantly higher resistance was observed during the following passage in intestinal juice under bile salt and pancreatic treatment. Recovery in viability occurs during passage in the terminal sections of the GIT, where the pH is alkaline. The capacity of protective biofilms formation and pathogens' inhibition were not significantly affected.

Conclusions:

Tested lactobacilli from katak revealed high transit tolerance with activity in simulated gut passage.

177 - IMMUNOBIOTIC LACTIPLANTIBACILLUS PLANTARUM MPL16 AND CRL1506 ENHANCE RESISTANCE TO ENTEROCOCCUS FAECALIS INFECTION IN VIVO

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Objective:

To evaluate the impact of Lactiplantibacillus plantarum MPL16 and CRL1506 feeding on the longevity of Caenorhabditis elegans and their ability to enhance resistance against Enterococcus faecalis infection in malnourished mice.

Methods:

Caenorhabditis elegans were fed with probiotics for 24 hours and then infected with E. faecalis 102. Survival rate was monitored daily, and bacterial counts were assessed. Intestinal distention was examined using transmission electron microscopy. BALB/c mice were subjected to a hypo-proteic diet for 21 days, followed by 7 days of re-nourishment with a conventional balanced diet or a diet supplemented with probiotics. Subsequently, mice were intraperitoneally challenged with E. faecalis 102. After 48h, CFUs were counted in various tissue samples.

Results:

Feeding C. elegans with L. plantarum MPL16 or CRL1506 increased their lifespan by approximately 20%, while E. faecalis feeding reduced their survival and affected their offspring. Pre-treatment of nematodes with CRL1506 and MPL16 delayed the onset of infection-related lethality (L50) by 24 hours and 48 hours, respectively, compared to the control group. MPL16 treatment resulted in a 1 log reduction in enterococci CFU/mL and restored reproductive capacity affected by enterococcal infection. In malnourished mice, probiotic supplementation significantly improved resistance to E. faecalis infection, evident from reduced CFU counts in intestinal lavage, feces, liver, spleen, and blood samples.

Conclusions:

The immunobiotic strains MPL16 and CRL1506 hold promise in preventing E. faecalis infections in susceptible hosts, as demonstrated in both the C. elegans and malnourished mouse models. These strains are potential candidates for future therapeutic interventions.

187 - FUNCTIONAL AND PROBIOTIC PROPERTIES OF LEUCONOSTOC MESENTEROIDES SJC113 PRODUCING EXOPOLYSACCHARIDES

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Objective:

This study was conducted to evaluate exopolysaccharide (EPS) producing lactic acid bacteria (LAB) strain - Leuconostoc mesenteroides SJC113 - and its functional and probiotic properties to be applied as potential starter culture.

Methods:

The functional and probiotic properties of Ln. mesenteroides SJC113 producing EPS was evaluated - these include the ability to grow in different NaCl concentrations, beta-galactosidase activity, antioxidant activity (radical scavenging activity-DPPH and hydroxyl scavenging activity), the ability to produce EPS in skim milk and sweet whey ant different sucrose concentrations (5, 10 and 20%), and gastrointestinal conditions (resistance to gastric acidity, bile salts and pancreatin).

Results:

Ln. mesenteroides SJC113 produces a dextran mucoid EPS (mostly alpha-1,6 glucose linkages). The strain showed a high tolerance to a wide range of NaCl concentration (2, 5 and 10 %), high production of beta-galactosidase (2368 ± 64 Miller units), medium scavenging rates of DPPH (12 ± 1. %) and hydroxyl scavenging activity (15.7 ± 0.7%) and high viability in simulated gastrointestinal conditions. EPS production in skim milk and sweet whey ranged from 0.96 ± 0.06 mg/mL to 3.36 ± 0.09 mg/mL, and 0.44 ± 0.08 mg/mL to 6.81 ± 0.51 mg/mL, respectively.

Conclusions:

The Ln. mesenteroides SJC113 showed good technologic and probiotic properties to be used as a starter culture in the food industry. This strain was also able to produce high amounts of EPS in both milk and whey media, presenting high prebiotic potential.

197 - EFFECTS OF LACTOBACILLUS CASEI ON GUT MICROBIOTA PROFILES OF HEALTHY PRE-TERM AND FULL-TERM NEWBORNS: A CLINICAL RANDOMIZED STUDY

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Objective:

The gut microbiota (GM) of premature infants has attracted growing attention because of its impact on the gut health at the early stage of life. The aim of this study was to determine the Lactobacillus casei DG® probiotic activity on GM modulation of healthy pre-term and full-term newborns within 48 hours from birth, to assess the GM ecological and functional profile and to evaluate the potential probiotics activity.

Methods:

A double-blind, placebo-controlled clinical trial was conducted. Sixty patients were enrolled and stratified into three birth weight-based groups, each of them was randomized 1:1 with L. casei DG® (Treated subjects) or placebo. Faecal samples were collected at different time points over 84 days and analysed by Real-Time PCR, targeted-metagenomics and gas chromatography mass spectrometry (GC-MS). A multivariate, univariate and correlation statistical analysis were applied to compare groups with placebo over time.

Results:

L. casei DG® was detected in treated subjects since administration starting point. An increase of Lactobacillus, butanoic and propanoic acids was observed during the first days of intake. A positive correlation ($p \leq 0.05$) was observed between L. casei DG® with Lactobacillus and Granulicatella and amongs butanoic acid with Ruminococcus, Prevotella, Collinsella, Faecalibacterium and propanoic acid with Oscillospira and Eggerthella, Bacteroides, Bifidobacterium.

Conclusions:

The meta-omics approach revealed that the administration of L. casei DG® has an effect on the GM ecology and functional activity. Butanoic and propanoic acids, have shown a positive correlation with beneficial bacteria such as Faecalibacterium, Oscillospira, Eggerthella and Bifidobacterium.

200 - HUMAN MILK AS A SOURCE OF POTENTIALLY PROBIOTIC BACTERIA

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Objective:

Isolate lactic acid bacteria (LAB) from human milk and investigate their antimicrobial activity and ability to produce alpha-aminobutyric acid (GABA) with a view to their potential use as probiotics.

Methods:

Breast milk samples of healthy women were aseptically collected, transported within sterile containers and processed immediately upon receipt. Samples were directly poured on de Man, Rogosa, and Sharpe (MRS) agar plates supplemented with 0.05% cysteine-HCl, which were incubated under anaerobic conditions at 37 °C for 2–5 days. All isolates that matched to the basic characteristics of the LAB group, Gram-positive, catalase, and oxidase-negative were used for identified by 16S rDNA sequencing. The antibacterial activity of the isolates was determined using the agar diffusion method against several indicators strains. To select strains that potentially produce GABA, a GAD colorimetric assay was performed. Strains that turned the color green to blue were recorded as positive for GABA production.

Results:

Seven strains, four Lactobacillus gasseri (strains BM8, BM9, BM10, BM13), one Limosilactobacillus fermentum (strain BM12), one Streptococcus infantis (strain BM16) and one Enterococcus faecalis (strain BM21), were identified by phylogenetic analysis.
Neutralized cell free-supernatant of strain E. faecalis BM21 showed antimicrobial activity against Listeria monocytogenes, indicating the production of a bacteriocin-like inhibitory substance (BLIS). Strain L. fermentum BM12 was positive for high GABA production.

Conclusions:

This work identified one strain of L. fermentum as high GABA producer and a E. faecalis strain as a BLIS producer. These strains isolated from human milk are potential probiotic candidates for application in the food and pharmaceutical industries.

203 - EFFECT OF POSTBIOTICS PRODUCED BY LACATOBACILLUS FERMENTUM (STRAIN LF53) ON CELL CYCLE OF HUMAN ENTEROCYTES AND KERATINOCYTES

Tanya Topouzova-hristova [(1)] - Veselina Moskova-Doumanova [(1)] - Ralitza Veleva [(1)] - Anita Vaseva [(1)] - Slavina Ivanova [(1)] - Svetla Danova [(2)]
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Objective:

Part of the beneficial effects of probiotics is also due to their products released into the environment, as well as to the postbiotics left behind. In complex naturally fermented foods, it is difficult to determine which effect is due to which component of the probiotics or postbiotics. The aim of our study was to check the effect of Lactobacillus fermentum metabolites and postbiotics on cell cycle parameters in two human cell lines – keratinocytes HaCaT and intestinal epithelial cells HT-29.

Methods:

Lactobacilli were cultured in standard MPS medium, and human cells were treated with samples of this medium after filtration and normalization of amounts to protein content. Cell cycle analysis was performed using Guava easyCyte flow cytometry system and Guava® Cell Cycle Reagent, Luminex. The proportions of cell populations in the different phases of the cell cycle were counted by flow cytometric measurement of DNA content.

Results:

Our results show a significant influence on the cell cycle of keratinocytes. We observed a clear redistribution of cells in the cell cycle phases and G1 arrest. Positive effect was observed in intestinal epithelial cells with an increase in the proportion of the cell population in a S period of interphase.

Conclusions:

The observed cell-specific effect on cell proliferation may be a good basis for future research on biomedical applications of L actobacillus fermentum postmetabolites.

204 - SET UP OF PROBIOTIC BLEND FOR IN OVO INJECTION TO BE USED IN POULTRY PRODUCTION CHAIN

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University of Catania, Agricultural, Food and Environment, Catania, Italy [1] - Nicolaus Copernicus University, Department of Microbiology, Faculty of Biological and Veterinary Sciences, Torun, Poland [2] - Nicolaus Copernicus University, Faculty of Health Sciences, Torun, Poland [3]

Objective:

The objective of the present project was to develop a synbiotic blend for in ovo injection to be applied in the poultry production chain. A prebiotic solution capable of enhancing the growth of a probiotic strain Lacticaseibacillus rhamnosus H25 was selected. In addition, its antimicrobial activity was evaluated in single and in combination with Bifidobacterium animalis subsp. lactis BLC01 strain against foodborne and non-food-borne pathogenic strains.

Methods:

Twelve prebiotics, including vegetable extracts and polysaccharides, were used in the experiment, and the growth rate was measured using a microplate reader (SpectraMax® ID3 Multi-Mode Microplate Reader from Molecular Devices®) at 600 nm, which was automatically checked every 2 hours for 24 hours. Antimicrobial activity of probiotic strain H25, alone and combined with Bifidobacterium animalis subsp. lactis BLC01, was tested using the agar well diffusion assay against thirteen pathogenic strains.

Results:

The probiotic strain showed excellent growth performance with all twelve prebiotics tested, especially in the presence of liquid seaweed extract and astragalus. Regarding antimicrobial activity, in the single condition, L. rhamnosus H25 strain showed moderate activity with almost all pathogens, while the blend formulation with probiotic strain B.animalis subsp. lactis BLC01 promoted antimicrobial activity, showing a strong activity against the tested pathogenic strains.

Conclusions:

Prebiotic formulations prove to be excellent growth promoters for probiotics, just as the use of a probiotic blend is able to enhance antimicrobial activity against pathogens. Therefore, the combination of prebiotics and probiotic blend could be a good strategy for the development of synbiotic formulations for the poultry production chain.

205 - SURVIVABILITY OF THE ENCAPSULATED PROBIOTIC LACTICASEIBACILLUS RHAMNOSUS CA15 (DSM 33960) STRAIN IN THE GASTROINTESTINAL TRACT THROUGH THE SHIME® MODEL

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Objective:

To evaluate the viability of the probiotic Lacticaseibacillus rhamnosus CA15 (DSM 33960) strain, under both fed and fasted conditions, using an in vitro human gastrointestinal microbial ecosystem (SHIME®) model. In addition, during the colonic phase and under fasted conditions, the viability of the probiotic CA15 strain, in presence of the antimicrobial Fluconazole, was studied.

Methods:

A SHIME® double-jacked reactor was used to sequentially simulate the stomach, small intestine, and colonic digestion according to the patented SHIME® conditions. The system was maintained at a temperature of 37 °C, under constant stirring and anaerobic conditions by nitrogen injection. The probiotic Lacticaseibacillus rhamnosus CA15 (DSM 33960) strain was tested as capsule, under both fasted and fed conditions, with and without the addition of the antimicrobial Fluconazole (200mg). Samples were collected from all GIT fractions and the viability of the probiotic CA15 strain was evaluated by both plate count and RT-qPCR by using strain-specific primers. In addition, in the colonic fraction, the profile of both short- and branched-chain fatty acids was investigated.

Results:

The probiotic Lacticaseibacillus rhamnosus CA15 (DSM 33960) strain showed, under both fasted and fed conditions, survival rate higher than 50%. The simultaneous administration of the antimicrobial Fluconazole, did not affect the viability of the encapsulated CA15 strain.

Conclusions:

The probiotic CA15 strain is suitable for oral administration, also during antibiotic therapy with Fluconazole, maintaining viability and functionality through colonic fraction.

PREBIOTICS

45 - MICROBIAL LEVAN BIOPOLYMER (AS PREBIOTICS) PRODUCTION AND ITS USE FOR THE SYNTHESIS OF AN ANTIBACTERIAL IRON OXIDE NANOCOMPOSITE

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Objective:
In this study, Levan biopolymer as prebiotics was used to synthesize a nanocomposite containing magnetic nanoparticles of iron with antibacterial effects.

Methods:
The effects of three factors at three levels of sucrose (5, 7, and 9 g), KH2PO4 (0.3, 0.5, and 0.7 g), and soy flour (3, 5, and 7 g) were evaluated to produce levan exopolysaccharide by Bacillus polymyxa PTCC1020. Nine experiments were designed with different environmental conditions via the Taguchi method. The nanoparticles of iron oxide were synthesized with the coprecipitation method. In addition, nanocomposites containing magnetic nanoparticles of iron and levan biopolymer were produced.

Results:
The highest level of levan extraction was observed with conditions of 5 g of soy flour (second level), 0.7 g of KH2PO4 (third level), and 5 g of sucrose (first level) as 27 g/L. The Fourier transform infrared analysis and ultraviolet–visible spectroscopy showed the formation of nanocomposites containing magnetic particles of iron. The results indicate that the synthesized nanocomposites had antibacterial effects on both Escherichia coli and Staphylococcus aureus.

Conclusions:
We concluded that levan and Fe3O4 could be used to synthesize antibacterial nanocomposites with high potential for various industrial applications.
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POSTBIOTICS & BACTERIAL METABOLITIES

4 - ISOLATION, CHARACTERIZATION, EFFET ON BIOFILM FORMATION OF BACTERIOCIN PRUDUCED BY LACTOCOCCUS LACTIS F01 ISOLATED FROM CYPRINUS CARPIO AND APPLICATION OF BIOPRESERVATION IN FISH SAUSAGE

Ulrich Daquain Fotso Techeu [(1)] - Edith Marius Foko Kouam [(2)] - Hector Kenfack Momo [(3)] - Laverdure Tchamani Piamé [(1)] - Romial Joël Ngouenam [(1)] - François Zambou Ngoufack [(1)] - ***Ulrich Daquain Fotso Techeu*** [(1)]
University of Dschang, Biochemistry, Dschang, Camerun [(1)] - *University of Dschang, Physiology Sciences and Biochemistry, Dschang, Camerun* [(2)] - *University of Bamenda, Nutrition , Food and Bioresource Technology, Bamenda, Camerun* [(3)]

Objective:
The aim of this work was the screening of bacteriocin-producing LABs isolated from fish, the characterization of the bacteriocin produced and evaluation of its potential to be used as bio-preservative(s).

Methods:
Sequencing of the 16S rRNA gene of the bacteriocin-producing strain was performed. Then a partial purification of the produced bacteriocin, using a combination of ammonium sulfate and chloroform-methanol precipitation was done. Its molecular weight was determined by SDS-PAGE. In addition, the hemolysis test, and its ability to inhibit biofilm formation were analyzed.

Results:
A total of 88 isolates of lactic acid bacteria including one (1) bacteriocin producer, which was identified as Lactococcus lactis F01 were collected. Regarding the SDS-PAGE profile, the secreted bacteriocin has molecular weight of about 3.5 kDa. The antimicrobial test showed that the bacteriocin inhibits pathogenic bacteria, 10 Gram-positive and 16 Gram-negative bacterial species. Moreover, it can inhibit biofilm formation from depending on the strain. The hemolytic activity of bacteriocin was observed at the concentration of 10 µg/ml of bacteriocin crude extract. In addition, it exhibited good thermal and pH stability with retained antibacterial activity of 85.25 % after treatment at 121°C for 20 min, as well as at a pH range between 2.0-10.0. Moreover, this bacteriocin showed the ability to inhibit the growth of bacterial culture load in fish sausage stored at 8 °C for 28 days.

Conclusions:
Considering the results obtained, bacteriocin could be potentially exploited as an alternative to chemical preservatives or as a substitute for antibiotics.

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43 - IN-VITRO AND IN-SILICO INSIGHTS INTO POTENTIAL GABA-PRODUCING INDIGENOUS LACTIC ACID BACTERIA

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Objective:

GABA facilitates communication between phylogenetically very different life forms by acting as a shared language, assisting in the homeostatic regulation of the enteric bacteria, and perhaps even influencing brain and behavior function. This study aims to identify major GABA producing probiotics, its in-vitro efficacy and functional annotation by whole-genome sequencing and comparitive genomic analyis.

Methods:

45 bacterial strains (20 Lactobacillus + 25 Bifidobacterium strains) were screened qualitatively and quantitatively for its GABA producing ability. In-vitro screening of strains was done in RAW 264.7 cells. Illumina (NOVASEQ 6000) based whole-genome sequencing was done, CLC Genomics Workbench 21 was used for genome assembly, and Rapid Annotation Server and Technology (RAST) was used for genome annotation following intraspecific comparitive genomics of selected strain.

Results:

Two high GABA producing strains LAB6 and LAB19 of indigenous origin were identified and two strains LAB7 and LAB31 produced moderate GABA. Some of the strains had potential anti-inflammatory activity against lipopolysaccharide-induced inflammation in RAW 264.7 cells, where the production of nitric oxide was reduced. However, LAB6 showed more potent in-vitro effects and its in-silico analysis revealed the presence of complete glutamate decarboxylase (GAD) gene system (gadA, gadB, and gadC). Whole genome analysis demonstrated the presence of beneficial probiotic traits like genes for acid and bile tolerance and host adhesion proteins.

Conclusions:

Postbiotic GABA producing LAB6 strain harbored canonical GAD operon and essential probiotic attributes making it a potential psychobiotic candidate.

174 - USE OF L. RHAMNOSUS IMC501 FOR THE PRODUCTION OF LACTIC ACID FROM RENEWABLE RESOURCES AND PURIFICATION OF EXOPOLYSACCHARIDES

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Objective:

The homofermentative probiotic strain Lactobacillus rhamnosus previously demonstrated to convert glucose from raw lignocellulosic material into L-lactic acid, with yields which vary between 0.38 and 0.97 g/g. Therefore, the aim of this work was to utilize grape stalks, for the production of lactic acid from L. rhamnosus IMC 501, due to the considerable demand in different industrial fields (e.g. food, pharmaceutical, etc). Moreover, by using a semidefined medium deprived of animal sourced components a preliminary protocol for exopolysaccharide purification was also evaluated.

Methods:

Steam explosion and alkaline hydrolysis were compared as biomass pretreatment methods, and a two-step enzymatic hydrolysis protocol with commercial enzymes (Cellic-cTec2, Novozymes) was optimized to improve the efficiency of cellulose conversion. Batch fermentations were conducted on 3 L Biostat CT plus reactors (Sartorius) to evaluate growth and lactic acid production on grape stalk hydrolysate with and without supplementation of yeast extract as additional nitrogen source. The exopolysaccharide secreted by L. rhamnosus in the supernatant was recovered by combining ultrafiltration on 10 kDa membrane, precipitation with organic solvents and final treatment with pharmaceutical grade activated charcoal.

Results:

A cellulose conversion efficiency of about 37% was obtained, that is one of the highest for this type of substrate described up to date. The strain could convert all glucose present in the grape stalk hydrolysate medium with a YLA/GLU of 0.99 and 0.98 g/g in the presence and absence of yeast extract, with a slight improvement of the glucose consumption rate in the supplemented medium. The exopolysaccharide was purified from the culture medium with a recovery of about 300 mg from 2L of supernant.

Conclusions:

We demonstrated the possibility to grow L. rhamnosus IMC501 on grape stalk hydrolysate without the need for additional medium components, and that the presence of vegetal biomass derived inhibitors (e.g. vanillin, furfural) did not affect growth and lactic acid production. The downstream process applied in this study allowed us to obtain a preliminary purification of the exopolysaccharide produced by L. rhamnosus IMC501 for further characterization and evaluation of biological activity.

175 - POSTBIOTIC EFFECT OF L. RHAMNOSUS GG ON DIARRHOEA AND OXIDATIVE STRESS INDUCED BY COVID19 SPIKE PROTEIN IN CACO2 CELLS

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Objective:

Diarrhoea is the most frequent gastrointestinal symptom of Covid-19, mediated by spike protein which acts as an enterotoxin inducing chloride secretion and an increase of reactive oxygen species (ROS). Treatment with the probiotic strain L. rhamnosus GG (LGG) is recommended for acute gastroenteritis. We tested the effects of a postbiotic preparation of LGG in an in-vitro model of Covid-19 induced-diarrhoea.

Methods:

Spike protein was added to Caco-2 monolayers mounted in Ussing Chambers and electrical parameters of ion fluxes (Isc and TEER) were determined. Oxidative stress was analyzed by standard tests: ROS levels (DCFDA), lipid peroxidation (TBARS) and GSH levels (DNTB). The same experiments were performed after pre-treatment with a post-biotic preparation (mLGG) and N-acetylcysteine (NAC), as control.

Results:

Spike induced an increase in Isc consistent with chloride secretion and secretory diarrhea. Pre-treatment with mLGG significantly reduced ion secretion (mLGG+Spike 0.9±0.32 vs Spike 2.9±0.3 $\mu A/cm^2$; $p=0.002$). Spike induced a 2-fold increase in ROS production and lipid peroxidation, and a change in glutathione levels. mLGG significantly reduced oxidative stress, namely ROS ($p<0.001$), lipid peroxidation ($p<0.001$) and glutathione levels ($p<0.001$), with an antioxidant effect similar to NAC.

Conclusions:

LGG counteracts Spike-induced diarrhoea by inhibiting the enterotoxic effect and oxidative stress. The LGG efficacy in postbiotic form depends on molecules secreted in the medium with a pharmacological-like direct action, including antioxidant properties. Because SARS-CoV-2 is a new agent of childhood gastroenteritis, the efficacy of LGG independent of etiology, is confirmed by our data.

206 - DO BACTERIAL POSTMETABOLITES AFFECT THE MITOCHONDRIA OF EUKARYOTIC CELLS?

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Objective:

To assess the effects of Lactobacillus fermentum Lf53 strain postbiotics on the mitochondrial functions of two eukaryotic cell lines.

Methods:

Post-microbial MRS media from 24h and 48h exponential culture of Lactobacillus fermentum Lf53 strain, isolated from traditional Bulgarian naturally fermented milk product were collected and centrifuged in order to obtain cell-free media. The amount of protein in the media was assessed calorimetrically by BCA-method. Postbiotic containing media were applied on two eukaryotic non-cancerous human cell lines (HaCaT – keratinocytes and HFF – fibroblasts) in concentrations ranging from 0,25mg/ml protein to 2mg/ml protein. The viability of cells after 48h of treatment was assessed by two distinct methods – classical MTT, measuring the mitochondrial activity and Cristal violet staining, measuring the protein content in the cells. Amount and distribution of mitochondria at the same time point was evaluated by confocal microscopy after staining with BioTracker488Green. In order to distinguish the effects of bacterial metabolites from those of MRS-media component the later was used as a control.

Results:

Increase in cell viability markers was observed at low treatment concentrations, diminishing in concentration-dependent manner. Effects of 24h exponential culture media were slighter in comparison to 48-cultute media. Highest concentration tested were toxic for the cells. Fluorescent assessment of mitochondrial redistribution within the cells revealed clustering in some of the cells, without changes of cell shape.

Conclusions:

Our results indicate for presence into the post-bacterial MRS of some component affecting mitochondrial function and distribution in eukaryotic cells.

SAFETY ASPECTS OF MICROBIOTA BASED THERAPIES

113 - IMPACT OF PROBIOTICS IN THE PROPHYLAXIS AND TREATMENT OF RESPIRATORY INFECTIONS LINKED TO COVID-19: SYSTEMATIC REVIEW AND META-ANALYSIS

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Objective:
Probiotics are living microorganisms that produce beneficial effects on host health when administered in sufficient quantities. According to several recent studies that rose with the high prevalence of SARS-CoV2, the use of these probiotics may have a positive influence on COVID-19 patients

Methods:
A predetermined search strategy was applied to seven databases: NCBI, PubMed, Science Direct, SpringerLink, Embase, CNKI and Cochrane Library for the search of human RCTs studies. Then, each included study was independently assessed for data extraction, quality and risk of bias and statistically analyzed. All analyzed data were pooled using the random-effects model and expressed as a SMD with a 95% CI. The P value (p) and heterogeneity (I^2) were assessed and quantified.

Results:
From 1111 identified studies, 05 ones treating a total of 282/375 participants were included in this meta-analysis that showed effects on: CRP (SMD=0.26 MG/L, 95% CI [0.10, 0.43], p= 0.002, (I^2=67%, p=0.03)). BMI (SMD=0.28 KG/m^2a, 95% CI [0.07, 0.50], p= 0.01, (I^2=67%, p=0.40)). T-cells (SMD=0.09 G/L, 95% CI [-0.07, 0.26], p= 0.26, (I^2=0%, p=0.73)). Albumin (SMD=0.28 G/DL, 95% CI [0.04, 0.52], p= 0.02, (I^2=7%, p=0.34)). IL-6 (SMD=0.67, 95% CI [0.45, 0.90], p= 0.00001, (I^2=94%, p=0.0001)). LDH (SMD=0.12mmol/L, 95% CI [-0.05, 0.30], p= 0.17, (I^2=55%, p=0.13)). And Ferritin (SMD=0.19mmol/L, 95% CI [-0.27, 0.66], p= 0.41, (I^2=77%, p=0.04)).

Conclusions:
This analysis suggests that the use probiotics in COVID-19 cases has a significant positive effect on measured parameters.

114 - META-ANALYSIS: PROBIOTICS, PREVENTION AND TREATMENT OF VIRAL INFECTIONS

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Objective:
Probiotics are living microorganisms intended to confer a health benefit when consumed. Emerging epidemiological evidence suggests that the use of probiotics may reduce the risk of infections and complications from viral infections. Our aim was to systematically examine the effect of probiotics on viral infections.

Methods:
We searched electronic databases as Science directe, Cochrane Library, NCBI, Springer-Link from the year 2019 through 2021 for randomized trials and cohort studies that systematically examined the effect of probiotics on viral infections. Data were pooled using the random-effect model and expressed as the mean standard difference (SMD) with a 95% confidence interval (CI). Heterogeneity was assessed and quantified.

Results:
Of the 316 reports that were reviewed, 04 clinical trials met the inclusion criteria. The meta-analysis shows that BMI (SMD = 0.07 kg / m2, 95% CI [-0.05, 0.19], p= 0.24, (I2 = 0%, p = 0.62)). Il-4 (SMD = 96.53 pg ml ^ (- 1), 95% CI [-93.87, 286.93], p =0.32, (I2 = 99%, p <0.00001)). Il-10 (SMD = 0.24 pg ml ^ (- 1), 95% CI [0.09, 0.39], p =0.002, (I2 = 8%, p = 0.30)). TNF-alpha (SMD = 0.27 pg ml ^ (- 1), 95% CI [0.15, 0.39], p<0.0001, (I2 = 0%, p = 0.98)). For the weight (SMD = 0.03 kg, 95% CI [-0.25, 0.31], p =0.84, (I2 = 0%, p = 0.43)). Egger's tests showed no significant publication bias.

Conclusions:
The use of probiotics for the prevention of viral infections has insignificant effects or needs to be further elucidated in the future.

BOTANICALS, PHYTOCHEMICALS, PHYTOMEDICALS & FOOD BIOACTIVE COMPOUNDS

20 - ASSESING THE INVASIVE POTENTIAL OF AILANTHUS ALTISSIMA: A COMPREHENSIVE REVIEW

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Objective:
The objective of this review is to provide a thorough assessment of the invasive potential of the Ailanthus altissima plant species. The review aims to analyze the biological, ecological, and environmental characteristics of the plant and to explore the mechanisms of its invasion and the impacts it has on biodiversity, ecosystem functioning, and human health. The review also aims to evaluate current control and management strategies and suggest future research directions. Ultimately, the objective of the review is to provide a comprehensive analysis of A. altissima as an invasive species and to offer valuable insights for researchers, policymakers, and environmental managers to better manage and control its spread

Methods:
To evaluate the invasive potential of A. altissima, the review examined the mechanisms of its invasion, such as seed dispersal, growth rate, and reproductive capacity. The impacts of A. altissima on ecosystems and human health were evaluated by analyzing studies on its competition with native species, effects on soil nutrient cycling, and potential health hazards associated with its pollen and sap. The review also evaluated current management and control strategies, such as physical, chemical, and biological control methods, and assessed their effectiveness in mitigating the spread of A. altissima. Finally, the review identified gaps in current knowledge and suggested future research directions to improve our understanding of A. altissima's invasive potential and to develop more effective control strategies.

Results:
The results of revealed that Ailanthus altissima is a highly adaptable and invasive plant species that poses a significant threat to native ecosystems worldwide. The review found that A. altissima exhibits a range of biological, ecological, and environmental characteristics that facilitate its invasion, such as rapid growth rate, prolific seed production, and the ability to grow in a wide range of soil types and environmental conditions.

Conclusions:
Overall, the review emphasizes the importance of effective management and control of A. altissima to protect native ecosystems and human health, and provides a valuable resource for researchers, policymakers, and environmental managers in the field of invasive species management.

33 - PRODUCTION OF PROTEOLYTIC ENZYMES BEARING ANTIOXIDANT POTENTIAL BORNE BY PLEUROTUS OSTREATUS (JACQ.) P. KUMM (BASIDIOMYCOTA, PLEUROTACEAE) IN SUBMERGED FERMENTATION

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UFAM, Universidade, Manaus, Brazil [1]

The present study has aimed to determine, as well as verify the Pleurotus ostreatus DPUA 1533 crude extract's proteolytic activity and antioxidant - cytotoxic. The mushroom was acquired from (supplied by) the Federal University of Amazonas DPUA Culture Collection and reactivated in, potato dextrose agar to obtain a viable culture. Cultivation was accomplished through the use of three different media in a 50 mL proportion containing, Malt (YM) and Sabouraud+yeast extract (SB+YE) 0.5% (w/v), at 150 rpm-, under 28°C for seven days. Relative protein concentration, proteolytic and antioxidant activity, along with cell viability, were ascertained through in vitro analyses. Under the evaluated conditions, the mushroom was able to excrete proteases in all media, showing a significantly higher specific proteolytic activity ($p<0.05$) in the SB+YE medium with 22.4±0.01 U/mL followed by 16.3±1.57 U/mL for the YM medium. SB+YE medium-cultivated P. ostreatus antioxidant capacity was 14.99%±0.03, of inhibition in ABTS, and 6.87%±0.03 in DPPH. In all cultures the extracts showed cell viability greater than 80%, - 84.1%±4.8, and 88.8%±0.1, in SB+YE and YM media, respectively. that all media presented favorable conditions for the growth of the fungus, was demonstrated, which proved (confirmed) that P. ostreatus is a proteolytic enzyme producer ($p<0.05$), presents no cytotoxicity, as well as safety for human consumption together with high potential for biocatalyst, and new bioproducts bearing, for the food and pharmaceutical industry due to its remarkable antioxidant activity.

77 - ETHANOL EXTRACTS OF GANODERMA PFEIFERRI, LAETIPORUS SULPHUREUS AND FOMES INZENGAE EXERT ANTI TUMORAL EFFECTS ON HEPATOCARCINOMA CELLS

Lara Lizzi [1] - Maria Giovanna Armillotta [1] - Federica Russo [1] - Martina De Mattheis [1] - Marco Leonardi [1] - Mirco Iotti [1] - ***Mara Massimi*** [1]
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Objective:

Polypores have long been recognized for their nutritional value and for their medicinal properties, for which there is increasing attention. They appear to exhibit a wide range of pharmacological properties, including antioxidant, anti-inflammatory, immunomodulatory and hepatoprotective activities, with less attention paid to the anti-oncogenic action. This study aimed to investigate the in vitro effects of ethanol extracts of Ganoderma pfeifferi, Fomes inzengae and Laetiporus sulphureus on in vitro proliferation, apoptosis, and migration activity of hepatocarcinoma cells.

Methods:

The cell lines HepG2 and Huh7 were treated with mushroom ethanol extracts for 48 or 72 hours. Inhibition of cell proliferation was evaluated by trypan blue test, cell migration by wound healing assays, and the expression of key molecules of cell cycle progression, apoptosis and invasion by western blot.

Results:

All extracts significantly inhibited HepG2 cell proliferation in a time- and dose-dependent manner, showing no significant toxicity at the concentrations that halved cell viability (IC_{50}). L. sulphureus exhibited the lowest IC_{50} but also the highest cytotoxicity at higher doses. All the extracts increased p27, p21, and p53 protein levels and promoted apoptosis by reducing Bcl-2 and increasing Bax, cleaved caspase-9, and cleaved caspase-3 protein expression. In addition, the extracts exhibited inhibitory effects on Huh-7 cell migration by increasing E-cadherin and decreasing Twist protein levels.

Conclusions:

Our findings suggest that these edible species may hold promise as adjuvants to increase efficacy and reduce toxicity of current treatments and offer a valuable contribution to the field of therapeutics for hepatocarcinoma (HCC), thus warranting further research and recognition.

100 - THE SKIN MICROBIOTA-MEDIATED BIODEGRADATION OF COMFREY ROOT EXTRACT

Natalia Melnyk [1] - Dominik Popowski [2] - Jakub Patryk Piwowarski [1] - Sebastian Granica [1]
Medical University of Warsaw, Microbiota Lab, Department of Pharmaceutical Biology, Warsaw, Poland [1] *- Waclaw Dabrowski Institute of Agricultural and Food Biotechnology - State Research Institute, Department of Food Safety and Chemical Analysis, Warsaw, Poland* [2]

Objective:

Comfrey root (Symphytum officinale) is a plant material traditionally used as an anti-inflammatory and wound-healing topical remedy for skin diseases. Also, it is the component of many popular ointments, creams, and tinctures applied directly to the skin. The research aims to verify the possible interaction of extract from Symphyti radix with human skin microbiota.

Methods:

Determination of the interaction between human skin microbiota and the extract was conducted in ex vivo conditions. The extract was incubated with skin microbiota collected from healthy volunteers. The composition of the extract and production of metabolites were analyzed and determined by an HPLC-DAD-MS. The influence of the extract on the microbiota composition was evaluated by sequencing of the 16S rDNA.

Results:

Changes in the composition of extract after incubation with skin microbiota for 24, 48, and 72h were assessed and showed that the skin microbial metabolism primarily focused on modifying pyrrolizidine alkaloids derivatives. The sequencing results revealed that the tested extract (at 2 mg/ml) have no influence on the biodiversity of the skin microbiota after 24 h incubation. However, some qualitative changes in the microbiota composition were observed.

Conclusions:

Microbiota-enhanced biodegradation of extract was observed. Some metabolites were detected. The results showed the extract alter skin microbiota composition. That may play a role in the activity of the extract in the treatment of skin diseases.

103 - EXPLORING THE PHYTOCHEMICAL COMPOSITION AND ANTIBACTERIAL ACTIVITY OF FABA BEAN PODS IN THE CONTEXT OF ITS UTILIZATION IN PIGS NUTRITION

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Objective:

Bacterial diarrhea among post-weaning piglets is one of the most important health conditions in pigs farming. Global restriction in antibiotic use in livestock forced us to seek new therapeutic strategies to maintain piglets gut health. The use of agricultural by-products such as faba bean pods (FBP, Vicia faba L.) can be considered as a sustainable approach to development of novel feed additives. The aim of the study was nutritional analysis of dried FBP as well as phytochemical and antibacterial evaluation of methanolic extract from FBP (eFBP).

Methods:

We have determined the nutritional composition of FBP and found that it is rich in crude fiber (206.7 g/kg), protein (144.3 g/kg), and potassium (27.78 g/kg). In eFBP, using Folin–Ciocalteu method we have measured the sum of phenolics (125.51 ug/mg).

Results:

Based on UPLC-DAD-MSn analyses of eFBP, we detected 35 compounds, 17 identified as derivatives of quercetin and kaempferol, along with levodopa, piscidic acid and hydroxyeucomic acid. Furthermore, we checked antibacterial activity of eFBP, and found dose-dependent growth inhibition of Escherichia coli ATCC25922 and Salmonella Typhimurium LT2 at concentrations of 0.250-8 mg/mL. Finally, we evaluated the effect of eFBP on the activity of porcine digestive enzymes amylase and lipase (IC50>4mg/mL).

Conclusions:

We have shown that FBP is a rich source of diverse polyphenols expressing antimicrobial effects, what makes this agricultural by-product a promising candidate for further development of novel feed additives applied to prevent post-weaning diarrhea in piglets.

104 - IN VITRO STUDY OF COMPOSITION AND BIOLOGICAL ACTIVITY OF LYTHRUM SALICARIA L. FOR POTENTIAL USE IN PIGLET NUTRITION

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Objective:

The aim of the study was to analyse the composition and biological activity of Purple loosestrife (Lythrum salicaria L.) aqueous extract (LSH) in order to develop novel therapeutic strategies targeted on maintaining piglets gut health to solve the biggest problem affecting piglet production - post-weaning diarrhoea.

Methods:

Total phenol (TPC) and tannins (TTC) contests were determined by Folin–Ciocalteu method. The minimal inhibitory concentration (MIC) of extract against Escherichia coli ATCC 25922 and Salmonella Typhimurium LT2 was verified by turbidimetric method. Enzymatic assays were conducted to determine the interaction of extract with porcine digestive enzymes: amylase and lipase. The extract was fractionated using column chromatography and phytoconstituents were identified with high-performance liquid chromatography coupled with mass spectrometer.

Results:

We found that LSH is a rich source of polyphenols (TPC=274.75 ug/mg) with tannins (TTC=268,06 ug/mg) as dominating compounds. LSH showed inhibitory activity against two most common gastrointestinal pathogens S. Typhimurium at concentration 500 ug/ml and dose dependent effect on E. coli (500-2000 ug/mL). Despite presence of tannins, LSH had no effect on porcine amylase, while for lipase IC_{50}=0.3546 mg/mL was established. Three dominating compounds, all being hydrolysable tannins, were identified and isolated: vescalagin, castalagin, and salicarinin A.

Conclusions:

The LSH was shown to be a good source of hydrolysable tannins with potential antibacterial properties. Revealed antimicrobial activity makes it a good candidate for development of novel feed additive applied to prevent post-weaning diarrhoea in piglets.

112 - IN VITRO, ANTIOXIDANT CAPACITY AND ANTIBACTERIAL PROPERTIES OF PROBIOTICS GROWN IN THE PRESENCE OF FABACEAE HONEY AS AN ENERGY SOURCE

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CNR, Institute of Food Science, Avellino, Italy [1] - Dept of Pharmacy, University of Salerno, Fisciano (SA), Italy [2] - DIAAA, University of Molise, Campobasso, Italy [3]

Objective:

Our work aimed to evaluate the influence of the astragalus honey on some activities of two probiotics, L. paracasei, and L. rhamnosus, in particular the cellular antioxidant activity and the antibacterial capacity expressed by their supernatants.

Methods:

Two commercial probiotics, L. paracasei and L. rhamnosus, were grown in MRS broth containing glucose 10% or astragalus honey 10%. The bacterial cells' capacity to act as OH radical scavengers was assessed. The supernatants were assayed against E.coli and S. aureus monitoring the growth of the pathogens in Luria Bertani broth containing 80 microliters/ml of MRS with glucose or astragalus. We also evaluated the capacity of the supernatants to inhibit the mature biofilm formation of E. coli and S. aureus through the crystal violet assay.

Results:

Astragalus honey increased the OH-scavenging efficacy of L. paracasei and L. rhamnosus. It caused an increase of the OH-radical scavenging activity of 5.52 times more in the case of L. paracasei and 6.53 times more in the case of L. rhamnosus, with respect to the control (growth in MRS+glucose). The supernatants of L. paracasei and L. rhamnosus showed an increase of the antibacterial capacity of 18.5% and 4.71%, against E. coli, respectively, and of 38.5% and 24.20% against S. aureus, respectively, compared to control. Astragalus honey also affected their biofilm-inhibitory activity.

Conclusions:

Astragalus honey meliorated the antioxidant and antibacterial capacity of the two probiotics, thus showing some interesting potential prebiotic effects, which we shall deeply study in future steps.

134 - CHROMATOGRAPHIC ANALYSIS AND HYPOGLYCEMIC ACTIVITY OF TWO MEDICINAL PLANTS

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Research Laboratory on Arid Zones, University of Sciences and Technology Houari Boumediene, Algiers, Algérie [1]

Objective:

Diabetes is growing rapidly worldwide, this is why scientific works must more focused on the search for new, less expensive and more effective alternatives. The present work aims to establish a scientific justification for the use of Moringa oleifera and Globularia alypum in herbal medicine for hypoglycemic effect and determine the bioactive compounds responsible for this therapeutic effect by HPLC (High-performance liquid chromatography) analysis.

Methods:

The glucose tolerance test evaluates the potential of Moringa oleifera and Globularia alpum infusion extract leaves at dose of 500mg/Kg of body weight in mice to reduce the concentration of glucose previously administered to the order of 4g/kg. The mice's blood sugar was measured at times (t): 30, 60, 120, 150 min on a drop of blood taken from the caudal end of the animals, using the glucometer. Methformin at 500mg/Kg was used as the reference drug. The bioactive compounds in the both infusion extracts were identified by HPLC analysis.

Results:

The glucose tolerance test shows that the infusions of Moringa oleifera and Globularia alypum are more effective in lowering blood sugar than metformin around 2.23, 1.05 and 1.02 units respectively for the three treatments. HPLC chromatogram indicated the simultaneous presence of kaempferol and rutin in both infusion of Moringa oleifera and Globularia alypum. These compounds are known for its inhibition of glucosidase activity in vitro by binding directly to the enzyme by hydrophobic bonding.

Conclusions:

This study justifies the traditional use of Moringa leifera and Globularia alypum as antidiabetic treatment.

135 - PHYTOCHEMICAL AND PHARMACOLOGICAL PROFILE OF PHENOLIC EXTRACTS OF POMEGRANATE PEEL (PUNICA GRANATUM)

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Objective:

This work aims to evaluate pharmacological properties of pomegranate peel extracts and establish their phytochemical profile.

Methods:

The pharmacological profile was determined by evaluating the antibacterial and cicatrizing power of three extracts (ethereal, butanolic extracts). The antibacterial activity of phenolic extracts of pomegranate peel at a dose of 500mg was carried out by the method of diffusion on agar medium against three bacterial strains. The cicatrizing effect of extracts of Punica granatum was evaluated by the excisional model in rats, the results were expressed by the percentages of reduction of the surfaces of the treated wounds using AutoCAD software. The phytochemical profile of pomegranate peel extracts was established by HPLC analysis.

Results:

The HPLC profiles revealed the richness of pomegranate peel extracts by phenols compounds such as quercetin, orientin, iso-orientin, apigenin, ferulic, acid. The antibacterial activity of pomegranate peel extracts showed that the butanolic was the most effective in inhibiting the growth of strains bacteria (Escherichia coli, Pseudomonas aeruginosa and Staphylococcus aureus) with inhibition diameters respectively 17, 22 and 25mm for butanolic extract. However, the ethereal extract showed the less antibacterial effect with inhibitory diameters in order to 13, 11 and 16mm respectively. The histological analysis of the healing effect of phenolic extracts of pomegranate bark revealed total healing of wounds treated with butanol with a 100% reduction in wounds, the ethereal extract reveals partial healing with 70% reduction in wounds.

Conclusions:

The present study shows that the phenolic extracts of pomegranate peel characterized by an interesting pharmacological properties.

140 - CAN PHYTOCHEMICALS (CAROTENOIDS) PREVENT DOXORUBICIN-INDUCED NEPHROTOXICITY?

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Objective:

Doxorubicin is an effective anticancer drug which has a toxic effect on a large number of organs including the kidneys. Carotenoids are thought to provide health benefits in decreasing the risk of disease by reducing oxidative stress, which is one of the mechanisms of doxorubicin-induced nephrotoxicity.

Methods:

In total, 60 animals were randomly divided into 6 groups. Animals were given saline (S), solvent (NADES – natural deep eutectic solvents, N, 1ml), carotenoids (C, 900 μg/kg), doxorubicin alone 4 doses (D, 2 mg/kg) or pretreated with solvent (ND) or carotenoids (CD). Kidney tissue was subjected to standard histological processing, staining and qualitative analysis. As signs of animal's general condition, we observed: quality and density of the hair and bleeding.

Results:

Kidney tissue morphology treated with solvent and carotenoids wasn't altered compared to the controle. In the kidneys of group D were found pronounced hypercellularity, atrophy and vacuolization in a large number of proximal tubules. In addition, the distal tubules were dilated, while areas of hemorrhage were present in the cortex. Morphological changes in the kidneys were accompanied by higher mortality and a worse general condition (thinned hair, traces of bleeding from the nose) in group D. Carotenoids/doxorubicin co-treatment alleviated the changes in the kidneys (moderate hypercellularity and rare vacuolization of the proximal tubules) as well as the general condition.

Conclusions:

Carotenoids pre-treatment showed a protective role on kidneys and the general condition. The continuation of research would be in the direction of finding the exact mechanism of carotenoids action.

143 - CHEMICAL COMPOSITION, ANTIOXIDANT AND ANTIPROLIFERATIVE ACTIVITY OF A POLYPHENOL-RICH FRACTION FROM PINUS SYLVESTRIS L. BARK

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Objective:

In Romania, wood of mature Pinus sylvestris L. trees is used in construction and furniture industries and bark is the main waste product. Since pine bark has medicinal uses in some Northern European countries even though not in Romania, this study aims to investigate possible therapeutic applications of pine bark waste by examining the chemical composition, anti-oxidant and anti-tumour effects of polyphenol-rich bark extracts on different tumour cell types.

Methods:

A raw extract and four extractive fractions were obtained from pine bark. They were all studied regarding polyphenolic content and profile using spectrophotometry and high-performance liquid chromatography. The anti-oxidant activity of the fractions was investigated using the DPPH, superoxide anion, hydroxyl radical scavenging activity and comet assays whereas the anti-tumour activity with the MTT assay, respectively.

Results:

Ethyl acetate fraction contained the highest amount of polyphenols; a taxifolin glucoside, procyanidin monomers and oligomers (dimers to tetramers) were the main compounds in this fraction. Ethyl acetate fraction proved to be an efficient scavenger of free radicals, although this fraction did not protect the normal immortalised MCF-10A breast cells from H_2O_2-induced oxidative damage. Nevertheless, it selectively reduced cancer cell viability (breast and colon cancer cell lines MCF-7 and CaCo2, respectively) without affecting the normal MCF-10A cell viability.

Conclusions:

The ability of ethyl acetate fraction to inhibit tumour cell growth and to scavenge free radicals reveals the importance of further studies on possible therapeutic applications of its antiproliferative and antioxidant potential.

153 - OPTIMIZATION OF THE ENZYMATIC-ASSISTED EXTRACTION PROCEDURE OF BIOACTIVE COMPOUNDS FROM SEA BUCKTHORN (HIPPOPHAE RHAMNOIDES L.) LEAVES

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Objective:

Sea buckthorn (Hippophae rhamnoides L.) leaves contain a significant amount of bioactive compounds that may possess natural therapeutic benefits for multiple applications. Various techniques are available for extracting bioactive fractions from leaves, including conventional and high-pressure methods. However, enzyme-assisted extraction (EAE) of sea buckthorn leaves using the cellulolytic enzyme complex Viscozyme L has not been comprehensively studied. This study aimed to optimize the critical parameters involved in the EAE of sea buckthorn leaves to achieve a high-yield extract with a concentrated amount of bioactive compounds.

Methods:

To determine the optimal conditions for EAE, the study employed a central composite design and response surface methodology to analyze the effects of four independent factors: pH, temperature, extraction time, and enzyme concentration, on two different responses. Furthermore, the changes in the cell wall morphology of SBL residue after EAE were observed through scanning electron microscopy (SEM).

Results:

Our findings indicate that under the optimal conditions (3:15 h of extraction, temperature 45 °C, pH: 4.9, and 1% Viscozyme L (v/w of leaves DW), EAE yielded 28.90 g/100 g DW of the water-soluble fraction and the total phenolic content 309.54 mg/100mL extract. Moreover, SEM images identified successful cleavage and hydrolysis of hydrolytic enzymes.

Conclusions:

This study enhances our knowledge of the extraction capabilities of sea buckthorn leaves and highlights the benefits of using enzyme-assisted methods to extract valuable bioactive compounds. Evolving high-quality sea buckthorn leaf extracts through enzyme-assisted extraction have the potential for various pharmaceutical, nutraceutical, and cosmeceutical applications.

161 - ANTIOXIDANT EFFECTS OF APPLE CIDER VINEGAR IN A METABOLIC SYNDROME RAT MODEL

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Objective:

The metabolic disorders characterizing the metabolic syndrome (MetS) are associated with oxidative stress that can be managed by natural antioxidants. The aim of this study is to assess the antioxidant activity of apple cider vinegar (ACV) in liver and kidney in an animal model of MetS induced by a cafeteria-fructose diet.

Methods:

Wistar rats received either the standard laboratory diet (S) or the cafeteria-fructose diet (CF) for 5 months. From the 4th month of experimentation, ACV was daily administered by intragastric gavage for 30 days at a rate of 3.5 ml/ kg/day (CFV). Throughout the experiment, monitoring of body weight was carried out. The determination of lipid peroxidation and the activity of antiradical defense enzymes was carried out at the end of the experiment in liver and kidney.

Results:

ACV caused a highly significant decrease ($p<0.001$) in body weight. It also counteracted the oxidative stress caused by the cafeteria-fructose diet in the CFV group compared to the CF group, by inducing a significant decrease ($p<0.001$) in the hepatic and renal levels of TBARS and hydroperoxides, and a highly significant increase ($p<0.001$) in the activity of superoxide dismutase (SOD), catalase and glutathione peroxidase (GPx) in liver and kidney tissues.

Conclusions:

The present study demonstrated that ACV was able to decrease the oxidative damage in liver and kidney caused by a cafeteria-fructose diet in the Wistar rat. This work, therefore, provides a promising therapeutic lead for the use of ACV in the correction of oxidative stress in the context of MetS.

164 - FERMENTATION WITH NATIVE MICROORGANISMS IN RAW, BLEACHED AND STERILIZED BROCCOLI PUREE AS A STRATEGY TO INCREASE THE SULFORAPHANE CONTENT

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Objective:

Apply to the fermentation with native microorganisms in broccoli puree demonstrating that fermentation is a viable strategy for the production of SFN a compound of high biological interest.

Methods:

Broccoli puree: Three pre-treatments were considered for the inflorescences: Raw broccoli, Sterilized broccoli sterilized at 121°C for 15 min and blanching broccoli in a thermoregulated bath at 57°C for 13 min. all samples was brought to a in a 1:3 ratio with sterilized water for puree formulation.
Starter cultures: A broccoli floret is taken and incubated at 37°C in MRS broth, to previgilate growth of lactobacteria, later glyceric, obtaining our stock culture.
Brocoli puree fermentation: each broccoli puree was inculted with the starter culture at a concentration of 10^8 CFU, fermentation was carried out in a shaker at temperature at 35°C for 20 day.
Sulforaphane content: SFN was quantified in reverse phase HPLC according to Mahn et al., 2020.

Results:

The SFN in all cases showed an increase because of fermentation, raw SFN without fermentation is 1.15±0.02 mg SFN/g m.s, increasing to 6.50±0.54, 9.74±0.33 and 467.91 mg SFN/g m.s. puree sterilized, raw, and bleached respectively. all the fermentations were showing a tendency to increase the SFN content, but at different times of sampling.

Conclusions:

Fermentation with native microorganisms increases the SFN content, showing better results in blanched broccoli puree. This may be due to the inactivation of enzymes that divert the SFN synthesis towards other degradation compounds. In addition, the bleaching conditions allow myrosinase to remain active endogenous broccoli

172 - MODIFICATIONS OF CHEMICAL COMPOSITION AND BIOLOGICAL ACTIVITY OF HAMAMELIDIS CORTEX EXTRACT AFTER INCUBATION EX VIVO WITH SKIN MICROBIOTA

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Objective:

Hamamelidis cortex (Hamamelis virginiana, HVC) is a pharmacopoeial herbal product with an established monograph of the European Medicines Agency, which classifies preparations of this plant material as traditionally used topically for the following indications: inflammation of the skin and mucous membranes of the oral cavity, skin dryness, haemorrhoids.

The aim of the study was to analyse the effect of the skin microbiota (SM) on the phytochemical composition of the aqueous HVC extract and to determine the effect of the HVC, its main compound, and its metabolite on inflammation in skin cells in vitro.

Methods:

The HVC and its main compound – hamamelitannin (compound was isolated and structure confirmed by NMR spectra) were incubated ex vivo for 48h with SM collected from healthy volunteers. Samples collected at 0, 6, 19, 24, and 48h were analysed by UHPLC-DAD-MS^n. The effect of the HVC, hamamelitannin, and the main metabolite on the inflammation of keratinocytes and fibroblasts was then investigated.

Results:

The main metabolite formed during the incubation of the extract and hamamelitannin with the SM was ellagic acid, despite the absence of hexahydroxydiphenoil group. While the extract and hamamelitannin inhibited the secretion of interleukins IL-6 and IL-8 by keratinocytes and fibroblasts, the produced ellagic acid stimulated their release.

Conclusions:

The SM influence the phytochemical changes of the Hamamelis virginiana bark extract, which can result in changes in its biological activity.

173 - THE INTERPLAY OF VAGINAL MICROBIOTA AND OAK BARK

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Objective:

Plant substances containing tannins, such as Quercus cortex (oak bark), have been used in traditional medicine for centuries to treat gynaecological conditions such as infections, inflammation and irritation. The aim of the study was to examine the effect of oak bark extracts on the taxonomic composition of the vaginal microbiota (VM) and to investigate the effect of the VM on the phytochemical composition of the tested extracts.

Methods:

Two preparations – traditional decoction and extract using Natural Deep Eutectic Solvents (NADES) – betaine and lactic acid were prepared and then incubated ex vivo with VM collected from female volunteers. The samples were analysed by UHPLC-DAD-MS^n before treatment and after 6, 12, and 24h of incubation with VM. After 24h, the VM was subjected to shotgun sequencing.

Results:

After 24h of incubation of VM with extracts, the relative abundance of Bacilli increased and Actinobacter decreased compared to the control group. The relative abundance of Lactobacillus was significantly higher after incubation with the extract prepared with NADES than with the traditional extract. The UHPLC-DAD-MS^n analysis showed that the tannins contained in the extracts were degraded or metabolized, while flavonoids, derivatives of rhamnetin, quercetin and taxifolin, were stable during incubation and were not metabolized by the VM.

Conclusions:

Due to the significant changes in both the chemical composition of the extracts and the taxonomic composition of the VM, these phenomena should be considered as playing part in therapeutic effectiveness of preparations containing oak bark.

201 - IMPACT OF CHLORELLA AND SPIRULINA TO REPLACE CONVENTIONAL PROTEIN FEEDS FOR SUSTAINABLE DAIRY COW DIET: META-ANALYSIS

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Objective:
In this study we will discuss the use of Chlorella and Spirulina as food supplements in the diet of dairy cows to improve milk production and quality.

Methods:
The study follows a meta-analysis type investigation to identify publications on the subject during the period from 2019 to 2022 in the three (03) databases: Springer Link, Science Direct, and Google Scholar.

Results:
Among the 585 publications identified, 04 were retained for analysis. Thus, the addition of C. vulgaris in the ration caused an increase in the daily quantity of milk from 13.58 Kg/d (R1: control ration) to 15.20 kg/d (R2: 2ml of C. vulgaris) and at 16.81 kg/d (R3: 4ml of C vulgaris), and for the second test, 29.7 kg/d for soybeans and 28.5 kg/d for FB (control rations) at 29.9 kg/d for the C vulgaris ration. In addition to the positive impact on the quantity of milk, the addition of C vulgaris showed interesting results on the rate of fat with rates of 36.2 g/kg, 37.4 g/kg for R2 and R3. And at 41.4 g/kg (C. vulgaris) versus 41 g/kg (soy) and protein improvement with 27.6 g/kg (R2) and 29 g/kg (R3) and 26.6 (soy), and also for the lactose rate: from 46.6 g/kg (soy) to 49 g/kg (R3) and 48 g/kg (R2). While Spirulina also demonstrated a marked improvement in milk production with 32.1 kg/d and 18.1 kg/d against 29.7 kg/d and 16.8 kg/d (controls) respectively, and an improvement in fat content of 41 g/kg (soya) to 45.0 g/kg (SPP) and also from 47.4g/kg (RSM) to 49.4g/kg (RSM+SPP). Similarly, proteins from 36.5 g/kg (RSM) to 37.1 g/kg (RSM+SPP) in addition to an improvement in lactose levels.

Conclusions:
These results argue for a strong prerogative of Chlorella and Spirulina to serve as quality food supplements to improve dairy performance.

202 - SOLID-STATE FERMENTATION OF BEE POLLEN - A STRATEGY TO IMPROVE THE BIOACTIVE COMPOUNDS AND BIOAVAILABILITY OF NUTRIENTS

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Objective:
The objective of this study was to use probiotic solid-state fermentation of bee pollen to obtain a product with an improved profile of bioactive compounds and enhanced bioavailability. The fermentation process utilized lactic acid bacteria, specifically L. plantarum and L. acidophilus

Methods:
Spectrophotometric methods were used for the determination of total polyphenols, flavonoids, antioxidant and antimicrobial activity. HPLC method was used for the quantification of individual bioactive compounds, such as polyphenols, flavonoids, and carotenoids. The bioavailability of the compounds was tested by in vitro digestion.

Results:
The results showed that there are significant differences between the chemical and bioactive composition of the bee pollen samples before and after the fermentation process. The fermentation process increased the value of bioactive compounds and their bioavailability. The total amount of polyphenols before fermentation was between 12.67-26.98 mg GAE /g sample and after fermentation, it varied between 19.56-78 mg GAE/g sample. Also, the fermentation process had a positive effect on the quantity of flavonoids from the samples. Samples of fermented pollen had a higher antioxidant and antimicrobial effect against the tested bacterial strains.

Conclusions:
Probiotic fermentation seems a promising option for increasing the value of bioactive compounds in pollen and their bioavailability, but additional research is needed to evaluate the effect of probiotic bacteria in the obtained product and their beneficial impact on health.

209 - THERAPEUTIC POTENTIAL OF TUALANG HONEY AND KELULUT HONEY ON INDOMETHACIN-INDUCED GASTRIC LESIONS

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Objective:
The study assesses the potential protective effects of the two Malaysian honeys (Tualang and Kelulut) on indomethacin-induced gastric ulcers in rats.

Methods:
Male Sprague-Dawley rats (n = 30) were randomly divided into 5 groups (n = 6).The control group and the indomethacin group were given distilled water; the positive control was given omeprazole at 40 mg/kg and the treated groups (Tualang and Kelulut Honey) at 2g/kg. The pre-treatment period was for 14 days. After the last dose, all groups except the control was given indomethacin to induced ulcer. Ulcer severity scoring (ulcer index), gastric oxidative enzymes (SOD, CAT, and GPX), malondialdehyde (MDA), cytokines and nitric oxide (NO) were measured to distinguish the effectiveness of two Malaysian honeys against gastric ulcer injury.

Results:
Decrease in ulcer index, MDA and NO concentration were observed with Tualang honey and Kelulut honey compared to the indomethacin group. While increased in SOD, CAT and GPX activities with Tualang and Kelulut honey compared to the indomethacin group were shown. There was a significant increase in IL-1β and TNF-α concentration in the indomethacin group compared to the normal control group. Both honey treated groups recorded a significant decrease in the levels of IL-1β and TNF-α. Histological observations found that the surface of the stomach mucosa was coated with mucus and was in an intact condition in the normal control group. The negative control group showed otherwise, the mucosa surface was clearly in an inflammatory state and the mucus secretion was also invisible.

Conclusions:
These findings suggested that Tualang and Kelulut honey effectively protects against gastric ulcers induced by indomethacin possibly due to the high flavonoid and phenol content in honey as cytoprotective actions.

INNOVATING FOOD TOWARDS SUSTAINABLE HEALTHY DIET

18 - DRIED OLIVE MILL WASTEWATERS OBTAINED BY SPRAY DRYING

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Objective:
In this work, we present the results relative to the phenolic compounds detected in dried olive mill wastewaters obtained by spray drying. Recently, a lot of research show that olive-derived phenols can exert pharmacological effects in the prevention of inflammation and oxidative stress. Olive phenols can also be used by the food industry as natural food additives with antioxidant and pharmacological properties and for extending the shelf life of food.
Olive mill wastewater from three-phase olive oil extraction process is a rich source of bioactive substances with various biological properties. We used olive mill wastewater as ingredients in the food industry for obtaining functional and nutraceutical new foods.

Methods:
Olive mill wastewater was collected during the crop year 2022/2023 from an olive mill located in Calabria, Italy, from the processing of olives of Carolea and Dolce di Rossano varieties after the centrifugation step using a three-phase mill. The drying process was achieved by means of industrial spray dryer. Qualitative and quantitative analyses were obtained by liquid chromatography tandem mass spectrometry, using an MSD Sciex Applied Biosystem API 4000 Q-Trap mass spectrometer.

Results:
The following phenol compounds have been identified and quantified in the obtained final dust: apigenin, catecol, hydroxytyrosol, tyrosol, vanillin, vanillic acid, caffeic acid, p-cumaric acid, ferulic acid, apigenin, diosmetin, luteolin, luteolin-7-O-glucoside, luteolin-4-O-glucoside, oleuropein, rutin, verbascoside, hydroxytyrosyl oleate.

Conclusions:
Therefore, olive mill wastewaters can produce an excellent dried extract rich in phenols with different biological properties by using a spray drier system at low temperatures.

60 - FRUITS JUICES SUPPLEMENTATION AND FERMENTATION WITH THE PROBIOTIC STRAIN LACTIPLANTIBACILLUS PLANTARUM DR7TM (CECT7481)

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Objective:

The population's demand for healthier foods is increasing. Fermentation can improve foods' nutritional profile but has been little explored in fruits, central players in a healthy diet. The aim of this study was to investigate the ability of the probiotic Lactiplantibacillus plantarum DR7™ (CECT7481) to ferment orange, apple, and peach juices, its stability and the production of bioactive compounds.

Methods:

Three different samples were analyzed for each fruit juice: original juice (B), juice with 10^9 CFU/serving (P) and juice with 10^9 CFU/serving fermented for 24-48h at 37 °C (FP). Stability analyses, including CFU enumeration, pH and total soluble solids (TSS), were performed throughout two months of cold storage at 4 ºC. Untargeted metabolomic analyses were performed by GC-MS and LC-MS to identify beneficial compounds. Finally, a hedonic analysis involving 51 participants assessed consumer acceptability of B, 24h and 48h FP orange juices.

Results:

P samples were stable throughout the study. FP samples showed an initial increase of CFUs accompanied by a change in pH, confirming the ability of the probiotic to ferment all juices. Metabolomic analyses identified several beneficial compounds in FP vs B samples, demonstrating increased nutritional value in DR7™-fermented fruit juices. The sensory evaluation showed that the 24h-FP and the B orange juices have comparable acceptance.

Conclusions:

Fruit juices are excellent carriers for the delivery of the probiotic L. plantarum DR7™ (CECT7481) and their fermentation results in tasty functional fruit juices enriched with health-promoting compounds.

86 - A COMPREHENSIVE ANALYSIS OF METABOLIC CHANGES AND HEALTH BENEFITS OF KOMBUCHA DURING FERMENTATION

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Objective:

This study comprehensively examined the fermentation process of sencha black tea to understand the developments and changes that occur during kombucha production. The objectives were to analyse the organic acid production, sugar content, antioxidant activity, and polyphenol content over a 10-day fermentation period.

Methods:

Daily samples of fermented sencha black tea were collected and analyzed using appropriate methods. Organic acids (malic, acetic, and oxalic) were evaluated and sugar content (sucrose, glucose, and fructose) was quantified and Antioxidant activity was assessed through DPPH, ABTS, and FRAP assays. The polyphenol content was determined by measuring gallic acid equivalents. HPLC was used to analyze gallic acid, epigallocatechin, and kaempferol levels.

Results:

Sugar content gradually decreased, with sucrose levels dropping from 1.39 g/100 ml to 0.00 g/100 ml by day 10. Organic acid production increased, particularly malic, acetic, and oxalic acids. Malic acid levels increased from 0.11 g/100 ml to 0.63 g/100 ml by day 10, and acetic acid reached 1.56 g/100 ml. Oxalic acid concentrations peaked at 1.31 g/100 ml on day 10. Antioxidant activity showed a progressive increase. The polyphenol content reached 103.9671455 mg of gallic acid/100 ml on day 6. HPLC analysis revealed dynamic fluctuations in gallic acid, epigallocatechin, and kaempferol levels.

Conclusions:

This study provides insight into the metabolic changes that occur during the fermentation of kombucha. The complexity of kombucha and its possible health advantages are highlighted by the drop in sugar content, along with increased generation of organic acids, improved antioxidant activity, and heightened polyphenol content. The dynamic alterations discovered through HPLC analysis highlight the complex nature of fermentation even more.These findings contribute to understanding the fermentation dynamics and health-enhancing properties of kombucha.

109 - WHITE BRINED CHEESE ENRICHED WITH FAVA (LATHYRUS CLYMENUM) BEANS AND PROBIOTICS

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Objective:
The main objectives of this study was to evaluate the compositional, antioxidant, and nutritional properties of fava beans and to examine its effect on chemical, mircobial and sensory properties of probiotic white brined cheese.

Methods:
For this perpose white brined cheeses from sheep milk were produced either with free probiotic cells as an adjuct culture or implemented within fava beans. The produced cheeses were evaluated regarding their physicichemical properties, digestibility, microbial stability and antioxidant capacity. Fianlly an orgalopepti review was conducted to acess the aceptabillity of produced white brined cheese.

Results:
The results showed high probiotic viability on cheese produced with incorporated fava beans which were represented by enhanced antioxidant capacity and high sensorial scores. Final products with incorporated probiotic cells could be characterized as probiotic thought 60 days of cold storage (4°C) retaining high viability scores (>10^7CFU/gr).

Conclusions:
The novel brined cheese with incorporated fava bean could show high commercialization potential providing enhanced fava nutritional characteristics in addition to a highly retained probiotic character.

132 - PRELIMINARY EVALUATION OF PREBIOTIC ACTIVITY OF BREWERS' SPENT GRAIN (BSG)-BASED FORMULATIONS OF PASTA

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Objective:
Brewers' spent grain (BSG), the main by-product of the beer industry, represents 85% of the total residues from the brewing process. BSG consists of the husks that covered the malted barley grains (Hordeum vulgare), in mixture with part of the pericarp and seed coat layers that are separated as residual solid material from the liquid wort after the mashing phase of beer production. Several factors limit BSG reuse in the food industry, such as the microbiological instability due to the high moisture, the presence of fermentable sugars and the poor technological and sensory characteristics. As a lignocellulosic material, its main constituents are fibers, and crude protein, with the remaining portion mainly represented by lipids. Its valuable composition, together with the low cost, make BSG an interesting material that has the potential to be used to produce goods with high added value, but only few commercial applications are currently available on the global market. Innovative uses of BSG in food production are increasingly being sought by the scientific and food industry communities.

Methods:
As there is an increasing interest in investigating dietary strategies able to modulate the gut microbial ecosystem which, in turn, may play a key role in human health, the aim of this study was prepare BSG-based formulations of pasta with different fortification level and the possibility of using it as a prebiotic. For this purpose, the prebiotic activity of BSG samples were evaluated in vitro using two probiotic Lactobacillus strains: L. casei and L. rhamnosus isolated from trademark products

Results:
Based on the in vitro growth study, BSG samples were found to be effective in selectively promoting the growth of Lacticaseibacillus rhamnosus strain as evidenced by the growth curves analysis.

Conclusions:
These results demonstrated that BSG-based formulations of pasta can help in restoring the balance of the gut microbiota. In conclusion, this study provides the basis for the development of sustainable nutrition and a healthy diet exploiting food waste.

156 - A PROTEOMIC INSIGHT OF CROSSTALK BETWEEN FOOD-ASSOCIATED LACTIPLANTIBACILLUS PLANTARUM C9O4 AND INFLAMED INTESTINAL EPITHELIAL CELLS IN AN IN VITRO INFLAMMATION MODEL

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Objective:

Chronic gut inflammation represents an emerging health concern with still a lack of successful therapies. Fermented foods and their associated lactic acid bacteria showed the potential to affect host health by modulating the immune and inflammatory response. This study is aimed at evaluating the crosstalk between food-associated Lpb. plantarum C9O4 and intestinal epithelial cells in an in vitro inflammation model.

Methods:

Healthy and inflamed NCM460 cells were exposed to Lpb. plantarum C9O4 for 4 hours. Inflammation was induced for 24 hours using an inflammatory cocktail consisting of 10 ng/ml TNF-α, 5 ng/ml IL-1β, and 10 ng/ml IFN- γ. Cytokines' modulation was performed through a high-throughput method for multiplex protein analysis. Intracellular proteomic changes were investigated by nanoLC-Orbitrap-MS/MS followed by bioinformatic functional analysis in which protein expression variability and Gene Ontology (GO) reclassification, using PANTHER database for molecular function and biological process, were performed to elucidate the molecular mechanisms involved in the Lpb. plantarum protective effect.

Results:

Cytokines profile shows the ability of C9O4 to significantly reduce levels of inflammatory biomarkers (i.e., IL-2, IL-5, IL-6, and IFN-γ) as well as to revert the apoptosis process in NCM460. Proteomic functional analysis reveals an active host-microbe interaction that highlights an immunoregulatory role of C9O4, able to revert the detrimental effects of IFN-γ through the JAK/STAT pathway, in which STAT1 seems to have a crucial role in Lpb. plantarum C9O4 mechanism of action in reverting the inflammatory effects.

Conclusions:

These results suggest a promising therapeutic role of fermented food-associated microbes for the management of gastrointestinal inflammatory diseases by inhibiting the JAK/STAT pathway.

176 - DIFFERENT PREBIOTIC BEHAVIOR OF THE AQUEOUS EXTRACT OF PISTACHIO LEAVES AMONG GENERA OF LACTOBACILLACEAE FAMILY

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Objective:

Pistachio (Pistacia vera L.) is a popular tree nut renowned for its distinct flavor and its nutritional values all over the world and especially in Sicily. In recent years, there has been growing interest in its potential as a prebiotic food, offering beneficial effects on gut health, because it is rich in dietary fiber, specifically the soluble ones. These kinds of fibers are known to resist digestion in the upper gastrointestinal tract, reaching the intestine intact where they serve as substrates for the growth of probiotic bacteria. Indeed, through fermentation by the gut microbiota, pistachio fiber produces short-chain fatty acids which have been associated with various health benefits, including improved gut barrier function, reduced inflammation, and enhanced nutrient absorption. The objective of the present study was to determine the effects of pistachio leaves on the gut microbiota with particularly attention to Lactobacilli.

Methods:

For this purpose, the preparation of the natural extract was performed by crushing the plant material until a homogeneous sample was obtained. The sample was then extracted in water at 90°C for 30 min. Subsequently, the extract was filtered by vacuum pump and stored in the dark at -20°C. Then, soluble polysaccharides extracted from pistachio leaves (SPEPL) via hot were used to evaluate the growth rates of Lactobacillus strains compared to MRS control to assess the prebiotic property of the substance.

Results:

The results suggested that pistachio leaf extract affects bacterial growth not always equally. In particular, L. paracasei showed a clear increase in growth in the presence of the extract. Unexpectedly, the non-significant influence on the growth rate of L. rhamonosus indicates that the extract does not contain substances that can be used as nutrients for this species.

Conclusions:

However, it can be concluded that further chemical-physical investigations will be necessary to better characterize this aqueous extract to understand the reason for the lack of favorable contribution to bacterial proliferation for specific species. Further research is warranted to explore the specific mechanisms underlying the prebiotic action of pistachio and its potential applications to design a synbiotic product in combination with Lactobacillus strains in promoting human health.

DIET, MICROBIOME AND HEALTH: PAST, PRESENT & FUTURE

48 - IMPROVEMENT OF THE NUTRITIONAL QUALITY OF BLACK BEAN (PHASEOLUS VULGARIS I.) POWDER DURING FERMENTATION: USE OF LACTIC STARTERS

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The objective of this study was to investigate lactic acid starters able to improve the nutritional quality of black bean powder (BBP) during fermentation. For this purpose, raw and cooked BBP was fermented with Lactobacillus acidophilus and BLHN7 isolate. After 120 hours of fermentation, the pH of medium was measured by pH meter, tannins and phytates by spectrophotometry, total proteins by the Kdjedhal method. The minerals by atomic absorption spectrophotometry and the total sugars by the phenol method. From these analyses, it was found that the pH decrease was not significantly different in BBP fermented with Lactobacillus acidophilus and BLHN7 isolate. This decrease in pH varied between 4.0 and 4.3. Principal Component Analysis (PCA) of the results shows the variability of nutritional parameters depending on the microorganisms used and the type of treatment applied to the BBP. However, a better increase in protein, iron and microbial growth is observed in the raw BBP fermented with Lactobacillus acidophilus. We observed an increase of 267, 240 and 118% respectively. It is also in the raw BBP that we observe a reduction of tannins and a small reduction of sugar content by 76 and 20% respectively. On the other hand, it is in the cooked BBP fermented with Lactobacillus acidophilus that phytates were reduced by 3.4% and magnesium increased by 180%. Calcium increased by 165% in cooked BBP fermented with BLHN7 isolate. Considering the effect of Lactobacillus acidophilus on the majority of the nutritional parameters studied, it would be interesting to use it to improve the nutritional quality of BBP as a dietary supplement for malnourished children.

62 - EVALUATION OF MICROBIAL DYNAMICS OF KOMBUCHA CONSORTIA UPON CONTINUOUS BACKSLOPPING IN COFFEE AND ORANGE JUICE

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Objective:
The kombucha market is diverse, and producers constantly test new components and flavours to satisfy customers' expectations. Replacing the original brewing medium, adding flavours, or using backslopping influence the composition of the symbiotic starter culture of bacteria and yeast (SCOBY). Yet, a deep characterisation of microbial and chemical changes in kombucha consortia in various unclassical growth media during backslopping has not been implemented. The study was aimed to develop and characterise new beverages based on SCOBY fermentation in unclassical growth environments.

Methods:
We studied the chemical properties and microbial growth dynamics of lactic acid bacteria-tailored (LAB-tailored) kombucha culture by 16S rRNA next-generation sequencing in coffee and orange juice during backslopping spanning for five cycles two to four days each.

Results:
Our data approved that tailored kombucha had a low abundance of LAB strains, but still it contained a higher amount of gluconic acid than the initial kombucha. Thus, we can assume that the added LAB influenced kombucha properties positively. In this study, we observed the dynamic changes in microbial composition during the backslopping cycles. Thus, backslopping changed the culture composition and accelerated the fermentation.

Conclusions:
This study gives an overview of pros and cons of backslopping technology for kombucha-based beverages production. Based on the research of two different media, this work provided valuable information regarding the aspects to consider for using backslopping method to produce novel kombucha drinks and what are the main drawbacks to solve it.

144 - PREVENTIVE EFFECT OF BARLEY BETA-GLUCAN CONSUMPTION ON RENAL ANGIOTENSIN II CONVERTING ENZYME (ACE2) EXPRESSION AND ON GUT MICROBIOTA IN OBESE RATS

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Objective:
Obesity is associated with microbial imbalances can be reestablished through, dietary therapy. Studies have demonstrated that dietary fiber has a positive effect on lipid disorders, increases Renal Agiotensin II Converting Enzyme (ACE2) and lowers high blood pressure by modulating the gut microbiota. The work aims to study the preventive effect of barley Beta-glucan consumption on lipid disorders and ACE2 expression in rats fed a high-fat-diet.

Methods:
24 male rats were divided into 4 groups, the 1st group presented a control, received a standard diet (CT), the 2nd group received a standard diet supplemented with 5% of Beta-glucan (CT+BG), the 3rd group received a high-fat diet (HFD), and the 4th received the same high-fat diet supplemented with 5% of Beta-glucan (HFD+BG). After 12 weeks of experimentation, the rats were sacrificed and biochemical assays were carried out. The renal ACE2 activity was measured using Fluorometric assay kit.-

Results:
A highly significant decrease was observed in total cholesterol, triglycerides, and Low Density Lipoprotein Cholesterol in (HFD+BG) group compared to (HFD) group. Moreover, a highly significant increase in ACE2 activity in the (HFD + BG) group compared to the (HFD) group, for the other groups no significant difference was observed.

Conclusions:
Our study promotes the Beta-glucan tested as a good substance for human health to improve biochemical parameters and ACE2 expression in obesity.

POLYPHENOLS

88 - IN VITRO INTERACTIONS OF PLANT EXTRACTS CONTAINING POLYPHENOLS DESIGNED TO PREVENT NASH WITH HUMAN GUT MICROBIOTA

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Objective:
Non-alcoholic fatty-liver is a widespread condition which, if untreated, can progress to non-alcoholic steatohepatitis (NASH). An interplay of western diet and gut microbiota has been reported to be involved in its development, but the role of the gut microbiota remains poorly described. In this context, plant extracts, rich in various bioactive molecules, appear promising in a multitargeted strategy. In this study, we investigated the interactions of Totum-448, a combination of plant extracts, containing polyphenols, designed to prevent NASH, with human gut microbiota, using batch colonic fermentation assays.

Methods:
Fresh stool from five healthy donors were used to inoculate batch vessels, treated or not with 1g/l Totum-448, and 24h fermentations were run. Microbial activity was followed by gas and short-chain fatty acid (SCFA) measurement, while composition was followed by qPCR analysis of selected bacterial populations. Totum-448 metabolites produced by microbiota metabolization were analyzed by UPLC-UV-MS.

Results:
No significant effect of Totum-448 on total gas and SCFA production was observed, together with no differences in gas profile and concentrations in acetate, propionate and butyrate. Total bacteria, gamma-Proteobacteria, Bacteroidetes and Firmicutes were not impacted by plant extracts. However, a very efficient metabolization of Totum-448 occurred regardless of stool donors, leading to the production of several polyphenol metabolites from plant extract precursors.

Conclusions:
These data suggest that Totum-448 has a limited impact on microbial activities, but confirm a key role of gut microbiota in plant extracts bioaccessibility, that needs to be further investigated in a more complex model of the human gut microbiome.

162 - BIOPROSPECTION OF COFFEE BY-PRODUCTS AS A SOURCE OF BIOACTIVE COMPOUNDS

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Objective:
During the processing of coffee cherry into coffee bean, a lot of by-products are generated. Despite of the wide variety, there are few studies addressing not only the coffee husk, but also immature and defective coffee beans as renewable sources of value-added products. The aim of this study was to evaluate the physico-chemical composition of coffee husk (CH), green coffee (GC), roasted coffee grain (RC) and commercial coffee powder (CCP) of a Brazilian coffee producer.

Methods:
Samples of GC, CH, RC were grounded in a blade mill through a sieve of 20 mesh, with exception of CCP. The moisture content was evaluated by infrared balance. Thereafter, soluble lignin content, insoluble lignin content, phenolic compounds, glucose, xylose, arabinose and acetic acid were determined on the basis of National Renewable Energy Laboratory (NREL) protocol, through an acid digestion method. HPLC was used in the samples analyses.

Results:
Total lignin content varied from 16.1 (GC) to 31.7% (CCP). Furthermore, glucana content ranged from 6.3 (CCP) to 27.8% (CH), xylana from 14.2 (RC) to 24.5% (CCP), arabinose from 1.2 (CH) to 5.0% (GC) and acetyl from 0.8 (CCP) to 2.7% (CH). Phenolic compounds profiles were distinct, depending on the sample. GC presented higher quantities of gallic acid and hydroxymethylfurfural; CH vanillin; RC vanillic acid, syringaldehyde and p-coumaric acid; CCP pyrocatechol, furfural and ferulic acid.

Conclusions:
The present study results demonstrated the presence bioactive and other compounds, which have high potential of different applications, mainly in the development of functional and new foods.

GUT BRAIN AXIS

107 - THE QUEST FOR PROBIOTICS WITH EFFECTS ON MENTAL HEALTH

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Objective:
We are only beginning to understand the network of biological systems that constitutes the bidirectional communication between gut bacteria and the brain. Communication pathways exist via chemical transmitters, neuronal pathways and the immune system enabling the gut microbiome to influence brain processes and mental health. Sustained peripheral inflammation drive altered immune signaling within the brain and reducing inflammation via the microbiota-immune-brain axis may improve brain health.

Methods:
Probiotics may influence the gut-brain-axis by improving the intestinal mucosal barrier, by inducing immune regulation, by modification of the gut microbiota, or by producing neurotransmitters that affects the brain via the vagus, or neuroendocrine pathways. At Chr Hansen we are exploring these mechanisms in vitro, in vivo, and in human trials. We have a large collection of bacterial strains with known effects on the intestinal barrier and the immune system, and with neurotransmitter secreting/stimulating capacity.

Results:
In a mouse model, a mixture of three strains reduced depression-like behavior with an efficacy comparable to fluoxetine. This and other strain combinations are now being tested in human proof-of-concept trials.
In patients with acute mania, consumption of a two-strain product reduced the rate of psychiatric rehospitalization 3-fold, and reduced rehospitalization time by 5 days compared to placebo. The probiotic benefit was increased in individuals with elevated levels of inflammation at baseline. These findings are further investigated in on-going trials.
Other clinical trials with Chr. Hansen probiotics have demonstrated beneficial effects on sleep patterns, stress levels and cognitive function.

Conclusions:
Probiotics have potential for improving mental health

186 - EVALUATION OF ECOLOGICAL AND FUNCTIONAL MODULATION OF THE GUT MICROBIOTA IN POST-STROKE RECOVERY PATIENTS

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Objective:

The gut-brain axis is a bidirectional communication system between the gut and the brain, whose perturbation can be involved in neurological damages. An imbalance within the gut microbiota (GM) coproduce a dysbiosis possibly related to risk factors for ischemic stroke such as diabetes, obesity, and hypertension. In particular, metabolites such as short chain fatty acids (SCFAs), indole and skatole can be involved in stroke outcomes. The aim of this study was to investigate changes in GM related metabolic activities after stroke event, and associations with clinical values.

Methods:

Faecal samples of 10 patients with stroke and 6 healthy subjects controls (CTRLs) were analysed in term of ecological profile by 16S rRNA and for functional profile by metabolomics with gas chromatograph coupled to a mass spectrometer (GC-MS). The gut permeability markers' zonulin was detected by ELISA.

Univariate and multivariate statistical analysis were performed for each metaomic dataset. Their correlations with clinical features and biochemical variables was performed by correlation analysis and non-parametric test.

Results:

Ruminococcaceae, Coriobacteriacea, Oscillospira were staristically associated with CTRLs, while Blautia, Akkermansia and Sutterella were related to patients. The metabolomic analysis revealed that high SCFAs characterized the profile of GM in stroke patients. Particularly, patients with lower motility showed the highest levels of SCFAs. On the contrary, complete depletion of indole was observed for the patients.

Conclusions:

Our findings highlighted the presence of altered microbial metabolites, especially SCFAs, with potential effects on patient's clinical outcomes.

189 - SYSTEMS MEDICINE FOR FUNCTIONAL STUDY OF THE GUT MICROBIOTA OF CHILDREN WITH AUTISM

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Objective:

Autism Spectrum Disorder (ASD) is a multifactorial neurological disorder characterized by language impairment, and repetitive behaviors. The bidirectional communication via gut-brain axis is driven by the gut microbiota (GM). We describe the GM functions of ASD patients, considering clinical, anamnestic and nutritional variables looking for new potential probiotics.

Methods:

Forty-one and 35 faecal samples collected from ASD and neurotypical children (controls, CTRLs), respectively, (age range, 3–15 years) were analysed by gas-chromatography mass spectrometry with solid phase micro extraction (GC-MS/SPME). The metabolomics data were correlated with operational taxonomic units (OTUs) from targeted-metagenomics and with subjects' metadata by statistical and computational models to compare ASD and CTRLs and to assess ASD confounding factors role such as: gastrointestinal (GI) symptoms, autism severity symptoms (ASS) and Child Behavior Checklist (CBCL) internalizing (INT) and externalizing (EXT) scales. The prediction of potential probiotics was performed by mathematical algorithms.

Results:

The ASD gut metabolic profile, compared with CTRLs, was characterized by high levels of SCFAs, ketones, indoles, alcohols and aldehydes. ASD without GI symptoms and with low ASS showed higher value of indole. The CBCL groups, showed 8 metabolites statistically expressed in ASD with CBCL-EXT risk versus no clinical symptoms, while 2 in those with CBCL-INT risk versus no clinical symptoms. The mathematical algorithms highlighted a decreasing of Bifidobacteria and Streptococci in ASD.

Conclusions:

Butanoic and propanoic acids were very higher in ASD, while indole was correlated those without GI symptoms and low ASS. These metabolites could play a potential role in postbiotic treatment.

GUT MICROBIOTA & IMMUNO-ONCOLOGY

58 - THE IMPACT OF ALCOHOL CONSUMPTION AND ORAL MICROBIOTA ON UPPER AERODIGESTIVE TRACT CARCINOMAS: A PILOT STUDY

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Objective:
Alcohol consumption is associated with oxidative stress and increased risk of carcinomas of the upper aero-digestive tract (UADT). Recently, it has been found that some microorganisms in the human oral cavity may locally metabolize ethanol, forming acetaldehyde, a carcinogenic metabolite of alcohol.

Methods:
In a cohort of patients firstly visited for UADT cancers, we estimated the alcohol consumption, by measuring Ethyl Glucuronide/EtG (a long-lasting metabolite of ethanol) in the hair and Carbohydrate-Deficient Transferrin/CDT (short-term index of alcohol intake) in the serum. Moreover, we analyzed, by culture-based methods, the presence of in the oral cavity, of Neisseria subflava, Streptococcus mitis and Candida albicans and glabrata, microorganisms generating acetaldehyde.

Results:
According to the EtG values, we correlated the alcohol drinking with the endogenous oxidative stress and the investigated microorganism presence. We show that 55% of heavy drinkers presented microorganisms generating acetaldehyde locally. Moreover, we found that the presence of oral acetaldehyde producing bacteria correlates with increased oxidative stress, compared to those of patients without such bacteria. As for the study of alcohol dehydrogenase gene polymorphisms (the enzyme transforming alcohol to acetaldehyde), we found that only the "CGTCGTCCC" haplotype was more frequent in the general population than in carcinoma patients.

Conclusions:
This pilot study suggests the importance to estimate the alcohol consumption (EtG), the presence of bacteria producing acetaldehyde and oxidative stress as a risk-factors for the onset of oral carcinomas

142 - ISOLATION AND EVALUATION OF BACILLUS SUBTILIS AND ENTEROCOCCUS HIRAE AS PROBIOTICS FOR FRESHWATER FISH FARMING

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Objective:
The objective of this work was to identify and characterize powerful autochthonous probiotics from the gastrointestinal tract (GIT) of a freshwater fish, Labeo rohita, to enhance the productivity of aquaculture.

Methods:
Forty-five isolates were obtained from healthy fish. Two isolates (KAF061 and KAF063) were chosen for evaluation of their safety characteristics, capability to survive in acidic environments, and colonizing capacity on the gut via pathogen exclusion. Their antioxidant activity was also tested. Molecular analysis was performed to identify the possible isolates, KAF061 and KAF063.

Results:
The two isolates exhibited strong antibacterial activity against fish infections, lack of hemolytic activity, gelatinase and lipase synthesis, and sensitivity to 85% of antibiotics. They were also non-toxic to the host animal, survived in acidic environments, and exhibited excellent colonizing capacity on the gut via pathogen exclusion. They also demonstrated considerable antioxidant activity. Molecular analysis identified KAF061 as Bacillus subtilis and KAF063 as Enterococcus hirae.

Conclusions:
KAF061 and KAF063 possess characteristics that make them potential probiotic candidates for aquaculture feed additives to improve productivity, minimize disease outbreaks, and increase nutrient absorption. The probiotics identified in this study, along with long-term effective water quality control and immunization, can significantly enhance the productivity of fisheries and reinforce their sustainability.

WOMEN MICROBIOME: A DIFFERENT WAY TO FEEL HEALTHY

90 - CHARACTERIZATION OF LACTOBACILLUS-STRAINS FOR VAGINAL WOMEN HEALTH

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Objective:
Vaginal eubiosis is characterized by beneficial lactobacillus-dominated microbiota. In contrast, vaginal dysbiosis, as bacterial vaginosis and vulvovaginal candidiasis, characterized by an overgrowth of multiple pathogens, is associated with an increased risk of adverse urogenital and reproductive health outcomes. Aim of this work is the evaluation of antipathogen capability of 4 probiotic strains Lactobacillus acidophilus (DSM 21717) LA02, Lactobacillus crispatus (DSM 33487) LCR04, Limosilactobacillus fermentum (DSM 32277) LF5 and Limosilactobacillus fermentum (DSM 19187) LF10, tested as alive and inanimate strains.

Methods:
Probiotic strains were firstly discriminated through FTIR analysis by IR Biotyper spectrometer (Bruker Optics-Daltonics GmbH) and phylogenetic classified by bioinformatic tool. Then, based on previous internal data demonstrating their potential antipathogen activity, it has been verified the probiotic inhibition of pathogens on 2 different eukaryotic models: VK2/E6E7 and 3D-model Reconstituted Human Vaginal Epithelium (RHVE) by testing pathogen survival and the effects of this competition on eukaryotic cells by analyzing cell viability and damage and cytokines response. In the end, it has been performed bioinformatic analyses of some genes of interest for vaginal wellness.

Results:
It has been found that probiotics, successfully characterized by FTIR analysis and phylogenetic classification, were able to inhibit the growth of pathogens. Additionally, they showed considerable cell protective effect when tested both as alive and inanimate strains.

Conclusions:
These results suggest that these probiotic strains, both as alive and inanimate, could be an excellent, non-invasive, adjuvant therapy in the treatment of vaginal infections and also a potential prevention strategy for women health.

111 - MAXIMIZING PROBIOTIC EFFICACY FOR VULVOVAGINAL CANDIDIASIS: THE ROLE OF CANDIDA ISOLATES AND RESEARCH CONDITIONS

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Objective:
The objective of this study is to investigate the importance of the used Candida isolate and research conditions, when developing probiotics for vulvovaginal candidiasis (VVC).

Methods:
First, virulence factors of various vaginal Candida albicans isolates were assessed to include only the most virulent strains in the subsequent anti-Candida experiments. This selection was based on growth, filamentation, cytotoxicity, adhesion, secreted aspartic protease and hemolytic activity. Hereafter, the efficacy of several probiotics was tested on these highly virulent Candida strains. By incorporating different vaginal Candida isolates, and using vaginal simulative medium, we strived to mimic the conditions in the host niche, as closely as possible. This provides us with a realistic view of the efficacy of the probiotics at the target site.

Results:
The virulence factors of the Candida isolates showed a large diversity. Moreover, the inhibitory effect of the tested probiotic strains varied substantially for the Candida strains tested, highlighting the importance of strain selection in probiotic research. Notably, big differences were observed between the effects on a lab strain and vaginal Candida isolates.

Conclusions:
These findings show the importance of utilizing multiple and relevant Candida strains in the development and selection of new probiotics. The Candida strains and experimental conditions used during the selection process of probiotic strains against VVC can have a major impact on the final clinical efficacy of probiotics.

154 - EFFICACY OF A MULTI-STRAIN PROBIOTIC FORMULATION FOR THE HEALTH OF POST-MENOPAUSAL WOMEN

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Objective:
During a woman's life, hormonal changes influence the homeostasis of the intestinal and vaginal microbiota. Such alterations cause bothersome infections that lead to inflammation, especially in the post-menopause period, when hormone levels drop dramatically.
Previous in vitro tests have shown that the antimicrobial and antiadhesive properties of L. plantarum PBS067, B. animalis subsp. lactis BL050 and L. rhamnosus LRH020 strains, contained in the probiotic formulation Femme, are useful in inhibiting the development of the most common urogenital pathogens. The aim of this study is to evaluate the efficacy of this multi-strain probiotic complex in post-menopausal women.

Methods:
50 post-menopausal women were enrolled in a clinical trial (ISRCTN15737648) to assess the inflammatory cytokine pattern and vaginal microbiota fluctuation after 28-day administration of the multi-strain probiotic formulation Femme (3B CFU/day). Vaginal well-being was measured using the Vaginal Health Index (VHI), while the inflammatory profile and vaginal microbiota were obtained by vaginal swabs analysis.

Results:
Clinical results showed an interesting decrease in menopausal symptoms. After probiotic administration, it has been observed: a 50% improvement in the VHI score ($p<0.001$), a reduction in inflammatory cytokines of 87.8%, 57.6%, and 40.8%, for IL-6, IL-1beta, and TNF-alpha, respectively ($p<0.05$), and a vaginal microbiota restoration, with an increase of 28% of lactobacilli abundance.

Conclusions:
These results suggested that Femme formulation is useful in menopause to reduce the risk of urogenital infections and improve vaginal dysbiosis.

DRUGS AND BUGS

79 - VIABILITY-PCR FOR QUANTIFICATION OF LACTOBACILLUS ACIDOPHILUS AND BIFIDOBACTERIUM BIFIDUM

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Objective:
To exert their beneficial effects, the microorganisms used in live biotherapeutic products (LBPs) and more generally in probiotic products must be viable and present in certain amounts.
The objective of the present study was to develop a molecular assay for the identification and enumeration of viable Lactobacillus acidophilus and Bifidobacterium bifidum, two microbial species frequently present in both LBPs and probiotic products.
The method, based on quantitative PCR (qPCR) coupled with the use of propidium monoazide (PMA) viability dye, is otherwise known as viability-PCR (vPCR).

Methods:
The vPCR method development involved: 1) determination of lethal conditions for the target microorganisms; 2) optimization of PMA concentrations for the selective detection of the microbial live cells; 3) application of qPCR combined with PMA pretreatment on mixtures of live and dead cells at known concentrations. Once set up, the vPCR was applied to the analysis of a commercial LBP product containing the two microorganisms.

Results:
The vPCR conditions proved effective for the selective quantification of the viable target microorganisms. For both microorganisms, the quantities determined by vPCR in the LBP product were significantly higher than those obtained by standard plate count, possibly because of the presence in the tested product of bacteria in the viable but non-culturable physiological state.

Conclusions:
The vPCR assay established in this work allowed the simultaneous identification, quantification and viability determination for both L. acidophilus and B. bifidum in approximately 5 hours, thus representing a reliable and time-efficient culture-independent alternative to conventional plate count.

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GENERAL INFORMATION

DATES & TIMES

September 16 - 19, 2023.

The Meeting will commence at 09.00 (CET) Saturday, September 16 and will conclude on Tuesday, September 19 at 12.30 (CET).

Invitations to participate are personal and non-transferable.

MEETING VENUE

September 16:
Auditorium della Tecnica, Via dell'Astronomia, 30 - 00144 Rome, Italy

September 17 - 19:
Auditorium della Tecnica,Viale Umberto Tupini, 65 - 00144 Rome, Italy

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www.centrocongressi.confindustria.it

LANGUAGE

September 16, il Corso FIMMG will be held in Italian - Translation service will not be provided.
September 17/18/19, the Meeting will be held in English - Translation service will not be provided.

DRESS CODE

Smart casual.

CLIMATE

September is one of the most beautiful months to visit Rome. Whilst approaching the end of summer, the weather in September is still warm and sunny. Temperatures range from a warm 25° degrees during the day and drop to a cool 15° degrees in the evening. A light weight jacket/cardigan/scarf is recommended for the evenings.

CLOAKROOM

If required, luggage can be left in the cloakroom at the venue.

REGISTRATION & NAME BADGES AVAILABLE AT THE ORGANIZING SECRETARIAT DESK

On-site registration and issuance of badges is available daily from:

- Saturday September 16: 08.00 - 14.00
- Sunday September 17: 08.00 - 19.00
- Monday September 18: 08.00 - 19.00
- Tuesday September 19: 08.00 - 13.00

Registration payment can be made by credit card or cash directly at the Organizing Secretariat desk.
For security purposes participants will be requested to present an identification document.
Participants and exhibitors will be required to wear name badges for access to the venue and all the meeting rooms.

Organizing Secretariat desk will be:
On September 16: floor R
From September 17 to Septembrer 19: exhibition area ground floor via dell'Astronomia.

REGISTRATION FEES (22% VAT included) - September 17/18/19

Participants	€ 400,00
Presenting Authors (abstract fee included)	€ 120,00
Biologists/Pharmacists/Chemists/Veterinarians	€ 200,00
Dieticians/Nutritionists	€ 200,00
Nurses	€ 120,00
IPA Members	€ 200,00
Mediterranean Task Force for Cancer Control Members	€ 150,00
Under 35*/ AGGEI Members	€ 150,00
Pediatric Day**	€ 200,00
Under 35 Pediatric Day	€ 100,00
Daily Registration	€ 200,00

* The applicant's registration form must be accompanied by a copy of an official document.

** If you are not registered to the Meeting.

REGISTRATION FEES
September 16 (FIMMG Session)

Participants by invitation only*

* Invitees to the FIMMG session are entitled to attend the meeting to be held September 17/18/19.

Registration fees include:

- Admission to scientific sessions, technical exhibition
- Final programme
- Access to B2B platform/meetings
- Coffee corner and lunches
- Opening ceremony and welcome cocktail on September 17
- Certificate of attendance
- Certificato ECM (agli aventi diritto)

BANKING AND CURRENCY EXCHANGE

The Italian monetary system is the Euro (€). Foreign currency can be exchanged at banks, currency exchange offices, hotels and the airport upon presentation of an identification document. All major credit cards are accepted in most hotels, restaurants and shops.

LIABILITY AND INSURANCE

The Organizing Secretariat cannot accept liability for personal injuries or for loss of, or damage to property belonging to Meeting participants (or accompanying persons) either during or as a result of the Meeting. Please check the terms and conditions of your health insurance.

CERTIFICATE OF ATTENDANCE

Certificates of attendance will be provided to all registered participants by the Organizing Secretariat desk.

FOOD AND BEVERAGES

Sunday September 17 - A buffet lunch will be served at the Meeting venue
Sunday September 17 - Welcome Cocktail will be served at the Meeting venue
Monday September 18 - A buffet lunch will be served at the Meeting venue
A free coffee corner will be available in the exhibition area

TRANSPORTATION AIRPORT INFORMATION

Rome is served by two international airports:
Rome Leonardo da Vinci International Airport, located in Fiumicino, 34 km from Rome's city centre.
Rome-Ciampino International Airport, located 15 km from Rome's city centre.

ACCESS TO THE MEETING VENUE FROM ROME LEONARDO DA VINCI INTERNATIONAL AIRPORT

- **Taxi:** The Meeting venue is located 23 km from the airport. Allow 30 mins by taxi, depending on traffic. The taxi fare costs € 50.00 (fixed fare).
- **Public transport:** Participants may take the Leonardo Express, a non-stop service which operates to/from https://www.trenitalia.com/en.html. From Roma Termini, participants can take Metro B to the Eur-Magliana stop. The trip takes about 17 minutes and costs 1.50 euros. Tickets can be purchased at the station. The Auditorium della Tecnica is a 3 minutes walk from the metro station.

ACCESS TO THE MEETING VENUE FROM ROME-CIAMPINO INTERNATIONAL AIRPORT

- **Taxi:** The Meeting venue is located 18 km from the airport. Allow 30 minutes by taxi, depending on traffic. The taxi fare costs € 30.00 (fixed fare).
- **Public transport:** Service Provider Terravision Bus Company. https://www.terravision.eu/airport_services.html?noredirect=en_US. Participants make take the bus to Rome Termini railway station. Allow approximately 40 minutes. The ticket costs € 6.00 and can be purchased either online or at the airport. From Roma Termini, participants can take Metro B to the Eur-Magliana stop. The trip takes about 17 minutes and costs 1.50 euros. Tickets can be purchased at the station. The Congress Center is a 3 minutes walk from the metro station.
- There is no train station at Rome-Ciampino International Airport.

TAXI SERVICES

We recommend using only licensed taxis located outside the airports and train stations. For taxi/shuttle services from the Meeting venue, please contact the Organizing Secretariat desk.
For reputable taxi companies, the following phone numbers are provided:

+39 06 3570 Radio Taxi
+39 06 5551 Samarcanda
+39 06 4994 La Capitale

Upon calling, the operator will provide the taxi identification number and indicate the time it will take the taxi to reach the caller.

UBER SERVICES

Uber remains legal to use in Rome; however, Italy only allows Uber Black (and Ubervans) as drivers must possess the car NCC license in order to operate. Due to the fact that there is no UberX or UberPOOL, Uber in Italy tends to be more expensive, on average, than taxis.

AUDITORIUM PARKING

- 7 min Piazzale Luigi Sturzo
- 8 min Eur garage - Via della chimica, 10
- 5 min Garage car parking - Viale dell'Urbanistica, 1

THE CITY OF ROME

Rome is the capital city of Italy and of the Lazio region. It has a population of approximately 2.8 million residents. The metropolitan area has a population of about 4 million. Rome is located in the central-western portion of the Italian peninsula, where the Aniene river joins the Tiber river.
An enclave of Rome is the State of the Vatican City, the sovereign territory of the Holy See. It is the smallest nation in the world, and the capital of the only religion to have representation in the United Nations (as a non-member observer state). Rome, refered to as Caput Mundi ("capital of the world"), la Citta Eterna ("the Eternal City"), Limen Apostolorum ("threshold of the Apostles"), la Citta dei Sette Colli ("the city of the seven hills") or simply l'Urbe ("the City"), is modern and cosmopolitan. As one of the few major European cities that escaped World War II relatively unscathed, central Rome remains essentially Renaissance and Baroque in character. The historic centre of Rome is listed by UNESCO as a World Heritage Site.

ORGANIZING SECRETARIAT

For additional information or queries, please address all correspondence to the Organizing Secretariat:

:e MEETING&CONSULTING

Via Michele Mercati, 33 - 00197 Rome, Italy
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probiotics2023@emec-roma.com
www.probiotics-prebiotics-newfood.com
www.emec-roma.com

SCIENTIFIC INFORMATION

ORGANIZING SECRETARIAT DESK AT THE MEETING VENUE WILL BE OPEN AS FOLLOWS:

DAY	DATE	FROM	TO
Saturday	September 16	08.00	14.00
Sunday	September 17	08.00	19.00
Monday	September 18	08.00	19.00
Tuesday	September 19	08.00	13.00

ORAL COMMUNICATIONS

Sessions are scheduled as follows

September 17
Aula Louis Pasteur 2
09.30 - 13.30

September 18
Aula Louis Pasteur 2
10.00 - 12.30
14.30 - 17.00

POSTERS

The E- poster area will be open from 10.30 on September 17 to 12.00 on September 19. The poster area is on the ground floor. The posters will be available on the meeting app.
Further information about the app is available on the meeting website.

SLIDES CENTERS

All speakers and authors must deliver their presentation to the slide centers 2 hours in advance or the day before their speech. Slides Center is located in Aula Urbanistica - Ground Floor.

ACCREDITAMENTO ECM

e meeting&consulting in qualità di Provider standard ha accreditato:

il corso FIMMG del giorno 16 settembre 2023 nell'ambito del **"12th Probiotics, Prebiotics & New Foods, Nutraceuticals and Botanicals - for Nutrition & Human and Microbiota Health"** per le seguenti categorie:

16/09/2023 – EVENTO ID: 387894

12TH PROBIOTICS, PREBIOTICS & NEW FOODS - CONOSCIAMO VERAMENTE I PROBIOTICI E PERCHE' DOVREMMO UTILIZZARLI?

Responsabile scientifico: Alberto Chiriatti

Durata/ore formative: 5 - **Crediti assegnati:** 1,5

Obiettivo formativo: 4 – Appropriatezza delle prestazioni sanitarie, sistemi di valutazione, verifica e miglioramento dell'efficienza ed efficacia. Livelli essenziali di assistenza (LEA)

Destinatari dell'iniziativa

Professione	Discipline
MEDICO CHIRURGO	Medicina generale (Medici di famiglia)

17-19/09/2023 – EVENTO ID: 388051

12TH PROBIOTICS, PREBIOTICS & NEW FOODS – NUTRACEUTICALS, BOTANICALS & PHYTOCHEMICALS FOR NUTRITION & HUMAN, ANIMAL AND MICROBIOTA HEALTH

Responsabile scientifico: Lucio Capurso; Alfredo Guarino

Durata/ore formative: 30 - **Crediti assegnati:** 6

Obiettivo formativo: 4 – Appropriatezza delle prestazioni sanitarie, sistemi di valutazione, verifica e miglioramento dell'efficienza ed efficacia. Livelli essenziali di assistenza (LEA)

Destinatari dell'iniziativa

Professione	Discipline
BIOLOGO	Biologo
CHIMICO	Chimica analitica
DIETISTA	Dietista; Iscritto nell'elenco speciale ad esaurimento
FARMACISTA	Farmacista pubblico del SSN; Farmacista territoriale; Farmacista di altro settore
MEDICO CHIRURGO	Allergologia ed immunologia clinica; Dermatologia e Venereologia; Endocrinologia; Gastroenterologia; Malattie metaboliche e Diabetologia; Malattie dell'apparato respiratorio; Malattie infettive; Medicina interna; Neonatologia; Oncologia; Pediatria; Reumatologia; Ginecologia e Ostetricia; Biochimica clinica; Farmacologia e Tossicologia clinica; Microbiologia e Virologia; Patologia clinica (laboratorio di analisi chimico-cliniche e microbiologia); Igiene degli alimenti e della nutrizione; Medicina generale (Medici di famiglia); Pediatria (Pediatri di libera scelta); Scienza dell'alimentazione e Dietetica

INFERMIERE	Infermiere
INFERMIERE PEDIATRICO	Infermiere pediatrico
VETERINARIO	Igiene degli allevamenti e delle produzioni zootecniche; Igiene prod.,trasf., commercial., conserv. e tras. alimenti di origine animale ederivati; Sanità animale

17/09/2023 – EVENTO ID: 387967

12TH PROBIOTICS, PREBIOTICS & NEW FOODS – PEDIATRIC DAY

Responsabile scientifico: Alfredo Guarino

Durata/ore formative: 9 - **Crediti assegnati:** 2,7

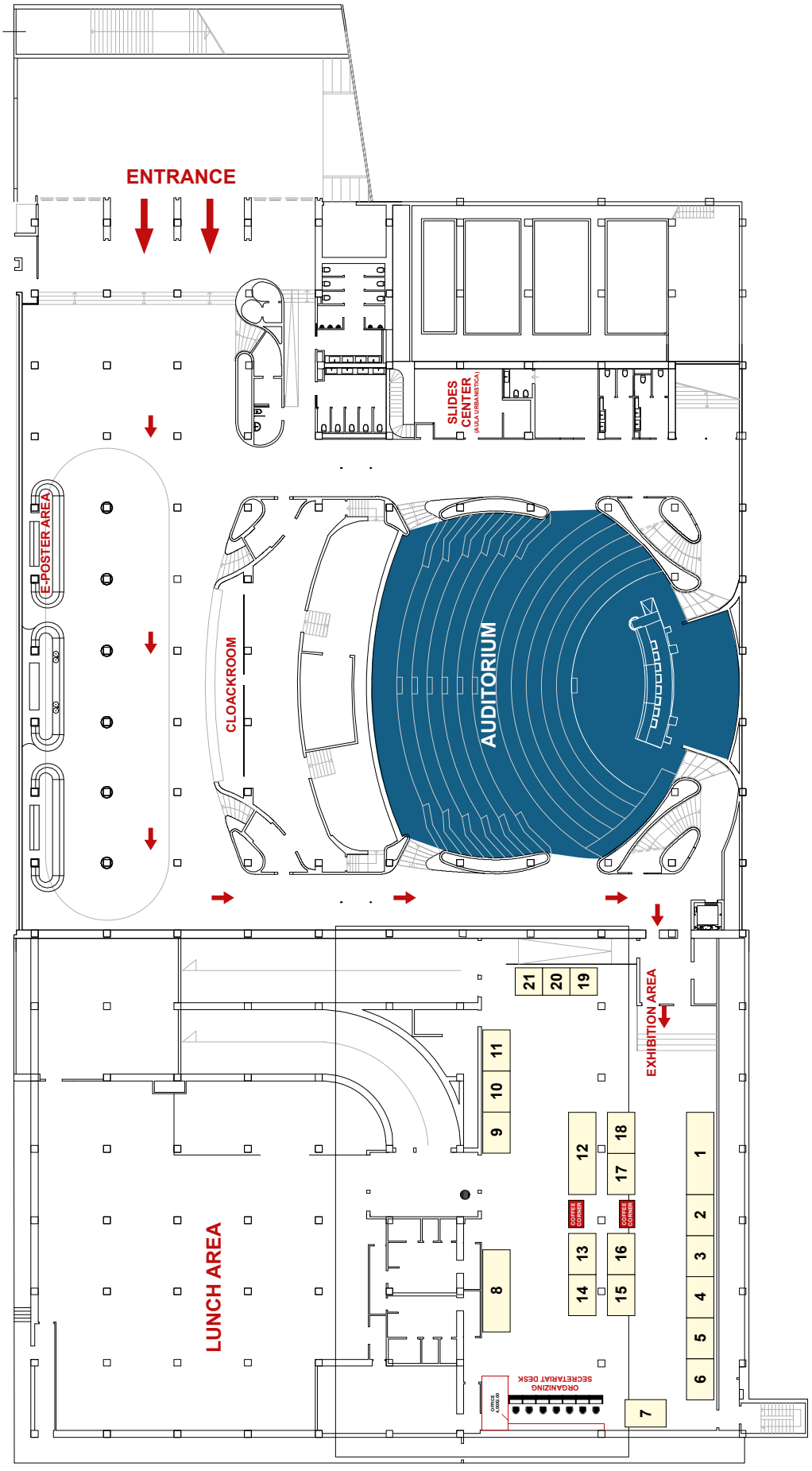
Obiettivo formativo: 4 – AAppropriatezza delle prestazioni sanitarie, sistemi di valutazione, verifica e miglioramento dell'efficienza ed efficacia. Livelli essenziali di assistenza (LEA)

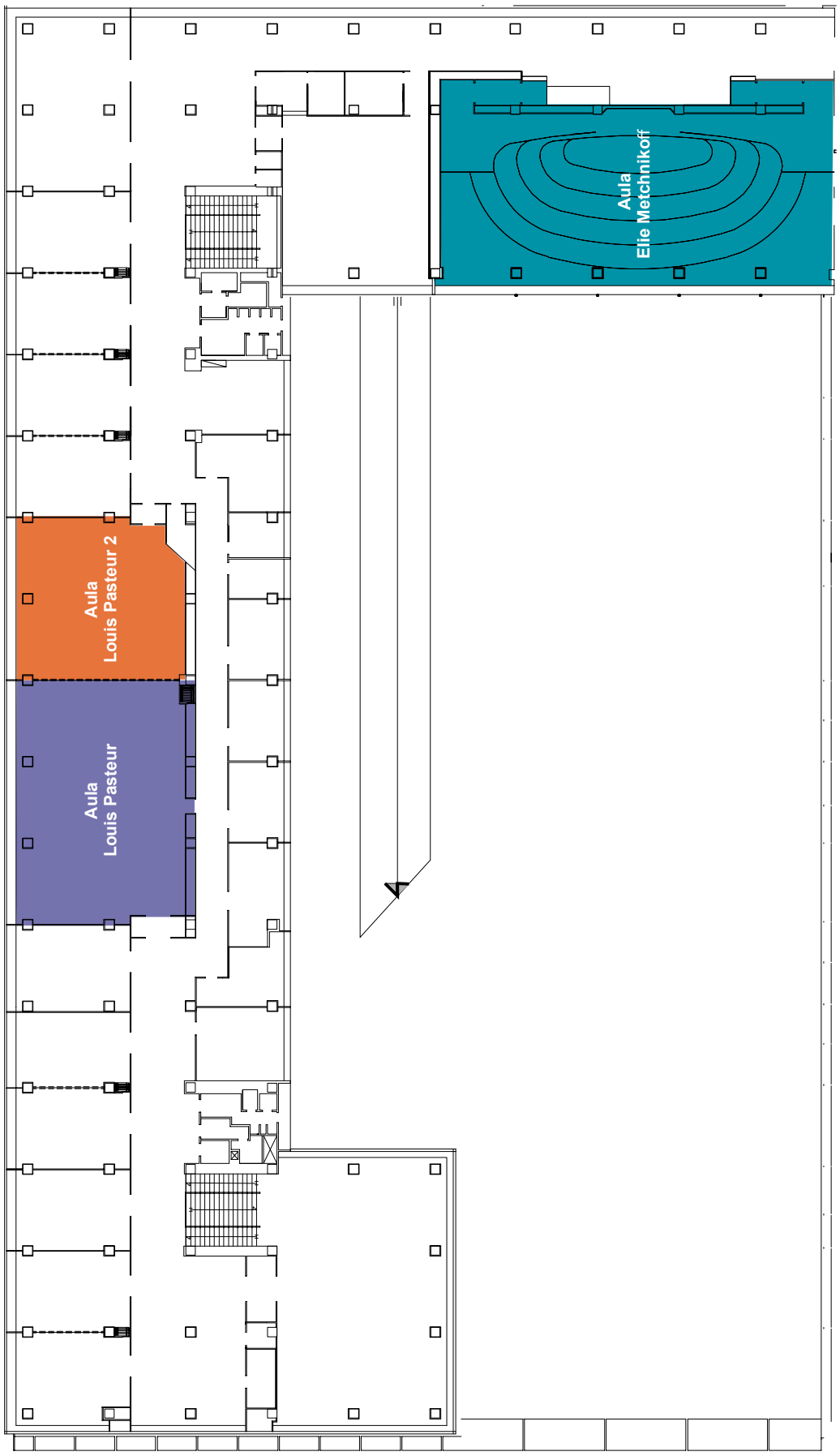
Destinatari dell'iniziativa

Professione	Discipline
BIOLOGO	Biologo
CHIMICO	Chimica analitica
DIETISTA	Dietista; Iscritto nell'elenco speciale ad esaurimento
FARMACISTA	Farmacista pubblico del SSN; Farmacista territoriale; Farmacista di altro settore
MEDICO CHIRURGO	Allergologia ed immunologia clinica; Dermatologia e Venereologia; Endocrinologia; Gastroenterologia; Malattie metaboliche e Diabetologia; Malattie dell'apparato respiratorio; Malattie infettive; Medicina interna; Neonatologia; Oncologia; Pediatria; Reumatologia; Ginecologia e Ostetricia; Biochimica clinica; Farmacologia e Tossicologia clinica; Microbiologia e Virologia; Patologia clinica (laboratorio di analisi chimico-cliniche e microbiologia); Igiene degli alimenti e della nutrizione; Medicina generale (Medici di famiglia); Pediatria (Pediatri di libera scelta); Scienza dell'alimentazione e Dietetica
INFERMIERE	Infermiere
INFERMIERE PEDIATRICO	Infermiere pediatrico

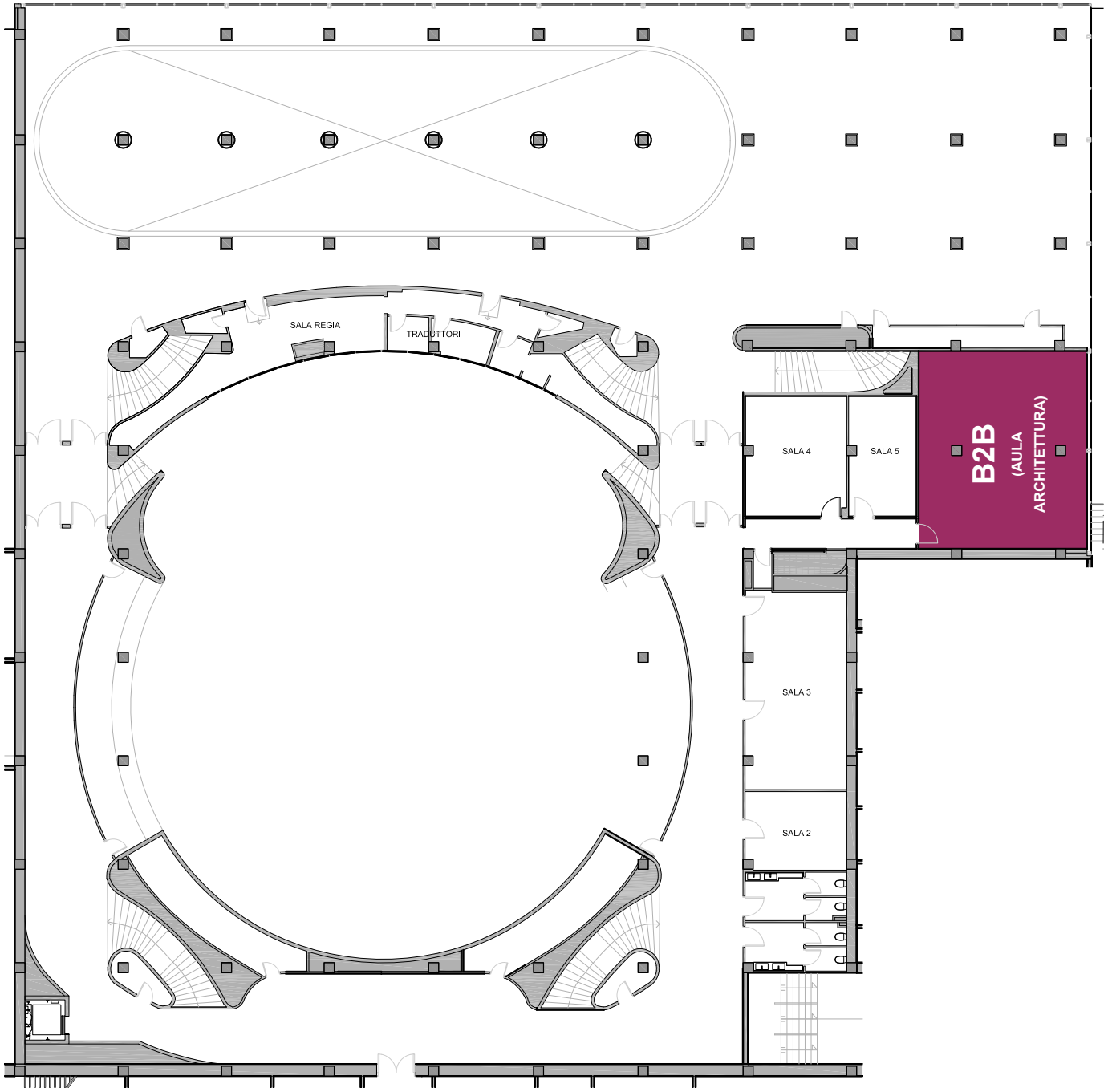
EXHIBITION AREA

STAND	AZIENDE
1	DICOFARM
2	PROBIOTICAL
3	BICT
4	GIULIANI
5	NAMED
6	CosmosID
7	FONDAZIONE ISTITUTO DANONE
8	DANONE NUTRICIA
9	SANOFI
10	SYNLAB ITALIA
11	BINC
12	AG PHARMA
13	PROBI AB
14	IFF – HEALTH
15	ISTITUTO ALLERGOSAN ITALIA
16	YAKULT ITALIA
17	OF MOM/COREEGROUP
18	IPA DAY GLOBAL
19	CEC Editore
20	CLOROFILLA editoria scientifica
21	POSTBIOTICA




Aula
Elie Metchnikoff
Aula
Louis Pasteur 2
Aula
Louis Pasteur

MEZZANINE


SALA REGIA
TRADUTTORI
SALA 4
SALA 5
B2B
(AULA
ARCHITETTURA)
SALA 3
SALA 2

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