ISAPP

International Scientific Association for **PROBIOTICS** and **PREBIOTICS**

2023 MEETING GUIDE

June 26-28, 2023

Denver, Colorado, USA

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Welcome

This is an exciting year for ISAPP and I would say for biotics in general. An icon in the field, Dr. Mary Ellen Sanders, is retiring as the Executive Science Officer of ISAPP. Mary Ellen is first and foremost a scientist who has helped shape and direct ISAPP since she was a founding member. She has kept us true to our mission, focused on the science. We hope this retirement is only from ISAPP and we still see her involved and influencing the field for years to come. Mary Ellen's innumerable contributions to the field will be celebrated this year and into the future with the launch of the Sanders Award for Advancing Biotic Science.

I am happy to begin this next phase for ISAPP under the leadership of our new Executive Director, Marla Cunningham. We are confident that Marla's attributes and energy are exactly what ISAPP needs at this time and look forward to working with her for many years. She will surely shape ISAPP with her own vision, which we are confident will benefit all in the field.

Daniel Merenstein, ISAPP President

Welcome to the 2023 ISAPP meeting in Denver, Colorado!

We are happy to once again have the opportunity to bring together scientists making advances in the field of biotics to create new connections, inspire new ideas and begin new collaborations.

There are plenty of opportunities to engage with your peers during the meeting. The meeting kicks off with interactive group discussions synthesising insights from recent scientific publications in the biotics field. Discussion groups the next day convene subject matter experts alongside broader meeting attendees to progress key questions of current relevance in the biotics field today and into the future. For member scientists, our pre-meeting innovation workshops connect industry and early career scientists to exchange knowledge and fertilise new perspectives. Our social event schedule provides opportunities to enjoy the company of like-minded scientists in historic Denver settings across two evenings.

Gather new insights from thought-provoking plenary lectures on interventions for microbiome maturation in early life as well as resilience in adulthood; vaginal and immune interactions; predictors of interindividual response and precision application of biotics; mechanistic and clinical advances in the gut brain axis field; exploration of microbe:microbe interactions upon probiotic administration, amongst other talks. Our popular late-breaking news schedule provides a forum to hear new developments, projects, and perspectives from attending scientists.

We hope you will find rewarding opportunities to learn and connect together within the ISAPP community. Thank you all for your participation and contributions, and please enjoy the meeting.

Marla Cunningham, ISAPP Executive Director

ISAPP

Being at the forefront of biotic science, ISAPP recognizes the importance of innovation to tackling the many scientific and clinical challenges facing the biotics field today. This year we are excited to debut a new workshop focused on innovation. For this workshop, the Industry Advisory Committee (IAC) and the Students and Fellows Association (SFA) have joined forces and initiated a new way to share knowledge and promote networking opportunities.

Workshop 1: Chaired by Marla Cunningham

Innovation in prebiotics: What's next?

Recent years have brought a surge of interest in prebiotic innovation. A broad range of microbiome-modulating compounds is being explored as candidate prebiotics, including nature-derived, modified, and synthetic substances. There is growing interest in the ability to select specific substrates to provide targeted modification of the microbiome as well as to identify determinants of individual response. At the same time, our knowledge continues to expand about the mechanisms of interaction of prebiotic substances with the host and microbiota. This workshop session will explore these and other concepts of innovation within the space.

Workshop 2: Chaired by Brendan Daisley

Latest advances in microbiome models and biotic screening techniques.

Microbiome models have made significant advancements in recent years, revolutionizing our understanding of the complex microbial communities inhabiting our bodies and the environment. These models can generate vast amounts of genomic, metagenomic, and metatranscriptomic data, allowing researchers to predict and simulate the interactions and functions within diverse microbial communities. By unraveling the intricate dynamics of microbiomes under controlled conditions, these models can provide valuable insights into the roles of microbes on human health, disease development, and ecosystem functioning. The workshop will explore innovative advancements in microbiome models as well as biotic screening techniques and their potential implications for the future, delving into topics such as the use of high-throughput bioreactor models, computational algorithms, data integration techniques, and their applications in personalized medicine, environmental conservation, and agricultural sustainability.

Workshop 3: Chaired by Daragh Hill

Looking to the future for food and biotics.

Fermented and prebiotic foods have grown in popularity in recent years, marketed for their health effects, including on the gut microbiome and immune system. The scientific, medical, and food industries are continuing to improve our understanding of how these foods may benefit our health, including which components are responsible for any health benefits. For example, fermented foods are not necessarily probiotic foods, with only some containing microbes that meet the strict criteria to be called a 'probiotic'. Future studies are still needed to confirm if these may be of therapeutic benefit, and who may benefit the most from consuming these products. This workshop session will explore if and how foods may be a vehicle to provide probiotics, prebiotics, and/or postbiotics.

Workshop 4: Chaired by Mariya Petrova

Probiotic application beyond the gut: What have we learned and what's next?

The last decade has marked the expansion of probiotic research (and the market) beyond the gut and gut-related conditions such as IBD, IBS, diarrhea, and constipation. With an increased understanding of the role of the human microbiota within other body sites, research has slowly turned towards other probiotic benefits and applications - from developing novel probiotic formulations for urogenital health, to skin products and formulations that can provide benefits via the gut-brain axis. The opportunities seem endless. This workshop session will explore these and other innovative applications of probiotics beyond the gut.

Microbiome endpoints for clinical trials.

The number of clinical trials focusing on the beneficial effects of different biotics has significantly grown in the last decade. During these clinical studies, a common area of investigation is the human microbiome and biotics' effects in modulating the microbiome. With the evolving nature of the field, many questions arise from scientists working in this area - choosing the best endpoints based on current knowledge, linking putative microbiome markers to health benefits, the impact of baseline microbiome status on response rates, going beyond taxonomic changes into metabolomic analysis, and many other questions. This year the IAC learning forum will provide a state-of-the-art synthesis of current knowledge and future directions for scientists designing and interpreting clinical studies with microbiome endpoints.

Industry Forum Speakers:

Jacques Ravel, University of Maryland School of Medicine, Institute for Genome Sciences, Baltimore, USA

Dr. Ravel is a Professor in the Department of Microbiology & Immunology and the Acting Director at the Institute for Genome Sciences (IGS), University of Maryland School of Medicine in Baltimore, MD. His laboratory research uses clinical genomics and systems biology approaches to develop improved strategy to manage gynecological and obstetrics conditions, including innovative live biotherapeutics drug formulations to manipulate the vaginal microbiome. By applying multi-omics approaches, his research is contributing to our improved understanding of the role of the vaginal microbiome in health and disease. He has published over 300 peer-reviewed articles. His work earned him to be elected to Fellowship of the American Academy of Microbiology (AAM) in 2012.

Sean Gibbons, Institute for Systems Biology, Seattle, WA, USA

Sean Gibbons is an Associate Professor at the Institute for Systems Biology (ISB), an affiliate Associate Professor in the Departments of Bioengineering and Genome Sciences at the University of Washington, and a data science fellow at the eScience Institute, in Seattle. His lab studies the human microbiome and its influence on health and disease, spanning the fields of ecology, evolution, microbiology, precision healthcare, and computational systems biology. The lab has recently developed community-scale metabolic modeling tools for engineering the metabolic outputs of the gut microbiome, which has potential applications to precision nutrition and personalized probiotics.
Website: https://gibbons.isbscience.org/

The interactive session provides an opportunity for scientists to discuss insights from recent papers which have moved the field forward in some way, with novel approaches, findings, perspectives, or challenges. All meeting participants will be divided into 12 tables, each discussing a different paper. Each table will have a leader who will coordinate the table discussion and report back to the full group at the end of the session.

The interactive session is chaired by Anisha Wijeyesekera, ISAPP Board Member, University of Reading, UK.

Table 1: Led by David Obis
VanEvery H et al. 2023. Microbiome epidemiology and association studies in human health.

Abstract: Studies of the human microbiome share both technical and conceptual similarities with genome-wide association studies and genetic epidemiology. However, the microbiome has many features that differ from genomes, such as its temporal and spatial variability, highly distinct genetic architecture and person-to-person variation. Moreover, there are various potential mechanisms by which distinct aspects of the human microbiome can relate to health outcomes. Recent advances, including next-generation sequencing and the proliferation of multi-omic data types, have enabled the exploration of the mechanisms that connect microbial communities to human health. Here, we review the ways in which features of the microbiome at various body sites can influence health outcomes, and we describe emerging opportunities and future directions for advanced microbiome epidemiology.

Table 2: Led by Kirstie Canene-Adams
Shalon D et al. 2023. Profiling the human intestinal environment under physiological conditions.

Abstract: The spatiotemporal structure of the human microbiome, proteome and metabolome reflects and determines regional intestinal physiology and may have implications for disease. Yet, little is known about the distribution of microorganisms, their environment and their biochemical activity in the gut because of reliance on stool samples and limited access to only some regions of the gut using endoscopy in fasting or sedated individuals. To address these deficiencies, we developed an ingestible device that collects samples from multiple regions of the human intestinal tract during normal digestion. Collection of 240 intestinal samples from 15 healthy individuals using the device and subsequent multi-omics analyses identified significant differences between bacteria, phages, host proteins and metabolites in the intestines versus stool. Certain microbial taxa were differentially enriched and prophage induction was more prevalent in the intestines than in stool. The host proteome and bile acid profiles varied along the intestines and were highly distinct from those of stool. Correlations between gradients in bile acid concentrations and microbial abundance predicted species that altered the bile acid pool through deconjugation. Furthermore, microbially conjugated bile acid concentrations exhibited amino acid-dependent trends that were not apparent in stool. Overall, non-invasive, longitudinal profiling of microorganisms, proteins and bile acids along the intestinal tract under physiological conditions can help elucidate the roles of the gut microbiome and metabolome in human physiology and disease.

Table 3: Led by Shalome Bassett
Wastyk HC et al. 2021. Gut-microbiota-targeted diets modulate human immune status.

Summary: Diet modulates the gut microbiome, which in turn can impact the immune system. Here, we determined how two microbiota-targeted dietary interventions, plant-based fiber and fermented foods, influence the human microbiome and immune system in healthy adults. Using a 17-week randomized, prospective study (n = 18/arm) combined with -omics measurements of microbiome and host, including extensive immune profiling, we found diet-specific effects. The high-fiber diet increased microbiome-encoded glycan-degrading carbohydrate active enzymes (CAZymes) despite stable microbial community diversity. Although cytokine response score (primary outcome) was unchanged, three distinct immunological trajectories in high-fiber consumers corresponded to baseline microbiota diversity. Alternatively, the high-fermented-food diet steadily increased microbiota diversity and decreased inflammatory markers. The data highlight how coupling dietary interventions to deep and longitudinal immune and microbiome profiling can provide individualized and population-wide insight. Fermented foods may be valuable in countering the decreased microbiome diversity and increased inflammation pervasive in industrialized society.

Table 4: Led by Vimac Nolla
Graham AE et al. 2023. The microbial food revolution.

Abstract: Our current food system relies on unsustainable practices, which often fail to provide healthy diets to a growing population. Therefore, there is an urgent demand for new sustainable nutrition sources and processes. Microorganisms have gained attention as a new food source solution, due to their low carbon footprint, low reliance on land, water and seasonal variations coupled with a favourable nutritional profile. Furthermore, with the emergence and use of new tools, specifically in synthetic biology, the uses of microorganisms have expanded showing great potential to fulfil many of our dietary needs. In this review, we look at the different applications of microorganisms in food, and examine the history, state-of-the-art and potential to disrupt current foods systems. We cover both the use of microbes to produce whole foods out of their biomass and as cell factories to make highly functional and nutritional ingredients. The technical, economical, and societal limitations are also discussed together with the current and future perspectives.

Table 5: Led by Elaine Vaughan
Freijy TM et al. 2023. Effects of a high-prebiotic diet versus probiotic supplements versus synbiotics on adult mental health: The "Gut Feelings" randomised controlled trial.

Abstract:
Background: Preliminary evidence supports the use of dietary interventions and gut microbiota-targeted interventions such as probiotic or prebiotic supplementation for improving mental health. We report on the first randomised controlled trial (RCT) to examine the effects of a high-prebiotic dietary intervention and probiotic supplements on mental health.
Methods: “Gut Feelings” was an 8-week, 2 × 2 factorial RCT of 119 adults with moderate psychological distress and low prebiotic food intake. Treatment arms: (1) probiotic supplement and diet-as-usual (probiotic group); (2) high-prebiotic diet and placebo supplement (prebiotic diet group); (3) probiotic supplement and high-prebiotic diet (synbiotic group); and (4) placebo supplement and diet-as-usual (placebo group). The primary outcome was assessment of total mood disturbance (TMD; Profile of Mood States Short Form) from baseline to 8 weeks. Secondary outcomes included anxiety, depression, stress, sleep, and wellbeing measures.

Table 5: con't

Results: A modified intention-to-treat analysis using linear mixed effects models revealed that the prebiotic diet reduced TMD relative to placebo at 8 weeks [Cohen's d = −0.60, 95% confidence interval (CI) = −1.18, −0.03; p = 0.039]. There was no evidence of symptom improvement from the probiotic (d = −0.19, 95% CI = −0.75, 0.38; p = 0.51) or synbiotic treatments (d = −0.03, 95% CI = −0.59, 0.53; p = 0.92). Improved anxiety, stress, and sleep were noted in response to the prebiotic diet while the probiotic tentatively improved wellbeing, relative to placebo. No benefit was found in response to the synbiotic intervention. All treatments were well tolerated with few adverse events.

Conclusion: A high-prebiotic dietary intervention may improve mood, anxiety, stress, and sleep in adults with moderate psychological distress and low prebiotic intake. A synbiotic combination of high-prebiotic diet and probiotic supplement does not appear to have a beneficial effect on mental health outcomes, though further evidence is required. Results are limited by the relatively small sample size.

Table 6: Led by Seema Mody

Leyrolle Q et al. 2021. Prebiotic effect on mood in obese patients is determined by the initial gut microbiota composition: A randomized, controlled trial.

Abstract:

Background and aims: Metabolic and behavioural diseases, which are often related to obesity, have been associated to alterations of the gut microbiota considered as an interesting therapeutic target. We have analyzed in a cohort of obese patients treated with prebiotic inulin versus placebo the potential link between gut microbiota changes occurring upon intervention and their effect on psychological parameters (mood and cognition).

Methods: A randomized, single-blinded, multicentric, placebo-controlled trial was conducted in 106 obese patients assigned to two groups: prebiotic versus placebo, who received respectively 16 g/d of native inulin or maltodextrin combined with dietary advice to consume inulin-rich or -poor vegetables for 3 months as well as to restrict caloric intake. Anthropometric measurements, food intake, psychological questionnaires, serum measures, and fecal microbiome sequencing were performed before and after the intervention.

Results: Inulin supplementation in obese subjects had moderate beneficial effect on emotional competence and cognitive flexibility. However, an exploratory analysis revealed that some patients exhibiting specific microbial signature -elevated *Coprococcus* levels at baseline- were more prone to benefit from prebiotic supplementation in terms of mood. Positive responders toward inulin intervention in term of mood also displayed worse metabolic and inflammatory profiles at baseline (increased levels of IL-8, insulin resistance and adiposity).

Conclusion: This study shows that inulin intake can be helpful to improve mood in obese subjects exhibiting a specific microbial profile. The present work highlights some microbial, metabolic and inflammatory features (IL-8, insulin resistance) which can predict or mediate the beneficial effects of inulin on behaviour in obesity.

Table 7: Led by Kristin Verbeke

Chen YE et al. 2023. Engineered skin bacteria induce antitumor T cell responses against melanoma.

Abstract: Certain bacterial colonists induce a highly specific T cell response. A hallmark of this encounter is that adaptive immunity develops preemptively, in the absence of an infection. However, the functional properties of colonist-induced T cells are not well defined, limiting our ability to understand anticommensal immunity and harness it therapeutically. We addressed both challenges by engineering the skin bacterium *Staphylococcus epidermidis* to express tumor antigens anchored to secreted or cell-surface proteins. Upon colonization, engineered *S. epidermidis* elicits tumor-specific T cells that circulate, infiltrate local and metastatic lesions, and exert cytotoxic activity. Thus, the immune response to a skin colonist can promote cellular immunity at a distal site and can be redirected against a target of therapeutic interest by expressing a target-derived antigen in a commensal.

Table 8: Led by Frederique Respondek
Wastyk HC et al. 2023. Randomized controlled trial demonstrates response to a probiotic intervention for metabolic syndrome that may correspond to diet.

Abstract: An individual's immune and metabolic status is coupled to their microbiome. Probiotics offer a promising, safe route to influence host health, possibly via the microbiome. Here, we report an 18-week, randomized prospective study that explores the effects of a probiotic vs. placebo supplement on 39 adults with elevated parameters of metabolic syndrome. We performed longitudinal sampling of stool and blood to profile the human microbiome and immune system. While we did not see changes in metabolic syndrome markers in response to the probiotic across the entire cohort, there were significant improvements in triglycerides and diastolic blood pressure in a subset of probiotic arm participants. Conversely, the non-responders had increased blood glucose and insulin levels over time. The responders had a distinct microbiome profile at the end of the intervention relative to the non-responders and placebo arm. Importantly, diet was a key differentiating factor between responders and non-responders. Our results show participant-specific effects of a probiotic supplement on improving parameters of metabolic syndrome and suggest that dietary factors may enhance stability and efficacy of the supplement.

Table 9: Led by Tami Mackle
Louie T et al. 2023. VE303, a Defined Bacterial Consortium, for Prevention of Recurrent Clostridioides difficile Infection: A Randomized Clinical Trial.

Abstract: Importance: The effect of rationally defined nonpathogenic, nontoxigenic, commensal strains of Clostridia on prevention of *Clostridioides difficile* infection (CDI) is unknown.
Objective: To determine the efficacy of VE303, a defined bacterial consortium of 8 strains of commensal Clostridia, in adults at high risk for CDI recurrence. The primary objective was to determine the recommended VE303 dosing for a phase 3 trial.
Design, Setting, and Participants: Phase 2, randomized, double-blind, placebo-controlled, dose-ranging study conducted from February 2019 to September 2021 at 27 sites in the US and Canada. The study included 79 participants aged 18 years or older who were diagnosed with laboratory-confirmed CDI with 1 or more prior CDI episodes in the last 6 months and those with primary CDI at high risk for recurrence (defined as aged ≥75 years or ≥65 years with ≥1 risk factors: creatinine clearance <60 mL/min/1.73 m2, proton pump inhibitor use, remote [>6 months earlier] CDI history).
Interventions: Participants were randomly assigned to high-dose VE303 (8.0 × 109 colony-forming units [CFUs]) (n = 30), low-dose VE303 (1.6 × 109 CFUs) (n = 27), or placebo capsules (n = 22) orally once daily for 14 days.
Main Outcomes and Measures: The primary efficacy end point was the proportion of participants with CDI recurrence at 8 weeks using a combined clinical and laboratory definition. The primary efficacy end point was analyzed in 3 prespecified analyses, using successively broader definitions for an on-study CDI recurrence: (1) diarrhea consistent with CDI plus a toxin-positive stool sample; (2) diarrhea consistent with CDI plus a toxin-positive, polymerase chain reaction–positive, or toxigenic culture–positive stool sample; and (3) diarrhea consistent with CDI plus laboratory confirmation or (in the absence of a stool sample) treatment with a CDI-targeted antibiotic.
Results: Baseline characteristics were similar across the high-dose VE303 (n = 29; 1 additional participant excluded from efficacy analysis), low-dose VE303 (n = 27), and placebo (n = 22) groups. The participants' median age was 63.5 years (range, 24-96); 70.5% were female; and 1.3% were Asian, 1.3% Black, 2.6% Hispanic, and 96.2% White. CDI recurrence rates through week 8 (using the efficacy analysis 3 definition) were 13.8% (4/29) for high-dose VE303, 37.0% (10/27) for low-dose VE303, and 45.5% (10/22) for placebo (P = .006, high-dose VE303 vs placebo).
Conclusions and Relevance: Among adults with laboratory-confirmed CDI with 1 or more prior CDI episodes in the last 6 months and those with primary CDI at high risk for recurrence, high-dose VE303 prevented recurrent CDI compared with placebo. A larger, phase 3 study is needed to confirm these findings.

Table 10: Led by Stefan Roos
Zou ZP et al. 2023. Biomarker-responsive engineered probiotic diagnoses, records, and ameliorates inflammatory bowel disease in mice.

Summary: Rapid advances in synthetic biology have fueled interest in engineered microorganisms that can diagnose and treat disease. However, designing bacteria that detect dynamic disease-associated biomarkers that then drive treatment remains difficult. Here, we have developed an engineered probiotic that noninvasively monitors and records inflammatory bowel disease (IBD) occurrence and progression in real time and can release treatments via a self-tunable mechanism in response to these biomarkers. These intelligent responsive bacteria for diagnosis and therapy (i-ROBOT) consists of E. coli Nissle 1917 that responds to levels of the inflammatory marker thiosulfate by activating a base-editing system to generate a heritable genomic DNA sequence as well as producing a colorimetric signal. Fluctuations in thiosulfate also drive the tunable release of the immunomodulator AvCystatin. Orally administering i-ROBOT to mice with colitis generated molecular recording signals in processed fecal and colon samples and effectively ameliorated disease. i-ROBOT provides a promising paradigm for gastrointestinal and other metabolic disorders.

Table 11: Led by Charles Budinoff
Rodriguez-Herrera A et al. 2022. Early-life fecal microbiome and metabolome dynamics in response to an intervention with infant formula containing specific prebiotics and postbiotics.

Abstract: This study examined fecal metabolome dynamics to gain greater functional insights into the interactions between nutrition and the activity of the developing gut microbiota in healthy term-born infants. The fecal samples used here originate from a randomized, controlled, double-blind clinical study that assessed the efficacy of infant formula with prebiotics and postbiotics (experimental arm) compared with a standard infant formula (control arm). A group of exclusively breast-fed term infants was used as a reference arm. First, conventional targeted physiological and microbial measurements were performed, which showed differences in fecal *Bifidobacterium* levels and corresponding activity (e.g., lactate levels). Next, the overall fecal microbiota composition was determined by 16S rRNA gene amplicon sequencing. The microbiota composition profiles showed several bacterial groups in the experimental arm to be significantly different from the control arm and mostly closer to the levels observed in the reference arm. Finally, we applied an untargeted UPLC-MS/MS approach to examine changes in the fecal metabolome. Fecal metabolome profiles showed the most distinct separation, up to 404 significantly different metabolites, between the study arms. Our data reveal that infant formula with specific prebiotics and postbiotics may trigger responses in the intestinal microbiota composition that brings the ensuing fecal metabolite profile of formula-fed infants closer toward those observed in breast-fed infants. Furthermore, our results demonstrate a clear need for establishing an infant gut metabolome reference database to translate these metabolite profile dynamics into functional and physiologically relevant responses.

Table 12: Led by Seppo Salminen

Ríus AG et al. 2022. Physiological responses of Holstein calves to heat stress and dietary supplementation with a postbiotic from Aspergillus oryzae.

Abstract: Increased ambient temperature causes heat stress in mammals, which affects physiological and molecular functions. We have recently reported that the dietary administration of a postbiotic from *Aspergillus oryzae* (AO) improves tolerance to heat stress in fruit flies and cattle. Furthermore, heat-induced gut dysfunction and systemic inflammation have been ameliorated in part by nutritional interventions. The objective of this study was to characterize the phenotypic response of growing calves to heat stress compared to thermoneutral ad libitum fed and thermoneutral feed-restricted counterparts and examining the physiologic alterations associated with the administration of the AO postbiotic to heat-stressed calves with emphasis on intestinal permeability. In this report, we expand previous work by first demonstrating that heat stress reduced partial energetic efficiency of growth in control (45%) but not in AO-fed calves (62%) compared to thermoneutral animals (66%). While heat stress increased 20% the permeability of the intestine, AO postbiotic and thermoneutral treatments did not affect this variable. In addition, AO postbiotic reduced fecal water content relative to thermoneutral and heat stress treatments. Heat stress increased plasma concentrations of serum amyloid A, haptoglobin and lipocalin-2, and administration of AO postbiotic did not ameliorate this effect. In summary, our findings indicated that heat stress led to reduced nutrient-use efficiency and increased systemic inflammation. Results suggest that the AO postbiotic improved energy-use efficiency, water absorption, and the intestinal permeability in heat stress-mediated increase in gut permeability but did not reduce heat stress-mediated rise in markers of systemic inflammation.

Jo-Ann Passmore, University of Cape Town, South Africa

Jo-Ann Passmore PhD is a Professor in the Division of Medical Virology, at the Institute for Infectious Diseases and Molecular Medicine (IDM), University of Cape Town, and Principle Medical Scientist with the National Health Laboratory Services. She heads the Mucosal Infections Group (MIG) in the Division of Medical Virology (www.passmore-lab.org.za). Jo-Ann is leading an African collaboration to evaluate temporal dynamics in vaginal microbiomes across menstrual cycle, in health and dysbiosis, to identify requirements for optimal vaginal health for women in Africa. This major African collaboration -VMRC4Africa – currently includes investigators from South Africa and Kenya. Jo-Ann recently was awarded the BMGF Calestous Juma Scientific Leadership Award to action VMRC4Africa, which aims to harness the vaginal microbiome from healthy women to improve reproductive health in Africa through development of live biotherapeutic products for BV treatment. In addition, Jo-Ann co-developed the Genital InFlammation Test (GIFT) for HIV prevention, with Dr. Lindi Masson at UCT, which is a social innovation aimed as a cheap, point-of-care lateral flow device to diagnose women with sexually transmitted infections or bacterial vaginosis and link them to treatment (www.GIFT.org.za). Jo-Ann's research group focuses on the role of genital tract inflammation and cellular activation on HIV risk in women, associated most commonly with undiagnosed sexually transmitted infections and bacterial vaginosis. She has published over 110 papers on mucosal immune responses and inflammation associated with HIV risk and progression and holds one patent.

June 26 - 14:30-15:00
The vaginal microecology, immunity and the potential of probiotic interventions.
Abstract: For the past decade, most major funding agencies in the US and UK developed clear strategic plans for investing in human microbiome research, which has yielded large volumes of publicly available sequence data - biased towards wealthier industrialized nations. Less progress has been made in understanding the relationship between microbial variability and health in LMICs, particularly in Africa, although the context and location of these "missing microbiomes" have important implications for disease management in African populations. This is particularly relevant to diseases and dysbiosis in African women that significantly impact HIV risk, fertility, and reproductive outcomes on the continent. Improving reproductive health using genital microbiome live biotherapeutic approaches relevant to women in Africa, including local bacterial strains that are commonly found in African women with optimal vaginal microbiota is key to understanding and preventing higher HIV risk and adverse birth outcomes. The aim of this talk will be to outline a major pilot initiative to enable high-quality, collaborative vaginal microbiome studies in South Africa and African partner countries, with capacity to do regionally relevant vaginal microbiome studies and contribute vaginal lactobacilli derived from Africa. Dr Passmore will present research on progress towards leveraging bio-banked cervicovaginal specimens from previous longitudinal cohort studies including South African women with stable vaginal microbiotas, to isolate and characterize vaginal Lactobacillus strains with health-promoting properties. In addition, she will summarize the parallel clinical studies currently underway in South Africa and Kenya to define what optimal vaginal microbiota looks like in women over two menstrual cycles.

Ophelia Venturelli, University of Wisconsin-Madison, USA

Dr. Ophelia Venturelli is an Assistant Professor in Biochemistry, Chemical & Biological Engineering, Biochemistry and Biomedical Engineering at UW-Madison. The Venturelli lab focuses on understanding and engineering microbiomes using systems and synthetic biology. The lab aims to combine high-throughput experiments and computational modeling to predict, design, and control microbiome functions. Dr. Venturelli began her appointment in 2016 after completing a Life Sciences Research Foundation Fellowship at UC Berkeley in the laboratory of Dr. Adam P. Arkin. She received her PhD in Biochemistry and Biophysics in 2013 from Caltech with Richard M. Murray, where she studied single-cell growth and gene expression dynamics and the role of feedback loops in a metabolic gene regulatory network. Dr. Venturelli has received numerous awards for her cross-disciplinary research including the Shaw Scientist Award (2017), Army Research Office Young Investigator Award (2017), Wisconsin Alumni Research Foundation Innovation Award (2019), and ACS Synthetic Biology Young Investigator Award (2023).

June 26 - 15:30-16:00
Design of dietary and bacterial therapeutic interventions to enhance the resilience and health-promoting properties of the human gut microbiome
Abstract: The human gut microbiome substantially expands our genome's capabilities and is a critical determinant of our health. In a healthy state, this gut ecosystem can provide beneficial functions. However, due to contrasting evolutionary objectives, disruptions to this ecosystem can alter the composition and functions of the community, which in leads to deleterious impacts on human health. Precision engineering of the gut microbiome holds tremendous therapeutic potential for personalized medicine. However, the complexity of this system including the hundreds of diverse bacterial species that reside in the gut, variability in the composition across individuals and unpredictable dynamic responses to environmental inputs have precluded our ability to effectively manipulate this system to our benefit. A detailed, mechanistic and quantitative understanding is critical for precisely manipulating the human gut microbiome. We seek to decipher the web of cellular interactions and molecular and ecological mechanisms driving the dynamic behaviors of gut microbiota. The ecological and molecular mechanisms will be exploited as novel control knobs to steer the system toward desired metabolic states.

By combining high-throughput bottom-up assembly of human gut communities with computational modeling, we decipher the interaction networks shaping community dynamics and health-relevant functions. We exploit the data-driven models to design communities with desired behaviors including tailored metabolite profiles and enhanced resistance to invasion by human gut pathogens. We demonstrate that complex dietary fibers can enhance the stability and resilience of human gut communities to perturbations by reducing the prevalence of negative inter-species interactions and promoting metabolic diversity. In sum, our work provides a foundation for exploring and exploiting the multifunctional landscapes of microbiomes.

Website: https://www.venturellilab.org/

Premysl Bercik, McMaster University, Hamilton, Ontario, Canada

Dr. Bercik is Professor of Internal Medicine and Gastroenterology at McMaster University, Hamilton, Canada. He is a clinician-scientist, with interests in both clinical and basic research in the microbiota-gut-brain axis, functional bowel disorders, neuro-immune interactions, and celiac disease. He published over 130 peer-reviewed papers; his current Google Scholar h-index is 66, with more than 19,000 citations. He was awarded the 2021 Research Excellence Award from the Canadian Association of Gastroenterology. His research in microbiome spans over 25 years, originating with studies on the role of H. pylori in acid secretion, followed by the role of commensal bacteria in gut motility and visceral sensitivity, and finally exploring interactions between the microbiota and brain function.

June 26 - 16:00-16:30

How the microbiome converses with the little brain and the big brain.

Abstract: Gut microbiota plays a key role in many aspects of human health, such as shaping the host immune system, modulating its metabolism, even affecting its behavior and brain function. There are multiple pathways, by which gut bacteria can affect the neural system, including direct communication through the vagus and spinal nerves, or indirect interactions through the immune or endocrine systems. Presence of bacterial pathogens can be detected within hours by the neural system, evidenced by activation of vagal ascending pathways, prior to mounting any significant immune response. The vagus nerve seems also to mediate beneficial effects of certain psychoactive probiotics. The innate immune system, through TLR signaling, is key in establishment of normal behavior and brain chemistry during the initial bacterial colonization, with intestinal dendritic cells playing a major role in this process, while the adaptive immune system appear to be more prominent later in life. Gut bacteria produce or affect metabolism of many neuroactive molecules, including short chain fatty acids and neurotransmitters, which affect not only the function of the gut but also the brain. Recent experiments demonstrated that bacterial production of histamine underlies chronic abdominal pain in some patients with Irritable Bowel Syndrome, through H4 receptor dependent pathways, which lead to mast cell chemotaxis and activation, with structural and functional changes in the enteric nervous system, resulting in visceral hypersensitivity.

2023 Glenn Gibson Early Career Researcher Prize winner talk
Paul Gill, Monash University, Melbourne, Australia

Dr. Paul Gill is currently a Postdoctoral Research Fellow in the Allergy and Clinical Immunology lab at the Department of Immunology, Monash University, Melbourne, Australia. His research explores the interaction between the gut microbiota and immune system, in the context of human health and disease. He completed his PhD at the Department of Gastroenterology at Monash University, where he studied the effect of microbial metabolites short-chain fatty acids on the human immune system and gut microbiota. He holds an honorary position at University College London, where he previously studied the role of the innate immune receptor NOD2 in Inflammatory bowel disease. His current research focuses on understanding the immune response to COVID-19 vaccination in immunosuppressed patients with Inflammatory bowel disease.

June 27 - 14:00-14:15
Investigating the effects of short-chain fatty acids on the immune system and gut microbiota of healthy humans
Abstract: Short-chain fatty acids (SCFA) produced from microbial fermentation of dietary fibre in the intestine have immune-modulating effects in animal models of disease. However, it has been difficult to translate pre-clinical results into human studies. This research aimed to determine effects of increased delivery of SCFA via dietary manipulation on the immune system and gut microbiota of healthy humans.
We conducted a blinded, randomized, cross-over dietary intervention in healthy adults (n=20), who consumed a high SCFA-producing diet and matched low-SCFA diet for 21 days with 21-day wash-out in between. Blood and faecal samples were collected at the end of each diet. Gas chromatography was used to measure SCFA. Gut microbiota composition was assessed using shotgun metagenomic sequencing. Flow cytometry was used for peripheral blood immuno-phenotyping.
Plasma and faecal SCFA were significantly higher on high-SCFA than on low-SCFA diet. High-SCFA diet associated with increased differential abundance of Bifidobacterium adolescentis, Anaerostipes hadrus and Ruminococcus bromii. Blood total B cells, mucosal-associated invariant T (MAIT) cells and CD8+ Tfh cells were significantly lower on high-SCFA than on low-SCFA diet. Changes in differential abundance of R. bromii negatively associated with changes to CD8+ Tfh cells, whilst changes in Aldercreutzia equolifaciens relative abundance positively associated with Tfh1 cells.
Delivery of SCFA using dietary intervention has discrete effects on gut microbiota and circulating immune cells in healthy humans. Further studies are required to determine if these changes alter immune function and have therapeutic benefit to those with inflammatory disease.
Website: https://research.monash.edu/en/persons/paul-gill

SFA Speaker
Anissa Armet, University of Alberta, Canada

Anissa Armet is a Registered Dietitian and PhD candidate in Nutrition and Metabolism at the University of Alberta in Canada, supervised by Drs. Jens Walter and Carla Prado. Anissa completed her Bachelor of Science in Nutrition and Food Sciences with distinction and an Integrated Dietetic Internship from the University of Alberta in 2018. Her current research focuses on how dietary fiber interventions modulate the gut microbiome and how this, in turn, impacts human health. She has a particular interest in whether the gut microbiome can be used to predict responses to dietary interventions and, therefore, inform personalized nutrition strategies to improve human health. Anissa is a recipient of numerous awards including the Killam Scholarship, the most prestigious graduate award administered by the University of Alberta.

June 27 - 14:15-14:30
Immunometabolic effects of physicochemically-distinct dietary fibers in adults with excess body weight: towards precision nutrition strategies
Abstract: see page 49

ISAPP

SFA Speaker
Soyolmaa Jamiyanpurev, Shinshu University, Japan

Soyolmaa Jamiyanpurev is a second-year master's student at Shinshu University, Japan in the laboratory of Prof. Takeshi Shimosato. Originally from Mongolia, her passion for lactic acid bacteria is deeply related to her nomadic background and exposure to traditional fermented foods such as “Airag (traditional fermented horse milk)”. She came to Japan to study the science of probiotics and pursued her undergraduate studies at the same university. Currently, her study mainly focuses on lactic acid bacteria and exploring ways to enhance their probiotic functions using Ribosome Engineering as an effective breeding strategy for probiotic lactic acid bacteria. She hopes to use a ribosome-engineered probiotic strain with enhanced properties and the potential practicality of RE in probiotic strain development for future industrial use.

June 27 - 14:30-14:45
Identification of novel immunomodulatory components in Lacticaseibacillus rhamnosus GG
Abstract: see page 39

Khurram Nasir, The Methodist Hospital and Weill Cornell School of Medicine, Houston, TX, USA

Khurram Nasir MD MPH Msc is the Chief of Cardiovascular Disease Prevention and Wellness as well as serves as the Chief Division of Health Equity & Disparities Research and Co-Director for Center for Outcomes Research at Houston Methodist. He is also the inaugural Director of the newly founded Center for Cardiovascular Computational Health & Precision Medicine (C3-PH). He is a Professor of Medicine at Weill Cornell Medical College and a Professor of Cardiology at Houston Methodist Academic Institute. Dr Nasir was recently appointed as Visiting Professor at London School of Economics. His clinical and research interests lies in the role of precision medicine and healthcare big data applications. His research endeavors are funded by two NIH RO1’s and various industry grants. He has published more than 850 high-impact articles published in top academic journals with h-index>100. He is currently Associate Editor for the journal “Circulation: Cardiovascular Quality and Outcomes”.

June 27 - 14:45-15:15
Re-imagining the Future of Healthcare Research Registries: Happening As We Speak
Abstract: The rapid generation of vast and diverse healthcare data holds immense potential for transforming the research enterprise, enabling accelerated learning and advancing the academic mission. To harness this potential, a paradigm shift is required, necessitating bolder approaches that move beyond the traditional and labor-intensive methods of creating data registries. This presentation aims to demonstrate the feasibility of developing a system-wide registry of patients with at-risk and established Atherosclerotic Cardiovascular Disease (ASCVD) within a large healthcare system using automated data extraction techniques. The purpose is to systematically identify disease burden, determinants, and care gaps while evaluating the spectrum of at-risk patients, thereby informing population health management and risk mitigation strategies.

The presentation will showcase the development of a real-time, interactive, dynamic, programmatically deidentified registry known as the EMR-based HM CVDLHS registry. This registry comprises approximately 750 variables stored in multiple tables, encompassing patient demographics, encounters, diagnoses, vitals, labs, medication use, and comorbidities. Rigorous measures were implemented to ensure logical and consistent definition of data elements, data quality assurance, and maintenance of structural integrity and uniformity. Using this approach, a total of 113,022 (9.6%) ASCVD patients were identified among 1,171,768 adult individuals in the registry, spanning the period between June 2016 and December 2022. Furthermore, the study employed multi-level groupings of patients based on laboratory test results and medication use to analyze outcomes of interest. By leveraging this framework, knowledge inference and reasoning queries surpass the limitations of Electronic Medical Record (EMR) data alone.

Khurram Nasir - abstract con't

These efforts highlight the transition from manual patient chart abstraction towards a unified registry framework that concurrently designs data collection tools and reporting mechanisms. It demonstrates that by utilizing automated extraction methods, valuable structured clinical data can be rapidly derived from EMRs, facilitating the creation of patient or specialty population registries. The adoption of such an approach promises to revolutionize research registries and accelerate the pace of medical advancements across all medical science domains.

Website: https://nasir.hmailabs.org

Lawrence David, Duke University, Durham, NC, USA

Dr. Lawrence David is an Associate Professor in Duke University's Department of Molecular Genetics and Microbiology and Co-Director of the Duke Microbiome Center. The David Lab studies relationships between diet, the gut microbiome, and human health. The lab is also interested in engineering new tools at the interface of nutrition and microbiology, including building genomic approaches for tracking food intake and microfluidic techniques for high-throughput assay of microbial metabolism. Lawrence was a Junior Fellow at the Harvard Society of Fellows, and he received a Ph.D. in Computational & Systems Biology from the Massachusetts Institute of Technology and a B.S. in Biomedical Engineering from Columbia University. Lawrence has been named one of the 10 Scientists under 40 years old to watch by ScienceNews and his work has been recognized with innovator and investigator awards from the Burroughs Wellcome Fund, the Searle Scholars Program, and the Arnold & Mabel Beckman, Hartwell, Alfred P. Sloan, Damon Runyon, and Chan Zuckerberg Foundations.

June 27 - 15:15-15:45
Impact and Personalized Responses to Prebiotics by Human Gut Microbiota
Abstract: Here, we test the effect of prebiotics on gut microbiota in the settings of health and conditions like obesity and graft-vs-host disease. To do so, we combine in vitro assays, animal and artificial human gut models, and dietary intervention trials. Our studies illustrate that while different prebiotics may vary in microbiome impact, inter-individual differences are also an important and consistent source of variation. This variation can be linked to habitual fiber intake as well as recent prebiotic consumption. Together, these findings suggest microbiome-based strategies for personalization of prebiotic intake.
Website: http://www.ladlab.org/

Jan-Peter Van Pijkeren, University of Wisconsin-Madison, USA

JP van Pijkeren is an Associate Professor at the Department of Food Science. Dr. van Pijkeren received a B.S. degree in Biotechnology and a M.S. degree in Biology from Leiden University, both in The Netherlands. He joined the laboratory of Dr. Paul O'Toole at the University of College Cork, Ireland, where he completed his Ph.D. training in Microbiology. During his postdoctoral training, Dr. van Pijkeren developed *Listeria monocytogenes* as a DNA delivery vehicle at the Cork Cancer Research Center, Ireland. After completing his second postdoctoral training under Dr. Robert Britton at Michigan State University, he started his own laboratory in 2013. Dr. van Pijkeren developed various genome editing tools for use in undomesticated lactobacilli, which are essential to pursue his long-term research goals. Studies in the van Pijkeren Laboratory focus mostly on the gut symbiont species *Limosilactobacillus reuteri*, until recently known as *Lactobacillus reuteri*. His research team aims to unravel the molecular mechanisms by which a gut symbiont interacts with members of the microbiome and the mammalian host. Knowledge gained from these studies is leveraged towards the development of next-generation probiotics for use in human medicine and agriculture.

June 27 - 15:45-16:15
Kill to prosper: intra-species competition of a probiotic
Abstract: Probiotics are routinely used to modulate the gut microbiota and can potentially impact host physiology. Survival of exogenously introduced microbes while passing through the gastrointestinal tract will in part depend on their resistance against host factors such as stomach and bile acids. In addition, probiotic survival will depend on the interactions with other members of the gut microbiome, including bacterial viruses. However, mechanistic knowledge underlying microbe-microbe and microbe-virus interactions in relation to gastrointestinal survival of probiotics is limited. The long-term goal of the Van Pijkeren Laboratory is to understand probiotic mechanisms and to leverage this knowledge toward the development of next-gen probiotics. Using in-house developed genome editing tools we investigate microbe-microbe and microbe-virus interactions in relation to gut fitness. Central to our work is the probiotic gut symbiont *Limosilactobacillus reuteri*. In this presentation, we will discuss the ecological relevance of a biosynthetic gene cluster and prophages in intraspecies interactions. The biosynthetic gene cluster we identified in select *L. reuteri* strains encodes an antimicrobial molecule, while prophages are universally present in the gut microbiome. By comparative genomics and genetics, we linked genotype and phenotype to provide insight in the intricate microbe-microbe and microbe-virus interactions. Such knowledge is critically important because of the significant impact the gut microbial community exerts on host health and may ultimately be leveraged to develop next-generation probiotics for precise and personalized applications.

IAC Speaker
Annemarieke van Opstal, Winclove Probiotics, Amsterdam, the Netherlands

Annemarieke van Opstal, PhD, is a medical biologist with a background in nutritional neuroscience and metabolic health. Previous doctoral and post-doctoral research work at the Leiden University Medical Center (Leiden, the Netherlands) includes clinical studies on brain function in healthy participants and patients with obesity, metabolic syndrome, and eating disorders. And includes studies on brain health and cognitive performance in patients with neurodegenerative disorders. Currently, Annemarieke is working as a Clinical Research Expert within the Patient-Centered Clinical Development department at Winclove Probiotics (Amsterdam, the Netherlands). In this role, she focusses on clinical studies that investigate the use of probiotics in the field of the gut-brain-axis and metabolic health, which includes topics such as depression, cognition, autism, and type 2 diabetes.

Annemarieke van Opstal, Winclove Probiotics, Amsterdam, the Netherlands - con't

June 28 - 8:00-8:15

Beneficial effects of multispecies probiotics on mood and cognition in clinical studies.

Abstract: The microbiota-gut-brain axis is proving more and more important in mood and cognition. Decline in cognitive functions such as memory and executive function are hallmarks of ageing, even in the absence of age-related disorders. Additionally, increased vulnerability to mental health disorders such as depression is common in older adults. Therefore, interventions targeting the gut microbiome might be beneficial to counter these effects in this population.

A recent (yet unpublished) randomised, placebo-controlled cross-over trial in 30 healthy older adults explored the effects of 8 weeks multispecies probiotic supplement (Ecologic® Barrier) on various cognitive domains, alongside mood measures. The study showed that probiotic supplementation led to less decrease in cognitive performance in the executive function domain during high cognitive demand compared to placebo. Other cognitive domains were not affected. Improvements were found in cognitive biases such as hopelessness, rumination, and aggression as measured with the Leiden Index of Depression Sensitivity (LEIDS-r) that contribute to reactivity to sad mood and therefore, vulnerability to depression.

These findings are in line with earlier studies with Ecologic® Barrier where the cognitive reactivity as measured by the LEIDS-r has shown the strongest effect while effects are not as consistently seen on clinical scales such as the BDI or HADS (Chahwan et al., 2019; Steenbergen et al., 2015). The results on cognitive function are also in line with an earlier study showing that Ecologic® Barrier improved cognitive function under stress (Papalini et al., 2019).

These results combined indicate that probiotics can have consistent effects on the vulnerability to sad mood or depression and protect against decreased cognitive performance under high demand or in a stressed condition. This suggests that choosing a sensitive (sub-clinical) outcome measure is important as these measures can show effects of probiotic supplementation that are not detected by all classic clinical questionnaires or cognitive tests.

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IAC Speaker
Jessica Van Harsselaar, BENEO-Institute, BENEO GmbH, Obrigheim, Germany

Dr. Jessica Van Harsselaar works as a Manager, Nutrition Science at the BENEO-Institute since 2017, where she is responsible for global scientific research activities on the nutritional and health benefits of Beneo's prebiotic dietary fibers. Jessica is a nutrition scientist, specializing in prebiotic research and the microbiota. Her interest for studying the human microbiome was sparked during her studies in Nutrition Sciences at the University of Gießen where she obtained her Master's degree in 2010. She continued her education at the University of Erlangen-Nuremberg, where she earned her PhD. Jessica is actively involved in international collaborative research projects including activities at the International Life Science Institute (ILSI).

June 28 - 8:15-8:30

Inulin-type fructans and 2'fucosyllactose alter microbial composition and alleviate stress-induced mood state in a working population: a randomized, controlled trial.

Authors: Peter P. J. Jackson[1], Anisha Wijeyesekera[1], Claire M. Williams[2], Stephan Theis[3] & Jessica Van Harsselaar[3]and Robert A. Rastall[1]
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2 University of Reading, School of Psychology and Clinical Language Science, Reading, RG6 6AL, UK
3 BENEO-Institute, BENEO GmbH, Wormser Str. 11, 67283 Obrigheim (Germany)

Abstract:
There is increasing interest in the bi-directional relationship between the gut and brain and how it can be affected to positively influence mood. Prebiotics like oligofructose, an inulin-type fructan, and candidate prebiotics like 2'fucosyllactose (2'FL), a human-milk oligosaccharide, are a means to selectively alter the gut microbiota by stimulating the growth of beneficial bacteria like bifidobacteria. As microbiota composition hasbeen associated with mood state, prebiotics may exert an influence on mood via the gut microbiota-brain axis. We aimed to compare the effects of the prebiotic oligofructose and candidate prebiotic 2'FL alone and in combination on microbial composition and mood state in a working population.

We conducted a 4-week, 4-arm, parallel, double-blind, randomized, placebo-controlled trial in 92 healthy adults with mild-to-moderate levels of anxiety and depression. Subjects were randomized to receive either oligofructose 8 g/day (plus 2 g/day maltodextrin), oligofructose 8 g/day plus 2'FL (2 g/day), 2'FL 2 g/day plus maltodextrin (8 g/day) or maltodextrin 10 g/day as a control. Changes in microbial load (FISH-FLOW) and composition (16s rRNA sequencing) were the primary outcomes. Secondary outcomes included bowel habits, cortisol awakening response and mood state parameters.

There were significantly greater increases in the taxa Bifidobacterium, Bacteroides, Roseburia and Faecalibacterium prausnitzii in the oligofructose and oligofructose/2'FL interventions (all $P < 0.05$). Significant improvements in Beck Depression Inventory, State Trait Anxiety Inventory, and Positive and Negative Affect Schedule scores and cortisol awakening response were detected across oligofructose, and 2'FL and oligofructose/2'FL combination groups (all $P < 0.05$). Both oligofructose and the oligofructose/2'FL interventions outperformed sole 2'FL and maltodextrin in improvements in several mood state parameters (all $P < 0.05$). The results of this study show that oligofructose and combinations of oligofructose/2'FL, can beneficially alter microbial composition along with improving mood state parameters.´

Plenary Speakers

Marie-Claire Arrieta, University of Calgary, Canada

Dr. Marie-Claire Arrieta is an Associate Professor in the Departments of Physiology and Pharmacology, and Pediatrics at the University of Calgary. Her research studies how the millions of microbes that inhabit an infant's gut (the early-life gut microbiome) contribute to human health or disease. Her research program conducts clinical and experimental research, aiming to understand the mechanisms behind host-microbiome interactions. Dr. Arrieta is co-author of the best-selling public book, Let Them Eat Dirt, and is involved in several science communication initiatives, including public talks, a second book, and a documentary film project.

June 28 - 8:30-9:00
Microbiome maturation in premature infants
Abstract: The effects of probiotics on premature infants are not well understood. In a randomized intervention trial, we show that a multi-strain probiotic mix accelerated microbiome maturation to resemble that of full-term infants and improved the metabolic and immune parameters, highlighting the critical ecological role of these species in the early life microbiome.

Website: Arrietalab.com

Bob Hutkins, University of Nebraska, USA

Bob Hutkins is the Khem Shahani Professor of Food Microbiology at the University of Nebraska. He received his Ph.D. from the University of Minnesota and was a postdoctoral fellow at Boston University School of Medicine. The Hutkins Lab studies bacteria important in human health and in fermented foods. His group is particularly interested in understanding factors affecting the persistence of beneficial bacteria in the gastrointestinal tract and how probiotics, prebiotics, and synbiotics can enhance health outcomes.

June 28 - 9:00-9:30
Association of live dietary microbes with health: A brief update
Abstract: A "Live Microbes Panel" was organized as an outcome of a Discussion Session held at the 2019 ISAPP meeting. The initial goal of the panel was to consider how to test the hypothesis that live dietary microbes could provide health benefits. The panel developed a classification system to organize more than 9,000 food codes listed in the NHANES database based on their live microbe content. More recently, this data was used to assess the relationship of these values with health outcomes reported in NHANES. Consumption of dietary microbes, mostly from fermented foods, was positively associated with several physiological parameters. However, before dietary guidelines could include a recommendation for live microbe foods, additional research, including RCTs or other clinical evidence will be necessary.

ISAPP

Hania Szajewska, Medical University of Warsaw, Poland

Bio: see page 58

June 28 - 9:00-9:30
The Role of Probiotics in Restoring Microbiota Composition and Function Following Antibiotic-Induced Perturbation.

Presented on behalf of the ISAPP Panel: T De Meij, S Forslund, B Johnston, R Knight, O Koren, P Little, J Łukasik, ME Sanders, K Scott, J Suez, H Szajewska, D Tancredi

Abstract: The International Scientific Association for Probiotics and Prebiotics convened a one-day expert meeting in London, UK, on March 8, 2023, with the objective of assessing the current state of the science regarding the probiotic-induced recovery of microbiota composition and/or function following antibiotic perturbation. The meeting aimed to determine whether there is evidence supporting the use of probiotics to improve or delay microbiome recovery after antibiotic treatment, and to identify key unanswered research questions in this area. Invited experts presented short talks addressing various aspects of the topic, including the harm caused by antibiotics, the impact on the human microbiome, and the resilience and plasticity of a healthy microbiota. The meeting explored the desirability and definition of microbiome restoration, the role of diversity and stability, and the outcomes of probiotic trials. A systematic review of clinical trials on probiotics and microbiome recovery was presented, emphasizing measurement methods. Limitations and approaches for assessing microbiome repair were discussed, along with the future direction of probiotics and antibiotic resistance genes. The meeting identified research gaps and outlined a paper to encourage researchers to address these gaps and provide guidance for future studies.

Karen Scott, Rowett Institute, University of Aberdeen, UK

Bio: see page 58

June 28 - 9:00-9:30
Prebiotic criteria.

Abstract: The concept of using dietary prebiotics to selectively enhance growth of specific members of the gut microbiota started in 1995, and in 2017 ISAPP published a consensus paper with a revised definition stating “Prebiotics are a substrate that is selectively utilized by host microorganisms conferring a health benefit”. This definition was deliberately designed to be broad enough to encourage innovation but remain true to the original intent. This new initiative was set up in 2022 to update and expand on some of the principles covered in the consensus paper. Key points considered were the levels and types of evidence required; details on characterisation, purification, stability and dose; how to demonstrate specific utilisation; how to show a health benefit; and how to address causality between selective utilization by the microbiota and health benefit. The aim was to identify the minimum criteria and make recommendations against which ‘putative prebiotics’ can be measured to ascertain if they are sufficiently characterized to be considered prebiotics.

This talk will update the current state of this initiative, and provide an opportunity for further comment from a wider audience.

Karin Allenspach, Iowa State University, Ames, USA

Karin Allenspach received her veterinary degree from the University of Zurich. She did an internship in small animal emergency medicine and critical care at Tufts University and a residency in small animal internal medicine at the University of Pennsylvania, and is a diplomate of the European College of Veterinary Internal Medicine. She was awarded a PhD in veterinary immunology from the University of Bern, Switzerland for her work on canine chronic enteropathies. Karin has published >125 peer-reviewed publications and has a current H factor of 41. She is currently employed as Professor in Internal Medicine and Translational Health at Iowa State University, Ames, USA, and is a PI of the SMART Translational medicine Lab at ISU, which focuses on the development and culture of adult stem stem-cell-derived organoids from various species. Her latest efforts have resulted in the founding of a start-up company (3D Health Solutions, Inc.) with the goal of commercializing assays for drug screening based on organoid methods.

June 28 - 9:30-10:00

Use of probiotics and prebiotics to restore microbiome homeostasis and treat GI diseases in companion animals

Probiotics are defined by the World Health Organisation (WHO) to be “live microbes which when administered in adequate amounts confer a health benefit to the host”. They are frequently, though not necessarily, commensal bacteria. The probiotic genera most often used in small animal practice are *Enterococcus, Lactobacillus, Bacillus* and *Bifidobacterium*, which are all normal inhabitants of the colonic flora. Prebiotics are components of the diet, most commonly fructo-oligosacchraides (FOS) that promote the growth of bacteria in the microbiome that are associated with health benefits, such as the production of beneficial short-chain fatty acids (for example, butyric acid).

The mammalian gastrointestinal tract contains > 100 trillion organisms comprising approximately 500 species, many of which have not been identified. These bacteria are parasites, commensals, or mutualists. Within hours after birth, the gastrointestinal tract is populated with numerous bacterial species, but *bifidobacteria* predominate in mammals. The change to a more complex diet after weaning allows the microbial population to diversify. Each organism strain appears to be associated with specific effects on other organisms and on the host, and specific cytokine profiles and biological effects result from these interactions. Gastrointestinal bacteria have co-evolved with their host and have become highly specialized over time. Composition of fecal microbiota in individual human beings and animals is unique but stable over time. Recent studies show evidence that a healthy composition of the microbiome in the intestine is important for the normal development of the gastro-intestinal immune system, and especially for adequate production of antigen-specific mucosal IgA.

The composition of the microbiome has been shown to be significantly altered in specific diseases in human beings as well as in dogs and cats. Specifically, increases in the amounts of *Enterobacteriaceae* species have been associated with acute and chronic diarrhea, such as inflammatory bowel disease in people as well as in dogs. For decades, it has therefore been hypothesized that the microbiome composition can be influenced by feeding probiotics and therefore shifting the microbiome to a more healthy or “normal” composition.

Mechanism of action of probiotics

Probiotics are able to modulate the host’s immune defences through multiple mechanisms. They may also have direct effects on microbial products like toxins, host products e.g. bile salts and food ingredients4. Probiotic products are recognized by host cells expressing pattern recognition receptors such as Toll like receptors (TLRs) on their surface. Binding of bacteria to the receptors triggers an intracellular signalling cascade leading to immune modulation. TLR binding has been shown to be species- and activity-specific with regard to the individual probiotics used, with the most important receptors activated by probiotics in this family including TLR2, TLR9 and NOD2. However, some in vitro and in vivo effects of probiotics were found not to require activation through TLRs. Deficiency in MyD88 abolished the investigated activities, thus it remains to be established whether other TLRs or a MyD88-dependent, but TLR-independent, pathways are involved. It has also been proposed that probiotics suppress the NF-κB activation pathway, which will have an effect on the levels of IL-12, the IL-10:IL-12 ratio, IL-6, TNF-α or IL-8 produced in the GI tract.

Karin Allenspach - abstract con't

Several *in vitro* studies have shown that probiotics can modulate the balance of Th1, -Th2- and Th17 –derived cytokines produced in the intestine. To this end, much attention has been paid to the abilities of probiotics to induce the development of T regulatory cells (Tregs). For instance, two *Lactobacillus strains* have been shown to stimulate human monocyte-derived immature dendritic cells (Dcs) and to trigger their differentiation into regulatory DCs; these cells were then able to induce IL-10 producing Tregs. However, in vitro studies are not always predictive of in vivo effects, particularly if the intestinal cell lines used for the assays are traditional 2dimensional assays (CaCo2 cells etc). Novel technologies using 3-dimensional culture of primary intestinal epithelial cells (so-called organoids) are much more translatable to the in vivo situation and show promise for high-throughput preclinical testing of probiotics (ref. 1).

Efficacy of probiotics in dogs and cats with diarrhea

Several studies have been performed in dogs and cats with acute diarrhea, and there is clearly some evidence that clinical signs disappear faster and/or with less use of additional supportive treatment when probiotics are used versus placebo (ref. 2,3,4,5). This has been shown with different probiotics and different clinical situations. Most studies report the use of *E. feacium*-containing probiotics as useful in the setting of acute diarrhea in dogs and cats. In one recent large-scale study in shelters, the frequency of diarrhea was significantly reduced in cats if probiotics were given prophylactically compared to placebo, however, the same was not true for dogs.

Chronic diarrhea (Inflammatory bowel disease) in dogs

Probiotics have been tested in dogs with chronic diarrhea in several recent trials (ref. 6,7). Although some parameters, such as the dysbiosis index, the number of cellular infiltrates in the intestine, as well as anti-inflammatory cytokines and tight junction proteins have been shown to be positively affected by the probiotics in some of these studies, the overall clinical effect of probiotics in chronic diarrhea cases seems to be minimal.

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Late Breaking News

The Late Breaking News session provides an opportunity for ISAPP industry scientists and invited experts to share interesting data, perspectives, or developments in 5-minute talks.

Late Breaking News is chaired by Gregor Reid, Lawson Health Research Institute, London, Canada.

16:45-16:50. An end and a beginning. Mary Ellen Sanders, ISAPP Executive Science Officer, Centennial CO, USA

16:50-16:55. Probiotics in the neonatal intensive care unit: a framework for optimizing product standards. Greg Leyer, Chr Hansens, Milwaukee, WI, USA

16:55-17:00. Postbiotic polemics: an action to move the field forward. Gabriel Vinderola, UNL-CONICET, Santa Fe, Argentina

17:00-17:05. Danone North America's qualified health claim petition to the FDA - Yogurt and type 2 diabetes risk reduction. Miguel Freitas, Danone North America, White Plains, NY, USA

17:05-17:10. Using genomics to track plant intake. Lawrence David, Duke University, Durham, NC, USA

17:10-17:15. Empowering women through their microbiome. Mariya Petrova, Winclove Probiotics, Amsterdam, the Netherlands

17:15-17:20. NIH activities and funding opportunities. Gabriela Riscuta, National Institutes of Health/National Cancer Institute, Bethesda, MD, USA

17:20-17:25. Microbial composition is conserved between paired faecal and rectal biopsy samples from healthy volunteers. Karen Scott, Rowett Institute, University of Aberdeen, UK

17:25-17:30. Is race relevant to human microbiome/probiotics research? Kingsley Anukum, Nnamdi Azikiwe University, Nnewi, Nigeria

17:30-17:35. Probiotic-derived EV as therapeutic effectors: biogenesis, host internalization and mechanistic targets. Graciela Lorca, University of Florida, Gainesville, USA

17:35-17:40. Potential of designed prebiotics for gut-brain axis health: case of Parkinson's disease. Thaisa Cantú-Jungles, Purdue University, West Layfayette, IN USA

17:40-17:45. Dissecting responses to probiotics with transcriptomics identifies unexpected mechanisms of action. Martin Desrosiers, Université de Montréal, Quebec, Canada

Group 1: Use of probiotics and prebiotics in agricultural and companion animals.
Chaired by: Kelly Swanson, University of Illinois – Urbana, USA and George Fahey, University of Illinois – Urbana, USA

Probiotics, prebiotics, and other biotic substances are not only effective ways to promote a healthy gastrointestinal tract, an effective immune system, and the overall health of humans, but also in agricultural and companion animals. As the oversight of antibiotic use intensifies, population density of animals and humans increases, and production strategies of agricultural animals are more heavily scrutinized, the importance of biotics and other health promotors will increase in the future. Because key differences exist in regard to gastrointestinal tract anatomy and physiology, dietary management and feeding strategy, and disease susceptibility, biotic types and amounts often differ according to host species and life stage. Despite these differences, the literature demonstrates the value of biotics in agricultural and companion animal species, but there is room for improvement and expansion. As knowledge of gastrointestinal microbiomes grows and the biotic field develops, more targeted and effective strategies for health promotion in these species is expected. The aims of this Discussion Group are: 1) to document successful use of probiotics, prebiotics, and other biotic substances to promote health or treat disease in agricultural and companion animals, and 2) to identify opportunities and challenges that may impact the future of this field. To achieve this goal, we have identified experts that will deliver short presentations relevant to the field. Following the presentations, the future needs, opportunities, and challenges will be discussed by all participants. The primary outcome of this activity is expected to be an opinion paper in a journal such as Trends in Microbiology, Frontiers in Microbiology, or something similar.

Group 2: What is the evidence that a biotic intervention can benefit healthy people?
Chaired by: Dan Merenstein and Dan Tancredi, University of California – Davis, USA

The FDA generally requires at least two adequate and well-controlled studies to establish effectiveness. However, that level of evidence seldom exists for most interventions – including biotics – when it comes to keeping healthy people healthy or preventing illness. If two RCTs are not available, the Bradford-Hill criteria for evidence of a causal relationship are often suggested to be applicable. Regardless, it is inherently difficult to demonstrate that any intervention can keep healthy people healthy, including diet, exercise, sleep, stress reduction, etc.

The U.S. Preventive Services Task Force (USPSTF) makes evidence-based recommendations for clinical preventive services, including screenings, counseling, and preventive medications. Their approaches are worth considering, and one can find their recommendations and grades for evidence here.

As an example, it is widely assumed that diet and exercise have a robust evidence base for preventing adverse cardiovascular conditions. However, the USPSTF gives only a C recommendation for behavioral counseling to increase diet and exercise for adults without cardiovascular risk factors. The USPSTF "recommends that clinicians individualize the decision to offer or refer adults without cardiovascular disease risk factors to behavioral counseling interventions to promote a healthy diet and physical activity." With regard to their assessment of the strength and quality of the evidence, the USPSTF "concludes with moderate certainty that behavioral counseling interventions have a small net benefit on CVD risk in adults without CVD risk factors."

Is there enough existing data in biotics for any preventive outcome to lead to the same or stronger conclusions as did the USPSTF for behavioral counseling interventions to promote a healthy diet and physical activity?

Group 2: What is the evidence that a biotic intervention can benefit healthy people? con't
Chaired by: Dan Merenstein and Dan Tancredi, University of California – Davis, USA

Questions for speakers to consider and try and address for their talks:
Scope: The focus of our discussion will be on endpoints studied in generally healthy populations. We will not discuss use of probiotics for UC, rheumatoid arthritis, at risk of developing NEC, etc.

1. What is the evidence that biotics can prevent disease or help maintain health?

2. Are there data from biotics interventions for one population that are sufficiently robust to enable extrapolation to another population? For example, are there data from a population with a disease that can be extrapolated to a population without that disease? Or are there data that can be extrapolated to a population with substantively different demographics? USPSTF uses an approach that allows a C level recommendation from extrapolated data. EFSA may allow extrapolation of benefits for certain subpopulation and outcomes (weight loss for obese patients) to the general population but not for other subpopulations and outcomes (joint function for patients with arthritis).

3. Are there subpopulations of the generally healthy population for whom biotics may prevent disease or help maintain health? For example, infants born via C-section, travelers at risk of traveler's diarrhea, etc.

4. Are there novel approaches that may provide evidence for keeping healthy people healthy? For example, using real world data, biomarkers of health, homeostasis of microbiota or clinical biomarker readouts, vaginal microbiota composition, etc.

5. Consider how adverse events and cost of intervention weighs on evidence assessment.

Group 3: Do probiotics improve health by changing the gut microbiome?
Chaired by: Maria Marco, University of California – Davis, USA and Dave Mills, University of California – Davis, USA

It is frequently stated that probiotics benefit health by modulating the microbiome. But is this actually true? Human studies frequently report that probiotics have limited to no effect on the composition of the intestinal microbiota. Mechanistic research has instead shown that compounds produced by probiotics act directly on host epithelial and immune cells to result in localized and distal health-modulatory effects. In this panel, we will discuss the latest findings on the molecular mechanisms governing probiotic-mediated effects through the digestive tract. The importance of the population size and persistence of the input probiotics, their impact on the resident microbiome, and the relative contribution of direct modulation of host responses will be discussed. The goal will be to better understand the population levels and activities of ingested microorganisms that align with improved probiotic efficacy.

Group 4: Is there an effective approach to rational design and validation of prebiotics to target members of the microbiota?

Chaired by: Bob Hutkins, University of Nebraska, Lincoln, USA and Bruce Hamaker, Purdue University, W. Lafayette, IN, USA

The human gut microbiome harbors multiple genes that are required for the digestion of prebiotics and other fibers, resulting in the production of end products that mediate gastrointestinal and systemic benefits to the host. Thus, the use of prebiotic interventions has been widely adopted as a strategy to modulate the gut microbiome and improve human health. However, considerable interindividual differences in gut microbial composition have resulted in variable responses toward these interventions. The existence of responders and nonresponders to these interventions emphasizes the need for personalized approaches to effectively redirect the gut ecosystem. In this discussion group, we will review strategies to address responder and nonresponder phenotypes in prebiotic and dietary fiber interventions. In particular, we will focus on targeted approaches to identify predictive features based on knowledge of fiber and prebiotic metabolism, metagenomes, and machine learning tools.

Group 5: How does the development pipeline differ between microbiome-based therapeutics and traditional probiotics for foods/supplements?

Chaired by: Sarah Lebeer, University of Antwerp, Belgium and Bruno Pot, Yakult Europe B.V., Almere, The Netherlands

Increased interest in the microbiome field has also boosted the interest in the clinical application of live micro-organisms to prevent or treat disease. According to the ISAPP consensus definition, these live microorganisms meet the criteria for probiotics, but there are differences with traditional probiotics for foods and supplements because the final products with these microorganisms will have to be registered as medicinal products to reach the market in the US and in Europe. The FDA has defined these products as “live biotherapeutic products” (LBP) and is one of the first authorities formulating important guidelines. (https://www.fda.gov/files/vaccines,%20blood%20%26%20biologics/published/Early-Clinical-Trials-WithLive-Biotherapeutic-Products--Chemistry--Manufacturing--and-Control-Information--Guidance-forIndustry.pdf). Since 2019, this category of drug products has also been included in the European Pharmacopoeia. In addition, in also other areas around the world, innovative microbiome-based drug products are explored and developed. For some background information, we refer to this publication of the Pharmabiotics Research Institute (PRI) (https://www.nature.com/articles/s12276-020-0437-6).

Group 6: Can C. difficile infections be prevented with bacteriotherapy?

Chaired by: Eamonn Quigley, The Methodist Hospital and Weill Cornell School of Medicine, Houston, TX, USA and Colleen Kelly, Brown University, Providence, RI, USA

This workshop will explore the latest information on an infection that represents a major challenge for health care throughout the world. This will include an update on basic pathogenesis of Clostridioides difficile infections including interactions with the microbiome, as well as with the host immune response. Here, biological factors that increase susceptibility or enhance resistance to Clostridioides difficile infection will be explored. In recent decades significant shifts have been observed in the epidemiology of Clostridioides difficile infections; a reappraisal of the current status of this infection and of Clostridioides difficile-associated disease (CDAD) is, therefore, important and timely with attention, in particular, being given to the relative prevalence of health care- vs community-acquired infections. A core component of the workshop will be the role of bacteriotherapy in the prevention and treatment of CDAD. Issues that will be addressed will include the potential of bacteriotherapy, in all of its forms, in both primary prevention and in the prevention of recurrence following successful treatment of an infection. An update on treatment strategies (and antibiotics, in particular) in the context of the emerging epidemiology and bacteriology of Clostridioides difficile will be provided and the latest information on fecal microbiota transfer (FMT) and live biotherapeutics will be shared and discussed.

SFA Discussion Group

7:45-8:30: SFA Keynote Presentation Learn to talk, walk and hope: tips for a career in life. Dr. Gregor Reid

8:30 - 8:45: Introductions from the SFA executive team

8:45 - 9:30: Lightning talks

9:30 - 9:45: Break

9:45 - 10:45:

- Orphan nisin immunity genes are widespread across the Bacillota. Ivan Sugrue
- Identifying novel probiotic candidates to counter kidney stone disease. Gerrit Stuivenberg
- Lactiplantibacillus plantarum Plantaricin EF is a probiotic effector that protects barrier function in intestinal epithelial cells through an intracellular cation-linked mechanism. Lei Wei

10:45-11:00: Break

11:00-11:30: How to leverage social media and maximize the reach of your scientific findings.
Kristina Campbell

11:30-12:15: Niche study area breakout groups

- Group 1: Probiotics and concept of using beneficial microbes for health
- Group 2: Prebiotics and concept of modulating fiber intake for health
- Group 3: Human microbiota and related bioinformatic analysis

12:15-12:45: Summary of discussions

12:45-1:00: Networking activities

ISAPP

The ISAPP IAC and SFA present the following poster abstracts.
Please note that the abstracts are grouped topically into four different sections which correspond with how the posters are located for viewing.

SECTION 1

Poster # 1 SFA

Poster title: SFA Informational Poster

Abstract: n/a

Poster # 2 SFA

Poster title: Optimization of the process for the degradation of raw shrimp waste and production of chitinase and chitin oligosaccharides having prebiotic potential

Authors and affiliations (presenter underlined): Rahul Warmoota (Panjab University Chandigarh, India), Shivam Singla (Panjab University, Chandigarh, India), Dr. Naveen Gupta (Panjab University, Chandigarh, India).

Abstract:
Introduction: Every year an enormous amount of waste is generated from seafood industry a major part of which is the shrimp waste. Available methods for the disposal of this waste; such as ocean dumping, chemical degradation etc. are not environment friendly. An eco-friendly and most suitable alternative is the biodegradation, employing microorganisms-producing enzymes such as chitinases. It will also lead to the production of various value-added products. In the present study, conditions were optimized for the optimum degradation of raw shrimp waste along with the production of chitinase using chitinolytic organism Bacillus sp. CH-2 isolated earlier in our laboratory. The hydrolysate produced after biodegradation of raw shrimp waste was analysed for various value-added products such as chitin oligosaccharides (COS). Methods: Bacillus sp. CH-2 was employed for the degradation of raw shrimp waste under submerged fermentation. Conditions for the optimal degradation were standardized using classical and statistical methods. Presence of COS was detected using techniques such as TLC. Prebiotic potential of COS of various degrees of polymerization was evaluated by in vitro fermentation of COS with various intestinal microorganisms. Results: Bacillus sp. CH-2 was able to do the effective degradation of raw shrimp waste. After statistical optimization there was 7.2 fold increase in the shrimp waste degradation and 35.52 fold increase in the chitinase yield. In TLC analysis COS of varied degrees of polymerization were found to be present in the hydrolysate. COS was found to have beneficial effect on the growth of various Lactobacillus sp. and also limits the growth of various enteric pathogens, therefore having huge potential as prebiotic agent.

Poster # 3 SFA

Poster title: An examination of the collateral damage caused to the gut microbiome by antimicrobials using an ex vivo distal colon model

Authors and affiliations (presenter underlined): Lauren Walsh (School of Microbiology, University College Cork, Cork, Ireland), (APC Microbiome Ireland, University College Cork, Cork, Ireland). Colin Hill (School of Microbiology, University College Cork, Cork, Ireland), (APC Microbiome Ireland, University College Cork, Cork, Ireland), R Paul Ross (School of Microbiology, University College Cork, Cork, Ireland), (APC Microbiome Ireland, University College Cork, Cork, Ireland), (Teagasc Food Research Centre, Moorepark, Co. Cork, Ireland).

Abstract:
Introduction: Antimicrobials are commonly ingested by humans as food preservatives (sodium benzoate, potassium sorbate, sodium nitrite, sodium sulfite), antibiotics (fidaxomicin and vancomycin), bacteriocins (nisin and thuricin CD), and pesticides (glyphosate). Collateral damage to the gut can be caused when antimicrobials exhibit a broad range of activity. This study examines the antimicrobials listed above and the level of disruption they cause to the gut microbiome. Methods: MIC's were determined for the pharmaceuticals against a range of antibiotic resistant and gut bacteria, and for the food preservatives and pesticide against various Lactobacillus strains. These in vitro experiments were done to determine which concentration would be used to treat the micro-Matrix™ mini fermentation system (an ex vivo model of the distal colon). Each well of the micro-Matrix was treated with a different antimicrobial and incubated for 24 hrs. DNA was extracted from samples and sent for whole metagenomic sequencing from which absolute abundance was determined. Results: All food preservatives were minimally active against all Lactobacillus strains tested. Glyphosate was not active against any strain at the concentrations tested. Thuricin CD exhibited low MIC's (<3.1 µg/ mL) for C. difficile and B. firmus. Whereas fidaxomicin, vancomycin and nisin demonstrated lower MIC's for all other strains tested when compared to thuricin CD. These results were mirrored in the micro-Matrix™ system. Conclusion: All pharmaceuticals, except for thuricin CD, demonstrated a significant degree of collateral damage to the gut. In contrast, while all food preservatives exhibited activity against commensal gut bacteria, this activity was not observed at concentrations reflective of that found in food.

Poster # 4 SFA

Poster title: *Lactiplantibacillus plantarum* Plantaricin EF is a probiotic effector that protects barrier function in intestinal epithelial cells through an intracellular cation-linked mechanism

Authors and affiliations (presenter underlined): Lei Wei (University of California, Davis, Davis, CA, USA); Maria Marco (University of California, Davis, Davis, CA, USA)

Abstract:
The two-peptide bacteriocin, plantaricin EF (PlnEF), made by *Lactiplantibacillus plantarum* is a potent antimicrobial with bactericidal activity due to its capacity to disrupt intracellular cation homeostasis. Recently, we showed that PlnEF elicits responses in intestinal epithelial cells that attenuate the effects of proinflammatory cytokines-mediated disruptions of intestinal epithelial cell function in a Caco-2 transwell model. To determine whether PlnEF alters intestinal cells in a manner similar to that observed for sensitive bacteria, we quantified the intracellular cation concentrations in Caco-2 cells using inductively coupled plasma mass spectrometry (ICP-MS). Exposure to 500 nM PlnEF for 32 h resulted in a significant 23.01% (2.11 x 10^10 to 1.62 x 10^10 atoms/cell) and 24.51% (2.48 x 10^11 to 1.87 x 10^11 atoms/cell) reduction in Mg2+ and K+, respectively.

Poster # 4 SFA con't

These changes were consistent with the 2- to 8-fold increase in expression of two genes encoding the divalent cation transport proteins, CNNM2 and CNNM4, which have an affinity for Mg2+ and homology to a putative binding site on the bacterial magnesium efflux protein CorC. Moreover, PlnEF treatment (500 nM) increased the expression of Caco-2 genes encoding tight junction proteins, CLDN1, CLDN3, CLDN4, occludin (OCLN), and ZO-1 and reduced the expression of pore-forming CLDN2 over time (reaching at least a 2-fold difference). These findings suggest that PlnEF is a probiotic effector that protects intestinal epithelial barrier integrity through a mechanism involving intracellular cation homeostasis.

Poster # 5 SFA

Poster title: Man's best friend: potentially novel antimicrobial compounds isolated from bacterial strains of canine source.

Authors and affiliations (presenter underlined): Michelle O' Connor (1. APC Microbiome Ireland, University College Cork, Cork, Ireland), Des Field (1. APC Microbiome Ireland, University College Cork, Cork, Ireland), Colin Hill (1. APC Microbiome Ireland, University College Cork, Cork, Ireland; 2. School of Microbiology, University College Cork, Cork, Ireland), R. Paul Ross (1. APC Microbiome Ireland, University College Cork, Cork, Ireland; 2. School of Microbiology, University College Cork, Cork, Ireland; 3. Teagasc Food Research Centre, Moorepark, Fermoy, Cork, Ireland).

Abstract:
Antimicrobial resistance (AMR) is a major risk to human and animal health requiring urgent attention. A contributing factor to AMR is the misuse/overuse of antibiotics adding to the development and spread of resistance mechanisms by pathogens. Greater efforts are needed not only to prevent additional AMR development but to reassess and identify alternative therapeutic options. One group of compounds that hold great promise is antimicrobial peptides (AMPs). AMPs produced by bacteria are termed bacteriocins, which can kill or inhibit bacterial strains closely-related or non-related to the producing strain. Notably, a diverse community of trillions of commensal bacteria inhabit the mucosal and epidermal surfaces of humans and animals and can be found in a multitude of sites; including the mouth, nose, skin, ears and intestines, many producing novel bacteriocins. Given their potent antimicrobial activity against pathogenic bacteria, immunomodulatory effects on their hosts, auto-regulation of their own production and self-immunity exhibited by the producing bacteria to their own peptides, this vast resource of bacteriocins and their beneficial characteristics show their potential as alternatives to traditional antibiotics in the fight against AMR. This study involves screening multiple sites from five canines in a bid to identify novel antimicrobial peptides which target a range of clinically relevant bacteria with a focus on drug-resistant pathogens particularly from veterinary settings.

Poster # 6 SFA

Poster title: Effects of commercial and traditional kefirs on apparent total tract macronutrient digestibility and fecal characteristics, metabolites, and microbiota of healthy adult dogs

Authors and affiliations (presenter underlined): Breanna N. Metras (University of Illinois at Urbana-Champaign), Patricia M. Oba (University of Illinois at Urbana-Champaign), Michael J. Miller (University of Illinois at Urbana-Champaign), and Kelly S. Swanson (University of Illinois at Urbana-Champaign).

Abstract:
Our objectives concerned the effects of commercial or traditional kefirs on apparent total tract macronutrient digestibility (ATTD) of a diet administered to healthy adult dogs and determine fecal characteristics, microbiota populations, metabolite, and immunoglobulin (Ig) A concentration. Dogs (n=12/group) were used in a replicated 3x3 Latin square design. A commercial diet was fed alongside allotments of 1 of 3 treatments: 2% reduced-fat milk treated with lactase (CNTL), commercial kefir (C-Kefir), or traditional kefir (T-Kefir) from 2% reduced-fat milk and kefir grains. Three 28-d periods were composed of a 22-d transition phase, a 5-d fecal collection phase, and 1 d for blood collection. Blood and fecal samples were collected for serum chemistry pH, dry matter, microbiota populations (16S rRNA gene amplicons), ATTD, metabolite, and IgA concentrations. Mixed Models procedure of SAS 9.4 was used, with main effects of treatment tested; significance set at $p<0.05$. T-Kefir had a higher ($p<0.0001$) CFU/mL count than CNTL and C-Kefir. Bacterial alpha diversity tended to be greater ($p=0.10$; Faith's PD) in dogs fed T-Kefir than CNTL. Beta diversity analysis (unweighted PCoA) identified a difference ($p<0.0004$) between dogs fed CNTL and C-Kefir. Dogs fed C-Kefir tended to have greater ($p=0.06$) relative abundance of Fusobacteriota; dogs fed T-Kefir had greater ($p<0.0001$) relative abundance of *Lactococcus*. Fresh fecal pH, DM, IgA and metabolite concentrations, and blood biomarkers were not affected by treatment. The supplementation of commercial or traditional kefir to healthy adult dogs had minor effects on fecal microbiota, fecal metabolite concentrations, stool quality, fecal IgA concentrations, and blood metabolites.

Poster # 7 IAC

Poster title: A water-soluble tomato extract rich in secondary plant metabolites lowers trimethylamine-n-oxide (TMAO) and modulates gut microbiota in overweight and obese adults

Authors and affiliations (presenter underlined): Ateequr Rehman [1], Gillian DunnGalvin [2], Shriram Patel [3], Timothy G. Dinan [4], Asim K. Duttaroy [5], Ruedi Duss [1], Robert E. Steinert [1, 6*]

1 DSM Nutritional Products, Kaiseraugst, Switzerland;
2 Atlantia Clinical Trials, Cork, Ireland;
3 SeqBiome, Cork, Ireland;
4 Atlantia Clinical Trials, Cork, Ireland, APC Microbiome Ireland, Cork, Ireland, Department of Psychiatry and Neurobehavioral Science, University College Cork, Cork, Ireland;
5 Department of Nutrition, Institute of Basic Medical Nutrition, Faculty of Medicine, University of Oslo, Norway;
6 Department of Surgery, Division of Visceral and Transplantation Surgery, University Hospital Zurich, Zurich, Switzerland

Poster # 7 IAC con't

Abstract:
Background and objective: Natural products rich in polyphenols have been shown to lower plasma trimethylamine-n-oxide (TMAO) known for its proatherogenic effects by modulating the intestinal microbiota. To further build evidence for polyphenols exerting a prebiotic effect, we aimed to determine the impact of a water-soluble tomato extract (Fruitflow®, FF), on plasma and urine TMAO, fecal microbiota, and plasma and fecal metabolites in humans.
Methods: Overweight and obese adults (n = 22, BMI 28–35 kg/m2) were included in a double-blind, placebo-controlled, cross-over study receiving 2x150 mg FF per day or placebo for 4 weeks with a 6-weeks wash-out between interventions. Stool, blood, and urine samples were collected to assess changes in plasma and urine TMAO as well as fecal microbiota, and fecal and plasma metabolites. In a subgroup (n = 9), postprandial TMAO concentrations were evaluated following a choline-rich breakfast (~450 mg).
Results: FF, but not placebo, reduced fasting levels of plasma (-1.5 μM, P ≤ 0.05) and urine (-19.1 μM, P ≤ 0.01) TMAO as well as plasma lipopolysaccharide (LPS) (-5.3 ng/mL, P ≤ 0.05) from baseline to the end of intervention. However, these changes were significant only for urine TMAO levels when comparing between the groups (P ≤ 0.05). Changes in microbial beta, but not alpha, diversity paralleled this with a significant difference in Jaccard distance-based Principal Component (P ≤ 0.05) as well as decreases in *Bacteroides, Ruminococccus*, and *Hungatella* and increases in *Alistipes* when comparing between and within groups (P ≤ 0.05, respectively). There were no between-group differences in SCFAs. An untargeted metabolomic analysis revealed TMAO as the most discriminant plasma metabolite between groups (P ≤ 0.05).
Conclusions: Our results support earlier findings that polyphenol-rich extracts can lower plasma TMAO in overweight and obese adults related to gut microbiota modulation suggesting a prebiotic effect.

Poster # 8 IAC

Poster title: The Microbial Metabolites Totipro® PE0401 Promoted Probiotic Bacteria Growth and Improved Intestinal Health in Human

Authors and affiliations (presenter underlined): Yi-Wei Kuo, Ching-Wei Chen, Yu-Chieh Hsu, Yu-Fen Huang, Chen-Hung Hsu, Jia-Hung Lin, Chi-Huei Lin, Cheng-Chi Lin, Tsai-Hsuan Yi, Yu-Wen Chu, Jui-Fen Chen, and Hsieh-Hsun Ho Research and Design Department, Glac Biotech Co., Ltd., Tainan City 744, Taiwan

Abstract:
Over the past few years, studies demonstrated the postbiotics (a preparation of inanimate microorganisms and/or their components that confers a health benefit on the host) played an important role in modulating intestinal microbiota. Evidences showed the single-strain postbiotics had positive effects on the health of host, but the functions of multi-strain postbiotics remained unclear. Therefore, this study was initiated from testing different combinations of metabolites and the 4 Mix postbiotic formula (named as Totipro® PE0401) was chosen for further investigation. Totipro® PE0401 consisted of metabolites from *Lactobacillus salivarius* AP-32, *L. acidophilus* TYCA06, *L. plantarum* LPL28, *Bifidobacterium longum* subsp. *infantis* BLI-02. The unique synergistic effect of Totipro® PE0401 was revealed on the expression of tight junction proteins (TJPs) in Caco-2 cells by Reverse Transcriptase PCR. The result indicated the potential of Totipro® PE0401 for strengthening the intestinal barrier. The pilot study displayed the daily oral supplementation of 600 mg Totipro® PE0401 significantly increased the defecation frequency and modulated gut microbiota in constipation subjects in 30 days. Notably, the genus *Akkermansia* increased in response to the supplementation of Totipro® PE0401. Moreover, the effect of Totipro® PE0401 on gut microbiota modulation was illustrated by growth assay *in vitro*, and the result validated the growth promoting effect of Totipro® PE0401 on various probiotic bacteria strains, e.g. *L. rhamnosus* GG and *Bifidobacterium animalis* subsp. *lactis* BB-12. In conclusion, Totipro® PE0401 was a specific combination of microbial metabolites, which enhanced the intestinal health via promoting intestinal barrier, bowl movement, and beneficial bacteria growth.

SECTION 2

Poster # 9 SFA

Poster title: Emerging evidence for probiotic-based disease management in honey bees

Authors and affiliations (presenter underlined): Brendan Daisley (University of Guelph, Guelph, Canada), Andrew Pitek (Western University, London, Canada), Christina Torres (University of California, Davis, Davis, USA), Robin Lowery (University of California, Davis, Davis, USA), Bethany Adair (Western University, London, Canada), Kait F Al (Western University, London, Canada), Bernardo Niño (University of California, Davis, Davis, USA), Jeremy Burton (Western University, London, Canada), Emma Allen-Vercoe (University of Guelph, Guelph, Canada), Graham Thompson (Western University, London, Canada), Elina Niño (University of California, Davis, Davis, USA), Gregor Reid (Western University, London, Canada).

Abstract:
Managed honey bee (*Apis mellifera*) populations play a crucial role in supporting adequate pollination of food crops but are facing unsustainable colony loss as the result of rampant disease spread within agricultural environments. Antibiotics have failed to resolve the issue so far, whereas mounting evidence from in vitro experiments suggests that select lactobacilli strains (some of which are symbionts in honey bees) can inhibit a broad range of important pathogens via multifaceted mechanisms. Focusing on three select strains of lactobacilli (LX3), our group has performed several probiotic field studies in distinct regions across North America. Cumulative evidence indicates that the LX3 strains can significantly improve resistance to disease outbreaks, partially mitigate the negative effects of antibiotics in bees, and increase queen egg laying – the latter of which has the potential to increase the number of bees present in a hive and thus overall pollination capacity which is relevant to agricultural crop yields. Furthermore, our studies show that certain effects derived from LX3 treatment are directly dependent on the way in which the strains were administered to the hive. This highlights that consideration of delivery method is essential for deriving an expected probiotic benefit in honey bees. Overall, the collective scope of this work is expansive and broadly relevant to microbial disease management in terrestrial ecosystems.

Poster # 10 SFA

Poster title: A method for the enrichment of bacteriocin-associated genes across the bacterial pangenome.

Authors and affiliations (presenter underlined): Dave Hourigan (APC Microbiome Ireland, Ireland).

Abstract:
Bacteria rarely live in isolation outside of the lab, usually inhabiting challenging ecosystems whilst having distinct ecological roles in their complex communities. Bacteriocins are ribosomally encoded antimicrobial peptides produced by bacteria with both broad and narrow spectrums of activity that can aid competition. Recent advancements in metagenomics have expanded our knowledge of the abundance and diversity of bacteriocin gene clusters whilst potentially giving us greater insight into their ecological role in these complex microbiomes. My research aims to investigate the proximity of genes or gene clusters to bacteriocin gene operons through Protein Family (PFAM) and Gene-Ontology functional enrichment to gain deeper insight into potential links between bacteriocin production and other bacterial properties. The non-redundant (nr) database was mined for lanthipeptide and circular bacteriocin (class IIc) gene clusters using RODEO2, a tool for evaluating the local genomic context of query proteins. PFAM co-localisation networks were constructed using “ggraph” and bacteriocin biosynthetic PFAMs were iteratively removed from the network to uncover PFAMs associated with bacteriocin biosynthetic gene clusters but not part of the core machinery. A negative control dataset was constructed using the refseq database without matches to known bacteriocin gene clusters as determined by blast hit vs BAGEL4 database, consisting of core and modification proteins (e-value; 1e-10). Protein domain and gene ontology enrichment analysis was performed using topGO.

Poster # 11 SFA

Poster title: Mining prebiotic active molecules using genetic analysis of plant foods with newly developed aims platform (automated in vitro microbiome screening)

Authors and affiliations (presenter underlined): Qinnan Yang (Univerisity of Nebraska-Lincoln), Mallory Van Haute (Univerisity of Nebraska-Lincoln), Nate Korth (Univerisity of Nebraska-Lincoln), Scott E. Sattler(USDA), John Toy(USDA), Devin J. Rose (Univerisity of Nebraska-Lincoln), James C. Schnable (Univerisity of Nebraska-Lincoln) & Andrew K. Benson (Univerisity of Nebraska-Lincoln).

Abstract:
The human gut microbiome has the capacity for metabolizing fibers, lipids, proteins, polyphenols and other molecular components and plays critical roles in gut health and wellness. The abundance of these, frequently uncharacterized, microbiome-active components varies within individual plant foods. To identify and characterize potential prebiotic active molecules that alter the composition and function of the human gut microbiome, we developed a high throughput AiMS platform (Automated in vitro Microbiome Screening). AiMS platform has the capacity to screen hundreds of different grains via in vitro digestion and fermentation in a high throughput manner. The platform also leverages the vast diversity of prebiotic-active molecules that are naturally present in cereal grains. One such grain is sorghum, one of the most widely consumed grains in the developing world. Accordingly, we used the AiMS platform to conduct in vitro fermentations with 294 sorghum recombinant inbred lines as fermentation substrates. After sequencing and quantitative trait loci (QTL) mapping, we successfully identified 10 loci in the sorghum genome that were associated with variation in the abundance of microbial taxa and/or microbial metabolites. Two loci co-localized with sorghum genes involved in regulating the biosynthesis of condensed tannins. Many plant polyphenols, including condensed tannins have recently been recognized to have prebiotic potential. Genetic analysis in near isogenic lines and molecular complementation showed that condensed tannins stimulate the growth of *Faecalibacterium*. Our work illustrates the potential for genetic analysis to systematically discover and characterize novel molecular components with prebiotic potential in plant foods.

Poster #12 SFA

Poster title: Development of a synergistic synbiotic containing arabinoxylan and Bifidobacterium longum using in vivo selection

Authors and affiliations (presenter underlined): Evan Jones (University College Cork, Cork, Ireland), Jens Walter (University College Cork, Cork, Ireland), Douwe van Sinderen (University College Cork, Cork, Ireland).

Abstract:
Colonization and metabolic activity of orally ingested bacteria in the colon rely on competitive ecological and niche-based factors that often limit functionality of commonly used probiotics. Synergistic synbiotics, which involve the parallel administration of a microorganism with its cognate substrate, have the potential to improve persistence and ecological performance of putative probiotic microbes. However, real synergism has not yet been established for synbiotics in human trials, and most synbiotic combinations have not been designed using an approach that accounts for the ecological constraints of the GI tract. Here we use in vivo selection (IVS) to identify strains of Bifidobacterium longum that are adapted toward the utilization of arabinoxylan (AX) in the human gut. To achieve this, bifidobacteria were quantitatively cultured from fecal samples collected during a human trial which showed that a high dose of corn bran AX

Poster #12 SFA con't

leads to a significant but highly individualised increase of *B. longum*. Isolates were randomly picked and genotyped by a high throughput gyrB sequencing method. Bacterial counts and strain composition were compared between baseline and week 6, and representatives of B. longum strains enriched in vivo by AX were then tested through in vitro fermentations to investigate their growth on AX and its constituents. Our initial findings showed that strains grew well on the arabinose branches and xylose monomers of AX, but not on xylo-oligosaccharides (XOS). Future work will explore growth on native AX, and involve whole-genome sequencing and comparative genomic analysis of selected strains to characterize the genetic basis of AX degradation. This study demonstrates an ecologically relevant process for selecting improved synbiotic combinations.

Poster # 13 SFA

Poster title: In Vitro Assessment Of Bacteriocins As Microbiome Modulators In A Simplified Human Intestinal Microbiota

Authors and affiliations (presenter underlined): Natalia S. Rios Colombo (APC Microbiome, University College Cork, Ireland), Mariana Perez-Ibarreche (APC Microbiome, University College Cork, Ireland), Lorraine A. Draper (APC Microbiome, University College Cork, Ireland), Paula M. O'Connor (APC Microbiome, University College Cork, Ireland), Des Field (APC Microbiome, University College Cork, Ireland), R. Paul Ross (APC Microbiome, University College Cork, Ireland), Colin Hill (APC Microbiome, University College Cork, Ireland).

Abstract:
Bacteriocins are antimicrobial peptides produced by bacteria of many genera that have been studied for decades as food bio-preservatives or as alternatives to antibiotics. Bacteriocins are often narrow spectrum and can kill target organisms without causing collateral damage to other bacterial populations. That is why bacteriocins are gaining credibility as precise modulators of the human microbiome. However, rigorous evidence is required to determine if bacteriocins can act as microbiome-editing tools to shape communities in a desirable direction. The aim of this project is to assess the effect of different bacteriocins on a Simplified Human Intestinal Microbiota (SIHUMI), using a set of bacteriocin-producing strains (Bac+) and their corresponding isogenic non-producers (Bac-). Bacteriocins from different classes and spectrum of activity were selected, including lantibiotics and pediocin-like peptides. SIHUMI is a bacterial consortium of seven diverse human gut species that can be individually tracked in a complex media using qPCR. The Bac+ and Bac- strains were superimposed on the SIHUMI system, and samples were taken at intervals up to 48 h for genomic DNA extraction. The genome copy number of each SIHUMI member was evaluated using specific primers. We were able to determine the behavior of the consortium over time and evaluate how the system is impacted by different bacteriocin producers. Our results show that it is possible to shape the composition of the community in a predictable way by targeting multiple members or specific members with either broad or narrow spectrum bacteriocins. While we recognize that SIHUMI is a simplified model, it provides useful insights into the possible mechanisms by which the microbiome could be shaped by bacteriocins.

Poster #14 SFA

Poster title: Endolysins targeting the IBD-associated bacterium Ruminococcus gnavus

Authors and affiliations (presenter underlined): Ellen Murray (School of Microbiology, University College Cork, Ireland), Ekaterina Khokhlova (APC Microbiome Ireland), Lorraine Draper (APC Microbiome Ireland), Andrey Shkoporov (APC Microbiome Ireland and School of Microbiology, University College Cork, Ireland) , Paul Ross (APC Microbiome Ireland and School of Microbiology, University College Cork, Ireland), Colin Hill (APC Microbiome Ireland and School of Microbiology, University College Cork, Ireland).

Abstract:
Introduction: *Ruminococcus gnavus* is a bacterium that has a strong correlation with Inflammatory Bowel Disease (IBD). In IBD patients, an overabundance of *R. gnavus* is associated with increased inflammation. Endolysin (lysin) therapy is a method of targeted microbiome editing. These phage-derived proteins can be used to target specific bacteria in the gut, such as *R. gnavus*, without causing collateral damage to microbiome composition. Lysins are peptidoglycan hydrolases that attack the structure of their host cell wall and result in cell lysis. Methods: Lysin genes were predicted in the genomes of R. gnavus temperate phages. Lysins were cloned into Escherichia coli for recombinant expression. Lytic activity against R. gnavus was assessed by spot assays, turbidity reduction assays, and kill curves. Host range was established using a panel of commensal gut strains. Observation of apparent lysin-resistant mutants of R. gnavus led to the generation of true mutants. DNA extraction of these cultures, and Illumina sequencing was used to compare their genomes to that of the sensitive parent strain of R. gnavus. Results: All cloned lysins showed activity against R. gnavus. Host range analysis was performed on 20 relevant strains. The lysins were specific for R. gnavus with some variations. We observed that after 20h there appeared to be growth of lysin-resistant mutants. Whole genome sequencing revealed SNPs in the genomes of these mutants that are associated with the bacterial stringent stress response. Conclusions: This study resulted in the isolation of lysins targeting R. gnavus. Future work will assess the potential issues of lysin-resistant mutants, and the viability of these lysins as therapeutics to restore microbiome composition in IBD patients.

Poster # 15 SFA

Poster title: Orphan nisin immunity genes are widespread across the Bacillota

Authors and affiliations (presenter underlined): Ivan Sugrue (APC Microbiome Ireland, University College Cork, Cork, Ireland), Colin Hill (APC Microbiome Ireland, University College Cork, Cork, Ireland), Paul Ross (APC Microbiome Ireland, University College Cork, Cork, Ireland).

Abstract:
Nisin is the prototypical lantibiotic, widely utilized as a food preservative and often suggested as an alternative to antibiotics. Nisin resistance proteins can be found in some pathogens and are a potential limiting factor for the use of nisin and nisin producing probiotics as therapeutics. The gut derived *Streptococcus hyointestinalis* DPC6484 produces nisin H but was thought to lack a nisin immunity system. However, it is highly resistant to diverse nisin variants, warranting further investigation. *S. hyointestinalis* DPC6484 was fully sequenced and the resulting 2.32 Mb genome was subject to BLASTp with known nisin resistance and immunity protein sequences. This identified a 5.2kb region encoding a lantibiotic immunity protein (nshI), transporter (nshFP), and a two-component regulator (nshRK) located elsewhere on the genome. The predicted genes were expressed in Lactococcus lactis MG1614 where they were found to confer resistance to nisin A. Protein BLAST and gene neighbouring algorithms were used to determine the prevalence of this novel resistance cluster, identifying three instances across Streptococcus genomes.

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A further 70 clusters were detected encoding nisin immunity (lanI), transport (lanFEG) and regulation (lanRK) genes spread throughout the phylum Bacillota, including the gut phyla Lachnospiraceae, Clostridaceae, Lactobacillaceae, Oscillospiraceae, Eubacteraceae and Streptococcaceae. Structures of putative protein sequences were predicted using Alphafold2 and found to be similar to known nisin variant immunity proteins. The unexpected prevalence of nisin immunity and resistance genes across the phylum Bacillota suggests a central role for nisin in the gut microbiome and may impact the potential application of nisin and nisin producers as bio-therapeutics.

Poster # 16 SFA

Poster title: Identification of novel immunomodulatory components in *Lacticaseibacillus rhamnosus* GG

Authors and affiliations (presenter underlined): Soyolmaa Jamiyanpurev (Department of Biomolecular Innovation, Institute for Biomedical Sciences, Shinshu University, Nagano, Japan), Fu Namai (International Education and Research Center for Food and Agricultural Immunology, Graduate School of Agricultural Science, Tohoku University, Miyagi, Japan), Suguru Shigemori (Department of Biomolecular Innovation, Institute for Biomedical Sciences, Shinshu University, Nagano, Japan), Takeshi Shimosato (Department of Biomolecular Innovation, Institute for Biomedical Sciences, Shinshu University, Nagano, Japan).

Abstract:
Introduction: Recently, probiotic lactic acid bacteria have been reported to have numerous functional properties, but it has been pointed out that their effects vary greatly among individuals. We previously applied ribosome engineering to *Lacticaseibacillus rhamnosus* GG to enhance its probiotic functions; one of the obtained mutants, MTK56N, showed enhanced immunomodulatory activity. In the present study, we attempted to identify the immunomodulatory components of MTK56N, and to elucidate the mechanism of action. Methods: We examined the bacterial lavage fluid of MTK56N, and constructed a genetically modified lactic acid bacteria (gmLAB) that produced chaperone protein DnaK (DnaK) and 60 kDa chaperonin (GroEL), which were suspected to be the responsible proteins. The immunomodulatory effects of the purified proteins were investigated using RAW264.7. In addition, RAW264.7 was incubated with each protein, and the expression levels of cytokine-encoding mRNAs and cytokine secretion were analyzed by RT-qPCR and ELISA, respectively. Results: Western blotting analysis confirmed that the constructed gmLAB expressed recombinant proteins in a nisin-stimulation-dependent manner. The levels of the pro-inflammatory cytokines TNF-Î± and IL-6 were significantly increased when the purified proteins were added. Moreover, the ELISA results indicated that each purified protein enhanced TNF-Î± and IL-6 secretion into the supernatant. Discussion: Our results indicated that the purified recombinant DnaK and GroEL proteins promoted the expression of TNF-α and IL-6 and exerted immunomodulatory effects in RAW264.7. Thus, DnaK and GroEL appear to be immunomodulatory components of MTK56N. We plan to elucidate the mechanisms of action of these bacterial surface proteins in future studies.

Poster # 17 IAC

Poster title: Science communication & education on biotics & the gut microbiome: a use-case with virtual reality technology

Authors and affiliations (presenter underlined): Sarah Moreira-Milheiro & David Obis, Danone Global Research and Innovation

Abstract:
Today, more than ever Science is changing the World. For this reason, it is important that science is explained in a simple and interactive way to as many people as possible. At the Danone Global Research and Innovation Center in Paris-Saclay, we have developed an innovative and immersive way to explain the science behind our products. We partnered with Healthskouts, Nozon – The Pack and ExecutXR, to create FLUX, a virtual reality program that allows users to explore the complex world of the gut microbiome. We wanted to develop an innovative, immersive and interactive communication program, to immerse our visitors in our world of biotics, fermentation, and gut microbiome. After an exploration of innovative communication techniques, the project team chose virtual reality, as it allows to create live and active experiences, and creates engagement and memories - what VR specialists call “emotional learning”. This technique also allows to make visible what is usually invisible. The virtual reality program is set up in a dedicated booth, providing visitors an immersive experience. With this tool, we now can take visitors on a journey through the gut and show them what they will not be able to see otherwise. The first two chapters developed in the program focus on the gut microbiota and the Danone strain collection. The 1st chapter of our project went live after the opening of our new R&I Center in Paris-Saclay in France in February 2023. FLUX is a key example the use of cutting-edge technology for scientific and education purposes to further explain the impact of nutrition on health and to help us shape the future of nutrition.”

Poster # 18 IAC

Poster title: *Bacillus clausii´s* mechanisms to protect the gut microbiome activity and composition after proton-pump inhibitor treatment, using the *in vitro* SHIME® technology

Authors and affiliations (presenter underlined): Zefferino Righetto[1], Cindy Duysburgh[2], Lynn Verstrepen[2], Mattia Van den Broeck[2], Dorothea M. Greifenberg[1], Beatrice Bois de Fer[3], Marcos III Perez[1], Peter Justen[3]

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2 ProDigest BV, Gent, Belgium;
3 Sanofi, Gentilly, France

Abstract:
Objectives and Study Proton pump inhibitors (PPIs) are commonly prescribed medications associated with changes in the gut microbiome and dysbiosis when used long-term. Probiotics, such as Enterogermina® (containing four strains of *Bacillus clausii*) reduce side effects from triple therapy with PPI + antibiotics. We aimed to assess the ability of this probiotic in preventing and/or treating the dysbiosis induced by PPI use.

Methods Faecal samples from six healthy donors were used to colonise a Triple-Mucosal-Simulator of the Human Intestinal Microbial Ecosystem® model with added ileal compartment. Changes in the microbial community composition and metabolite production were measured for PPI alone (control), PPI + Enterogermina (preventative), and Enterogermina treatment after PPI (curative). Differences were assessed by one-way ANOVA with Tukey’s multiple comparisons test.

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Results The model was shown to replicate some of the effects of long-term PPI use. There were significant changes in microbial diversity and an increase in butyrate levels in the preventative and curative arms, indicative of a beneficial effect to gut health. Probiotic use countered some of the effects of PPI use: *Streptococcus bovis* levels increased in the control arm but reduced following probiotic treatment.

Conclusion These results show that probiotic treatment with *B. clausii* may have beneficial effects on the gut microbiota following PPI treatment.

SECTION 3

Poster # 19 SFA

Poster title: Introducing a CRISPR-Cas9 based prime editing system for precision mutagenesis in lactobacilli

Authors and affiliations (presenter underlined): Dieter Vandenheuvel (University of Antwerp), Tom Eilers (University of Antwerp), Jelle Dillen (University of Antwerp), Eline Cauwenberghs (University of Antwerp), Peter Bron (University of Antwerp) & Sarah Lebeer (University of Antwerp).

Abstract:
The Lactobacillaceae are key players in different ecological habitats, like food fermentations or important in the healthy state of diverse human, plant, and animal niches. Contrary to the industrial and medical importance of lactobacilli, there is surprisingly little known about the genetic factors behind these beneficial effects. One reason for this can be found in the limited amount of tools available for genetic modification, especially precision mutagenesis. Methods: Here, we employ a recent advancement on the classical CRISPR-Cas method, called 'prime editing'. Prime editing uses an nCas9-reverse transcriptase fusion protein, capable of selectively identifying a genetic target and replacing it with a desired mutation. The system will target two genes, the pili-related spaC gene and the nucleotide related thyA gene, resulting in easily screenable phenotypes. These genes will be knocked out with the introduction of in-frame stop codons. Results: First, the nCas9-reverse transcriptase fusion gene was codon optimized for lactobacilli, and synthetically produced. The fusion gene was cloned into an expression vector for lactobacilli. As a proof of concept, this system will now be introduced in *Lacticaseibacillus rhamnosus* GG, the type strain of the genus and one of the best studied probiotics. Discussion: After successful introduction in this type strain, the system will be introduced in other non-model strains isolated from food and the human vaginal niche in order to facilitate functional molecular studies.

Poster # 20 SFA

Poster title: Characterising *Lactobacillus* strains from African women with persistently optimal vaginal microbiota - framework for an African vaginal probiotic product development platform

Authors and affiliations (presenter underlined): Anika Chicken (Institute of Infectious Disease and Molecular Medicine (IDM), University of Cape Town, Cape Town, South Africa), Jo-Ann Passmore (IDM, University of Cape Town, Cape Town, South Africa; NRF-DST CAPRISA Centre of Excellence in HIV Prevention, Cape Town, South Africa; National Health Laboratory Service (NHLS), Cape Town, South Africa) Anna-Ursula Happel (IDM, University of Cape Town, Cape Town, South Africa), Christina Balle (IDM, University of Cape Town, Cape Town, South Africa), Linda-Gail Bekker (Desmond Tutu HIV Centre, University of Cape Town, Cape Town, South Africa), Katherine Gill (Desmond Tutu HIV Centre, University of Cape Town, Cape Town, South Africa), Heather B. Jaspan (IDM, University of Cape Town, Cape Town, South Africa; Seattle Children's Research Institute, Seattle, USA; University of Washington Department of Paediatrics and Global Health, Seattle, USA) and Brian Kullin (IDM, University of Cape Town, Cape Town, South Africa).

Abstract:
Bacterial vaginosis (BV) is associated with significant health risks in cisgender women (CW). The high rates of BV reoccurrence following antibiotic treatment necessitates the development of alternative treatments. While probiotic products are promising in this regard, there is an urgent need for the development of improved vaginal products containing strains with proven beneficial properties capable of persistently colonising the female genital tract. We collected vaginal specimens at 3 visits from a total of 86 CW (aged 15-19 years; uCHOOSE cohort). Strains were selectively isolated from participants with longitudinally stable L. crispatus-dominant communities (CST I) using VALENCIA and assayed for their ability to inhibit a BV-associated bacteria. Whole genome sequencing was performed on 3 isolates and their resistance to antibiotics used in BV treatment was determined. A total of 337 isolates were obtained from 3 participants with longitudinally stable CST I communities. Almost all isolates (n = 323 [95.8%]) showed some inhibition of P. bivia ATCC 29303 and local P. biva strains growth. Overall, 6 different bacteriocin related proteins (Class III: 3; Class II: 1; LAPs: 1) were identified. No resistance genes were identified (ResFinder & CARD) but all selected strains were phenotypically resistant to metronidazole. The proportion of CW with longitudinally stable, optimal vaginal communities in our setting is relatively low. However, targeting these women for the isolation of potential probiotic bacteria yielded a large number of isolates with inhibitory activity against a BV-associated pathogen, which can be characterised further. Phenotypic variation among isolates illustrates the importance of screening multiple strains of the same species per sample.

Poster # 21 SFA

Poster title: Healthy aging: Molecular bases for the development of a bioinnovative food prototype with psychobiotics

Authors and affiliations (presenter underlined): Pablo Cataldo* (CERELA-CONICET, Tucumán, Argentina); Bulacios, G*(CERELA-CONICET, Tucumán, Argentina); Naja, J (CERELA-CONICET, Tucumán, Argentina); Elean, M (CERELA-CONICET, Tucumán, Argentina); Posse de Chaves, E (Departments of Pharmacology and Medicine and the Centre for Neuroscience, Faculty of Medicine and Dentistry, University of Alberta, Edmonton, Canada); Taranto, MP (CERELA-CONICET, Tucumán, Argentina); Beauquis, J (IBYME-CONICET, Universidad de Buenos Aires, Argentina); Hebert, EM (CERELA-CONICET, Tucumán, Argentina) and Saavedra L (CERELA-CONICET, Tucumán, Argentina).

Poster # 21 SFA con't

Abstract:
One consequence of the increase in longevity is the appearance of diseases associated with aging such as dementia. Alzheimer's disease (AD) is the most common type of dementia. Currently, there is no definitive treatment for AD, cholinesterase inhibitors and memantine are the current mainstays of the treatment. Numerous nutritional interventions for AD are currently under study. To date, there is scientific evidence on the use of psychobiotics, those probiotics that provide a potential benefit to mental health. This work represents the first report on the daily oral administration (30 days) of *Lactobacillus delbrueckii* subsp. lactis CRL 581 (1x10E8), an in vitro AChE inhibitor and *Levilactobacillus brevis* CRL 2013 (1x 10E9), a GABA producer strain, on oxidative stress and cholinergic dysfunction in a scopolamine-mice model. Scopolamine, a cholinergic receptor blocker, produced memory loss, cognitive impairment and increased AChE activity, mimicking those alterations observed in AD. Administration of CRL581 showed a decrease in AChE activity in brain homogenates of scopolamine-treated mice; CRL2013 increased catalase activity and the amount of reduced glutathione. In addition, both strains were able to reduce malondialdehyde, an end-product of lipid peroxidation, considered to be one of the markers of reactive oxygen species generation. Shot-gun proteomic analysis of scopolamine- and psychobiotics-brain homogenates revealed unique differential expression patterns. Our results show that both strains evaluated here ameliorate oxidative stress markers in a scopolamine-mice model supporting the development of a functional supplement containing genetically and functionally characterized psychobiotics for non-pharmacological intervention of those affected with AD.

Poster # 22 SFA

Poster title: The gut microbiome, mild cognitive impairment, and probiotics: a randomized clinical trial in middle-aged and older adults

Authors and affiliations (presenter underlined): Mashael R. Aljumaah (University of North Carolina; Chapel Hill, NC, USA; North Carolina State University; Raleigh, NC, USA; King Saud University; Riyadh, Saudi Arabia) Urja Bhatia (Kent State University, USA), Jeffery Roach (University of North Carolina; Chapel Hill, NC, USA), John Gunstad (Kent State University, USA), M. Andrea Azcarate-Peril (University of North Carolina; Chapel Hill, NC, USA)

Abstract:
Advancing age coincides with changes in the gut microbiome and a decline in cognitive ability. Psychobiotics are microbiota-targeted interventions that can result in mental health benefits and protect the aging brain. This study investigated the gut microbiome composition and predicted microbial functional pathways of middle-aged and older adults that met criteria for mild cognitive impairment (MCI), compared to neurologically healthy individuals, and investigated the impact of probiotic *Lactobacillus rhamnosus* GG (LGG) in a double-blind, placebo-controlled, randomized clinical trial. A total of 169 community-dwelling middle-aged (52-59 years) and older adults (60-75 years) received a three-month intervention and were randomized to probiotic and placebo groups. Participants were further subdivided based on cognitive status into groups with intact or impaired cognition and samples were collected at baseline and post supplementation. Results: Microbiome analysis identified *Prevotella ruminicola, Bacteroides thetaiotaomicron*, and *Bacteroides xylanisolvens* as taxa correlated with MCI. Differential abundance analysis at baseline identified *Prevotella* as significantly more prevalent in MCI subjects compared to cognitively intact subjects (ALDEx2 P= 0.0017, ANCOM-BC P= 0.0004). A decrease in the relative abundance of the genus *Prevotella* and *Dehalobacterium* in response to LGG supplementation in the MCI group was correlated with an improved cognitive score. Our study points to specific members of the gut microbiota correlated with cognitive performance in middle-aged and older adults. Should findings be replicated, these taxa could be used as key early indicators of MCI and manipulated by probiotics, prebiotics, and symbiotics to promote successful cognitive aging.

Poster #23 SFA

Poster title: Protocol for the chemo-gut trial: a double-blind randomized controlled trial investigating the effects of a multi-strain probiotic on gut microbiota, gastrointestinal symptoms, and psychosocial health in cancer survivors

Authors and affiliations (presenter underlined): Julie M. Deleemans (University of Calgary Cumming School of Medicine, Calgary, Canada), Athina Spiropoulos (University of Calgary Cumming School of Medicine, Calgary, Canada, Raylene Reimer (University of Calgary Cumming School of Medicine, Calgary, Canada), Safiya Karim (University of Calgary Cumming School of Medicine, Calgary, Canada), Bill Richardson (Patient and Family Advisory Network Cancer Care Alberta, Alberta Health Services, Calgary, Canada), and Linda E. Carlson (University of Calgary Cumming School of Medicine, Calgary, Canada).

Abstract:
Background: Survivors of cancer experience chronic gastrointestinal (GI) and psychosocial symptoms, and reduced gut microbial diversity. This may compromise therapy compliance and reduce well-being. No studies have investigated probiotics for managing GI and psychosocial symptoms and the gut microbiota in post-treatment cancer survivors.

Aims: to investigate the effects of a probiotic vs. placebo on (1) abdominal pain and depressive symptoms (primary outcomes); (2a) GI (i.e. gas/bloating, diarrhea, constipation) and psychosocial symptoms (i.e. anxiety, cognitive function, fatigue, and general health; and (2b) gut microbiota composition; (3) relationships between microbiota, GI and psychosocial symptoms.

Methods: This double-blinded, placebo-controlled, 2-arm, randomized trial will recruit N=66 participants for a 12-week trial. Adult survivors diagnosed with a solid tumour or blood cancer who completed chemotherapy, and show elevated GI or psychosocial symptoms will be included. The probiotic capsule contains Lactobacillus helveticus Rosell®-52, Bifidobacterium longum Rosell®-175 and Lacticaseibacillus rhamnosus Rosell®-11 strains ingested orally once daily. Stool samples are collected at baseline and week-12 and analyzed using GA-Map dysbiosis test and 16s rRNA gene sequencing. GI and psychosocial surveys are completed at baseline, weeks 6 and 12. Descriptive statistics, paired samples t-tests, linear mixed models, and Spearman's correlation analyses will be used.

Implications: Our findings may improve symptom management and treatment adherence, while our commitment to patient-centered knowledge translation via creating patient materials (e.g. infographics, personal results summary) will enable patients to make informed decisions about their health.

Poster #24 SFA

Poster title: Investigating the effects of the infant probiotic Bifidobacterium infantis and human milk oligosaccharides on the severity of anaphylaxis in a mouse model of peanut allergy

Authors and affiliations (presenter underlined): Morgan Cade (School of Biological Sciences, University of Nebraska, USA; Nebraska Food for Health Center, USA), Tasneem Ali (School of Biological Sciences, University of Nebraska, USA), Emily Plotnik (School of Biological Sciences, University of Nebraska, USA), Anthony Juritsch (Department of Food Science and Technology, University of Nebraska, USA; Nebraska Food for Health Center, Nebraska), Kristin Beede (Department of Food Science and Technology, University of Nebraska, USA), Robert Schmaltz (Department of Food Science and Technology, University of Nebraska, USA), Jeffrey Price (Department of Food Science and Technology, University of Nebraska, USA; Nebraska Food for Health Center, Nebraska), Bethany M. Henrick (Department of Food Science and Technology, University of Nebraska, USA; Evolve Biosystems, USA), Amanda Ramer-Tait (Department of Food Science and Technology, University of Nebraska, USA; Nebraska Food for Health Center, Nebraska).

Abstract:
Interactions between gut microbes and early-life immune programming may influence the development of food allergies, providing a potential explanation for the rapidly increasing prevalence of pediatric peanut allergy. Supplementation with Bifidobacterium has been shown to induce oral tolerance in conventional mouse models of food allergy; however, it has not been tested in mice harboring an early-life human microbiome. We hypothesized that treatment with *B. infantis* EVC001 + human milk oligosaccharides (HMO) would limit the severity of anaphylaxis in an infant microbiome-associated mouse model of peanut allergy and expand regulatory T cells (Treg). Germ-free mice received a human infant microbiome lacking Bifidobacterium and were then orally sensitized to peanut for five weeks. Beginning at colonization, mice were gavaged daily with either 1 x 10^8 CFU *B. infantis* or PBS and given drinking water with or without 5% w/v of the HMO Lacto-N-neotetraose (LNnT) for the duration of the study. Treatment with *B. infantis* + LNnT significantly decreased fecal pH and cecal acetic acid levels, increased abundances of *B. infantis* and lowered anaphylactic scores after challenge compared to sensitized mice treated only with B. infantis.
No differences were observed in plasma levels of mast cell protease-1, total IgE, and peanut-specific IgE or in splenic Treg numbers. These results suggest that supplementation with LNnT enhances the ability of B. infantis to limit innate immune responses related to anaphylaxis but may not alter the peripheral adaptive immune response to peanut tested here. Moreover, our infant microbiome-associated mouse model of peanut allergy provides a novel framework for testing the efficacy of live therapeutic strategies in limiting allergic responses.

Poster #25 SFA

Poster title: Identifying novel probiotic candidates to counter kidney stone disease

Authors and affiliations (presenter underlined): Gerrit A. Stuivenberg (Western University, London, Canada), John A. Chmiel (Western University, London, Canada), Polycronis P. Akouris (Western University, London, Canada), Kait F. Al (Western University, London, Canada), Gregor Reid (Western University, London, Canada), Jeremy P. Burton (Western University, London, Canada).

Abstract:
We have recently shown that the gut microbiota derived uremic toxins p-cresyl sulfate, indoxyl sulfate, and their precursors enhance calcium oxalate (CaOx) kidney stone production in vitro and in vivo. As these toxins build-up, they contribute to the production of reactive oxygen species which accelerate stone formation. Probiotic therapies can exploit the wealth of microbial diversity to reduce toxin accumulation and mitigate kidney stone incidence. Using in vitro culture techniques, we identified strains of lactobacilli and bifidobacteria that could resist or reduce uremic toxins in relevant culture media. Toxin clearance was measured using HPLC. To determine if uremic toxin resistance and clearance was associated with the ability to reduce CaOx kidney stone burden in vivo, the strains were assessed individually using an established *Drosophila melanogastor* model. We identified four bifidobacterial strains that could internalize uremic toxins and over ten strains of lactobacilli that could resist high concentrations of the toxins. Oral supplementation of toxin-clearing strains reduced stone burden in flies exposed to uremic toxins compared to controls. We also showed that all the uremic toxins tested increased reactive oxygen species in the Malpighian tubules (i.e., fly kidney) of exposed flies and some strains reduced this oxidative stress. This work highlights why dosing with certain probiotic strains may be clinically useful in kidney stone disease. The oral supplementation of toxin clearing probiotics may be useful in minimizing the incidence and recurrence of CaOx kidney stones and should be evaluated in humans. In addition to reducing stone burden, these strains have the potential to normalize the dysbiotic gut microbiota observed in stone formers.

Poster #26 IAC

Poster title: Selective and preferential utilization of human milk oligosaccharides by probiotics

Authors and affiliations (presenter underlined): Leonie Jane Kiely [a,b,c,d], Kizkitza Busca [b], Jonathan A. Lane [b], Douwe van Sinderen [c,d] and Rita M. Hickey [a,c*]

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Abstract:
Human Milk Oligosaccharides (HMOs) are complex sugars with proven health benefits for the developing infant. These glycans survive gastrointestinal transit intact and supply metabolic substrate necessary for beneficial bacteria to establish and thrive. Several members of the infant associated *Bifidobacterium* genus have been shown to selectively utilise HMOs, however, utilisation by other early colonizers is less explored. This study aimed to genotypically and phenotypically characterise HMO utilisation (8 commercially available HMO blend) of 23 clinically documented commercial probiotic strains, including *Bifidobacterium*,

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Lactobacillus and *Pediococcus* strains. Genome profiling to identify glyco-genes, including enzymes and transporters, was initially used to predict probiotic HMO utilisation. Phenotypic profiling included growth analyses, preferential HMO utilization and metabolomics through the use of High pH Anion Exchange Chromatography with Pulsed Amperometric and High Pressure Liquid Chromatography with Refract Index detection. Our findings highlighted preferential utilization and strain specific superior growth for infant-associated Bifidobacterium strains. Overall, glycomics 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 *Bifidobacterium* strains, to <5% for several *Lactobacillus* and *Pediococcus* strains. This research gives insight into the complex relationship between HMO and infant associated bacteria in the early stage of life.

Poster #27 IAC

Poster title: A real-world study evaluating use of *Bacillus clausii,* treatment outcomes and patient satisfaction in Italian community pharmacies.

Authors and affiliations: Corrado Giua[1], Flora Romano[1], Enrico Keber[1], Paolo Pellegrino[2], Marcos Perez[3], Peter Justen[4], Maria-Chiara Uboldi[2] on behalf of SGCP[1]*

Presented by: Daniel Marquez

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SGCP group of clinical pharmacists that pursued the experiment:
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Abstract:
Introduction: Patients worldwide self-manage ailments like diarrhea and antibiotic-associated symptoms using probiotics. Pharmacists are in a strategic position to investigate the reasons behind probiotic self-medication and patient-reported outcomes. The aim of this study is to evaluate usage of a *B. clausii* strains O/C, N/R, SIN, T 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 come back to the pharmacy when symptoms had subsided (T1), but no later than 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.

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Results: Overall, 268 pts 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, the most common 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.

Conclusion: This is the first pharmacy-based study in Italy that provided real-world picture of usage of probiotics like *B. clausii* strains O/C, N/R, SIN, T 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.

SECTION 4

Poster #28 SFA

Poster title: Investigating select substrates on a gut microbial community using an ex vivo fermentation model

Authors and affiliations (presenter underlined): Cathy Lordan (Teagasc Food Research Centre), Geoffrey McCarthy (Teagasc Food Research Centre), Rita M. Hickey (Teagasc Food Research Centre), Mark Fenelon (Teagasc Food Research Centre), R. Paul Ross (APC Microbiome Ireland), Paul D. Cotter (APC Microbiome Ireland).

Abstract:
The contribution of the gut microbiota to health and disease is becoming increasingly apparent due to developments in both DNA sequencing and cultivation techniques. There has been a lot of focus on enhancing the growth of desirable microbes, especially bifidobacteria and lactobacilli, using prebiotics, i.e., non-digestible food substrates which are selectively utilised by beneficial bacteria. However, there remains much to be learned about the direct impact that different substrates have on the gut microbiota at the community level. In this study, we employed an ex vivo colonic model to test a range of substrates, including a formulated beverage, in various combinations on a gut microbial community. Ex vivo models provide a reproducible, rapid, and inexpensive means of assessing the colonic microbiota. Samples were obtained at 0h and 24h to establish the impact of these substrates before and after fermentation. Shotgun metagenomic sequencing was applied to unravel the composition and functional changes between time points. A combination of computational approaches were used, including species-level taxonomic classification, functional potential, and the generation of metagenome-assembled genomes. Substrates differed in their impacts on the microbiota, but some consistent patterns were revealed, such as oligosaccharides supporting the increased abundance of bifidobacteria and lactobacilli. Species-level alpha diversity was best maintained with lactose, a whey protein concentrate and xylo-oligosaccharide (XOS) combination, and XOS alone. This provides the basis for additional testing to determine the taxonomic and potential functional effects these substrates have on the gut microbial community.

Poster # 29 SFA

Poster title: Immunometabolic effects of physicochemically-distinct dietary fibers in adults with excess body weight: towards precision nutrition strategies

Authors and affiliations (presenter underlined): Anissa M. Armet (University of Alberta, Canada), Fuyong Li (University of Alberta, Canada; City University of Hong Kong, China), Edward C. Deehan (University of Alberta, Canada), Daria Nikolaeva (Skolkovo Institute of Science and Technology, Russia; University College Cork, Ireland), Benjamin Seethaler (University of Hohenheim, Germany), Junhong Liu (University of Alberta, Canada), Janis L. Cole (University of Alberta, Canada), Yuan-Yuan Zhao (University of Alberta, Canada), Jonathan M. Curtis (University of Alberta, Canada), Spencer D. Proctor (University of Alberta, Canada), Stephan C. Bischoff (University of Hohenheim, Germany), Wendy V. Wismer (University of Alberta, Canada), Catherine J. Field (University of Alberta, Canada), Jeffrey A. Bakal (University of Alberta, Canada), Dan Knights (University of Minnesota, USA), Carla M. Prado (University of Alberta, Canada), and Jens Walter (APC Microbiome Ireland, University College Cork, Cork, Ireland).

Abstract:
Prebiotic dietary fibers (DF) elicit clinical benefits, but with significant inter-individual variation. It is unknown to what degree DF strategies can be improved through personalization based on the individual's gut microbiome. Our objective was to compare the immunometabolic effects of high doses of physicochemically-distinct DFs in adults with excess body weight and determine if individual microbiome signatures predict these effects using machine learning. In a six-week, parallel-arm, randomized controlled trial, adults with BMI 25-35 kg/m2 added 25g (females) or 35g (males) of one of three DFs to their usual diet daily: acacia gum (AG; soluble, fermentable; n=75), resistant starch type 4 (RS4; insoluble, fermentable; n=75), or microcrystalline cellulose (MCC; insoluble, non-fermentable control; n=45). A multi-omics approach was applied to assess clinical markers and microbiome composition, genes, and metabolism. AG and RS4 increased flatulence and overall gastrointestinal symptoms ($q<0.05$, linear mixed models), and AG increased fecal acetate ($q<0.01$), propionate ($q<0.05$), and total short-chain fatty acid levels ($q<0.01$). RS4 increased the anorexigenic hormone peptide YY ($q<0.001$), and AG decreased the orexigenic hormone ghrelin ($q<0.05$). Both AG ($q<0.001$) and MCC ($q<0.001$) reduced fecal calprotectin, a marker of gut inflammation. Coefficients of variation in immunometabolic markers ranged from 30-243%, signifying large inter-individual variation in responses to DF supplementation. We are currently exploring if baseline microbiome signatures and other metadata can predict clinical outcomes using machine learning. If successful, this study will help establish a framework to improve health through personalized DF use based on individual gut microbiome features.

Poster # 30 SFA

Poster title: In vitro effects of human milk oligosaccharides (HMOs) on gut microbiota in irritable bowel syndrome (IBS)

Authors and affiliations (presenter underlined): Patricia Sanz Morales (University of Reading, UK), D. Robertson (University of Surrey, UK), A. Wijeyesekera (University of Reading, UK), C.L. Boulangé (Nestlé S.A., Switzerland), G. Major (Nestlé S.A., Switzerland), G. Gibson (University of Reading, UK).

Abstract:
IBS is the most common gastrointestinal disorder in the Western world and a major public health concern. Despite extensive research, the psychological and physiological factors that contribute to the aetiology of IBS remain poorly understood. Recent evidence has presented HMOs as a potential treatment for IBS

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symptoms. We hypothesise that gut bacteria are integral contributors to cognitive as well as intestinal health, and that dietary interventions such as HMOs, which are known to positively alter the gut microbiota, have the potential to improve symptoms in IBS patients. This study will assess the impact of different HMOs on gut microbiota to streamline a novel IBS therapy. An in vitro HMO intervention, using a lab human gut model system is used to assess the potential therapeutic modulation of the microbiota in IBS. Molecular phenotyping using gas chromatography (GC) and fluorescent in situ hybridisation of fermentation samples provides assessment of impact of the intervention on gut microbial composition and activity. All 3 subtypes of IBS are under investigation, and one taken forward to a human study. Preliminary results for two healthy controls, two IBS-D, an IBS-C and an IBS-M donor show that the HMOs Lacto-N-tetraose, Lacto-N-neotetraose (LNnT) and 3'-sialyllactose have a bifidogenic effect. An HMO mix increases bifidobacteria in both healthy donors, IBS-D and IBS-C. Additionally, preliminary GC results show that in IBS-M, LNnT and 2'-fucosyllactose are the most successful in stimulating butyrate production. HMO supplementation shows promising results in altering the gut microbiota. Various HMOs produce different prebiotic effects on bacterial counts and short chain fatty acids and their potential in IBS needs to be confirmed in a prospective clinical trial.

Poster # 31 SFA

Poster title: Immunomodulatory effects of galacto-oligosaccharides

Authors and affiliations (presenter underlined): Yunan Hu (Department of Nutrition, Gillings School of Global Public Health, University of North Carolina, Chapel Hill, NC, USA; UNC Microbiome Core, Center for Gastrointestinal Biology and Disease (CGIBD), School of Medicine, University of North Carolina, Chapel Hill, NC, USA), Jason W. Arnold (Department of Medicine, Division of Gastroenterology and Hepatology, School of Medicine, University of North Carolina, Chapel Hill, NC, USA; UNC Microbiome Core, Center for Gastrointestinal Biology and Disease (CGIBD), School of Medicine, University of North Carolina, Chapel Hill, NC, USA; Duke Microbiome Center, Department of Molecular Genetics and Microbiology, School of Medicine, Duke University, Durham, NC, USA), Johanna M. Smeekens (Department of Pediatrics, Division of Allergy and Immunology, School of Medicine, University of North Carolina, Chapel Hill, NC, USA). Michael D. Kulis (Department of Pediatrics, Division of Allergy and Immunology, School of Medicine, University of North Carolina, Chapel Hill, NC, USA), Ellyce T. San Pedro (Joint Department of Biomedical Engineering, University of North Carolina, Chapel Hill and North Carolina State University, Raleigh, NC, USA), Scott T. Magness (Joint Department of Biomedical Engineering, University of North Carolina, Chapel Hill and North Carolina State University, Raleigh, NC, USA), M. Andrea Azcarate-Peril (Department of Nutrition, Gillings School of Global Public Health, University of North Carolina, Chapel Hill, NC, USA; Department of Medicine, Division of Gastroenterology and Hepatology, School of Medicine, University of North Carolina, Chapel Hill, NC, USA; UNC Microbiome Core, Center for Gastrointestinal Biology and Disease (CGIBD), School of Medicine, University of North Carolina, Chapel Hill, NC, USA).

Abstract:
Food allergies in infancy have become a growing public health concern. According to the CDC, food allergies are estimated to impact over 8% of children in the US. Galacto-oligosaccharides (GOS), structurally similar to human milk oligosaccharides, modulate the gut microbiota and have beneficial effects on host health. In an early pilot experiment, GOS feeding resulted in non-statistically significant reductions in peanut-specific IgE, anaphylaxis, intestinal permeability, and increased relative abundance of *Akkermansia* and *Bifidobacterium* in peanut-sensitized CC027/GeniUnc mice. Here, we showed in mice and primary human intestinal cells that GOS induced the expression of Lgals-1, which encodes Galectin-1 (Gal-1), a

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glycoprotein with immunomodulatory effects and an established role in suppressing allergic asthma. We first confirmed differential expression of Lgals-1 in mice fed GOS compared with control diets by reverse transcription-quantitative (q) PCR. GOS significantly increased Lgals-1 expression in the colon of young but not old mice. Computational molecular docking predictions confirmed the binding affinity between GOS and Gal-1, suggesting a direct interaction. We also showed that GOS interacted directly with human primary intestinal cells inducing Lgals-1 expression. Additionally, we showed that GOS induced Lgals-1 expression in the human intestinal cells by enhancing *Bifidobacterium*, providing an indirect induction pathway of Lgals-1 by GOS. Our study lays the groundwork for mechanistic research exploring a potential prebiotic role in modulating the immune system, specifically for preventing or treating food allergies.

Poster # 32 SFA

Poster title: Gut microbiome composition and metabolic capacity differ by FUT2 secretor status

Authors and affiliations (presenter underlined): Alexander W. Thorman (University of Cincinnati, Cincinnati, USA), Grace Adkins(St. Jude's Graduate School of Biomedical Sciences, Memphis, USA), Shannon C. Conrey (University of Cincinnati, Cincinnati, USA)(Cincinnati Children's Hospital Medical Center, Cincinnati, USA), Allison R. Burrell (University of Cincinnati, Cincinnati, USA)(Cincinnati Children's Hospital Medical Center, Cincinnati, USA), Ying Yu (The University of Tennessee Health Science Center, Memphis, USA), Brendon White (Cincinnati Children's Hospital Medical Center, Cincinnati, USA), Rachel Burke (Centers for Disease Control and Prevention, Atlanta, USA), David Haslam (Cincinnati Children's Hospital Medical Center, Cincinnati, USA), Daniel C. Payne (Centers for Disease Control and Prevention, Atlanta, USA), Mary A. Staat (Cincinnati Children's Hospital Medical Center, Cincinnati, USA), David S. Newburg (University of Cincinnati, Cincinnati, USA) and Ardythe L Morrow (University of Cincinnati, Cincinnati, USA)(Cincinnati Children's Hospital Medical Center, Cincinnati, USA).

Abstract:
Risk of several gut diseases is influenced by a major polymorphism in the fucosyltransferase2 (FUT2) gene, but its impact on the microbiome of infants is understudied. In individuals with an active FUT2 enzyme (“secretors”), the intestinal mucosa is abundantly fucosylated, providing a rich endogenous source of fucose for mutualist bacteria. Similarly, maternal secretor status influences the abundance of fucosylated human milk oligosaccharides. Non-secretors lack the ability to create this enzyme and therefore have lower gut and milk fucosylation. We compared the impact of maternal secretor status, measured by FUT2 genotype, and infant secretor status, measured by FUT2 genotype and phenotype, on early infant fecal microbiome samples collected from 2-month-old breastfed and non-breastfed infants enrolled in the PREVAIL term birth cohort (n=211). Infant secretor status (22% non-secretor, 24% low-secretor, and 54% full-secretor) was more strongly associated with the infant microbiome than it was with the maternal FUT2 genotype. Alpha diversity was greater in full-secretors compared to the low- ($p=0.031$) or non-secretor infants ($p=0.045$). Three distinct microbial enterotypes corresponded to infant secretor phenotype ($p=0.022$) and to the dominance of *Bifidobacterium breve, Bifidobacterium longum*, or neither ($p<0.001$). Infant secretor status was also associated with microbial metabolic capacity, specifically, bioenergetics pathways. These patterns were modified by exclusive breastfeeding. We conclude that infant secretor status and breastfeeding status, but not maternal secretor status, is associated with infant microbial colonization and metabolic capacity. These findings indicate that the glycans help establish early colonizers of the gut.

Poster # 33 SFA

Poster title: Dietary inulin modulates host iron utilization and gut microbiota in high-iron milk formula fed neonatal piglets

Authors and affiliations (presenter underlined): Jungjae Park (University of California, Davis, USA), Yapa Wickramasinghe (University of California, Davis, USA), Karen Kalanetra (University of California, Davis, USA), David A. Mills (University of California, Davis, USA), Peng Ji (University of California, Davis, USA).

Abstract:
Iron nutrition imposes impacts on the mammalian physiology and gut microbiota, and host-microbe interactions are thought to be important in early-life development. Iron supplementation or fortification is a common method to resolve iron deficiency (ID) or iron deficiency anemia (IDA). However, iron-fortified infant formula provides excessive amount of iron compared to breastmilk and may have adverse effects on infant growth and development. The gut health is implicated in the adverse outcomes of neonatal iron supplementation, and dietary iron overexposure may exacerbate inflammation and dysbiosis because iron is an essential nutrient for bacterial growth and function and modulates gut microbiota. This study examined the efficacy of dietary inulin and inulin in combination with *Ligilactobacillus agilis* YZ050 (L. agilis YZ050) on the host iron utilization and gut microbiota in response to iron-fortified milk diet in a neonatal piglet model with the four dietary treatments: an iron-adequate formula (AI), a high-iron formula (HI), the HI formula supplemented with inulin (HIP), the HIP formula with L. agilis YZ050 (HIS). While HI formula resulted in hepatic iron overload and increased iron concentration in the colon digesta and feces, use of HIP and HIS formulas diminished iron deposition in the liver, colon digesta, and feces in piglets. We observed significantly different gut microbial clusters between non-inulin (AI and HI) and inulin (HIP and HIS) diet piglets and similar shifts in gut microbiota in HIP and HIS. Our findings shed light on appropriate use of dietary supplements and insights needed to purposely modulate gut microbiota via establishment of beneficial microbes linked to inulin and L. agilis YZ050 to mitigate risks of systemic iron overload at infancy.

Poster # 34 SFA

Poster title: Metabolism Of Human Milk Oligosaccharides By Infant Gut Microbiota

Authors and affiliations (presenter underlined): Simone Renwick (University of California San Diego, CA, USA), Annalee Furst (University of California San Diego, CA, USA), Lars Bode (University of California San Diego, CA, USA), Emma Allen-Vercoe (University of Guelph, ON, Canada).

Abstract:
The third largest solid component of human milk is a set of structurally diverse, complex carbohydrates known as human milk oligosaccharides (HMOs). Following consumption, HMOs enter the colon undigested, performing several functions critical to gut microbiota development. However, because of challenges in obtaining HMOs, research into the impact of HMO metabolism on microbial community structure and function is limited. Regardless, commercially available infant formula is already being supplemented with artificial 2-fucosyllactose (2-FL), a highly abundant HMO structure produced by most women. The aim of this study was to characterize the impact of pooled HMOs (pHMOs) and 2-FL on the composition and function of infant fecal-derived microbial communities. Seven communities were seeded from infant stool in bioreactors designed to mimic the conditions of the human distal colon. Steady-state communities were treatment with 4 g/L pHMOs, 0.5 g/L 2-FL, or a control under batch fermentation conditions. Degradation of 19 HMO structures was evaluated by HPLC-glycoprofiling while resultant changes in composition and metabolic output were assessed using metataxonomics (16S rRNA gene

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sequencing) and metabonomics (NMR) respectively. Despite the heterogeneity in composition, all communities maintained the capacity to degrade the majority of detectable HMO structures. Metataxonomic and metabonomic profiling demonstrated significant shifts in the composition and metabolic output of the communities as a result of pHMOs-treatment compared to 2-FL and the control, while 2-FL yielded results similar to the control. Overall, this study has considerably expanded our knowledge of HMO gut microbiota interactions and has provided deeper insights into the addition of HMOs to infant formula.

Poster # 35 IAC

Poster title: A randomized, double-blind, placebo-controlled study to evaluate the effects of chicory inulin on bowel habit and intestinal microbiota in adults with functional constipation

Authors and affiliations (presenter underlined): Carrie A.M. Wegh [1, 2*], Marie-Luise Puhlmann[1, 2*], Veerle Dam [3], Andrea Doolan[4], Diederick Meyer[3], Marc A. Benninga[5], Clara Belzer[1], Elaine E. Vaughan[3], Hauke Smidt[1]

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*both contributed equally

Abstract:
Background: Constipation is a widespread condition that substantially affects quality of life. Prebiotics may potentially alleviate symptoms by intestinal microbiome modulation. We investigated the effect of prebiotic inulin intake in adults with functional constipation (FC) on stool frequency and consistency, constipation symptoms (PAC-SYM), quality of life (PAC-QOL), and intestinal microbiota composition by 16S rRNA gene sequencing.

Methods: A randomized, double-blind, placebo-controlled, cross-over trial with a 2-week run-in followed by two 4-week intervention periods with 12g inulin or placebo separated by a 4-week washout in 40 adults with FC according to Rome III Criteria.

Results: Subjects were 37±11 years old and 92.5% were female. No within-individual differences between inulin and placebo were detected, however, a remarkable carry-over effect of inulin was observed in nearly all secondary outcomes. Therefore, we analyzed the run-in and first intervention period as a parallel trial reporting between group-differences. Median weekly stool frequency and mean consistency increased after inulin intake compared to placebo (4.0 [2.75, 4.50] vs 2.50 [2.38, 3.50], p=0.046) and (2.72±0.22 vs 2.24±0.14; p=0.04), respectively. PAC-SYM and PAC-QoL scores also improved only after inulin intake, as reflected in less rectal tearing and burning (inulin -0.66 vs placebo -0.47, p=0.036), and improved treatment satisfaction (inulin -1.23 vs placebo -0.53, p=0.05). Relative abundances of several bacterial genera were modulated only by inulin (p>0.10). Bifidobacteria relative abundance increased by 1.3 fold (p=0.02; q=0.36), as well as Anaerostipes and Subdoligranulum spp. increased, while there was some decrease in several genera of the Ruminococcaeae family.

Conclusion: Daily consumption of 12g inulin has potential to alleviate (functional) constipation. Observed effects are concomitant with changes in intestinal microbiota composition reflected in an increase in relative abundance of potential butyrate producers and a reduction in constipation-associated genera of the Ruminococcaeae family.

Poster # 36 IAC

Poster title: Summary of research studies revealing health-related effects of a specific prebiotic galactooligosaccharides mixture

Authors and affiliations (presenter underlined): Ged Baltulionis, Clasado Biosciences, Georgina Dodd, Lucien Harthoorn, Clasado Biosciences

Abstract:
Galactooligosaccharides (GOS) are a naturally occurring fermentable fibre and lactose-derived food ingredient, recognized as a prebiotic. GOS has demonstrated the ability to shift the gut microbiota balance towards a profile rich in bifidobacteria and decreased abundance of pathobionts, which is associated to multiple health benefits. The efficacy and safety of a specific prebiotic GOS, called Bimuno®, is supported by over 100 scientific publications, including over 20 clinical trials. Multiple studies have shown that bifidobacteria are selectively grown in the large intestine and levels are increased within 7 days following administration of this GOS. A large body of scientific evidence has shown that this GOS can improve gastrointestinal health and associated quality of life, strengthen anti-pathogenic activity, improve immune function, and enhance cognitive health related to stress, mood and anxiety. More specifically, evidence has revealed an array of positive gastrointestinal-related effects such as reduction in digestive discomfort, bloating and abdominal pain, improvement of bowel habits in people with IBS or maintaining regularity in healthy populations. Studies have also shown that this specific GOS reduces the adhesion of pathogens to gut wall cells and increases the circulation of internally secreted substances that prevent invasion of pathogens or reduce incidence of travellers' diarrhoea. The positive effects by the GOS on the innate immune system is exemplified by increased levels of anti-inflammatory cytokines and decreased levels of proinflammatory cytokines. Lastly, the modulation of the gut-brain axis by this GOS has been evident from reduction of the stress hormone cortisol in healthy individuals and reduction of anxiety with better quality of life in IBS cohorts. Given GOS' useful properties as a food ingredient, including its stability and versatility, there is growing interest in including GOS as a functional ingredient. We will showcase the properties and functionalities of this specific prebiotic GOS using selected examples.

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Poster # 37 IAC

Poster title: ILSI Europe prebiotic task force: investigating the potential of prebiotics to rebalance and maintain health

Authors and affiliations: The Prebiotic Task Force - Chakrabarti,A[1]; de Vos, P[2]; Dodd, GF[3]; Forssten, S[4]; Guillemet, D[5]; A; Meynier, A[6]; Respondek, F[7]; Stahl, B[8, 9]; Thabuis, C[10]; Theis, S[11] ; Vaughan, E[12]; Venlet, NV[13]; Verbeke, K[14]

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7 CP Kelco, France;
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9 Danone Nutricia Research, Netherlands;
10 Roquette, France;
11 BENEO GmbH, CRDS Nutrition Science, Germany;
12 Sensus BV (Royal Cosun), Netherlands;
13 ILSI Europe, Belgium;
14 Translational Research Center for Gastrointestinal Disorders (TARGID)

Presented by: Frederique Respondek

Abstract: The Prebiotic Task Force of the International Life Sciences Institute (ILSI) Europe advances the science and understanding of prebiotics and their health benefits. The Task Force aims to provide scientific evidence to support the development of prebiotic-containing foods and dietary supplements that can improve gut health and overall well-being.
Last year, the Task Force published three new peer-reviewed papers and one concise monograph. Scientific activities included: A narrative review, providing an overview of the role of non-digestible carbohydrates in the human diet, their impact on the gut microbiota, and their potential as prebiotics, with a particular emphasis on structure-related activities and in vitro models; (2) A Perspective review, describing state-of-the-art tools for harnessing the microbiome for precision health, such as pro- and prebiotic dietary solutions amongst others, and a corresponding future vision of healthcare; (3) A concise monograph, available in 7 languages, providing an easily accessible introduction to the abundant scientific knowledge on prebiotics, probiotics and the intestinal microbiota and how they impact the human host; (4) Perspectives on what we know, what we need to investigate, and how to put knowledge into practice in the microbiota-gut-brain axis.
Currently, a systematic review of the role of prebiotics in bacterial and viral infection and vaccination efficiency is ongoing. The review will give the current status for prebiotics impact on infections, both prevention or recovery, and in supporting vaccination efficacy, for academics and industry scientists in this field.
This year, the Task Force will focus on highlighting the need to perform studies in healthy participants that test the potential “rescuing” effects of prebiotics under conditions where cognition may be transiently compromised as well as, organise a multi-stakeholder workshop to discuss evidence describing the communication channels linking microbiome modulation and modulation of host physiological pathways responsible for improved health and reduced disease risk. The current routes to make a prebiotic claim will be identified and participants will co-build and design a roadmap to progress scientific support for prebiotic health effects and health claim substantiation.

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Daniel Merenstein, Georgetown University, ISAPP President

Dr. Daniel Merenstein is a Professor with tenure of Family Medicine at Georgetown University, where he also directs Family Medicine research. Dr. Merenstein has a secondary appointment in the undergraduate Department of Human Science, in the School of Health. Dr. Merenstein teaches two undergraduate classes, a research capstone and a seminar class on evaluating evidence based medical decisions. He has been funded by PCORI, NIH, USDA, Foundations and Industry. The primary goal of Dr. Merenstein's research is to provide answers to common clinical questions that lack evidence and improve patient care. Dr. Merenstein is a clinical trialist who has recruited over 2,000 participants for 10 probiotic trials since 2006. He is an expert on probiotics, on antibiotic stewardship in outpatient settings, and also conducts HIV research in a large women's cohort. He sees patients in clinic one day a week. Dan lives in Maryland with his wife and 4 boys.

Maria Marco, University of California, Davis, ISAPP Vice President

Maria Marco is a Professor in the Department of Food Science and Technology and Chair of the Food Science Graduate Group at the University of California, Davis. She received her PhD in microbiology from the University of California, Berkeley, and then was a postdoc and project leader at NIZO Food Research, The Netherlands. Dr. Marco has 20 years of experience investigating fermented foods, probiotics, and diet-dependent, host-microbe interactions in the digestive tract. Her laboratory at UC Davis is broadly engaged in the study of food and intestinal microbiomes and the ecology and genetics of lactic acid bacteria.

Gabriel Vinderola, Dairy Products Institute, Faculty of Chemical Engineering (UNL), ISAPP Secretary

Gabriel Vinderola graduated from the Faculty of Chemical Engineering at the National University of Litoral (Santa Fe, Argentina) in 1997 and obtained his Ph.D. in Chemistry in 2002 at the same University. He is presently Principal Researcher at the Dairy Products Institute (CONICET-UNL) and Adjoint Professor at the Biotechnology and Food Technology Department of the Faculty of Chemical Engineering (National University of Litoral). He participated in the development of the first commercial cheese carrying probiotic bacteria from Latin America, released in the market in 1999. In 2011, he was awarded the prize in Food Technology for young scientists, by the National Academy of Natural, Physic and Exact Sciences from Argentina. His interests are technological and microbiological aspects of lactic acid bacteria, bifidobacteria, fermented foods, and probiotics. He has joined several research groups in Brazil, Canada, Spain, Italy, France, Germany, and Finland. He has co-edited the fifth edition (2019) of the book Lactic Acid Bacteria: Microbiological and Functional Aspects. He is engaged in communication of science to the general audience.

Daniel Tancredi, University of California, Davis, ISAPP Treasurer

Daniel J. Tancredi, PhD, is Professor in Residence of Pediatrics in the University of California, Davis School of Medicine. He has over 25 years of experience and over 300 peer-reviewed publications as a statistician collaborating on a variety of health-related research. A frequent collaborator on probiotic and prebiotic research, he has attended all but one ISAPP annual meeting since 2009 as an invited expert. In 2020, he joined the ISAPP Board of Directors. Colin Hill and Daniel co-host the ISAPP Podcast Series "Science, Microbes, and Health". On research teams, he develops and helps implement effective study designs and statistical analysis plans, especially in settings with clusters of longitudinal or otherwise correlated measurements, including cluster-randomized trials, surveys that use complex probability sampling techniques, and epidemiological research. He teaches statistics and critical appraisal of evidence to resident physicians; graduate students in biostatistics, epidemiology, and nursing; and professional scientists. Dan grew up in the American Midwest, in Kansas City, Missouri, and holds a bachelor's degree in behavioral science from the University of Chicago and masters and doctoral degrees in mathematics from the University of Illinois at Chicago. He lives in the small Northern California city of Davis, with his wife Laurel Beckett (UC Davis Distinguished Professor Emerita), their Samoyed dogs Simka and Milka, and near their two grandkids.

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Colin Hill, APC Microbiome Ireland

Colin Hill has a Ph.D in molecular microbiology and is a Professor in the School of Microbiology at University College Cork, Ireland. He is also a founding Principal Investigator in APC Microbiome Ireland, a large research centre devoted to the study of the role of the gut microbiota in health and disease. His main interests lie in the role of the microbiome in human and animal health. He is particularly interested in the effects of probiotics, bacteriocins, and bacteriophage. In 2005 Prof. Hill was awarded a D.Sc by the National University of Ireland in recognition of his contributions to research. In 2009 he was elected to the Royal Irish Academy and in 2010 he received the Metchnikoff Prize in Microbiology and was elected to the American Academy of Microbiology. He has published more than 600 papers and holds 25 patents. He was president of ISAPP from 2012-2015. More than 80 PhD students have been trained in his laboratory. Google Scholar.

Sarah Lebeer, University of Antwerp

Sarah Lebeer is a research professor at the Department of Bioscience Engineering of the University of Antwerp, Belgium. She has studied bioscience engineering, with a specialisation in cell and gene technology/food & health, and obtained her Master at KU Leuven (Belgium). In 2008, she obtained a PhD degree with a topic on the mode of action of gastro-intestinal probiotics in inflammatory bowel diseases and a scholarship in the team of Prof. Jos Vanderleyden (KU Leuven). After a postdoc on the interaction between lactobacilli, viruses, and mucosal immunology, in November 2011, she was offered a tenure-track position at the University of Antwerp. Since then, she is leading the Laboratory for Applied Microbiology and Biotechnology of the ENdEMIC research group. In 2020, she was awarded an ERC Starting Grant that enables her to gain more in-depth knowledge of the evolutionary history and ecology of lactobacilli. This rationale was also an important driving force to revise the Lactobacillus genus taxonomy with a large international consortium. Within the ERC project, Sarah has also launched the Isala citizen-science project to gain new insights into the role of vaginal lactobacilli for women's health. Since 2018, Sarah is an academic board member of the International Scientific Association on Probiotics and Prebiotics. Communicating about beneficial microbes and probiotics for experts and laymen is an important inspiration for her daily work.

Eamonn Quigley, Houston Methodist Hospital and Weill Cornell Medical College

Eamonn M M Quigley MD FRCP FACP MACG FRCPI MWGO is David M Underwood Chair of Medicine in Digestive Disorders and Chief of the Division of Gastroenterology and Hepatology at Houston Methodist Hospital. A native of Cork, Ireland, he graduated in medicine from University College Cork. He trained in internal medicine in Glasgow, completed a two-year research fellowship at the Mayo Clinic, and training in gastroenterology in Manchester, UK. He joined the University of Nebraska Medical Center in 1986 where he rose to become Chief of Gastroenterology and Hepatology. Returning to Cork in 1998 he served as Dean of the Medical School and a PI at the Alimentary Pharmabiotic Center. He served as president of the American College of Gastroenterology and the WGO and as editor-in-chief of the American Journal of Gastroenterology. Interests include IBS, gastrointestinal motility and the role of gut microbiota in health and disease. He has authored over 1000 publications and has received awards and honorary titles world-wide. Married for over 40 years to Dr Una O'Sullivan they have 4 children and three grandchildren. Interests outside of medicine include literature, music and sport and rugby, in particular; Dr Quigley remains a passionate supporter of Munster and Irish rugby.

Board of Directors

Seppo Salminen, University of Turku, ISAPP Past President

Prof Seppo Salminen is a Professor at the Faculty of Medicine and director of the Functional Foods Forum, University of Turku, Finland. He has been visiting professor at RMIT University, Melbourne, Australia, and BOKU University, Vienna Austria. His main research interests are probiotics, prebiotics, and intestinal microbiota modulation as well as functional foods and health and regulatory issues in novel foods and health claims. He has been active in the International Life Sciences Institute Europe, the International Dairy Federation, and the International Scientific Association for Probiotics and Prebiotics (past President and current Board Member). He received his MS at Washington State University (USA) in 1978, MSc from the University of Helsinki in 1979, and PhD from the University of Surrey (United Kingdom) in 1982. He has around 500 journal articles and several textbooks and book chapters and he has received several international awards including the ISF-Institute Pasteur Metchnikoff Price, Swiss Price on Modern Nutrition and the Grand Prix du Yoplait.

Karen Scott, Rowett Institute, University of Aberdeen

Karen Scott is a Professor of Research in the Gut Microbiology Group at the Rowett Institute, University of Aberdeen. She leads a research team investigating the (molecular) mechanisms by which key members of the gut microbiota interact with the diet and host, at different life-stages. The fermentation products of gut bacteria contribute to gut health and are differentially expressed on different substrates, including prebiotics. In vitro bacterial growth studies utilising our large culture collection of gut anaerobes (in pure culture, mixed culture, fermentor systems, and also with human cells) and bioinformatic analyses illustrate niche-specific processes and bacterial interactions. She has numerous highly cited publications and has attracted multiple research council and commercially funded grants.

Kelly Swanson, University of Illinois

Kelly Swanson is Interim Director of the Division of Nutritional Sciences and the Kraft Heinz Company Endowed Professor in Human Nutrition at the University of Illinois Urbana-Champaign. His laboratory studies the effects of nutritional intervention on health outcomes, identifying how nutrients impact host physiology and gut microbiota, with primary emphasis on gastrointestinal health and obesity in dogs, cats, humans, and rodent models. Much of his lab's work has focused on dietary fibers, prebiotics, probiotics, synbiotics, and postbiotics. Over the past 2 decades, he has established an internationally recognized research program, highlighted by $25 million in research support, 155 invited lectures at scientific and professional meetings, 240 peer-reviewed journal articles, and 15 research and teaching awards. He has trained over 40 graduate students and post-doctoral fellows, hosted 15 international visiting scholars, and mentored 40 undergraduate research projects. In addition to research, Kelly teaches 3-4 classes each year to undergraduate and graduate students and has been named to the university's 'List of Teachers Ranked as Excellent by Their Students' 30 times. He also serves on advisory boards for many companies in the human and pet food industries as well as non-profit organizations, including the Institute for the Advancement of Food and Nutrition Sciences (IAFNS) and ISAPP.

Hania Szajewska, The Medical University of Warsaw, Department of Paediatrics

Hania Szajewska, MD, is Professor and Chair of the Department of Paediatrics at the Medical University of Warsaw. Among her various functions, she served as the Editor-in-Chief of the Journal of Pediatric Gastroenterology and Nutrition; a member of the Council, and then as the General Secretary of the European Society for Paediatric Gastroenterology, Hepatology and Nutrition (ESPGHAN); the Secretary of the ESPGHAN Committee on Nutrition. Most recently, she joined the Board of Directors of the International Scientific Association for Probiotics and Prebiotics (ISAPP). Prof. Szajewska has broad interests in paediatric nutrition but her research focuses on the effects of early nutritional interventions on later outcome (especially food allergy); and the gut microbiota modifications such as with various biotics (probiotics, prebiotics, synbiotics, postbiotics). She is or has been actively involved in several European Union-funded research projects. She is an enthusiastic advocate for the practice of evidence-based medicine. She has co-authored more than 350 publications. In 2020 and 2021, Prof. Szajewska has been ranked as one of the world's top 2% most-cited researchers.

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Kristin Verbeke, KU Leuven

Kristin Verbeke graduated from the KU Leuven, Belgium as a pharmacist in 1991. She obtained a PhD in Pharmaceutical Sciences at the Laboratory of Radiopharmaceutical Chemistry in 1995 and subsequently spend a postdoctoral period in developing radioactively labelled compounds. In 2002, she was appointed at the department of gastroenterology of the Medical Faculty of the Leuven University where she got involved in the use of stable isotope labelled compounds to evaluate gastrointestinal functions. Within the University Hospitals Leuven, she is responsible for the clinical application of diagnostic 13C- and H2-breath tests. Her current research interest specifically addresses the microbial bacterial metabolism in the human colon. Her team has developed several analytical techniques based on mass spectrometry and stable isotope or radioisotope technologies to evaluate several aspects of intestinal metabolism and function in humans (transit time, intestinal permeability, carbohydrate fermentation, protein fermentation, metabolome analysis). Collaborative research has allowed showing an aberrant bacterial metabolism in patient groups with end stage renal failure, inflammatory bowel diseases, irritable bowel disorders and alcohol abuse. These collaborations all have resulted in high quality peer-reviewed papers. In addition, she showed the impact of dietary interventions (modulation of macronutrient composition, pre- or probiotic interventions) on the microbial metabolism and its impact on health. As a PI, she acquired grant support from the university and different funding bodies and successfully completed these projects. Similarly, she supervised several PhD projects that all resulted in the achievement of a PhD degree. Her research resulted in over 200 full research papers. Together with colleague Prof. J. Delcour, she was the beneficiary of the W.K. Kellogg Chair in Cereal Sciences and Nutrition (2010-2020). She is the president of the Belgian Nutrition Society, the vice-chair of the Leuven Food Science and Nutrition Center, and the co-chair of the Prebiotic task force at ILSI Europe. Furthermore, Kristin Verbeke is the editor of the journal Gut Microbiome and member of the editorial board of Gastrointestinal Disorders.

Anisha Wijeyesekera, University of Reading

Anisha Wijeyesekera, PhD is a Lecturer in Human Microbiome Studies and Director of Postgraduate Research Studies, in the Department of Food and Nutritional Sciences at the University of Reading, UK. Her research interfaces analytical chemistry with microbiology and nutrition, for functional assessment of the gut microbiota. Dr. Wijeyesekera's research includes in vitro as well as in vivo human studies. She applies metabolic profiling approaches to generate metabolic readouts of the gut microbiota using in vitro gut model systems, as well as molecular phenotyping of human biological samples for better insight into host-gut microbiota interactions. The ultimate aim of her research is to identify potential targets for therapeutic modulation through dietary intervention (in particular, prebiotics and probiotics), and capturing the impact of such interventions on gut and overall health. Dr. Wijeyesekera's research portfolio includes projects funded by research councils, charities/societies, and the food industry. Dr. Wijeyesekera joined the ISAPP Board of Directors in 2021. She is also a member of the Academic Board for the Royal Society of Chemistry's Community of Analytical Measurement Sciences, and the London Metabolomics Network Committee.

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Board of Directors

Marla Cunningham, Executive Director

Marla Cunningham is the Executive Director of ISAPP. Prior to 2023, Marla was an industry scientist within the ISAPP community and brings over 20 years of experience in the probiotic, prebiotic, and natural products industry, working across innovation, clinical research, product development, regulatory compliance, and education. She trained as a healthcare practitioner in complementary medicine and has written and presented extensively for clinical audiences on the implementation of biotic-related science. Marla has broad scientific literacy across the fields of biotic substances, microbiome, gut health, nutrition, and human physiology, and brings a passion for harnessing science to deliver beneficial changes in health for our community and our planet.

Mary Ellen Sanders, Executive Science Officer

Mary Ellen Sanders, PhD has served in several roles within ISAPP. She was the founding president, executive science officer and executive director and will be retiring from ISAPP on June 30, 2023. She is also a consultant in the area of probiotic microbiology. She works internationally with food and supplement companies to develop new probiotic products and offers perspective on paths to scientific substantiation of probiotic product label claims. She is the current chair of the United States Pharmacopeia's Probiotics Expert Panel, was a member of the working group convened by the FAO/WHO that developed guidelines for probiotics and serves on the World Gastroenterology Organisation Guidelines Committee preparing practice guidelines for the use of probiotics and prebiotics for gastroenterologists.

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SFA Executive Committee

Brendan Daisley, PhD, University of Guelph, SFA President

Research Interests: I am interested in how probiotic science can be applied to favourably impact human, wildlife, and overall planetary health. A major focus of my current work is to elucidate mechanisms by which beneficial strains of bacteria can directly and/or indirectly improve immunity, detoxification of pesticides, and the nutritional status of honey bees. Through this work, I hope to contribute to a sustainable future by developing a framework of how microbial-based solutions can be used to support the health of important pollinator insects that are critical to the global food supply.

Daragh Hill, PhD, APC Microbiome Ireland & University College Cork, SFA Vice President

Current Research: I am interested in how bacteria can be used to promote health in a range of different ways. I currently work in dairy fermentation and bacteriocins. In particular on the products of bacterial growth which could have a beneficial effect on health either directly or through food. Exopolysaccharide, polyol, and bacteriocin production by lactic acid bacteria are my main areas of focus.

Dieter Vandenheuvel, PhD, University of Antwerp, Belgium & Shinshu University, Japan, SFA Treasurer

Research interests: My research focuses on the functional annotation of unknown genes and gene clusters in lactobacilli through genetic modification. My research interests include genetics, bacteriophage research, functional and molecular characterization, and pharmaceutical processing of biologicals (such as spray drying probiotics).

Cathy Lordan, PhD, APC Microbiome Ireland, SFA Secretary

Current Research: My research is based on human milk oligosaccharides (HMOs), found in breast milk, and their impact on the early life gut microbiota, with a specific focus on Bifidobacterium. I am looking at how HMOs impact both composition and functional potential of the infant microbial community, including the metabolites they produce as a result of HMO availability. Profile: https://www.linkedin.com/in/cathy-lordan-61a379b7/

Sarah Ahannach, PhD, University of Antwerp, Belgium, SFA Director of Outreach and Community Engagement

Research interests: I am interested in the deeper understanding of women's microbiome and how microbial management and cutting-edge microbiome analyses can improve women's health and safety. A major focus of my work is studying the inner workings of the vaginal ecosystem (Isala project), vitamin-producing bacteria, and applying microbiome analysis to forensics with a focus on sexual assault cases (GeneDoe project). I hope to contribute to knowledge on the stability and dynamics of the female microbiome by presenting novel understandings for future intervention studies to unravel underlying mechanisms; the development of probiotics and biotherapeutics; and for developing novel tools that could be used in diagnostics and criminal investigations.

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David Hourigan, APC Microbiome Ireland, SFA Director of Communications and Development

Research Interests: My research is centered around the role of bacteriocins, which are small ribosomally encoded antimicrobial peptides produced by bacteria, and their subsequent role within the microbiome. My research focuses on exploiting their effectiveness as selective antibacterial agents to curate the microbiota to tackle AMR and climate change. Interests include functional, ecological, and evolutionary genomics, microbial ecology, and bacterial competition.

Breanna Metras, SFA Local Organizer

Research Interests: I am interested in how fermented foods can affect the host gut microbiome and how current federal regulations impact fermented food production. A major focus of my current work is better understanding the differences between grain and commercially produced kefir. My research has consisted of microbial plating, animal models, and in vitro fermentation to determine how compositional and microbial differences in kefir may affect host health. Through this work, I hope to contribute evidence that shows improved regulations in labeling and characterizing fermented foods are needed so they might retain authenticity when produced large scale.