2012 ISAPP Meeting Report
October 1-3, 2012
Cork, Ireland

Incoming ISAPP President and local meeting organizer Colin Hill opened the conference with a traditional Gaelic greeting, "Cead Mile Failte," which means "one hundred thousand welcomes." And welcome ISAPP they did. The Irish hosts for the 10th ISAPP meeting October 1-3, 2012 on the University College Cork campus and at the River Lee Hotel in Cork, Ireland, succeeded in setting the stage for a meeting that's scientific rigor was matched only by the fun had by all.

This by-invitation meeting was attended by 109 delegates, including 40 scientists from the ISAPP Industry Advisory Committee, 43 invited delegates, 10 members of the ISAPP Board of Directors and 6 Student Fellow Association members. Twenty countries (Australia, Belgium, Canada, China, Denmark, Germany, Spain, Finland, France, Ireland, Italy, Mexico, Netherlands, New Zealand, Poland, Sweden, United Kingdom and United States) were represented. The details of the 3-day program are found in Appendix A. The slides presented in all sessions are posted for meeting participants, at a password-protected site.

At each ISAPP meeting the Board of Directors meets to discuss the past accomplishments and future directions for the organization. Details can be found in the 2012 Annual Report.

2011-2012 ISAPP Board of Directors, in Cork Ireland. Back row, left to right, Glenn Gibson, Todd Klaenhammer, Colin Hill, George Fahey, Phoukham Phothirath, Ravi Menon and Francisco Guarner. Front row, Mary Ellen Sanders, Gregor Reid and Karen Scott.

This year the board underwent several changes in personnel. Several positions shifted within the board, with Colin Hill taking over for Glenn Gibson as president, Karen Scott agreeing to serve as vice president and George Fahey as treasurer. Francisco Guarner rotated off the board, and will be sorely missed. Glenn moved to the past president position. There are three new members of the board: Seppo Salminen (University of Turku, Finland), Eamonn Quigley (currently at the APC, but moving in January to the Methodist Hospital in Houston TX) and Juliet Ansell (New Zealand Institute for Plant & Food Research, Palmerston North). These individuals expand the expertise and geographical representation of the board and ISAPP is indebted to them for agreeing to serve in these positions. ISAPP expressed appreciation to those who served over the past year (see photos below).

Colin Hill presents gifts to: Glenn Gibson. His plaque reads: "In Appreciation for Service to ISAPP, Glenn Gibson, Ph.D., whose insights, creativity and commitment led to the formation of ISAPP, whose scientific excellence established ISAPP as the premier, science-based, global organization for probiotics and prebiotics, whose leadership over the past 10 years defined ISAPP, and whose good humor made ISAPP enjoyable for (almost) all involved. ISAPP will forever be indebted to Glenn Gibson, the person and scientist. ISAPP Founder, President 2009-2012, Vice President 2002-2009
Meeting Host, Henley, UK 2003." **Mary Sally Cudmore and Andrea Doolan**, for their herculean efforts as local organizers; and Francisco Guarner. His plaque reads: "In Appreciation for Service to ISAPP, **Francisco Guarner**, M.D., Ph.D., who brought scientific excellence with clinical experience and insights to the ISAPP organization and programs, whose leadership and ideas helped ISAPP reach important clinical audiences, and whose exceptional service and commitment to ISAPP was unparalleled and will be sorely missed. Member of Board of Directors 2003-2012; Meeting Host, Barcelona, Spain 2010."

ISAPP delegates unwind at the ISAPP-sponsored social event for the meeting, a tour of Middleton Distillery, followed by dinner, traditional Irish music and Irish dancers. Around table, Tamar Ringel-Kulka, Gregor Reid (standing), Yehuda Ringel, Jacoline Gerritsen, Jose Garcia, Paul Blatchford, Juliet Ansell and Tomoyuki Sako. In background, Duane Charbonneau, Karen Scott, Dan Merenstein, and 2 accompanying guests, Frank Weaver and Dymphna Hill.

2012 Industry Advisory Committee Members

ISAPP is fortunate to be sponsored by top-notch probiotic and prebiotic companies, globally. Through their generous support, ISAPP has the funds to conduct its annual meetings. ISAPP expresses appreciation for the support of the 2012 IAC companies:

Abbott Laboratories
Agropur Cooperative
Beneo-Orafti
Biocodex
BioGaia
Bio-K+ International
CA Dairy Research Found
Cargill
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The Coca-Cola Company
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Mead Johnson Nutrition
Merck
Nestle
NIZO
Nutricia Research
Pfizer
Probi
Probiotics International Ltd. (Protexin)
Procter & Gamble
Valio
Winclove
Yakult

Fredrik Backhed

Plenary Lectures. The meeting featured an expanded plenary lecture program this year, in part to take advantage of the wealth of scientific expertise associated with the Alimentary Pharmabiotic Centre. **Fredrik Bäckhed**, University of Gothenburg, Sweden started off the session with a presentation titled "How gut microbiota are altered in metabolic diseases and what mechanisms are involved in interacting with the host." Fredrik addressed the findings that gut microbiota of individuals with obesity and type-2 diabetes is altered. Obesity is associated with reduced microbial diversity and increased capability to harvest energy from the diet. The gut microbiota may promote low grade inflammation, a condition linked to obesity, diabetes and cardiovascular disease. **Douwe van Sinderen**, APC, Ireland followed with a talk on "Linking genes to pro- and prebiotics." He described traits in bifidobacterial genomes linked to their ability to colonize and persist in the mammalian gut, such as pili and surface exopolysaccharides. **Harry Flint**, Rowett Research Institute, Aberdeen, next delivered a lecture on "Metabolite cross-feeding among the human colonic microbiota." Harry reminded us all of the complexity of the colonizing microbiota interactions, as reflected in competition for resources such as hydrogen, vitamins and biosynthetic precursors. He emphasized the importance of metabolic function of the


Douwe van Sinderen

Harry Flint

microbiota being more important than the presence of specific species, but also acknowledged that microbial specialists, "keystone species," are important as primary degraders.

The next presentations were focused on "Gut microbiota transplant." Two eminent gastroenterologists, **Christina Surawicz**, University of Washington, Seattle and **Elaine Petrof**, Queen's University, Canada, took the pro and con positions, respectively, on this issue. Christine presented examples of successful treatment from her own practice using fecal microbiota transplant (34 patients in all) for recurrent C. difficile colitis and was convinced of its utility as a therapeutic intervention, although acknowledging that there are many unanswered questions that need to be studied. Elaine agreed, but noted several problems with fecal microbiota transplant, including lack of standardization, risk of infection transmission from the donor and limitations in donor screening turnaround times when patients are acutely ill. Elaine postulated that a better approach is a "synthetic stool," comprising a defined combination of bacterial species that can restore balance to the patients' disturbed microbiota.

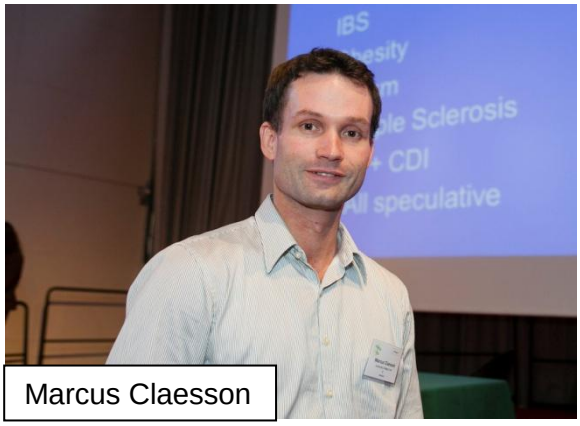
Christina Surawicz and Elaine Petrof

The program switched focus from gut microbes to oral microbes with a presentation by **Howard Jenkinson**, University of Bristol, UK on "The oral microbiota – what is healthy and can we play with it?" Howard described the oral microbiota as a unique collection of species, most of which are not found elsewhere, that vary in composition from one site to another in the same mouth. Although some lactic acid bacteria have been studied for oral applications, they have often been derived from probiotics designed for gut applications and are likely not optimal. Furthermore, Howard warned that increased acid production in the oral cavity is undesirable. Probiotic interventions in the oral cavity may exploit natural anti-microbial compounds, biomimetics (QS inhibitors, receptor analogs), anti-adhesins (antibodies, adhesintopes), or direct bacterial interference. **John Cryan**, APC, Ireland, took on the challenge of describing the role of the microbiome-gut-brain axis in stress-related disorders. Microbiome-gut-brain communication occurs through neural, hormonal, and immunological mediators. Fascinating new studies describe the added role of microbes in brain function and host behavior, including stress responses. Stress, especially early in life, alters composition of the microbiota;


John Cryan

microbiota in early life is critical for brain development, normal behavior and visceral pain; and probiotic administration has effects on stress, anxiety, depression and central gamma-amino-butyric acid receptor levels. Cryan postulated that modulation of the gut microbiota with biotherapeutics may target stress-related CNS disorders, including possibly stress-induced cognitive deficits. However elucidation of mechanisms and validation of animal studies in humans are important research goals.

The next lecture topic was "Gut microbiota, diet and health in the elderly population" by **Marcus Claesson**, APC, Ireland. This presentation focused on the findings from the Eldermet study. This study documented that the microbiota of older people displays greater inter-individual variation than that of younger adults. Furthermore, the microbiota of elderly in long-stay care was significantly less diverse than that of community dwellers, and these changes correlated with increased frailty. Microbiota changes across location were mirrored by changes in health parameters. Findings from Eldermet suggest that diet shapes gut microbiota, which impacts health in elderly people.



Marcus Claesson

The plenary session concluded with a lecture by the always-provocative **Fergus Shanahan**, APC, Ireland, who spoke on "Translating the microbiota to healthcare - where are the gaps in knowledge and future directions?" Fergus overviewed many key probiotic discoveries, while emphasizing that understanding mechanisms of action is key to advancing the field and the importance of translating animal research into well designed human trials (mice are not men). Fergus then railed against many examples of flawed concepts and bad language in the probiotic field. Some examples included unculturable microbes (not yet cultured is more accurate); boosting the immune system (this can be dangerous; modulation of the immune system is more correct); dysbiosis (this implies that we know what the starting point was, and that there was a change from this "good" state to a worse state; it implies we know what is wrong with colonizing microbial populations, but science isn't there yet); and finally, the term "probiotic,". Fergus feels this term has outlived its usefulness, partly because it's misunderstood by so many, and partly because the requirement of health benefits by the FAO definition is so nondescript as to be meaningless. Much food for thought in this presentation.

Late Breaking News Session. The Late Breaking News convened immediately after the plenary lectures. This is a rapid fire session where speakers can present 3 slides in 5 minutes on topics of interest to meeting participants. Lectures aim to be provocative, and highlight new data, new perspectives or new concerns related to the probiotic and prebiotic fields. The 2012 Late Breaking News speakers are listed in Table 1.

Table 1. Late Breaking News Schedule

Title of talk	Speaker
Increasing serum propionate by prebiotics reduces cancer cell proliferation in the liver	Laure B. Bindels
Concise Monograph on Prebiotics and Probiotics	Artur Ouwehand
Monitoring immune modulation by nutrition in the general population: identifying and substantiating effects on human health	Phoukham Phothirath and ILSI Europe
An opportunistic pathogen isolated from an obese human gut microbiota induces obesity in germfree mice	Liping Zhao

In vitro effect of polydeoxycholic acid on gut microbiota parameters	Adele Costabile
Who lives there?	Jose F. Garcia-Mazcorro
When our microbiota becomes drunk...	Nathalie Delzenne
Novel models for parallel testing of factors like pro- and prebiotics	Christophe Lacroix
Host-specific adherence of *Lactobacillus reuteri* contributes to ecological fitness *in vivo*	Steven Frese
How ISAPP saved me $100,000 = 77,790 Euro	Andi L. Shane
Challenging the "strain-specificity" dogma in a new approach to regulators	Ross Crittenden, Chairman of Global Alliance for Probiotics (GAP)
Challenging EFSA with Challenge Models	Delphine Saulnier
Microbiota interaction with secondary plant compound resveratrol	Charles Franz
Early markers of colic in young infants based on intestinal microbiota analysis	Willem de Vos

Discussion Groups[1]. Six discussion groups were convened all day on day 2 of the meeting. The participants in each group are shown in Table 3, and short summaries of each discussion follow.

Group 1. *What makes a prebiotic a prebiotic (and how do you know)?*

Chaired by Glenn Gibson and Bob Hutkins

Group 1 focused on prebiotics, and was organized around a series of presentations designed to fuel discussion:

- The original prebiotic concept from 1995 to ISAPP - Gibson
- Why structure affects function - Rastall
- Using biomass for bioactivity - Hotchkiss
- How to test for a prebiotic effect: in vitro, animals, humans or all? – Venema and Lacroix
- Prebiotics and functionality – Lacroix and Venema
- Examples of extra intestinal effects - Reimer, Garcia
- Prebiotics for companion animals - Fahey
- What does molecular biology tell us - Goh; van Sinderen
- What do patients tell us - Whelan
- New generation prebiotics, including anti-adhesive activities - Hutkins
- Expansion of the concept (cross feeding, co-metabolism) - Ansell
- Industry discussion: What are the next generation of prebiotics and why? Where are the claims, what is feasible? – Schoterman.

Various prebiotic definitions were discussed and how the concept has evolved from targeting the colonic microbiome, through to the entire gastrointestinal tract and finally the ISAPP definition, which specifies fermentation as a key criterion. There were views that this should be altered to include prebiotics that are non-fermentable e.g. anti-adhesive forms. This was seen as an opportunity to expand current biological activities. Moreover, there was the view that pathogen reduction could be included (and virulence attenuation) as well as stimulation of positive microorganisms. Structure and function

[1] Thanks to discussion group chairs for providing summaries of each discussion group.

relationships were becoming clearer with effects upon microbial diversity, determinations of selectivity and enhanced biological activity being major outcomes Immune modulation and metal chelation were further facets.

Biomass can be a useful, and economic, means of generating new prebiotics. Pectic oligomers from citrus were used as a model example. Issues over small volume testing and the need to identify promising candidates before addressing scale up were described. Testing aspects were then discussed – their advantages and disadvantages. This ranged from batch culture fermenters to multiple stage models (3 stage, TIM, SHIME), immobilized systems, animal, cellular studies and human trials. Analytical processes around microbiota characterization and functionality were compared. Human studies were seen as the definitive outcome, including ^{13}C labeling. New target microbes (aside from bifidobacteria and lactobacilli) were suggested.

For extra intestinal effects, the group looked at existing publications on atopic disease, respiratory infections, vaginal issues, oral disease, adiposity, liver damage and skin infections. The general outcome was that microbiota modulation was the key mechanism that linked these interactions.

In pet food applications, the market potential for prebiotics is huge. Health targets are similar to those of humans. Issues include monomeric composition, chain length, linkages, branching, microbiota beyond bifidobacteria, metabolic function, mechanisms of health effects.

Molecular biology has unraveled some of the explanations for prebiotic influences e.g. gene clusters to show transporters, regulators, permeases, hydrolases, lacS. In *Lactobacillus ruminis,* fermentation studies have been aligned to genome annotations, showing an energy efficient and rapid transport of GOS. In bifidobacteria, functional genome analyses have demonstrated uptake of trisaccharides (ABC transport). In infants, HMOs have unique compositions not relevant to the babies. These can be targeted by bifidobacteria. There is a need to go beyond genus level specificity. Combined or consecutive prebiotics may improve selectivity.

Questions relating to patients were then raised. For example, are prebiotics related to disease treatment or health maintenance? If a prebiotic does not change the microbiota, then is it something else? Case study trials in IBD were presented on patient access to prebiotics and information. Their knowledge of prebiotics was extremely poor, compared to probiotics.

The group then discussed the next generation of prebiotics (anti-adhesive activities, etc). The comparator was HMO, which both reduce adherence of pathogens and act as prebiotics. Studies with GOS have used pyrosequencing to demonstrate varying species level effects. This has relevance for infant formulae.

Prebiotic aspects of whole foods and their complexity was covered. Kiwi fruit trials were described where cross feeding and co-metabolism had been investigated. Suggestions on other prebiotic influences, aside from bifidobacteria, were made and included metagenomics, metabonomics, gene expression, mRNA global sequencing, bile deconjugation, enzyme profiles, lipids, phenolics.

It was concluded that FOS and GOS were accepted prebiotics by the current definition. This was confirmed by a range of model systems that cumulated in human studies. The reasoning was their size, structure, non-digestibility, complementary activities towards bifidobacteria (specific enzymes, location). The above discussion suggested how prebiotics could move forward with a wider expansion of

the concept, target populations, expanded microorganisms, health benefits, application of new technologies and improved consumer understanding being the main goals.

Group 1 participants

Group 2. ***From Clinical Trials to Clinical Guidelines: Reconciling the Evidence***
Chaired by Dan Merenstein and Michael Cabana

The discussion group focused on a key question: How can clinicians and consumers use the existing probiotic literature to guide clinical care?

Probiotic literature is broad-based, but at the same time, limited. Clinicians and consumers need better guidance on how to leverage the existing probiotic literature to guide clinical care.
Clinicians are increasingly relying on experts and professional organizations to provide guidelines and recommendations for probiotics and prebiotics; however, there are relatively few well-done RCTs conducted for probiotic and/or prebiotic interventions in humans. The current published literature regarding the use of probiotics for the prevention of NEC illustrates the difficulty and issues in translating clinical trial information to consensus and clinical guidelines. NEC is a horrible condition in which traditional medicine has limited evidence-based options for treatment. Many probiotic studies have shown impressive outcomes with a variety of strains for preventing NEC.

We spent the first few hours reviewing NEC, discussing how physicians use systematic reviews and meta-analyses and reviewed 10 relatively well done NEC articles. We had a heated debate about if probiotic usage should be standard of care to prevent or decrease the risk of NEC. In the end no consensus was reached, although 9 out of 14 favored using probiotics routinely. One of the participants, who has extensive experience on FDA panels approving drugs and for CMS reviewing coverage, commented that this is typical of any decision and that generally 9 out of 14 would be enough for the FDA to approve a drug.

Different members of this discussion group, who formed different conclusions, plan to write 2-3 papers covering this discussion.

1. Why practice needs to change immediately, discussing how the evidence is robust and that placebo controlled trials are no longer ethical.
2. Why practice doesn't change for things not championed by a pharmaceutical company.

3. Why practice can't change yet and what additional information is needed to move this forward.

Group 3. ***How can we manipulate the human gut microbiota to affect host metabolism?***
Chaired by Fredrik Backhed and Patrice Cani

What do we know from animal models? There has been extensive work in animal models during the past ten years on how pro- and prebiotics modulate host metabolism. In rodents, it has been shown that the gut microbiota can regulate adiposity, satiety, inflammation, glucose metabolism and energy expenditure. We are also starting to identify which components of the bacteria and/or dietary fibres that are important. As we have gained more knowledge on the mechanisms from *in vivo* experiments, there is a growing need to translate the results into humans. However, there is a lack of good, double-blind, placebo-controlled clinical trials that can prove causality of pro- and prebiotics on modulating human metabolism.

Evidence from recent and ongoing human trials. At present, high quality human trials are starting to demonstrate the potential for gut microbiota manipulations in preventing or treating disease. For instance, prebiotics given to obese humans led to a reduced waist/hip ratio and to a huge increase in *Bifidobacterium* and *Faecalibacterium prausnitzii,* both bacteria were correlated to a significant decrease in serum lipopolysaccharides. Additionally, probiotics have been shown to be able to affect plasma lipid profiles in humans, mainly on low-density lipoprotein (LDL) levels. Nutrigenomics analysis from duodenal biopsy obtained in subjects after probiotics interventions (randomized, placebo-controlled double-blind, cross-over design with several *Lactobacillus*) suggest that *Lactobacillus acidophilus* affects host cholesterol metabolism.In traditional Chinese medicine, the herb berberine has been used to treat bacterial diarrhea. Recent studies have now shown that berberine can also lower blood cholesterol and improve glucose homeostasis in humans, whether this effect is mediated by altering the gut microbiota composition remains to be studied. It is believed that berberine reduces the abundance of bacteria in rats, as shown by sequencing of the gut microbiota that showed reduction or even disappearance of many bacterial groups along with reduced inflammation. Fecal microbiota transplant (FMT) is a new and upcoming method for treating disease using the gut microbiota. A recent study showed that FMT could be used to improve insulin sensitivity in Type II diabetes patients who received feces from lean people. However, not all patients responded to the treatment, illustrating the complexity of individual variation in humans. Taken together, these findings suggest that it may be possible to treat and prevent human metabolic disorders by targeting the gut microbiota.

Designing the optimal clinical trial. How do you design a good clinical trial to study causality of probiotics and prebiotics in metabolic disease? Long-term trials are needed to address this question, as well as careful consideration of methodology, relevant end-points and appropriate control experiments.

Methodology. Studying different environments in the gut and not only fecal samples will improve the quality of human studies. However, obtaining these samples (e.g. for from the ileum) is a challenge for the moment. As microbiology techniques continue to advance, we are now able to also cultivate previously uncultured organisms including anaerobic bacteria. Colonization and growth of bacteria is also highly substrate-specific, which must be taken into account. Furthermore, we can now genetically modify specific bacterial strains to study mechanisms. For instance, removal of lipoteichoic acid from lactobacilli increases their anti-inflammatory activity. Using transcriptomics we can further increase our understanding of how bacteria affect gut gene expression profiles. However, transcriptome

profiles differ more between individuals as compared to the transcriptional changes seen after probiotic administration, making such studies difficult to interpret.

End-points and biomarkers. Satiety might not be the best biomarker in humans, since obese patients tend to have reduced sensitivity to satiety. Instead, fat mass and inflammatory markers, liver steatosis and insulin resistance, but also key biomarkers measured in the gut microbiota might be more appropriate markers.

Control experiments. Using heat-killed bacteria as a control to live probiotics could give mechanistic insights, as well as using antibiotics targeted at a specific microbe. In terms of FMTs, autologous transplants can be used as a good control. It would be of interest to also use fecal transplants from obese individuals to lean people as a control treatment, but this is unlikely to pass the IRB. Also, dietary habits must be closely monitored as this will have a large impact on the gut microbiota composition. Standardization of design and protocols is urgently needed to facilitate comparisons between microbiome studies. To prove causality, it is also important to separate secondary responses of the gut microbiota to pro- or prebiotic treatments from the actual, causative changes. Mechanistic insights will likely require animal experiments.

Strain-specific effects need to be communicated to the public, industry and scientific society
The genus *Lactobacillus* consists of 180 species and the growing scientific data point to the fact that we can no longer group all lactobacilli in one probiotic basket. There are clear species- and even strain-specific differences in how these organisms affect the host. Different strains of the same species can affect metabolism via completely different mechanisms and even have opposing effects. Hence, it is of utmost importance to make this fact known to the public, the industry and the scientific community. Otherwise, we will see confusing reports on how all lactobacilli are “good” or “bad”.

Conclusion
It is possible that the term “probiotic” might become obsolete as we develop and understand how we can manipulate the gut microbiota to affect metabolism. Some “probiotic” bacteria might in fact work through inhibition of other pathogenic bacteria or bacteria that associate with increased risk of disease – these bacteria could even be called the next generation of antibiotics. The future of the pro- and prebiotic field will most likely be to target sub-groups of patients with a specific disease.

Group 4. *How do the microbiota and pro/prebiotics influence nutritional status?*
Chaired by Karen Scott and Nathalie Delzenne

The discussion focussed on efforts to improve nutrition in under-nourished children, pregnant mothers and the elderly. The different target groups require different strategies, partly due to differences in the commensal microbiota, and different strategies are required to address the problem in the developing world, compared to the developed world. Additionally, new simple diagnosis of the early stages of under-nutrition, and knowledge of when to treat, would make treatments more effective.

Mechanisms to improve maternal and childhood nutrition in the developing world include initiatives to set up sustainable kitchens to provide fermented milk products to the local community. This provides employment for the mothers, aswell as much-needed food for the children. Other trials on specific prebiotic and probiotic supplements illustrate the difficulties in choosing combinations for maximum efficacy, and in defining appropriate end-points. This could only be improved by a better understanding of the mechanisms by which such interventions work, and some of these investigations can be done in model systems. New genomic information may also help understand mechanisms. For instance *Lactobacillus reuteri* possesses pathways for the synthesis of essential amino acids, folate and also some

B vitamins. Whether any of these are important in the apparent ability of *L. reuteri* to alleviate diarrhoea better than L. *casei* remains to be seen.

Childhood under-nutrition has long-term health consequences in the aberrant development of the immune system and cognitive function, as well as enhanced risks of later development of coronary heart disease and diabetes.

Changes in the composition of the gut microbiota in elderly individuals have been linked to poorer health, and seem to be triggered by dietary changes, particularly on entering care home accommodation. Increasing the diversity of the general diet, and including probiotic and prebiotic products, could be a simple and cheap way of redressing the balance. The loss of muscle as an older person becomes frail is similar to that observed in cachexia in some cancers. In this case, mouse models have been used to show that Lactobacillus supplementation can reduce inflammation. Probiotic yoghurt has also been included in the nutritional rehabilitation of patients recovering from anorexia nervosa (who also demonstrate extreme muscle wastage), and alters the ratio of the CD4/CD8 markers to improve health.

Shorter discussions on the role of the microbiota in alleviating incommunicable diseases and in improving nutrient uptake followed. Although reduced nutrient absorption has clear adverse effects on health, there has been substantially less research in this area. Calcium absorption and bone density can be improved by prebiotic (soluble corn fibre) supplementation while iron uptake has been increased with consumption of specific probiotics.

Group 4 Participants

Group 5. *New opportunities for use of probiotics and prebiotics for the prevention and treatment of disease*

Chaired by Eamonn Quigley and Francisco Guarner

Two large-scale research projects aimed at deciphering the structure and function of the human gut microbiota, namely the NIH's Human Microbiome project and the European MetaHIT project, will have concluded their tasks by the end of 2012. Thanks to advances in sequencing technologies as well as in the bioinformatic tools needed to analyze massive amounts of data, these projects, as well as other research initiatives, are providing deeper insights into the microbial communities that inhabit the human gut and, thereby, will allow the identification of changes that are associated with disease states. A better knowledge of the contributions of microbial symbionts to host health will certainly help in the design of new interventions to promote symbiosis and prevent disease.

A number of disease states have been associated with changes in the composition of the gut microbiota. Experimental and human data on the metabolic syndrome suggest that changes in gut microbiota composition may play a role in the disorder (Qin et al, 2012). Other instances of associations between human disease and particular gut microbiota characteristics have been provided by Crohn's disease, ulcerative colitis, irritable bowel syndrome, celiac disease, childhood-onset asthma and even psychological disorders such as autism (Manichanh et al, 2012; Cho and Blaser, 2012). Consistency between studies is still poor for some of these examples. Obviously, such associations do not necessarily indicate a causative role for the microbiota in the pathogenesis of disease, as they could rather be a consequence of the disease. The group suggested that follow-up descriptive studies and, particularly, intervention studies aiming at restoring the normal composition of the gut microbiota will be required. There is a growing interest in developing strategies that will improve the compositional and functional quality of the human gut microbial ecosystem for health benefits. The future of a healthy human gut microbiota may include the restoration of our ancestral microbial ecology (Cho and Blaser 2012). Different interventional approaches are emerging, including techniques for microbial reconstitution by fecal microbiota transplantation, the design of synthetic stool preparations by selection and culture of critical species, and the use of novel probiotics and prebiotics. A paradigm is the case of *Faecalibacterium prausnitzii*, a predominant constituent of the normal human gut microbiota, which produces mediators with important anti-inflammatory influence on the intestinal mucosa, and has been shown to be in reduced abundance in Crohn's disease and ulcerative colitis (Sokol 2008; Manichanh 2012).

There are a number of problems for the design of studies to test the efficacy of gut microbial ecosystem restoration for the prevention of disease. First, since prevalence of the above mentioned disorders is generally low, large sample sizes of healthy population and long time interventions will be needed in order to prove the benefit. Timing is another critical point, as some interventions may only be effective early in life ("the pivotal window of opportunity"). It may also be difficult to determine what will be a successful outcome in terms of meaningful benefit. A modest benefit achieved by a safe intervention may generally be perceived as meaningful. Finally and primarily, intensive research is still needed in order to identify, characterize and produce optimized intervention products aimed at restoring human gut microecology for prevention and treatment of disease, be it as foods or drugs.

1. Qin J et al. Nature 2012
2. Manichanh C, et al Nature Rev 2012
3. Cho I, Blaser MJ. (2012) The human microbiome: at the interface of health and disease. Nat Rev Genet 13(4):260-70. doi: 10.1038/nrg3182. Review
4. Sokol H, Pigneur B, Watterlot L et al. (2008) Faecalibacterium prausnitzii is an anti-inflammatory commensal bacterium identified by gut microbiota analysis of Crohn disease patients. Proc Natl Acad Sci U S A 105,16731–16736.

Group 6. *Strain Identity*
Chaired by Mary Ellen Sanders and Todd Klaenhammer

When does a probiotic strain change from being a safe and efficacious strain for a specific use into one that is not safe or not efficacious for that use? Although scale-up, fermentation conditions, growth substrates, cryoprotectants, food formulation or storage time are likely to generate detectable differences in genes (mutations, genome rearrangements, etc), gene expression patterns or metabolic output, when do these changes become substantive, warranting a re-examination of safety or efficacy? To what extent should expensive and time consuming testing be required to confirm bioequivalency when there is only a small likelihood that the efforts will reveal differences in the safety or efficacy profiles? What type of testing – short of full safety assessments or human efficacy trials - would be reasonable and meaningful assessment of the likelihood that safety or efficacy profiles have changed?

This group discussed these difficult issues, with the aims of providing scientific perspective to regulators as well as identifying needed research.

Eric Johansen discussed the importance of genetic characterization of probiotic bacteria, emphasizing that full genomic sequencing should be a minimum level of characterization for commercial strains. Genomic sequencing today is only €300 (compared to €200,000 in 2005). Genomic sequencing allows comparison among different strains of the same species, providing an approach to link phenotypic differences to genotypes. Also, the genome sequence can be an important part of safety assessments, as genes of concern – such as transmissible antibiotic resistance genes – can be identified. If undesirable genes are detected, different approaches can be used to rid the strain of these genes. Eric also shared his perspectives on physiological characterization of probiotic strains, including the value of measuring growth characteristics, expression arrays and immunological assays. However, he concluded that genomics is the ultimate tool for strain characterization to differentiate closely related strains, rule out presence of undesirable genes and identify of mutations in variants.

David Pridmore discussed his experience with isolation of a lactate dehydrogenase mutant of a production strain of *L. johnsonii*. He described a series of physiological and genetic assessments that are useful to determine how the mutant compares with the parent strain, including microscopic morphology, 16S sequence, resistance to in vitro GI tract assay, carbohydrate fermentations profile, H_2O_2 production and antibiotic resistance pattern. Although not all inclusive, this battery of tests gives a good indication if the mutant strain has not changed in important parameters. Such tests may provide a first level assessment to determine if mutations or changes in processing are substantive. David also pointed out that although changes in growth conditions may alter the properties of the resulting probiotics, the changes may be irrelevant when we consider that reprogramming of the probiotics after consumption is likely more important for probiotic function.

Greg Leyer described studies conducted to gain insight into genetic stability of bacteria through processing. He described clear differences in expression during exponential growth due to growth medium changes. In fact, he found that different growth media and growth phases influence genetic expression more than small genetic differences, such as exists among different strains of the same species. Harvesting cells during exponential phase resulted in more differences than stationary phase in eight different media. Evidence of genetic stability emerged from a study following a *S. thermophilus* strain through 100s of multiple transfers - no changes in the *S. thermophilus* crspr region were detected.

Maria Marco cautioned us to not forget the importance of the host on probiotic gene expression. Host factors such as diet, microbiota and host genetics that impact microbes in vivo may dwarf changes induced by production conditions or the matrix. Also, the food, beverage, or dietary supplement matrix in which the probiotic is consumed can influence the survival, and therefore, the function of the probiotic in the intestine.

It was clear from these talks, and other evidence presented by, Duane Charbonneau and Todd Klaenhammer, that industrial processing, product environment and the consuming host will induce changes in gene expression profiles and microbial physiology, but that assessing the significance of these changes vis a vis probiotic efficacy was a difficult task.

In trying to understand the importance of production and matrix changes and their implications for product efficacy, several guiding principles were used:

- The goal is reasonable certainty, not 100% assurance, of functional equivalence
- Any changes should not compromise delivery of live probiotics to site of action
- Impact of consumer diet, genetics, microbiota likely to dwarf impact of changes due to different delivery matrices
- An array of functional, physiological tests may provide a "performance map" of biological activity – determine probiotic performance in the new matrix compared to the old matrix
- Any *regulatory* requirements should have a reasonable potential to add to the overall safety and, if that potential is very low, additional testing is unnecessary.
- In foods, there is precedent that food ingredients can be delivered in different matrices, without negation of claim of health benefit

For safety, the group concluded that it was unlikely that processing or delivery matrix changes could transform a safe microorganism to an unsafe one. Furthermore, spontaneous mutations or undirected genetic shifts were also unlikely to result in safety concerns. However, one instance where a safety concern could arise was shared. For example, whereas histadine decarboxylase in a probiotic used in a dried supplement product would not pose a safety risk, use of that same probiotic for aged cheese may result in unsafe levels of biogenic amines production. The European QPS approach as a baseline for assessing probiotic safety was accepted by the group. However, care must be taken to understand dose and non-food uses of microbes deemed safe on this list.

For efficacy, the group concluded that a system of describing categories of change would be helpful. Matrices could be grouped, for example, as dairy products, freeze dried products, spray dried products, etc. Then changes of matrix within the category would not require additional testing. Regarding production changes, minor fermentation or matrix changes such as growth carbohydrate or inert formulation ingredients would not warrant any further testing. However, changes between categories would require testing, such as tests to measure impact on viability in product. Additionally, a human study documenting survival through intestinal transit may need to be conducted. However, repeating a clinical efficacy trial should not be required.

The group plans to further develop these concepts in a focused paper, hopefully contributing to framing the discussion further with regulatory bodies.

Table 2. Discussion group participants.

Last Name	First Name	Affiliation	Country
1. Consensus group on what really is a prebiotic and why. Chair: Glenn Gibson, Co-chair: Bob Hutkins			
George	Fahey	University of Illinois	USA
Glenn	Gibson	University of Reading	United Kingdom
Gunhild	Kozianowski	BENEO Group	Germany
Margriet	Schoterman	FrieslandCampina Domo	the Netherlands
Juliet	Ansell	New Zealand Institute of Plant & Food	New Zealand
Jose Francisco	Garcia Mazcorro	Facultad de Medicina Veterinaria,	Mexico
Christophe	Lacroix	ETH Zurich	Switzerland
Raylene	Reimer	University of Calgary	Canada
Yong Jun	Goh	North Carolina State University	USA
Koen	Venema	TNO Healthy Living	The Netherlands
Bob	Hutkins	University of Nebraska	USA
Arland	Hotchkiss	US Department of Agriculture-Agricultural	USA
Robert	Rastall	Department of Food and Nutritional	UK
Kevin	Whelan	King's College London	UK
Douwe	Van Sinderen	Alimentary Pharmabiotic Centre &	Ireland
2. Translation of clinical evidence to recommendations. Chair: Dan Merenstein, Co-chair: Michael Cabana			
Michael	Cabana	University of California, San Francisco	USA
Steven	Davis	abbott nutrition	USA
Arthur	Ouwehand	Active Nutrition, DuPont Nutrition &	Finland
Douwina	Bosscher	Cargill	Belgium
Niklas	Larsson	Probi AB	Sweden
François-Marie	Luquet	Bio-K+ International inc.	Canada
Alexandra	Meynier	Kraft Foods	USA
Hania	Szajewska	The Medical University of Warsaw	Poland
Alex	Krist	Virginia Commonwealth University	USA
Frank	D'Amico	Duquesne University / UPMC Family	USA
Daniel	Tancredi	University of California, Davis	USA
Dan	Merenstein	Georgetown University	US
Amnon	Lahad	Hebrew University, Jerusalem, Israel	Israel
Girish	Deshpande	NEPEAN HOSPITAL SYDNEY AND	AUSTRALIA
Andi	Shane	Emory University	USA
Tamar	Ringel-Kulka	University of North Carolina	USA
Josef	Neu	University of Florida	USA
Kurt	Selle	NCSU	USA
3. How can we manipulate the human gut microbiota to affect host metabolism? Chair: Fredrik Bäckhed, Co-chair:			
Fredrik	Bäckhed	University of Gothenburg	SWEDEN
Colin	Hill	APC	Ireland
Jan	Knol	Danone Research	The Netherlands
Bo	Mollstam	BioGaia AB	Sweden
George	Tzortzis	Clasado	UK

Ravi	Menon	The Bell Institute of Health & Nutrition -	USA
David	Hayashi	Kraft Foods today as of Oct 1st Mondeleze	US
Johan	Van Hylckama	Danone Research	FRANCE
Frida	Fåk	Gothenburg University	Sweden
Paul	Cotter	Teagasc Food Research Centre	Ireland
Patrice D.	Cani	Université catholique de Louvain	Belgium
Willem M	De Vos	Wageningen and Helsinki University	Netherlands
Max	Nieuwdorp	AMC-UvA, department of Internal	the Netherlands
Harry	Flint	Rowett Institute, University of Aberdeen	United Kingdom
Carel	leRoux	Conway Institute, University College	Ireland
John	Cryan	University College Cork	IRELAND
Michiel	Kleerebezem	Wageningen University	Netherlands
Liping	Zhao	Shanghai Jiao Tong University	China
Sarah	O'Flaherty	North Carolina State University	USA
4. How do the microbiota and pro/prebiotics influence nutritional status? Chair: Karen Scott, Co-chair: Nathalie Delzenne			
Gregor	Reid	Lawson Health Research Institute	Canada
Karen	Scott	Rowett INstitute of Nutrition and Health	UK
Delphine	Saulnier	NIZO	The Netherlands
Eduardo	Schiffrin	Nestlé, Research & development	Switzerland
Kerstin	Holmgren	Probi AB	Sweden
Saskia	Van Hemert	Winclove b.v.	the Netherlands
Natalie	Lamb	Probiotics International Ltd	UK
Tomoyuki	Sako	Yakult Europe B.V.	The Netherlands
Lori	Lathrop Stern	Pfizer Consumer Healthcare	USA
Maciej	Chichlowski	Mead Johnson Nutrition	USA
Paul	Sheridan	Rowett Institute of Nutrition and Health	UK
Howard	Jenkinson	Professor of Oral Microbiology	United Kingdom
Connie	Weaver	Purdue University, Department of	USA
Esther	Nova	Institute of Food Science and Technology	Spain
Paul	O'Toole	Univ College Cork	IRELAND
James	Bunn	Alder Hey Childrens NHS Foundation Trust	UK
Nathalie	Delzenne	université catholique de Louvain	Belgium
Marcus	Claesson	University College Cork	Ireland
5. New opportunities for use of probiotics for the prevention and treatment of disease. Chair: Eamonn Quigley,			
Francisco	Guarner	University Hospital Vall d'Hebron	Spain
Phoukham	Phothirath	Nestlé	Switzerland
Janine	Barlow	Probiotics International limited	UK
Irene	Lenoir-Wijnkoop	Danone Research	France
Melanie	Lalonde	Bio-K+ International inc.	Canada
Emilie	Fargier	BIOCODEX	France
Adam	Baker	Chr Hansen A/S	Denmark
Eamonn	Quigley	Alimentary Pharmabiotic Centre,	Ireland
Christina	Surawicz	U of WA	US
Timothy	Dinan	University College COrk	Ireland

Helen	Whelton	University College Cork	Ireland
Flavia	Indrio	University of Bari	Italy
Harsharn	Gill	RMIT University	Australia
Charlie	Daly	Alimentary Pharmabiotic Centre (APC)	Ireland
Philippe	Langella	INRA	France
Fergus	Shanahan	Alimentary Pharmabiotic Centre, UCC	Ireland
Elaine	Petrof	Queen's University	Canada
Yehuda	Ringel	University of North Carolina	USA
Marianne	Fraher	APC	Ireland
6. How does genetic content and variability impact the safety and efficacy of probiotic microbes? Chair: Mary Ellen Sanders, Co-chair: Todd Klaenhammer			
Mary Ellen	Sanders	Dairy & Food Culture Technologies	USA
Todd	Klaenhammer	NC State University	USA
Maeve	Murphy	General Mills Inc	USA
Eamonn	Connolly	BioGaia AB	Sweden
Rosaline	Waworuntu	Mead Johnson Nutrition	USA
Nicolas	Pagé	Nestlé	Switzerland
Eric	Johansen	Chr Hansen A/S	Denmark
Duane	Charbonneau	The Procter and Gamble Company	USA
Gregory	Leyer	DuPont Danisco	USA
Tami	Mackle	Pfizer	USA
Pascal	Molimard	Merch Medication Familiale	FRANCE
Julie	Audy	Agropur	Canada
Jacoline	Garritsen	Winclove b.v.	The Netherlands
Ross	Crittenden	Valio	Finland
David	Pridmore	Nestec SA	Switzerland
Bruno	Pot	Institut Pasteur de Lille	France
Maria	Marco	University of California, Davis	USA
Paul	Ross	Teagasc Food Research Centre	Ireland
Seppo	Salminen	Functional Foods Forum	Finland
Charles	Franz	Max Rubner institute, federal Research	Germany
Emma	Call	North Carolina State University	United States

Methods for exploring the microbiome: microbiome, transcriptomic and metabolome approaches and what they tell us about the effects probiotics and prebiotics can have on the host.[2]
Course organizer and instructor: Paul O'Toole, UCC, Ireland

This course was organised to provide information on interpreting data generated by microbiome, transcriptome and metabolome analyses, with a view to understanding how such approaches can assist in understanding the effects of probiotics and prebiotics on the host. The two hour course was divided roughly into four sections, three presented by different members of staff from the Department of Microbiology and Alimentary Pharmabiotic Centre at UCC, with the final presentation from Professor Michiel Kleerebezem from Wageningen University in the Netherlands.

In the 'Cells and Organisms' section Dr Paul O'Toole explained that closely related bacterial strains (including probiotic strains) can have nearly identical genomes but different phenotypes – which can sometimes be explained by different transcriptomes. Put simply, two bacteria may possess virtually the same complement of genes, but express different genes under different growth conditions giving them quite different activities. Thus you cannot use the genotype to infer the phenotype – otherwise known as epigenetics. This talk finished with the importance of including analysis of the microbiota in understanding the links between human genomics and risk of disease.

The second part (given by Dr Marcus Claesson) focussed on the human gut microbiota, and the techniques used to analyse it. There were explanations of the methods, and which to use when, as well as the output, which varies from phylum level classification (Bacteroidetes:Firmicutes) down to family or genus level. There are differences in classification between OTU (Operational Taxonomic Unit), approximating to a bacterial family, and a COG (Cluster of orthologous genes) which is a functional classification. Such comparisons indicate that whilst the microbiome composition may vary greatly between individuals, there is considerable conservation of the metabolic function. This was followed by discussions in small groups as to the importance of some of these key aspects – one being whether outliers =individuals who do not 'fit the pattern' - may represent a valuable resource for improving our understanding of the links between the microbiota and health.

The third session (given by Dr Ian Jeffrey) used an example paper to explain how the output from a microbial compositional analysis can be interpreted – and what the data really means. The different sequence processing pipelines were compared and the pros and cons of each highlighted. The different ways of presenting the output from large datasets were shown, and explained, including cluster analysis (PCA plots compared to dendrograms). Again the contrast between phylogenetic variation and functional redundancy within the gut microbiota of individuals was raised.

The final session (Professor Kleerebezem) focussed on probiotics, and how they can modulate the human genome transcriptome. Three different species of Lactobacillus had distinct responses in terms of human gene expression. The challenge is to link the responses to known data from clinical interventions involving the same bacterial strains. However the effect also varies between individuals – with inter-individual variation often exceeding the response to the intervention. Thus it may be very difficult to predict with certainty what an individual response to a probiotic intervention will be, although there is also evidence of conserved responses among healthy individuals.

[2] Thanks to Karen Scott for providing summary.

Each of the presentations was very clear and all were very interactive, allowing frequent interruptions to clarify points. This was essential for the course attendees to get the most out of the course, although unfortunately it meant that there was not enough time to complete the interactive workshop type activities that had been planned.

IAC/BOD meeting. Chair: Ravi Menon

The antitrust policy statement was read at the beginning of the meeting.

Student and Fellows Association Program[3]

The 2012 ISAPP Student and Fellow Association Conference was held from September 29th to October 1st in Cork, Ireland. This overlapped with the annual ISAPP meeting and allowed SFA to interact with ISAPP Scientists and Industry Members, many of whom have shown interest in attending SFA events and leading panel discussions geared towards young scientists. This was an excellent opportunity to meet possible employers both in Academia and Industry as well as learn firsthand from leaders in the field. This year 40 SFA members from North America, Europe, Africa and the Middle East participated in the meeting, along with many local UCC students. In addition to a poster session set up prior to the plenary session, the SFA program featured six speakers who spoke on a variety of topics related to science in industry, academia, mentorship, and how to start a career. Three students presented in the Late Breaking News session. The full program and abstracts from the poster session are available in the SFA Program 2012.

ISAPP-SFA members at the 2012 meeting at Cork, Ireland

[3] Information obtained from SFA officers and SFA website

10th Meeting of the
International Scientific Association for Probiotics and Prebiotics

River Lee Hotel and University College Cork

Cork, Ireland

October 1-3, 2012

Meeting information website

PROGRAM

Date/time	Event	Location
Sunday, September 30		
noon – 15:30	Board of Directors (BoD) meeting (BoD only)	River Lee Hotel, Tower Room
14:00-15:30	Registration desk	River Lee Hotel lobby
15:30 – 16:30	Industry Advisory Committee (IAC) meeting (IAC only)	River Lee Hotel, Western Room
19:00	BoD+IAC+local hosts BBQ dinner (BoD+IAC+local hosts only)	Weir Room, River Lee Hotel
Monday, October 1		
8:00-11:00	Registration desk	Devere Hall, UCC Campus
8:30-9:30	BoD+IAC meeting (BoD+IAC only)	
9:30	SFA posters set up*	
10:00-11:00	Coffee and poster viewing with authors*	
	Plenary lecture session*	
11:00– 11:15	Welcome. Glenn Gibson, University of Reading, UK, ISAPP President Colin Hill, Incoming ISAPP President and Local Host, UCC and APC, Ireland	
11:15-12:45	Chair (Session 1). Karen Scott, Rowett Research Institute, Aberdeen	
11:15-11:45	How gut microbiota are altered in metabolic diseases and what mechanisms are involved in interacting with the host. Fredrik Bäckhed, University of Gothenburg, Sweden	
11:45 – 12:15	Linking genes to pro- and prebiotics. Douwe van Sinderen, APC, Ireland	
12:15-12:45	Metabolite cross-feeding among the human colonic microbiota. Harry Flint, Rowett Research Institute, Aberdeen	
12:45 – 14:00	Lunch and poster viewing	
14:00-15:30	Chair (Session 2). Todd Klaenhammer, North Carolina State University, Raleigh, USA	
14:00-14:30	Gut microbiota transplant a. Pro position. Christina Surawicz, University of Washington, Seattle b. Con position. Elaine Petrof, Queen's University, Canada	
14:30-15:00	The oral microbiota – what is healthy and can we play with it? Howard Jenkinson, University of Bristol, UK	
15:00-15:30	Mind altering microbes: Role of microbiome-gut-brain axis in stress-related disorders. John Cryan, APC, Ireland	
15:30-16:00	Coffee and poster viewing	
16:00-17:00	Chair (Session 3). Michael Cabana, University of California-San Francisco, USA	
16:00-16:30	Gut microbiota, diet and health in the elderly population. Marcus Claesson, APC, Ireland	

16:30-17:00	Translating the microbiota to healthcare - where are the gaps in knowledge and future directions? Fergus Shanahan, APC, Ireland	
17:30	Reception*	
17:45-18:45	Late Breaking News*. Chair: Gregor Reid, University of Western Ontario, Canada	
19:00	Dinner** (ISAPP invited participants and IAC only)	Aula Maxima, UCC campus
Tuesday, October 2		
8:30 – 15:30 pm, including working lunch	**Discussion Groups****	River Lee Hotel
	1. Consensus group on what really is a prebiotic and why. Chair: Glenn Gibson, Co-chair: Bob Hutkins	Victoria Room
	2. Translation of clinical evidence to recommendations. Chair: Dan Merenstein, Co-chair: Michael Cabana	Peake Room
	3. How can we manipulate the human gut microbiota to affect host metabolism? Chair: Fredrik Bäckhed, Co-chair: Patrice Cani	Western Room
	4. How do the microbiota and pro/prebiotics influence nutritional status? Chair: Karen Scott, Co-chair: Nathalie Delzenne	Blarney Room
	5. New opportunities for use of probiotics for the prevention and treatment of disease. Chair: Eamonn Quigley, Co-chair: Francisco Guarner	Coachford Room
	6. How does genetic content and variability impact the safety and efficacy of probiotic microbes? Chair: Mary Ellen Sanders, Co-chair: Todd Klaenhammer	Exhibition Room
16:00	**Middleton Distillery, Tour, Whiskey Tasting, Dancing and Dinner. Buses depart from River Lee Hotel at 16:00.**	River Lee Hotel to Middleton Distillery
23:00	**Buses return to River Lee Hotel.**	River Lee Hotel
Wednesday, October 3		
8:30 – 12:00	**Wrap-Up Session***.** Chair: George Fahey, University of Illinois, USA	Devere Hall
10:00-10:30	**Coffee break*****	
12:00-12:20	**Interactive discussion***:** Categories of probiotics, Gregor Reid, Univ Western Ontario, Canada	
12:20 pm	**General meeting adjourned**	
12:20 – 13:30	Lunch***	
13:30 pm – 16:30	**IAC Learning Forum (IAC only)** Methods for exploring the microbiome: microbiome, transcriptomic and metabolome approaches and what they tell us about the effects probiotics and prebiotics can have on the host. Course instructor: Paul O'Toole, UCC, Ireland ***Pre-course sign up required***	Bioinformatics Teaching lab, Food Science Building UCC
13:30 pm – 16:30	**Tour of Teagasc***, the agriculture and food development authority in Ireland. Dr. Paul Ross, (Head of Teagasc Food Programme), will lead a tour of the Moorepark Food Research Centre, highlighting research and development activities and possibilities. Transportation will be arranged. Please RSVP to Mary Ellen Sanders mes@mesanders.com. **All participants welcome.**	Teagasc Food Research Centre, Moorepark, Fermoy, County Cork
16:30 – 17:30	**Board of Directors Meeting (BoD only)**	BioSciences Institute, Room 1.38, UCC

* IAC, SFA, APC and ISAPP invited participants
** IAC and ISAPP invited participants only
*** IAC, APC and ISAPP invited participants

Session Descriptions

Late Breaking News Session Description

This session is an opportunity for people to give short presentations (3 slides/5 min) on late breaking news topics. These presentations range from 'hot' off-the-bench news from their lab/clinic to controversial or important issues on the science, politics, funding, business or humorous aspects of the field of probiotics or prebiotics. Hosted bar and munchies will be provided in an informal atmosphere. All meeting participants are welcome to present, including students, fellows and industry representatives. ***Extra slides or going over time will not be tolerated***. To be scheduled for a LBN presentation, please send title and short abstract to Gregor Reid gregor@uwo.ca. To avoid delays, slides must be submitted prior to the session so they can be preloaded and ready to go. Gregor reserves the right to delete slides if more than 3 are submitted.

Wrap-Up Session

Presentations (30 min each) provide an overview from each discussion group from chairs of all 6 discussion groups to all meeting participants.