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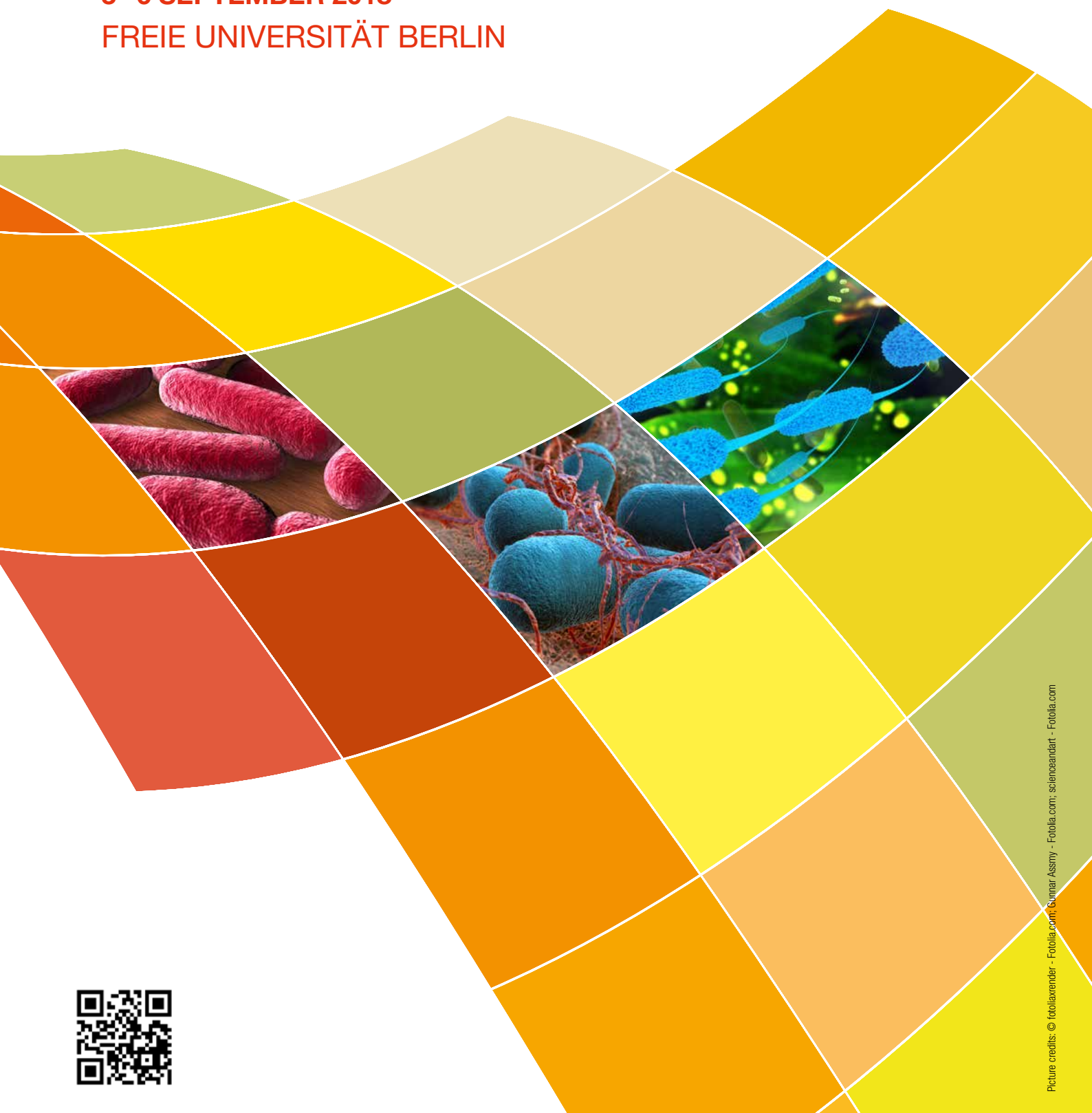


FoodMicro

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Conference Theme: "Biodiversity of Foodborne Microbes"

BOOK OF ABSTRACTS

Exploring biodiversity in microbial ecosystems along the food chain

P1.43

A pilot study of the role of corn dextrin and milk peptides supplementation on faecal microbiota in healthy adultsModesto M.¹, Di Paola M.², Quagliariello A.³, Sansosti C.¹, Cavani L.¹, Prati G.M.⁴, Fornari F.⁴, De Filippo C.⁵, **Mattarelli P.**¹¹University of Bologna, Department of Agricultural and Food Science, Bologna, Italy, ²University of Florence, Department of Biology, Sesto Fiorentino, Florence, Italy, ³Bambino Gesù Children's Hospital, Unit of Human Microbiome, Rome, Italy, ⁴Piacenza Hospital, U.O. di Gastroenterologia ed Epatologia, Piacenza, Italy, ⁵National Research Council, Institute of Agricultural Biology and Biotechnology, Pisa, Italy

The gastrointestinal microbiota has an important role in human health. Dietary interventions are of great interest to modulate the composition and metabolic functions of the gut microbial communities and to improve health, and prevent or treat diseases. Consumption of prebiotics is one dietary strategy for beneficial manipulation of the gut microbiota, because it allows increasing the fibre intake, especially in people with western dietary habits, who do not take the recommended daily amount of fiber. Interestingly, milk peptides can also positively affect the beneficial gut microorganisms. The present work is a pilot study aimed to investigate the effect of a prebiotic supplementation on composition and metabolic activity of microorganisms living in the human gut. In this trial, 12 healthy subjects received 10g/die of supplement Biotransit®, composed by corn derived dextrin and milk peptides, produced and marketed in Italy by Depofarma (Italy), for 4 weeks with a 2 weeks washout. Outcome measures were assessed at four time points (before the supplementation T0-1, T0-2, at the end of intervention, T30 and after washout, T45), including gut microbiota profiling by 16S rRNA gene sequencing and intestinal functional metabolism measuring faecal Short Chain Fatty Acid concentrations (SCFAs). The effects of the Biotransit supplementation on bifidobacteria were also assessed with culture dependent techniques. Gut microbiota analysis revealed that Biotransit® supplementation after 30 days did not exert effects on the overall gut microbiota structure. Although no significant differences on alpha diversity were obtained, we observed an increase of diversity after 30 days of treatment. Beta diversity analysis, calculated on Bray-Curtis distances revealed significant differences comparing T0 vs T45 and T30 vs T45. Interestingly, at T45, we found an enrichment of *Porphyromonadaceae*. Biotransit® induced quantitative changes in cultivable bifidobacteria with increased amount at T45, even if the total number of species has not been influenced. Biotransit® supplementation is also associated to an increase total SCFAs concentration in T30 and T45, in particular related to acetate, propionate and butyrate ($p < 0.05$). Future study will be aimed to follow the time course of the persistence of this effect after the end of treatment.

Keywords: Microbiota profile, peptides, fibers, Bifidobacterium, SCFAs