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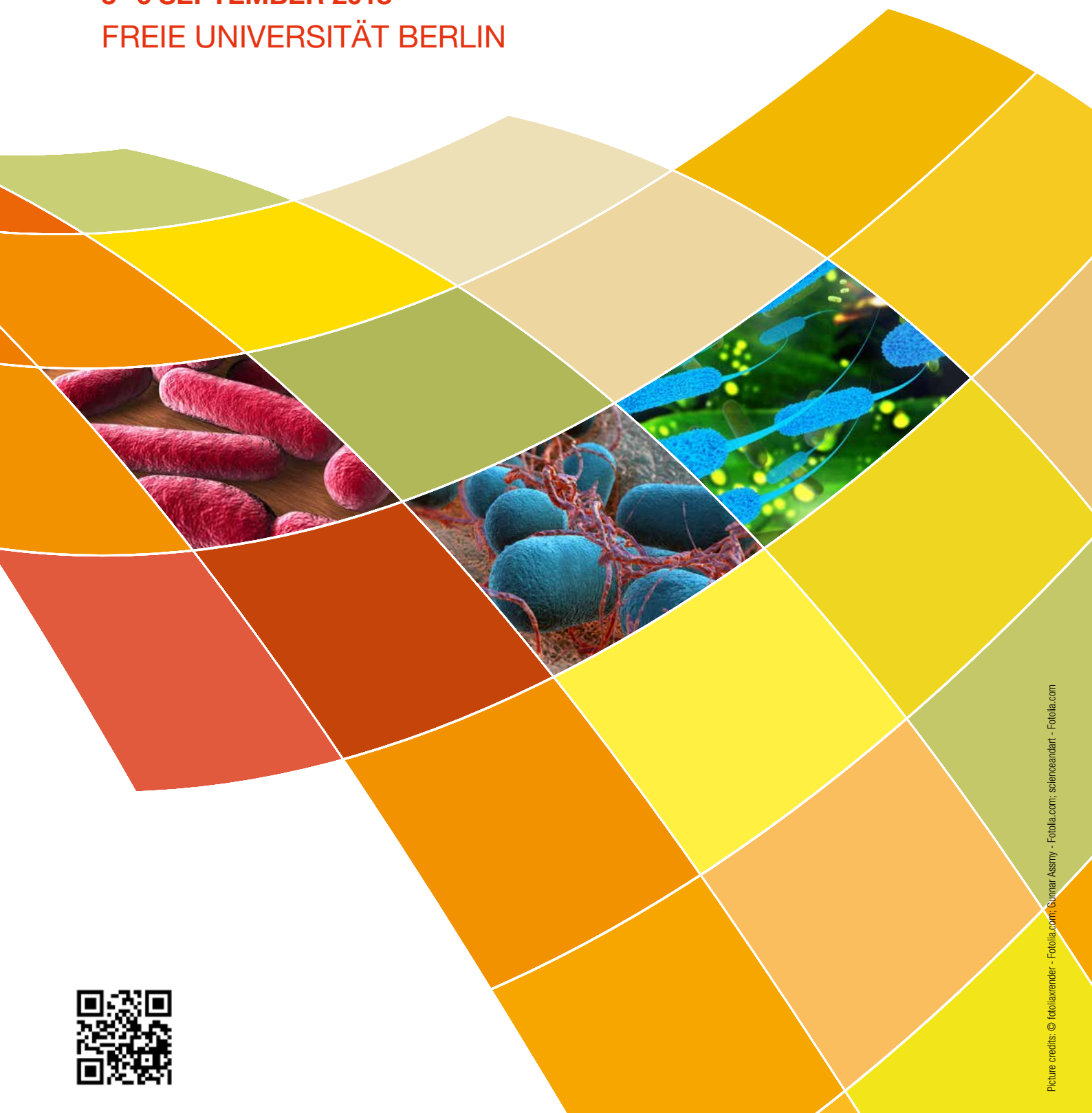


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Conference Theme: "Biodiversity of Foodborne Microbes"

BOOK OF ABSTRACTS

Exploring biodiversity in microbial ecosystems along the food chain

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Microbial diversity of Brazilian native fish during chilled and frozen storageBaptista R.C.¹, Ferrocino I.², Pavani M.³, Guerreiro T.M.³, Catharino R.R.³, Cocolin L.², Sant'Ana A.S.¹¹University of Campinas, Department of Food Science, Campinas, Brazil, ²University of Turin, Department of Agricultural, Forest and Food Science, Grugliasco, Italy, ³University of Campinas, Nucleus of Experimental Medicine and Surgery, Campinas, Brazil

Pacu (*Piaractus mesopotamicus*), patinga (female *Piaractus mesopotamicus* x male *Piaractus brachypomus*) and tambacu (female *Colossoma macropomum* x male *Piaractus mesopotamicus*) highlight as native species of significant economic importance for Brazilian fish farming, being well accepted by the consumers. Spoilage Specific Organisms are directly influenced by storage conditions of the product and the development of undesiderate microbes, being responsible for the production of undesirable off-flavors, associated with spoilage. Thus, this study aimed to assess the microbiota involved in the spoilage of pacu, patinga and tambacu and in order to understand how they can affect the quality of these fishes. Changes in bacterial diversity of these three fish species, during ice or frozen based storage for one year, was studied through 16S rRNA amplicon based sequencing. The development of volatile organic compounds (VOCs) as well as the production of microbial metabolites assessed by nuclear magnetic resonance (NMR) were also investigated. The microbiota of the Brazilian fish was composed mainly by *Pseudomonas fragi*, *Brochothrix thermosphacta*, *Acinetobacter*, *Acinetobacter johnsonii*, *Bacillus*, *Lactobacillus plantarum*, *Kocuria* and *Enterococcus*. No significant differences were observed between fish species ($P < 0.05$). The results showed the presence of methane, propanoate, butanoate, sulfur, arginine and proline in higher amounts in frozen stored samples compared to ice stored samples. *Kocuria*, *P. fragi*, *L. plantarum*, *Enterococcus* and *Acinetobacter* were positively correlated with the metabolic pathways with the ether lipid metabolism. *B. thermosphacta* and *P. fragi* were related with metabolic pathways involved in aminoacid metabolism (arginine, alanine and proline metabolism). *P. fragi* was the most prevalent spoilage bacteria at in both conditions followed by *B. thermosphacta*, which can contribute to determine the final characteristics of the products. Moreover, the main OTUs identified in fish samples were positively correlated with the production of off-flavour. In particular *P. fragi* was linked with the presence of hexanol, nonanal, octenol and ethyl-hexanol. Improved storage conditions is needed, possibly coupled with antimicrobial packaging in order to achieve a simultaneous inhibition of more spoilage microbial groups and to preserve the microbiological quality of fish during storage.

Keywords: Microbial ecology, Fish spoilage, 16S rRNA sequencing, volatile organic compounds (VOCs).