

O FOOD 3

Gut microbiota diversity of omnivore, vegetarian and vegan healthy subjects by culture dependent and rRNA DGGE profiling

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In the last decades several studies report the importance of improving the knowledge of how lifestyle factors such as diet, age or geographic site influence the change in gut microbiota. In particular, diet habits appear to be an important factor affecting the gut microbiota. Three main dietary habits are worldwide diffused: omnivore, ovo-lacto-vegetarian and vegan. The aim of this study was to assess the fecal microbiota of 153 volunteers (51 per category) recruited from North to South Italy between 30-50 years of age and with a male:female ratio approximately 1:1. The fecal microbiota was assessed at species level by RNA-based-DGGE and by using conventional enumeration on selective agar plates. The similarity matrixes obtained from dendrograms analysis of the RNA-DGGE fingerprints were used to build Projection on Latent Structures - Discriminant Analysis (PLS-DA). Concerning the dietary habits it was possible to observe a gradient of samples driving a certain degree of separation of omnivore from non-omnivore subjects. When the samples were grouped based on the dietary habits, the PLS-DA models showed a trend of differentiation based on geographical origin of the samples. It was observed that the fecal microbiota of ovo-lacto-vegetarian and vegan volunteers showed significantly lower counts of *Bacteroides fragilis* and LAB group. The food consumed can have an impact on fecal microbiota, long-term diets associated with low levels of protein and animal fat intake decrease the levels of the genera *Bacteroides* and the absence in vegan diet of food such as yogurt and cheese, decrease the gut LAB populations. All together, these findings confirm that the food consumed, more that the dietary habits, and geographical origin can have an impact on fecal microbiota. This work can be the basis for further research regarding the identification of biological, molecular and metabolic markers specific to the type of diet.

Poster presentations

P FOOD 1

New insights into the ecology of supralittoral sediments detritivores from the analysis of gut microbiota of talitrid amphipods

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Talitrid amphipods (sandhoppers and beach fleas) are supralittoral zone dwellers and obtain most of their food from stranded materials, which include detrital marine angiosperms and macroalgae, as well as occasional death animals. Here, we report the characterization of gut microbiota of *Talitrus saltator*, *Talorchestia ugoi*, *Sardorchestia pelecyaniformis*, *Orchestia montagui*, collected in Sardinia (Italy). Microbiota were analyzed by metabarcoding analysis on amplified 16SrRNA V4 region and by quantification of family 48 glycosyl hydrolases genes, which are involved in cellulose degradation. Obtained results indicated the presence of a complex bacterial flora, including several members of Verrucomicrobia in four out of the five species. Moreover, different gut microbiota taxonomic assemblages among the selected talitrid species were found. In particular, *O. montagui* (which lives in close contact with *Posidonia banquettes*) gut microbiota was found to be the most different with respect to those of the other talitrids, being more abundant in members of Firmicutes, Planctomycetes and Actinobacteria, and containing the highest level of family 48 glycosyl hydrolases genes. We conclude that talitrid amphipods harbor a complex gut microbiota which may be related to the habitat the different species colonize