Study of the fecal microbiota as affected by omnivore, vegetarian or vegan diets through culture dependent and independent analysis

Ferrocino Ilario[1]; Di Cagno Raffaella[2]; De Angelis Maria[2]; Neviani Erasmo[3]; Lazzi Camilla[3]; Vannini Lucia[4]; Turroni Silvia[5] and Cocolin Luca[1]

(1) University of Torino, Dept Agric, Forest & Food Sci, Italy
(2) University of Bari Aldo Moro, Dept Soil Plant & Food Sci, Italy
(3) University of Parma, Dept Food Sci, Italy
(4) University of Bologna, Alma Mater Studiorum, Dept Agric & Food Sci, Italy
(5) University of Bologna, Alma Mater Studiorum, Dept Pharm & Biotechnol, Italy

Diet is the main reservoir of microbes and, especially, is the nutrient source for the host and related intestinal microbiota. Excluding obvious geographic differences, three main dietary habits are worldwide diffused: omnivore, 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. Volunteers were requested to collect feces samples in a time of spam of 3 weeks, once per week. Each week the feces samples were used to evaluated the main microbial populations by using selective culture media. The microbiota was assessed at species level by using PCR-DGGE analysis of 16S rRNA gene of DNA extracted directly from feces. Reverse transcription (RT)-PCR-DGGE has been also performed in order to obtain a more complete picture of the microbiota in the main dietary habits. The results of the microbial counts on specific media were analyzed by using one-way analysis of variance (ANOVA). Loads of *Bacteroides* spp., *Corynebacteria* spp. and LAB were higher in the omnivore group, while counts of *Pseudomonas* spp. were higher in the vegetarian group. Counts of *Bifidobacterium* spp. and LAB were lower in vegan group if compared with the other ones. PCR-DGGE and RT-PCR-DGGE fingerprints where then subjected to cluster analyses. The dendrogram of similarity obtained showed a clear difference between global and live population in feces samples. On the other hand the results showed a low similarity between volunteers regardless of the type of diet. Only geographic site seems to influence the composition of the 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.

Keywords: Fecal microbiota; Diet; Plate counts; DGGE; (RT)-PCR-DGGE