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Impact of diet on the salivary microbiome and metabolome

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The choice of ovo-lacto-vegetarian or vegan diets is increasing worldwide. Therefore, understanding how long-term dietary habits can shape the human microbiome and possibly predispose to illness is an important goal. In this study, we analyzed the salivary microbiota of 161 healthy individuals following omnivore (O), ovo-lacto-vegetarian (VG) or vegan (V) diets through 16S rRNA gene amplicon pyrosequencing. Moreover, metabolomic profiling of saliva using 1H-NMR and GC-MS/SPME was carried out. A core microbiome shared by 98% of individuals was identified, including 12 microbial genera: Prevotella, Porphyromonas, Streptococcus, Granulicatella, Gemella, Veillonella, Fusobacterium, Leptotrichia, Neisseria, Haemophilus, Actinomyces and TM-7 class. Despite our results suggest that diet has no effect in shaping salivary microbiome, the grouping of subjects in three "salivary types" (ST) was found, driven by the abundance of the core genera. ST1 was characterized by higher abundance of Neisseria and Fusobacterium, ST2 was distinguished by Prevotella and ST3 by Streptococcus and Gemella; Porphyromonas was associated to both ST1 and ST3. Moreover, species co-occurrence/exclusion patterns revealed that core microbial genera of Firmicutes (including Streptococcus, Gemella and Granulicatella) or Bacteroidetes (Prevotella and Porphyromonas) tend to dominate the salivary microbiome and exclude other bacterial taxa. Metabolomic analysis identified diet-related biomarkers that enabled a significant discrimination between the 3 groups of individuals on the basis of their diet. Formate, urea, uridine and 5-methyl-3-hexanone could discriminate O salivary metabolome, whereas 1-propanol, hexanoic acid and proline were characteristic of non-omnivore diets. These results suggest that the salivary metabolome can be discriminating for diet, while salivary microbiota has a remarkable inter-individual stability and do not vary with dietary habits.