

Extended Abstract

Characterization of Bacterial Metabolites in Parotid, Submandibular/Sublingual and Whole Saliva of Healthy Subjects †

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Metabolome is the comprehensive assembly of metabolites in biologic tissues and/or fluids. The study of metabolic profiles may give important information about the health status. Recently, many researches have been focused on saliva diagnostics, based in its abundant production and easier way of collection [1].

The present study reports the differences in concentration of bacterial short-chain fatty acids (SCFA) in 3 different types of saliva (parotid–PS; submandibular/sublingual–SMS; whole saliva–WS) and serum. Moreover, urea concentration, a nitrogen source, has been correlated to bacterial metabolism in PS, SMS, WS.

Ten healthy males and 10 females, aged between 20 and 25 years, were enrolled. Subjects with hyposalivation (modified Saxon's test < 5 mL/5 min) and/or with evidence of periodontal disease (periodontal screening and recording–PSR > 3 in one of the sextant) and/or caries (decay missing filled teeth–DMFT > 5 teeth with active carious lesions) were excluded. Subjects with full mouth bleeding score (FMBS) and full mouth plaque score (FMPS) > 25% were treated through non-surgical periodontal therapy, 15 days before saliva collection. Saliva and serum samples were collected between 9 and 11 a.m. Subjects were asked to avoid intense workout for 12 hours before collection, as well as food, beverage different from water and toothpaste or mouthwash. The metabolic profile was evaluated by Proton Nuclear Magnetic Resonance (¹H-NMR). Statistical analysis was performed through contingency tables, using the chi-squared test ($p < 0.05$ significant of association).

Among the metabolites identified in saliva, the SCFA-formate (1C), acetate (2C) and propionate (3C) were produced by bacterial flora. Acetate was the most abundant metabolite in all types of saliva followed by propionate and formate. The acetate concentration determined was 2556.4 μ M in WS, 676.4 μ M in PS and 354.4 μ M in SMS. In serum, acetate concentration is 56.9 μ M indicating the endogenous contribution of the total amount of this metabolite. Propionate was 14 times less concentrated in PS and SMS and 9 times less in WS than acetate. Formate is produced by a different metabolic pathway and were present in lower concentration and 57.7 μ M in WS, 27.2 μ M in PS and 22.9 μ M in SMS. Differences of the 3 metabolites in the 3 typologies of saliva are statistically very significant ($p < 0.0001$).

When each SCFA is compared to urea (acetate vs. urea; propionate vs. urea and formate vs. urea) differences are statistically very significant ($p < 0.00001$), indicating an inverse relationship among the three different typologies of saliva.

To the best of our knowledge this is the first study which takes into account the metabolic contribution of SCFA to the SMS composition. Three of the metabolites most commonly produced by *bacteria* spp. are found in significantly higher concentration in WS respect to PS and SMS, indicating a differential presence of *bacteria* spp., among the three types of saliva.

Particularly, the very high concentration of acetate supports the hypothesis of the presence in the oral cavity of peculiar species of “acetogenic” *bacteria*.

Conflicts of Interest: The authors declare no conflict of interest.

References

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