

Targeted Proteomics on Taste Tissue and Determination of Saliva Total Proteins.

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Saliva is pivotal for digestion, taste, microbial defense and maintenance of the oral cavity. These functions are provided through a complex mixture of electrolytes, proteins, and buffer ions dissolved in water principally excreted from the three major salivary glands.

Protection against microorganisms through saliva is provided by anti-bacterial, anti-fungal and anti-viral proteins such as immunoglobulins, histatins, cystatins etc. [1]. Tooth and oral cavity maintenance employing salivary compounds works at different levels such as protection against demineralization, remineralization, lubrication and buffer functions.

Interaction between saliva and food, the most obvious property, acts on three different levels. Pre-digestion of food occurs in the mouth with enzymes such as amylase, a broad range of proteases, lipases, DNase and RNase. Tasting is made possible through the presence of saliva allowing diffusion of foodborne tastants to receptors [2]. Bolus formation [1] requires saliva as lubricant to facilitate swallowing and transfer through the esophagus. Despite only three major salivary glands it is obvious that salivary proteins are of more diverse origin and that their composition and relative abundance are highly dynamic. For example, as part of the oral tissue involved in tasting also the von Ebner glands, located beneath the circumvallate papillae contribute to the secretion of saliva. Likewise, any other taste-related tissue might secrete proteins that will eventually end up in saliva.

To identify salivary proteins specifically involved in gustatory signal transduction we analyzed human fungiform papillae cDNA libraries using a genomic approach and total salivary protein using a proteomic approach. In a first round of random screening both complementary approaches identified numerous candidate proteins either as a list of ESTs derived from large scale sequencing of the cDNA libraries [3] or as a direct image of all salivary proteins derived through peptide mapping and LC-ESI-MS/MS analysis on human saliva. In a second, targeted round of screening specific PCR-primers were designed based upon the proteins found in

saliva to challenge the cDNA library and to verify their origin and possible involvement in gustatory signal transduction.

In addition to several proteins known to be major constituents of saliva such as lipocalins and calgranulin various other known and previously undescribed proteins seem also to originate from gustatory tissue.

REFERENCES

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