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Data Article

Data from human salivary proteome – A resource of potential biomarkers for oral cancer

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ABSTRACT

Salivary proteins are an important source for developing marker-based assays for oral cancers. To get an insight into the proteins present in human saliva, we applied multiple strategies involving affinity-based depletion of abundant proteins, fractionation of the resulting proteins or their tryptic peptides followed by LC–MS/MS analysis, using high resolution mass spectrometry. By integrating the protein identifications observed by us with those from similar workflows employed in earlier investigations, we compiled an updated salivary proteome. We have mapped the salivary proteome to the published data on differentially expressed proteins from oral cancer tissues and also for their secretory features using prediction tools, SignalP 4.1, TMHMM 2c and Exocarta. Proteotypic peptides for the subset of proteins implicated in oral cancer and mapped to any two of the prediction tools for secretory potential have been listed. The data here are related

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to the research article “Human saliva proteome – a resource of potential biomarkers for oral cancer” in the Journal of Proteomics [1].

1. Value of the data

- Proteins identified, compiled from published LC–MS/MS analysis and the data from our recent analysis represent an updated salivary proteome.
- The list of salivary sub-proteome includes proteins which are reported to be differentially expressed in oral cancer tissue specimens and have secretory potential.
- A high confidence list of proteins along with their proteotypic peptides is supported by their relevance in oral cancer and predicted secretory features.
- This subset would serve as an important reference for developing targeted analysis for clinical applications.

Specifications table

Subject area	Biology
More specific subject area	Saliva proteomics or proteome
Type of data	Tables, excel files
How data was acquired	Fourier Transform LTQ-Orbitrap Velos mass spectrometer (Thermo Fischer Scientific, Bremen, Germany) equipped with Proxeon Easy nLC was used for LC–MS/MS analysis Proteome Discoverer 1.4 and SEQUEST search engine Human RefSeq 60 database Human Oral Microbiome Database (HOMD)
Data format	Analyzed
Experimental factors	Human saliva proteomic analysis, processing and fractionation of salivary proteins, mass spectrometry, data analysis
Experimental features	Human saliva from healthy subjects was subjected to depletion of high abundant proteins by starch affinity and/or antibody affinity for plasmatic proteins or enrichment of low abundant proteins by capturing with hexapeptide library. Pre-fractionation of proteins by SDS-PAGE followed by in-gel tryptic digestion or SCX chromatography of tryptic peptides from in-solution digested total proteins. Mass spectrometry was carried out using high resolution MS platform.
Data source location	Bangalore, India
Data accessibility	Analyzed datasets are directly provided with this article

2. Data, experimental design, materials and methods

2.1. Sample collection and processing

The study was approved by the Institutional Ethics Committee. The procedure for collection and processing of saliva was adapted from earlier reports [2,3]. Briefly, unstimulated saliva samples (5 ml) were collected from healthy subjects of either sex in the age group between 20 and 50 years, with written informed consent. The individuals selected were without any risk habits like tobacco chewing, smoking or alcohol abuse. Samples were collected in the morning after rinsing the mouth with water and with subjects refraining from food/drink for at least 1 h prior to the collection. All the samples were centrifuged at 2000 rpm, at 4 °C for 10 min to remove the cells. The supernatant was then collected and centrifuged at