

## **Establishment of 2-D proteomic map from human saliva**

### **Abstract**

Saliva is increasingly used as a diagnostic fluid due to its relatively simple and minimal invasive collection. In order to create a reference map for comparative studies on normal and pathological condition of human diseases, globally expressed salivary proteins were studied using twodimensional electrophoresis. To investigate the effect of meal taking on the proteome profile, the whole saliva samples were collected from an individual before and after meal. In addition, the variation among different individuals was also investigated. Two-dimensional electrophoresis results had separated around 400 protein spots. Comparative proteomic analysis of human salivary proteins before and after meal showed that 17 protein spots were altered. Out of these, two spots were found to decrease and 15 spots were found to increase. Whereas from the comparative proteomic profile among four different individuals revealed only three differentially expressed proteins. These findings suggested that the variation of 2-D proteome map among different individuals may not be significant. However our observation had shed light on important aspects that have to be considered before commencing salivary proteomic studies especially related to the timing of saliva sampling, ethnicity, individuality, oral hygiene, eating and dietary habits and even environmental factors.