# PRELIMINARY PROTEOMICS ANALYSIS SHOWED ADENOID CYSTIC CARCINOMA MOLECULAR SUBTYPES

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## INTRODUCTION

Adenoid cystic carcinoma (AdCC) is characterized by indolent and slow growing, but eventually fatal. AdCC is composed of epithelial and myoepithelial cells and are subdivided into 3 histological groups: cribriform, tubular, and solid patterns. The diagnosis of AdCC remains a challenge due to the high variation in histological subtypes and overlapping features. L ocal recurrences, metastases, and perineural invasion are eventually expected. Along with a morphologic examination, biomarkers can be used to increase diagnostic accuracy and for prognosis and treatment. We conducted a proteomics analysis of AdCC tumors to identify and propose a protein profile classification with future clinical applications.

## MATERIALS AND METHODS

Proteomics analyses of 12 tissue samples from AdCC patients were performed. The mass spectrometry (MS) analyses were carried out using the nanoElute nanoflow chromatographic system, from Bruker Daltonics, Bremen, Germany, coupled online to a hybrid trapped ion mobility spectrometry-quadrupole time-of-flight mass spectrometer-timsTof Pro. The raw files were processed in the MaxQuant software, version 2.4.0.0. The Perseus analysis software, version 2.0.9.0 (Tyanova and Cox, 2018), was used to filter the proteomic results. We used R software for Heatmap and the Fisher Exact test to evaluate the significance of an association between the cluster of the heatmap and demographics and clinical data.

## RESULTS AND DISCUSSION

About 7164 proteins were identified and quantified through MS analyses. We use the hierarchical clustering method to classify the different clusters. Analysis of proteomics indicated that AdCC divides into four distinct groups. Association of categorical clinical, molecular data and overall survival (OS) with AdCC subgroups was evaluated and a possible difference was shown. Cluster 1 was enriched for tumors with cribriform and solid component and was more likely to be in the major salivary gland origin. In contrast, samples in cluster 2 and 3 contained more tumors with cribriform histology and were more likely to originate from the minor and major salivary glands. Cluster 4 showed a predominant solid histology and 66.7% of the samples originated from the minor salivary gland. Others clinical data was analyzed and similar literature with the AdCC characteristics were observed, such as perineural invasion, distant metastases with the lung the most involved site. Cluster 1 and 4 samples exhibit worse OS than cluster 2 and 3 in which present both tubular and cribriform patterns that generally have a better prognosis. OS analysis for histologic subtype showed a better prognosis in cribriform subtype with corroborate with the literature.

## CONCLUSIONS

Our findings used a very effective and efficient proteomics tools to screen a molecular profile in AdCC. We have detected distinct clusters which could provide more clues for the diagnosis of these tumors; however, is necessary to add a major number of samples in the analysis for a biomarker discovery.

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