Paraskevi Chairta et al., J Clin Cell Immunol 2017, 8:6(Suppl)
DOI: 10.4172/2155-9899-C1-042

Comparative proteomic analysis of affected and non-affected areas of systemic sclerosis skin biopsies

Paraskevi Chairta[1], Paschalis Nicolaou[1], Kleitos Sokratous[1], George M Spyrou[1], Christine Galant[2], Frédéric Houssiau[2], Bernard R Lauwerys[2] and **Kyproula Christodoulou[1]**
[1]Cyprus Institute of Neurology & Genetics, Nicosia, Cyprus
[2]Université catholique de Louvain, Bruxelles, Belgium

Statement of the Problem: Systemic sclerosis (SSc) is an autoimmune rheumatic disease characterized by vasculopathy, inflammation and fibrosis. It is a complex and heterogeneous disease, as many organs of the body may be affected and symptoms vary among individuals. As the aetiology and pathogenesis of the disease are currently unclear, its prognosis and diagnosis are challenging and thus up to date there is no cure for SSc. Therefore, the purpose of this study is to discover specific proteomic biomarkers gaining insights into the mechanisms implicated in SSc pathogenesis and facilitating the early prognosis, more accurate diagnosis and therapeutic targeting of the disease.

Methodology & Theoretical Orientation: Human biopsies were obtained from affected and non-affected skin areas of SSc patients and have been classified based on histological criteria. Proteins were extracted from human skin biopsies, purified, reduced, alkylated and digested with trypsin. Purified peptides were analyzed on a Waters SYNAPT G2Si HDMS instrument operated in ion mobility mode using a UDMSE approach. Data were processed by the Progenesis QI and functional annotation analysis performed using multiple bioinformatics resources.

Findings: Proteomic analysis led to identification and quantification of more than 1500 differentially expressed proteins. Differential expression of approximately 1000 out of these proteins including interferons and interleukins, have statistically significant fold Change of ≥1.5 or ≤0.667. Further pathway analyses showed that the identified dysregulated proteins were involved in multiple pathways including, antigen processing and presentation and complement pathway, which is known to be associated with autoimmune diseases.

Conclusion & Significance: Using MS-based proteomic analyses of SSc human skin biopsies, we identified several proteins that might be implicated in the pathogenesis and development of SSc. The most differentially expressed proteins as well as differentially expressed proteins that are involved in autoimmunity-related pathways could be considered as potential SSc biomarkers.

This work has received support from the EU/EFPIA/ Innovative Medicines Initiative Joint Undertaking PRECISESADS grant no 115565.www.precisesads.eu

Biography

Paraskevi Chaitra is a PhD student in Medical Genetics at Cyprus School of Molecular Medicine (CSMM). She is working on Proteomics and Genetics of Systemic Sclerosis. The proteomics part is carried out through the PRECISESADs project. Human skin biopsies were obtained from SSc patients voluntarily participating in the project by the collaborating clinicians. Samples are sent to CING where they are analyzed using mass spectrometry. The genetics part is carried out on Cypriot SSc patients and healthy volunteers, and the samples are analyzed using Restriction Fragment Length Polymorphism and SNaPshot techniques. Her life goal is to undertake critical research and provide essential services to people who suffer from complex diseases such as systemic sclerosis. Through her PhD project, she aims to discover specific proteomic and genetic biomarkers to facilitate an early prognosis, diagnosis and therapeutic targeting of SSc.

paraskevich@cing.ac.cy

Notes: