

## 5th International Conference on

## **Clinical & Experimental Cardiology**

April 27-29, 2015 Philadelphia, USA

## MALDI imaging for determining the protein network associated with atrial fibrillation

Salah A Mohamed<sup>1</sup>, Junfeng Yan<sup>1</sup>, Oliver Klein<sup>2</sup>, Thorsten Hanke<sup>1</sup>, Beate Godau<sup>3</sup>, Hans H Sievers<sup>1</sup>, Jens Cordes<sup>3</sup> and Herbert Thiele<sup>4</sup>

<sup>1</sup>UKSH-Campus Luebeck, Germany

<sup>2</sup>Berlin-Brandenburger Centrum for Regenerative Therapien Campus Virchow-Klinikum, Germany

<sup>3</sup>University Medical Center Schleswig-Holstein, Germany

<sup>4</sup>Fraunhofer MEVIS, Germany

**Background:** Atrial fibrillation (AF) is associated with increased risks of stroke, cardiac failure, and mortality. We used a comprehensive proteomics approach matrix-assisted laser desorption/ionization and mass spectrometry imaging (MALDI-MSI) to understand the complex cellular processes and networks in the pathology of AF.

Material and Methods: Left atrial appendage tissue resected routinely during MAZE procedure in surgery were collected of patients with paroxysmal (n = 9, mean age  $69.0\pm3.1$  years), persistent (n = 18, mean age  $67.0\pm2.7$  years), and long-standing persistent (n = 19, mean age  $71.0\pm2.0$  years) arrhythmia. 9 sections of each phenotype were prepared from paraffin blocks and transferred onto Indium-Tin-Oxide slides suitable for MALDI-MSI. Sections were dewaxed and trypsin solutions were applied directly onto the section using an automated spraying device. Spectra were acquired at a mass range of m/z 800-3500Da and lateral resolution of 80  $\mu$ m. Two hundred laser shots were acquired per pixel and random walk of 50/position. Data analyses were performed using SCiLS Lab software.

**Results:** Component analysis of MALDI Imaging data by probabilistic latent semantic analysis results in a clear discrimination in the first 3 components of atrial fibrillation as shown in figure 1. Intensity distribution of given m/z values, which are discriminative for the considered cluster, was determined to distinguish between paroxysmal vs persistent AF (mean,  $4.08\pm1.21$  vs  $1.59\pm0.12$ , p = 0.09), and persistent vs long-persistent AF ( $1.59\pm0.12$  vs  $6.85\pm3.02$ , p = 0.02). Follow-up with case-controlled assessment of neurological events was shown, that persistent AF showed its vulnerability for neurological attacks, compared paroxysmal and long-persistent AF (56% vs 13% and 42%, p = 0.001).

**Discussion:** Tissue-based proteomic approach provides clinically relevant information that may be beneficial in improving risk stratification in AF patients.

## **Biography**

Salah A. Mohamed, Laboratory and Group Leader in Department of Cardiac and Thoracic Vascular Surgery, University Clinic of Schleswig-Holstein, Campus Luebeck in Germany, the group dedicated research interests to aortic and aortic valve diseases, Atrial fibrillation, aging, and biomarker. He has published more than 25 papers in reputed journals and has been serving as an editorial board member of repute.

salah.mohamed@uksh.de

**Notes:**