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HIGH RESOLUTION 2-DE-BASED PROTEOMIC ANALYSIS OF HUMAN ATRIAL FIBRILATION

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Introduction. Atrial Fibrilation (AF) is the most common cardiac arrhythmia found in clinical practice. It is associated with significant mortality and morbidity from stroke, tromboembolism and heart failure. It is caused by chaotic electrical impulses in the atria of the heart and results in a heart rate fast and irregular and loss of coordination between the atria and the ventricles. Our aim is to identify new biomarkers that will allow a better understanding of the molecular factors that trigger AF using high resolution 2-DE to compare the atrial proteome between subjects with AF and controls with sinus rhythm (SR).

Methods. Human atrial appendage tissues from 16 patients that underwent heart surgery with AF or SR were snap frozen in liquid nitrogen. The tissue was homogenized in lysis buffer using a mortar and a pestle. Proteins were precipitated with TCA/Acetone, and separated by 2-DE (500 µg per gel). First dimension was with 24 cm, pH 4-7 IPG strips. Second dimension was by 10% SDS-PAGE. Gels were stained with SyproRuby. Samples were grouped according to the clinical characteristics of the patients. Images corresponding to 8 gels (4 AF and 4 SR) were analysed using Ludesi REDFIN software. Proteins present in spots of interest are identified by MALDI-TOF/TOF.

Results. Our analysis allowed the detection of over 2,000 spots per gel. Following differential image analysis, we found 22 spot differences between the AF and SR group in the 4-7 pI range. The fold change was at least 2, and $p<0.05$ after ANOVA test was applied on normalised spot volumes.

Conclusions. We have standardised sample preparation conditions to achieve high resolution proteome maps of atrial tissue. Proteins identified from the 22 spot differences detected between the AF and the SR groups will be further studied and validated as potential biomarkers for AF.