

**Introduction and objectives:** Malignant pleural effusion (MPE) is a rapidly rising healthcare burden and critically hampers the patients' survival and quality of life. Current treatments aim to palliate symptoms and talc pleurodesis remains a standard therapeutic modality. There is little high quality data in prediction of successful pleurodesis and therapeutic biomarkers are desperately needed.

**Aim:** To identify and validate novel therapeutic biomarkers for successful pleurodesis in MPE.

**Methods:** Clinical data and pleural fluid from MPE patients prior to treatment were prospectively collected as part of the randomised TIME2 trial. Patients were classified based on the treatment outcome (success/failure based on study datasets). Pleural fluid on enrolment (Success n=15, Failure n=11) were assessed with mass spectrometry profiling after depletion of the 12 most abundant proteins. Full protein profile analysed with R software and ELISA technique was performed for the validation of the results.

**Results:** Mass spectrometry identified 1,154 proteins, 97 of which were statistically different (two tailed t-test,  $p < 0.05$ ) between the two groups. The Vascular Cell Adhesion Protein 1 (VCAM1,  $p < 0.001$ ) and Angiopoietin-related protein 4 (ANGPTL4,  $p < 0.01$ ) were constantly overexpressed in the success group. Both proteins are biologically relevant associated with the adhesion and ANGPTL4 is involved in angiogenesis and vascular leakage.

**Conclusions:** Based on a unique biobank and clinical database, we have identified 2 therapeutic biomarkers that may stratify patients' management. These results require validation which is underway using a retrospective (TIME1 trial) and prospective (SIMPLE study) datasets