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A combined proteomic and transcriptomic approach shows diverging molecular mechanisms in thoracic aortic aneurysm development in patients with tricuspid- and bicuspid aortic valve

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Abstract

Aortic aneurysm is one of the major diseases that affect the aorta. The disease involves degradation of the extracellular matrix eventually leading to a dilatation and rupture of the vessel wall, a potentially lethal condition if not treated on time. The focus of present study is thoracic aortic aneurysm (TAA). There are several different etiologies of TAA involving aneurysm associated with bicuspid aortic valve (BAV) disease. TAA is a widespread complication in individuals having BAV disease that is a common congenital disorder present in 1-2% of the population. Studies have indicated that increased susceptibility of aneurysm formation associated with BAV is regardless of the presence or absence of hemodynamically significant valve dysfunction.

In order to better understand the underlying molecular mechanisms of TAA, 2D DIGE gel electrophoresis, LC-MS/MS, and GeneChip Human Exon 1.0 ST Affymetrix arrays followed by multivariate data analysis (MVA) of human biopsies were used in order to investigate proteomic and transcriptomic differences in dilated and non-dilated TAA with BAV and TAV.

Our results show that TAV and BAV patients have diverging protein expression level patterns in dilated and non-dilated aorta tissues. Furthermore, our results suggest that dilatation in TAV and BAV patients has different gene expression and alternative splicing fingerprints. Diverging protein expression and alternative splicing patterns observed between the two valve types indicate that dilatation in patients with TAV has different underlying molecular mechanisms compared with BAV patients.

Biography

Sanela Kjellqvist has completed her Ph.D 2008 at the age of 29 years from Uppsala University and postdoctoral studies 2012 from Karolinska Institutet. She has published 16 papers in reputed journals in the area of protein biochemistry and bioinformatics. Her main research interest is transcriptomics, proteomics and bioinformatics in cardiovascular diseases.