

P12. Transcriptomic Study Of The Myxomatous Mitral Valve Prolapse (MMVP)

Alexia Hulin¹; Charles Lambert¹; Christophe Deroanne¹; Betty Nusgens¹; Alain Colige¹; Marc Radermecker²

¹Laboratory of Connective Tissues Biology, GIGA-Cancer, Liège, Belgium; ²Department of Cardiovascular and Thoracic Surgery, University Hospital of Liège, Liège, Belgium

OBJECTIVES: Degenerative mitral valve is characterized by the bulging of abnormally thickened, redundant mitral leaflet(s) into the left atrium during systole. A long term consequence is a backflow of blood in the left atrium leading to left ventricular enlargement and ultimately heart failure. In the idiopathic myxomatous degeneration the segment P2 of the posterior leaflet is mostly affected. Histologically, it is characterized by an excess of proteoglycans-rich deposits in the spongiosa while the outer layers display collagen and elastic fibers disorganization. In a first approach, the establishment of a profile of selected genes expression is needed for a better understanding of the pathology.

METHODS: Analysis by RT-PCR was performed on a selection of extracellular matrix genes. Myxomatous P2 segments (n=5) were obtained during surgery and normal P2 segments collected from hearts rejected for transplantation (n=6).

RESULTS: Among the 28 investigated genes, the expression of type I collagen and lumican, a small leucine-rich proteoglycan involved in the control of collagen fibers size and stability, was significantly increased in MMVP. The hyaluronan synthase 2, a critical enzyme driving hyaluronan synthesis, was significantly decreased. A similar decrease was observed for CD44, a hyaluronan and collagen receptor and for MMP14, an extracellular matrix degrading enzyme, also involved in MMPs activation and cleavage of CD44.

CONCLUSIONS: These results indicate that the redundant leaflets in MMVP can be related not only to an increased extracellular matrix synthesis but also to a reduction of degradation leading to a proteoglycans accumulation such as versican. Further studies using microarray analysis are in progress.

modified gene expression in MMVP

