

PW2-1

Laser capture microdissection and comparative microarray expression analysis identified vessel-specific molecular markers of the ductus arteriosus and aorta in fetal rats

Bokenkamp R. (1), Van Bremp R. (2), Van Munsteren J.C. (3), van de Wijngaert I. (4), De Hogt R. (4), Finos L. (5), Goeman J. (5), Gittenberger-de Groot A.C. (6), Poelmann R. (3), Blom N.A. (1), DeRuiter M.C. (3)

Departments of Pediatric Cardiology(1), intensive care(2), anatomy and embryology(3), medical statistics and bioinformatics(5), cardiology(6) Leiden University Medical Center, Leiden , The Netherlands and Johnson and Johnson Pharmaceutical Research and Development, Beerse, Belgium

Introduction: Closure of the ductus arteriosus (DA) is a crucial step in the transition from the fetal to the postnatal circulation. Patent DA is one of the most common cardiovascular anomalies in children causing morbidity especially in premature infants. Little is known about the molecular mechanisms regulating the unique remodeling process of the DA.

Objective: We aimed to identify genes that specify the DA in the fetus and differentiate it from the non-closing aorta.

Methods and results: Comparative microarray analysis of laser-captured microdissected endothelial (ECs) and vascular smooth muscle cells (SMCs) from the DA and aorta of fetal rats identified vessel-specific transcriptional profiles. The linear model of microarray analysis (LIMMA) revealed a strong age-dependency of gene expression in the samples from embryonic day 18 and 21. Among the DA-dominant genes the regulator of the G-protein coupled receptor 5 (*RGS5*) and the homeobox transcription factor *DLX1* exhibited the highest and most significant level of differential expression. The aorta showed a significant preferential expression of the Purkinje cell protein 4 (*PCP4*) gene. The results of the microarray analysis were validated by real-time quantitative PCR. Finally, immunohistochemistry at day 21 documented differential expression of the proteins encoded by the three newly identified genes in DA and aorta.

Conclusion: In conclusion, our study confirms a DA and aorta-specific transcriptional profile in ECs and SMCs. For the first time we recognized the preferential expression of *RGS5* and *DLX1* in the fetal DA. These genes may represent novel molecular targets for the regulation of fetal DA maturation and postnatal DA closure.