Transcriptional Profiles in the Chicken Ductus Arteriosus During Hatching

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The ductus arteriosus (DA) of oviparous animals differs from mammals' in the embryonic gas exchange system and its anatomy. We performed transcriptional analysis of chicken DA, attempting to elucidate the similarity and diversity in the mechanism of DA closure among species.

Chicken DA proximal to the pulmonary arteries (proximal DA) closes after hatching while the DA proximal to the aorta (distal DA) remains open even after hatching [1]. Histological analysis revealed that the ductal wall of the proximal DA became thicker with fragmented elastic fibers from embryonic day (ED) 19. Therefore, we performed microarray analysis with proximal DA, distal DA, and aorta from chicken embryo at ED19. Clustering analysis found that the expression pattern of distal DA was similar to that of proximal DA than that of aorta although

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distal DA has a similar structure to aorta. Subsequent pathway analysis with DAVID [2] revealed that proximal DA had enhanced expression of the melanogenetic genes compared with distal DA and aorta (Table 40.1). This result appears reasonable because proximal DA shares its developmental origin, neural crest, with melanocytes. Although several known genes such as transcription factor AP-2 beta (tfap2b) [3] were highly expressed in proximal and distal DA, we newly found proximal-DA-dominant genes. Further investigation would be required to understand the role of these genes in DA closure not only for the chick but also for mammals.

Table 40.1 KEGG pathway analysis by DAVID from chicken DA microarray

Gene symbol	Gene name	Proximal DA/aorta	Distal DA/aorta	Note
Proximal DA dominant pathways				
Melanogenesis/tyrosine metabolism				
DCT	Dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)	1.44∗	1.06	
EDNRB2	Endothelin receptor B subtype 2	1.31∗	1.07	(1)
TYR	Tyrosinase (oculocutaneous albinism IA)	1.54∗	0.94	(1)
TYRP1	Tyrosinase-related protein 1	1.48∗	1.03	
WNT11	Wingless-type MMTV integration site family, member 11	1.33∗	1.14	
Arachidonic acid metabolism				
CYP2C45	Cytochrome P-450 2C45	1.44∗	1.02	
HPGDS	Hematopoietic prostaglandin D synthase	1.56∗	1.02	
PTGS2	Prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	1.31∗	1.21	
DA dominant pathways				
Focal adhesion/ECM-receptor interaction				
FIGF	c-fos-Induced growth factor (vascular endothelial growth factor D)	1.50∗	1.29∗	(2)
KDR	Kinase insert domain receptor (a type III receptor tyrosine kinase)	1.34∗	1.32∗	(2)
LAMA4	Laminin subunit alpha 4	1.33∗	1.24	
LAMB1	Laminin, beta 1	1.36∗	1.27∗	
TNC	Tenascin C	2.15∗	1.82∗	
VWF	von Willebrand factor	1.39∗	1.31∗	
CHAD	Chondroadherin	1.24	1.22∗	
ITGA1	Integrin, alpha 1	1.28	1.21∗	
VEGF signaling pathway				
HSPB1	Heat shock 27kDa protein 1	1.34∗	1.21∗	
KDR	Kinase insert domain receptor (a type III receptor tyrosine kinase)	1.34∗	1.32∗	
PTGS2	Prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	1.31∗	1.21∗	
PLCG2	Phospholipase C, gamma 2 (phosphatidylinositol-specific)	1.17	1.20∗	

The asterisk indicates that the component genes appeared in the result of DAVID analysis
(1) Only appeared in "melanogenesis,"
(2) Only appeared in "focal adhesion"

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