JSPCCS-AHA Joint Session

Sat. Jul 11, 2026 9:10 AM - 10:50 AM JST | Sat. Jul 11, 2026 12:10 AM - 1:50 AM UTC | Room1（Conference Hall A）

[AHAJS] JSPCCS-AHA Joint Session（III-AHAJS）

Basic Science in Congenital Heart Disease: Morphology, Genetics & Molecular Mechanisms

Chair:Antonio Cabrera(The Ohio State University,Nationwide Children's Hospital)

Chair:Yoshihide Mitani(Prinatal Care center, Mie University Hospital)

[III-AHAJS-3] Deciphering the Pathogenesis of Aortic Dissection Through Vascular-Extravascular Cell Interactions

○Hiromi Yanagisawa (Life Science Center for Survival Dynamics, TARA, University of Tsukuba)

Keywords：Aortic dissection、Fibrillin-1、Hereditary thoracic aortic disease

Aortic dissection (AD) is characterized by the separation of medial layers of the aorta following an intimal tear. AD is a major cause of death in patients with connective tissue disorders such as Marfan syndrome, yet the molecular mechanisms underlying its onset and progression remain incompletely understood. Recently, we established a mouse model of AD based on a novel missense mutation in the fibrillin-1 gene (FBN1) identified in a Japanese male patient with familial AD. The corresponding mutation located in the first hybrid domain of Fbn1 was introduced into mice, and vascular pathology was systematically examined in homozygous animals. Approximately 50% of homozygous mice died within 5 weeks after birth due to aortic rupture. Histological analysis revealed endothelial cell activation preceding the massive accumulation of immune cells in the intima. Single-cell RNA sequencing demonstrated a marked increase in macrophage clusters, including MHC class II–positive pro-inflammatory macrophages (M1) at the onset of dissection and CCR2+ bone marrow-derived macrophages with M1- and M2-like phenotypes as AD progressed. In addition, fibrillin-1 expression was decreased in the aortic media, whereas aberrant subendothelial fibrillin-1 expression was increased during the progression. Notably, TGF-β signaling was downregulated in the AD aortas. This novel mouse model recapitulates key pathological features of human AD and provides a unique opportunity to investigate the early pathological events underlying AD.