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Association of miR-196a2, miR-27a, and miR-499 polymorphisms with isolated congenital heart disease in a Chinese population

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ABSTRACT. We hypothesized that single nucleotide polymorphisms (SNPs) in certain microRNAs contribute to congenital heart disease (CHD) phenotypes. Five hundred and seventy-three subjects were enrolled in this study. DNA extracted from peripheral blood cells was used for SNP genotyping of miR-196a2 (rs11614913), miR-27a (rs11671784, rs895819), and miR-499 (rs3746444). Allele and genotype association analyses were performed to evaluate the

correlation between certain microRNA SNPs and three phenotypes of isolated CHD: atrial septal defect (ASD), ventricular septal defect (VSD), and patent ductus arteriosus (PDA). All the participants carried a homozygous CC variant of miR-27a (rs11671784). The homozygous CC variant of miR-196a2 (rs11614913, T>C) was negatively associated with ASD compared with the wild-type TT variant (OR = 0.379, 95%CI = 0.209-0.686, P = 0.001). The miR-196a2 C allele was negatively associated with ASD compared with the T allele (OR = 0.646, 95%CI = 0.491-0.849, P = 0.002). The statistically significant results were further confirmed by dominant and recessive model assays. SNPs of miR-27a (rs895819, T>C) and miR-499 (rs3746444, A>G) showed diverse association with ASD, VSD, or PDA, but the differences were not statistically significant. The rs11614913 (T>C) SNP of miR-196a2 is associated with ASD, and the homozygous CC variant and the C allele are protective factors associated with ASD. The homozygous CC variant and the C allele of the rs11614913 (T>C) SNP of miR-196a2 are associated with a significantly reduced risk of ASD.

Key words: Single nucleotide polymorphisms; Congenital heart disease; microRNA; miR-196a2