Association between \textit{RNF41} gene c.-206 T > A genetic polymorphism and risk of congenital heart diseases in the Chinese Mongolian population

Y. Zhang\textsuperscript{1,2*}, S.Q. Jin\textsuperscript{1*}, W.X. Li\textsuperscript{4}, G.Q. Gao\textsuperscript{5}, K. Zhang\textsuperscript{1} and J.L. Huang\textsuperscript{2}

\textsuperscript{1}Department of Pathophysiology, Baotou Medical College, Baotou, China
\textsuperscript{2}The Central Laboratory, Shenzhen Second People’s Hospital, Shenzhen University First Affiliated Hospital, Shenzhen, China
\textsuperscript{3}Department of Cardiology, The First Affiliated Hospital of Baotou Medical College, Baotou, China
\textsuperscript{4}Department of Pediatric Cardiology, Beijing Anzhen Hospital Affiliated the Capital Medical University, Beijing, China
\textsuperscript{5}Department of Emergency, The Central Hospital of Wulanchabu City, Wulanchabu, China

*These authors contributed equally to this study.
Corresponding author: Y. Zhang
E-mail: susanyuan821@163.com

Received November 18, 2015
Accepted January 18, 2016
Published June 17, 2016
DOI http://dx.doi.org/10.4238/gmr.15028089

ABSTRACT. This study aimed to explore the association between ring finger protein 41 (\textit{RNF41}) c.-206 T > A variant and susceptibility to congenital heart disease (CHD) in the Chinese Mongolian population. The association between \textit{RNF41} gene c.-206 T > A polymorphism and CHD was examined in two independent case-control studies consisting of 219 CHD patients and 208 healthy controls. Genotype was determined by direct sequencing of PCR products. We found that the genotype frequencies of \textit{RNF41} c.-206 T > A differ significantly
between the two groups (P < 0.05). The TT and TA genotypes in the CHD group were 80.67 and 19.33%, respectively. On the other hand, the frequencies of TT and TA in the control group were 94.44 and 5.56%, respectively. Furthermore, the allelic frequencies of CHD patients (T, 90.34%; A, 9.66%) were significantly different as compared with those of non-CHD controls (T, 97.22%; A, 2.78%; \( \chi^2 = 4.031, P = 0.041 \)). Our study demonstrates that the \textit{RNF41} c.-206 T > A polymorphism may be a risk factor for congenital heart disease in the Chinese Mongolian population.

**Key words:** Congenital heart diseases; E3 ubiquitin ligase; Genetic variant; \textit{RNF41}; Mongolian