



Association between functional polymorphisms in the nitric oxide synthase 3 gene and pediatric acute respiratory distress syndrome

L. Wei^{1*}, Y. An^{2*} and J. Wang²

¹Department of Pediatrics, Shaanxi Provincial People's Hospital, The Third Affiliated Hospital of Xi'an Jiaotong University, Xi'an, Shaanxi Province, China

²Pediatric Intensive Care Unit, Xi'an Children's Hospital, Xi'an, Shaanxi, Province, China

*These authors contributed equally to this study.

Corresponding author: J. Wang

E-mail: zhangruiguo98@126.com

Genet. Mol. Res. 15 (3): gmr.15038401

Received January 7, 2016

Accepted June 2, 2016

Published September 16, 2016

DOI <http://dx.doi.org/10.4238/gmr.15038401>

Copyright © 2016 The Authors. This is an open-access article distributed under the terms of the Creative Commons Attribution ShareAlike (CC BY-SA) 4.0 License.

ABSTRACT. Nitric oxide mediates multiple physiological functions, including neurotransmission, immune regulation, angiogenesis, antiplatelet activity, and surfactant maturation or secretion. Mice deficient in the nitric oxide synthase 3 (*NOS3*) gene displayed defective lung vascular development and fatal respiratory distress. Polymorphisms in *NOS3* have been reported to be associated with respiratory distress syndrome (RDS). The role of *NOS3* polymorphisms as a risk factor for pediatric acute respiratory distress syndrome (PARDS) was evaluated by analyzing the possible functional single nucleotide polymorphisms (SNPs) in the regulatory and coding regions of *NOS3*. Samples from 216 PARDS patients and 225 healthy control subjects were genotyped

at 4 SNP loci (rs11771443 and rs3918188 in the promoter region, rs1799983 in exon 7, and rs7830 at the intron24-exon23 boundary). Statistically significant differences were observed in the allelic or genotypic frequencies of the rs1799983 and rs11771443 polymorphisms in *NOS3*. The T and G alleles of rs1799983 and rs11771443 were associated with a significantly higher risk of PARDS compared to the C allele ($P = 0.030$) and the T allele ($P = 0.004$), respectively. Strong linkage disequilibrium was observed in one block ($D' > 0.9$). Subjects with PARDS displayed significantly fewer T-C haplotypes ($P = 0.013$) in block 1 (rs1799983-rs11771443). These findings indicate that *NOS3* polymorphisms play a definitive role in PARDS, and therefore may be useful for future genetic or neurobiological studies on RDS.

Key words: Pediatric acute respiratory distress syndrome; Nitric oxide synthase 3; Single nucleotide polymorphisms