



JMS (ISSN 1682-4474) is an International, peer-reviewed scientific journal that publishes original article in experimental & clinical medicine and related disciplines such as molecular biology, biochemistry, genetics, biophysics, bio-and medical technology. JMS is issued four times per year on paper and in electronic format.

For further information about this article or if you need reprints, please contact:

Mochammad Hatta,
Molecular Biology and Immunology
Laboratory for Infectious Diseases,
Faculty of Medicine,
Hasanuddin University, Makassar,
Indonesia

Tel: +6285299432233

Research Paper

J. Med. Sci., 17 (3): 133-139
July-September, 2017
DOI: 10.3923/jms.2017.133.139

Association of Typhoid Fever Severity with Polymorphisms NOD2, VDR and NRAMP1 Genes in Endemic Area, Indonesia

^{1,2}Ressy Dwiyantri, ¹Mochammad Hatta, ³Rosdiana Natzir,
³Sutji Pratiwi, ^{1,2}Muhammad Sabir, ^{1,4}Yadi Yasir, ¹Rizki Amelia Noviyanthi,
¹Ade Rifka Junita, ^{1,4}Nataniel Tandirogang, ^{1,4}Masyhudi Amir, ¹Matius Fias,
^{1,2}Juhri Saning and ⁵Burhanuddin Bahar

Only small proportions of *Salmonella enterica* serovar Typhi (S. Typhi), in endemic areas, exposing individuals develop typhoid fever symptoms. Identification of polymorphisms NOD2, VDR and NRAMP1 genes is mandatory for a better understanding of typhoid fever molecular pathogenesis and thus to the development of novel strategies for the prevention of infection. The aim of this study was to determine whether genetic polymorphisms in nucleotide oligomerization binding domain 2 (NOD2), vitamin D receptor (VDR) gene and natural resistance-associated macrophage protein 1 (NRAMP1) genes are involved in host susceptibility to severity of typhoid fever. The genotyping of eight regions were applied in the genes; NOD2, VDR and NRAMP1, using PCR-RFLP. A multivariate analysis on 426 mild and 35 severe state of typhoid fever patients. All patients living in the geographically isolated village of South Sulawesi, Middle Sulawesi, Southeast Sulawesi, East Borneo and Papua islands which was an endemic areas in Indonesia. Data were analyzed using Microsoft Excel and Stata 9.2. The G/C and C/C alleles of exon 8 in NOD2 gene were strongly associated and more frequently found in the patients with severe typhoid fever than in mild typhoid fever ($p=0.027$ and 0.014 , odds ratio = 16.7 and 27.9 , 95% confidence interval = $3.4 - 25.7$ and $2.6 - 37.1$ in G/C allele and C/C allele), respectively. In contrast, No evidence for the association of VDR and NRAMP1 genes polymorphisms with severity state of typhoid fever. The polymorphism of exon 8 in NOD2 gene; heterozygotes or homozygotes for a G-C change in codon 2722, was related to susceptibility to typhoid fever in clinical severity of this disease. Polymorphisms of exon 8 in NOD2 gene; heterozygotes or homozygotes for G/C in codon 2722 were related to susceptibility to typhoid fever in clinical severity.

Key words: Nucleotide-binding oligomerization domain 2(NOD2), vitamin D receptor (VDR), natural resistance-associated macrophage protein 1 (NRAMP1), typhoid fever

¹Department of Medical Microbiology, Faculty of Medicine, Molecular Biology and Immunology Laboratory for Infectious Diseases, Hasanuddin University, Makassar, Indonesia

²Department of Medical Microbiology, Faculty of Medicine, Tadulako University, Palu, Indonesia

³Department of Biochemistry, Faculty of Medicine, Hasanuddin University, Makassar, Indonesia

⁴Department of Microbiology and Immunology, Faculty of Medicine, Mulawarman University, Samarinda, Indonesia

⁵Department of Biostatistic and Public Health, Faculty of Public Health, Hasanuddin University, Makassar, Indonesia