

Identify genetic hypomethylation and upregulation of toll-like receptors in Kawasaki disease

Huang Y.H., Li S.C., Kuo H.C.

*Department of Pediatrics and Kawasaki Disease Center, Kaohsiung Chang Gung Memorial Hospital and
Chang Gung University College of Medicine, Kaohsiung, Taiwan*

Introduction: Kawasaki disease (KD) is an acute febrile systemic vasculitis of childhood characterized by profound elevated levels of proinflammatory and inflammatory cytokine. Toll like receptors (TLRs) act as the sensor arm of the innate immune system and induce proinflammatory cytokine expressions. The aim of this study is to survey TLR1-10 in different stages of KD and controls.

Methods: A total of 18 KD patients including before intravenous immunoglobulin (IVIG), at least 3 weeks after IVIG treatment, 18 health and 18 febrile controls were enrolled for survey. GeneChip® Human Transcriptome Array 2.0 was used with 6 cases pooling methods and Infinium HumanMethylation450 BeadChip Kit to evaluate methylation patterns of CpG markers on TLRs.

Results: KD patients showed significantly differential expression of mRNA levels of TLRs compared to health and febrile controls, while only TLR 3 and 7 were not different between KD patients and controls. After IVIG treatment, the mRNA levels of TLRs except TLR3 were significantly down-regulated in the KD patients. On the contrary, the methylation status of CpG sites of TLR1, 2, 4, 6, 8, 9 demonstrates reverse tendency between two stage of KD samples and controls.

Conclusion: TLRs especially TLR1, 2, 4, 6, 8, 9 may involve in the immunopathogenesis of KD. These results provide first evidences by TLRs that a bacterial-like inflammatory response play important role in KD.