NOD2/CARD15 variants in Malaysian patients with sporadic colorectal cancer

Abstract

Colorectal cancer (CRC) is one of the most common types of cancer in both developed and developing countries. This disease is triggered by and progresses via the sequential accumulation of multiple genetic alterations. In addition, the interaction between low-penetrance genes and environmental factors can also increase the risk of developing CRC. Since inflammatory bowel diseases (IBDs) are one of the predisposing factors for CRC, IBD-related genes might, to a certain extent, be associated with cancer initiation. The nucleotide oligomerization domain 2/caspase activating recruitment domain 15 gene (NOD2/CARD15) is the most well-established gene to be associated with increased susceptibility to Crohn's disease. Thus, various studies have been performed to investigate the potential contribution of this gene to CRC risk. In this study, we aimed to determine the frequency of the Arg702Trp, Gly908Arg, 3020insC, Pro268Ser, and JW1 variants of NOD2/CARD15, and to investigate their association with CRC susceptibility. A total of 130 CRC patients and 212 healthy controls were recruited for this study. Subsequently, real-time polymerase chain reaction with TaqMan was performed for the genotyping of these NOD2/ CARD15 variants. None of the NOD2/CARD15 variants was statistically associated to CRC susceptibility in our Malaysian population. Our findings were remarkably similar to those of other Asian cohorts, which indicated that these NOD2/CARD15 variants exhibit genetic heterogeneity between Caucasian and Asian populations.