

The Distribution of HLA-C* 14:02 Allele in Thai Population to See Risk Factors for Severe COVID-19

Authors : Naso Isaiah Thanavisuth, Patompong Satapornpong

Abstract : Introduction: Covid-19 has been a global pandemic for some time now, causing severe symptoms to patients that received the virus. However, there has been no report on this gene in the Thai population. Objective: Our aim in this study is to explore and compare the frequency of HLA-C allele that is associated with severe COVID-19 symptoms in Thais and other populations. Method: 200 general Thai population were enrolled in this study. The genotyping of HLA -C alleles were determined by the polymerase chain reaction with sequence-specific oligonucleotide probes (PCR-SSOP) and Luminex®IS 100 system (Luminex Corporation, Austin, Texas, USA). Results: We found that the frequency of alleles HLA-C* 01:02 (16.00%), HLA-C* 08:01(10.50%), HLA-C* 03:04 (10.25%),HLA-C* 07:02 (10.00%), HLA-C* 03:02 (9.25%), HLA-C* 07:01 (6.75%), HLA-C* 04:01 (5.00%), HLA-C* 06:02 (4.00%), HLA-C* 04:03 (4.00%), and HLA-C* 07:04 (3.75%) were more common in the Thai population. HLA-C* 01:02 (16.00%) allele was the highest frequency in the North, Center, and North East groups in Thailand, but there was the South region that was not significantly different when compared with the other groups of the region. Additionally, HLA-C*14:02 allele was similarly distributed in Thais (3.00%), African Americans (1.98%), Caucasians (2.08%), Hispanics (1.71%), North American Natives (1.34%) and Asians (5.01%) by p-value = 0.6506, 0.6506, 0.6506, 0.6135 and 0.7182, respectively. Conclusion: Genetic variation database is important to identify HLA can be a risk factor for severe COVID-19 in many populations. In this study, we will support the research of the HLA markers for screening severe COVID-19 in many populations.

Keywords : HLA-C * 14:02, COVID-19, allele frequency, Thailand

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