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During the 2009 H1N1 pandemic patients with severe illness were found in many countries around the world. This study was conducted to determine if an individual's HLA class I and class II genotype is associated with the severe response to H1N1 infection. A total of 76 patients were recruited from multiple hospital ICUs from across Canada. Genomic DNA was isolated from patients and HLA class I and II genes were amplified using gene specific primers. A sequence-based genotyping method was to genotype HLA class I and class II genes using CodonExpress, a computer software program. The frequencies of HLA class I and class II alleles in the ICU patients were compared with general population allele frequencies in the MHC database using SPSS 13.0. The frequency of DRB1*04:07:01, DRB1*08:02:01, B*51:01:01, and C*15:02:01 of ICU H1N1 positive aboriginal patients was much higher than in the H1N1 negative aboriginal patients. DRB1 and DQB1 homozygotes were significantly higher in the H1N1 positive individuals when compared to the H1N1 negative individuals. This information may aid in identifying high risk groups in future influenza pandemics.

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Analysis of HLA class I and class II antigens of ICU patients with severe response to H1N1 infection in the 2009 H1N1 pandemic

Chris Czarnecki National Microbiology Laboratory, Canada