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Frequencies of KIR3DL1/S1 and their cognate HLA-B Bw4 ligands in H1N1/09 ICU patients

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Influenza A (H1N1/09) pandemic flu virus caused an onset of cases late into the first quarter of 2009 and a subset of patients were found to develop severe illnesses in many countries around the world. Natural Killer (NK) cells play an important role in the innate immune responses, as part of the first line of defense to infectious pathogens, by destroying virally-infected cells. NK cell activation and function depend on a broad array of receptors, such as the Killer-cell receptors (KIR) and their interactions with specific HLA class I molecules. KIR genes are highly polymorphic. Given the independent genetic diversities of KIR and HLA genes, there likely exist combinations of KIR/HLA that can variably influence the efficacy of NK cell response towards the control of viral loads. In the study, we genotyped 51 H1N1/09 intensive-care unit (ICU) patients with severe cases of H1N1/09 infections and 105 uninfected aboriginal individuals. We found an increased proportion of KIR3DL1/S1-Bw6 homozygotes pairings overall among ICU patients, in addition to several specific KIR3DL1 alleles that were highly prevalent. Relative to world populations of similar ethnic background (Venezuelan Amerindians (VA) and worldwide Caucasians (CA)), speculative differences were found among various KIR3DL1/S1 alleles. 3DL1*00101 was enriched among ICU aboriginals (P=8.4x10^{-10}, Pc=6.7 x10^{-9}) and 3DL1*00401 (P=2.6x10^{-5}, Pc=3.6 x10^{-4}) was enriched in ICU non-aboriginals. Overall, our results also indicate a large proportion of null KIR3DL1/S1 and HLA-B interactions exist among H1N1/09 ICU patients and a disproportionate pattern of KIR3DL1/S1 allele distribution.