ORT.30 - The rs12252C polymorphism in the human *IFITM3* gene has no association with severity of influenza A(H1N1)pdm09 infection in Brazilian patients

Jéssica Santa Cruz de Carvalho Martins[1]*; Cristiana Couto Garcia[1]; Marilda M. Siqueira[1]; Aline da Rocha Matos[1].

1Fiocruz/IOC.

Introduction: Respiratory infection caused by the influenza virus continues to exacerbate morbidity and mortality rates worldwide. The group of young immunocompetent adults were severely affected during the 2009 influenza A(H1N1)pdm09 pandemic. Therefore, it is necessary to understand host factors that are associated with the severity of this infection. Interferon induced transmembrane protein 3 (IFITM3) is produced during the activation of innate immunity in response to viral infections. This protein, in influenza, prevents the fusion of the viral membrane with the host endosome membrane, interfering in the release of viral genetic material into the cytoplasm of the infected cell. The rs12252C SNP in the *IFITM3* gene results in the deletion of 32 amino acids, generating a truncated protein, which has been associated with worse clinical outcomes during influenza infection.

Objective: Our aim was to investigate the rs12252 SNP frequency in Brazilian influenza A (H1N1)pdm09 samples and its correlation with the severity of the infection.

Methodology: There were investigated 341 respiratory samples positive for influenza A(H1N1) pdm09, classified according to their symptoms in influenza like illness (ILI, n=118) and severe acute respiratory infection (SARI, n=223) cases. Genomic DNA was extracted and genotypes for rs12252C were determined using the 5' nuclease assay (TaqMan®). PCR amplification was carried out on 5-20ng DNA using 1X TaqMan® universal PCR master mix. TaqMan® assays were ordered using the Thermo Fisher assays-on-demand service. The samples were separated into 3 clusters: allele 1homozygous (TT); heterozygous (TC); and allele 2 homozygous (CC).

Results: The different clinical groups presented similar distribution of TT, CT and CC genotypes and T or C allele frequencies. Additionally, we did not observe any association between the genotypes and clinical symptoms associated with influenza complications, as dyspnea, respiratory distress and oxygen saturation <95%. Interestingly, the distribution of the allele C was higher in samples from Brazilian South region, but there was no association with the presence of C allele and disease severity in the samples from this region.

Conclusion: The rs12252C SNP in the *IFITM3* gene does not influence the susceptibility to influenza A (H1N1) pdm09 severe disease or mortality in individuals from Brazil.

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