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Ana Filipa Maia Rodrigues
Fernando Pessoa University, Portugal

Co-Authors

AM. Santos, R. Marino, AM. Ferreira,
ME. Barreira and JM. Cabeda
Fernando Pessoa University, Portugal

Rhinovirus infection is influenced by polymorphisms in the immune system related genes TOLLIP and IL6

Rhinovirus are picornavirus with over 150 serotypes and 3 species. Although usually causing common colds, in Asthma, COPD and elders it may cause life-threatening disease. Both environmental and genetic susceptibility factors may play a role in rhinovirus epidemiology.

In the present study we evaluated the influence of immune-system related genetic variations (TOLLIP rs5743899, IL6 rs1800795, IL1B rs16944, TNFA rs1800629) in the modulation of rhinovirus infection susceptibility.

Blood samples and monthly nasal swabs were collected from 89 volunteers. DNA and RNA were purified with Qiagen column based kits. Viral RNA was quantified by RTqPCR on Lightcycler 1.1 (Roche). Polymorphisms were genotyped by PCR-RFLP.

TOLLIP and IL6 polymorphisms (but not IL1B and TNF) were found to influence rhinovirus nasal detection. TOLLIP-G individuals were more often year-long rhinovirus free ($p < 0.048$). Additionally, if TOLLIP-G individuals were excluded from analysis, non-IL6-C individuals showed higher rhinovirus titers ($p < 0.028$). This fully agrees with molecular mechanisms as free Rhinovirus particles, are detected by TLR2 which is inhibited by TOLLIP. TOLLIP-G decreases TOLLIP expression, increasing TLR2 and protecting from Rhinovirus infection. TOLLIP G also sustains production of IL6 needed for viral clearance post-infection. However, in the absence of the TOLLIP G allele, and of the IL6-C allele there is low IL6 production leading to a poorer Immune response and higher viral titers.

31035@ufp.edu.pt

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