03.01 - Molecular pathology and functional genomics

# 29294
# Genetic risk for covid-19 outcomes in COPD

Genomics, Mutations, Viruses

**R. Marçalo[1], S. Neto[1], M. Pinheiro[1], A. Rodrigues[2], N. Sousa[2], M. Santos[3], P. Simão[4], C. Valente[5], L. Andrade[5], A. Marques[6], G. Moura[1]**

**[1]Genomics Lab, Department of Medical Sciences & iBiMED, University of Aveiro - Aveiro (Portugal), [2]Life and Health Sciences Research Institute (ICVS), School of Medicine, University of Minho - Braga (Portugal), [3]iBiMED, Department of Medical Sciences, University of Aveiro - Aveiro (Portugal), [4]Pulmonology Department, Unidade Local de Saúde de Matosinhos - Porto (Portugal), [5]Pulmonology Department, Centro Hospitalar do Baixo Vouga - Aveiro (Portugal), [6]Lab 3R - Respiratory Research and Rehabilitation Laboratory, School of Health Sciences, University of Aveiro (ESSUA) - Aveiro (Portugal)**

There is strong individual variability in both susceptibility and clinical response to covid-19 infection. People with chronic obstructive pulmonary disease (COPD) constitute one of covid-19 risk groups for poor outcomes upon infection. This study contributes to unveil the underlying reasons for such outcomes by looking at the genetic background of people with COPD.

255 people with COPD (66±9y; 72%♂; FEV1 53.01±20.31pp) and 243 controls (67±10y; 80%♂; FEV1 100.46±19.19pp) were clinically characterized and genotyped using saliva samples. Covid-19 associated SNPs from the literature (susceptibility: rs286914/rs12329760; severity: rs657152/rs11385942) were assessed and their allelic frequencies used to calculate the probability of having multiple risk alleles in both groups. Polygenic risk analysis was also conducted.

No differences in genetic risk for covid-19 susceptibility or severity were found between groups (all p-values > 0.01), either considering individual risk alleles, allelic combinations or polygenic risk scores (Fig. 1).

These results suggest a low genetic contribution for the poor covid-19 outcomes observed in people with COPD.

This work was supported by FEDER (Fundo Europeu de Desenvolvimento Regional) funds through the COMPETE 2020, Operational Programme for Competitiveness and Internationalization (POCI), and by Fundação para a Ciência e a Tecnologia, I.P. (FCT) under the projects PTDC/DTP-PIC/2284/2014; PTDC/BIA-MIC/31849/2017 and UIDP/04501/2020.

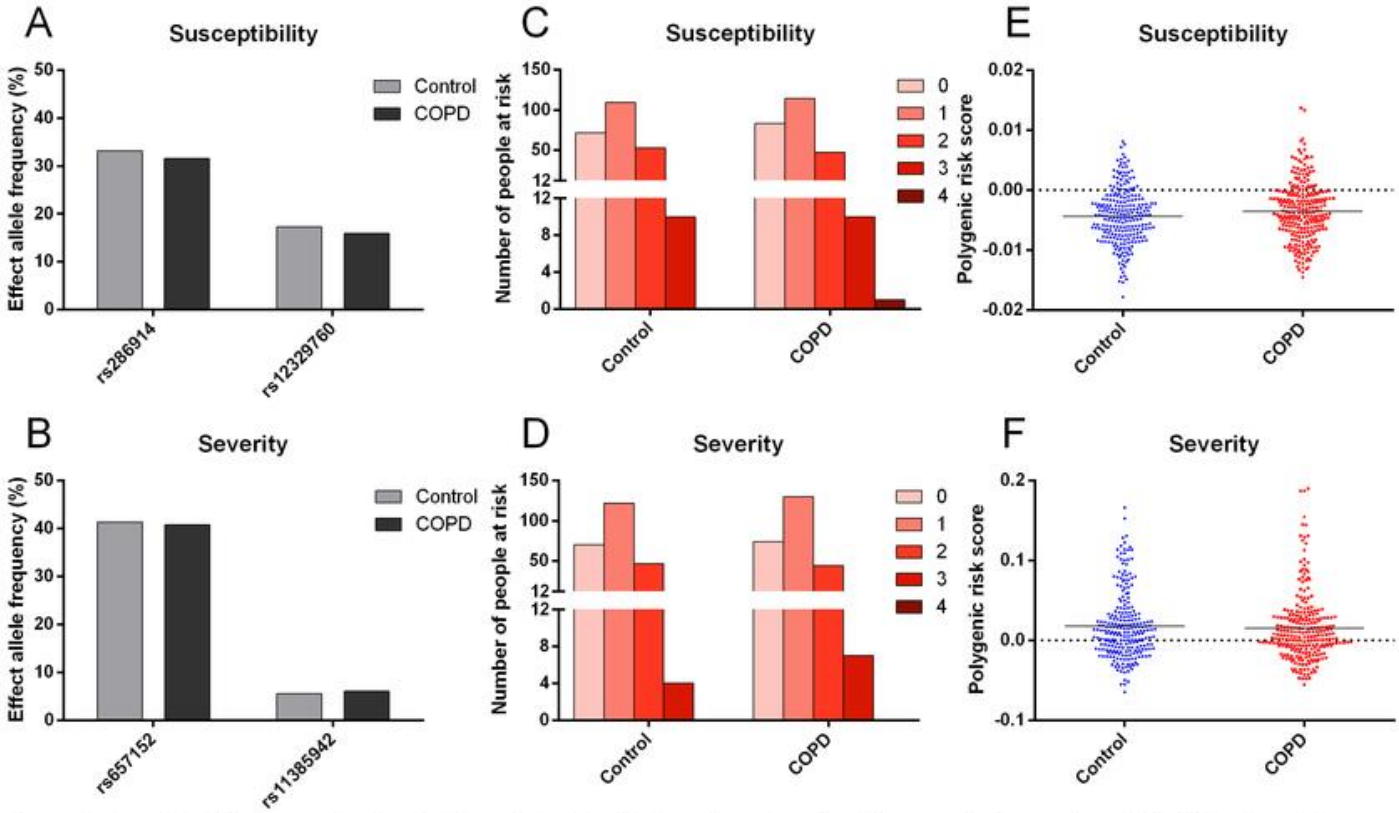


Figure 1 - A and B: Allele frequencies for significant SNPs; C and D: Number of people with a cumulative number of risk alleles; E and F: Polygenic risk assessment. Top panel (A/C/E): genetic risk for covid-19 susceptibility; bottom panel (B/D/F): genetic risk for severe covid-19. 0 to 4: sum of effect alleles for each covid-19 outcome.