Genetic risk for COVID-19 outcomes in COPD and differences among worldwide populations

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People with chronic obstructive pulmonary disease (COPD) constitute one of COVID-19 risk groups for poor prognosis upon infection. Variability in predisposition and clinical response to COVID-19 exist but our understanding of these factors in the COPD population is limited. This study explored the genetic background as a possible answer to COVID-19 infection response heterogeneity, either for the poor prognosis in people with COPD or across healthy worldwide populations.

Significant SNPs (susceptibility: rs286914/rs12329760[1–3]; severity: rs657152/rs11385942[4]) were selected from the literature and their allelic frequencies[5,6] used to calculate the probability of having multiple risk alleles in both our COPD cohort and each worldwide population. A polygenic risk analysis was conducted in the COPD cohort for the two mentioned phenotypes, and for hospitalization and survival to COVID-19 infection.

No differences in genetic risk for COVID-19 susceptibility, hospitalization, severity or survival were found between people with COPD and the control group (all p-values>0.01), either considering risk alleles individually, allelic combinations or polygenic risk scores. Alternatively, all populations, even those with European ancestry (Portuguese/Spanish/Italian), showed significant differences from the European population in genetic risk for COVID-19 susceptibility and severity (all p-values<0.0001).

Our results indicated a low genetic contribution for COVID-19 infection predisposition or worse outcomes in people with COPD. Also, our study unveiled a high genetic heterogeneity across major world populations for the same alleles, even within European subpopulations.

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