DECIPHERING COPD AS A RISK GROUP FOR COVID-19: CAN WE BLAME GENETICS?

Rui Marçalo, PhD student
Department of Medical Sciences, University of Aveiro
Contact: ruifilipemarcalo@ua.pt

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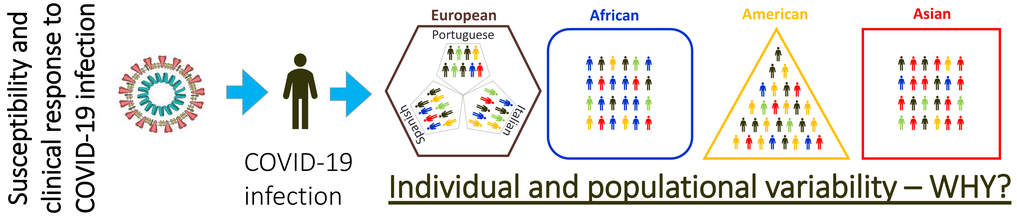
Marçalo, R.[1, 2], Neto, S.[1], Pinheiro, M.[1], Rodrigues, A.J.[3], Sousa, N.[3], Santos, M.A.S.[1], Simão, P.[4], Valente, C.[5], Andrade, L.[5], Marques, A.[2], and Moura, G.R.[1] gmoura@ua.pt

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

Background

- Chronic obstructive pulmonary disease (COPD) is associated with a poor prognosis upon COVID-19 infection[1].
- High populational variability observed in COVID-19 related outcomes[2].



Aim

- To explore the genetic background as a possible contributor to COVID-19 infection response heterogeneity, either for the poor prognosis in people with COPD or across healthy worldwide populations.

Methods

Identification of COVID-19 associated genetic variants (susceptibility and severity)[3-5]

Assessment of risk allele frequency (Portuguese cohort genotyping and online databases)[6, 7]

Computation of bi-allelic risk scores and polygenic risk scores

Statistical analyses

SNPs associated with susceptibility to COVID-19 infection: rs286914 and rs12329760.
SNPs associated with severe COVID-19 with respiratory failure: rs657152 and rs11385942.

Results

- We found no differences in genetic risk for COVID-19 susceptibility or severity between people with COPD and the control group (all p-values > 0.01) (figure 1);
- Every population showed a significant difference from the European population in both genetic risk for COVID-19 susceptibility and severity (all p-values < 0.0001) (figure 2).

Table 1. Sociodemographic, anthropometric and clinical characteristics of participants.

Characteristics	Baixo Vouga cohort		Portuguese cohort
	COPD (n=255)	Control (n=243)	Control + Minho (n=623)
Age (years)	68 [61, 74]	67 [60, 72]	66 [58, 72]
Gender (Male), n (%)	203 (79.61%)	176 (72.43%)	359 (57.62%)
Body mass Index (Kg/m²)	25.97 [23.44, 29.73]	27.32 [24.91, 29.75]	27.53 [25.08, 30.22]
FEV_1 (Litres)	1.32 [0.94, 1.81]	2.58 [2.11, 3.06]	n.d.
FEV_1/FVC	53.02 [41.24, 61.94]	83.90 [78.01, 89.02]	n.d.

N (%) - number of individuals and corresponding percentage; remaining data is presented as medians with interquartile range in square brackets. FEV1 - Forced Expiratory Volume in 1-sec in litres; FVC - Forced Vital Capacity in litres; n.d. - no data available.

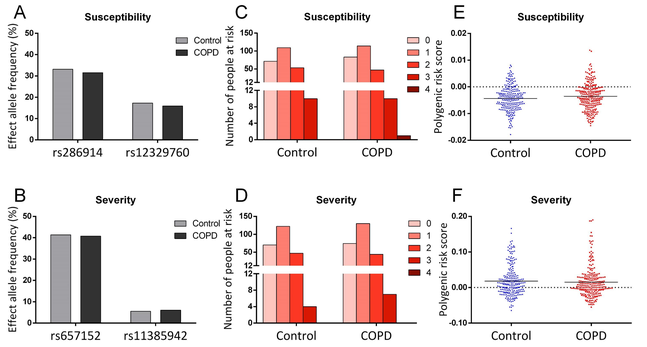


Figure 1. A and B: Allele frequencies for significant SNPs; C and D: Number of people with a cumulative number of risk alleles; E and F: Polygenic risk assessment. Top panel (A/C/E): genetic risk for COVID-19 susceptibility; bottom panel (B/D/F): genetic risk for severe COVID-19. 0 to 4: sum of effect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

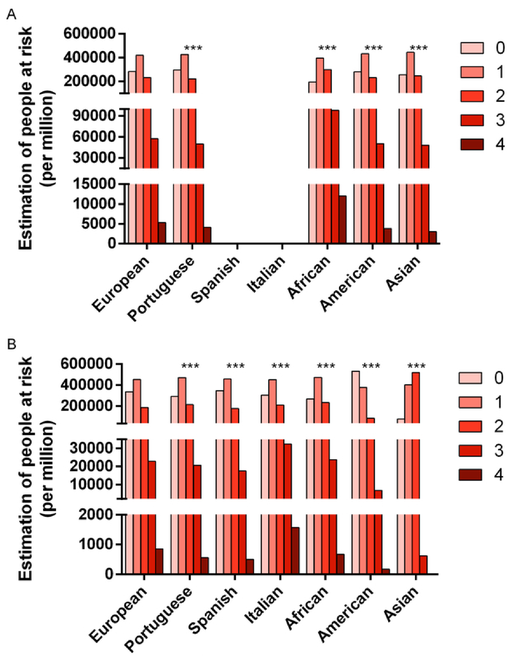


Figure 2. Estimation on the number of people with a cumulative number of risk alleles in the world major populations for A - susceptibility for COVID-19 infection (rs286914 + rs12329760) and B – severe COVID-19 with respiratory failure (rs657152 + rs11385942). 0 to 4 represent the sum of effect alleles for each COVID-19 associated phenotype. ***: p-value<0.0001. Statistical analyses were performed using the European population as reference.

Conclusions

- Low genetic contribution for COVID-19 infection predisposition or severe COVID-19 in people with COPD.
- High genetic heterogeneity across worldwide populations for the same alleles, even in ancestry sharing populations as Portuguese, Spanish and Italian populations (all European subpopulations).

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Acknowledgements

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