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The worldwide covid-19 genetic risk scenario

Genomics, Mutations, Viruses

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Populations respond differently to the current global pandemic of covid-19. This study explores the role of individual factors in the differential response to covid-19, by looking at the genetic background of worldwide populations.

Significant SNPs (susceptibility: rs286914/rs12329760; severity: rs657152/rs11385942) were selected from the literature and their allelic frequencies used to calculate the probability of having multiple risk alleles in each population. Portuguese (n=623), Spanish (n=9761) and Italian (n=6363) populations data are observed values, whereas data for world populations are estimations based on public information.

All populations, even those with European ancestry (Portuguese/Spanish/Italian), were significantly different from the European population in both covid-19 susceptibility and severity (all p-values < 0.0001)(Fig. 1).

Our study highlights a genetic heterogeneity across world populations, especially within European subpopulations. There is a need to build a European genetic map so that differences in the distribution of relevant alleles can be easily accessed and used to better manage the populations, ultimately, safeguarding those under higher genetic risk.

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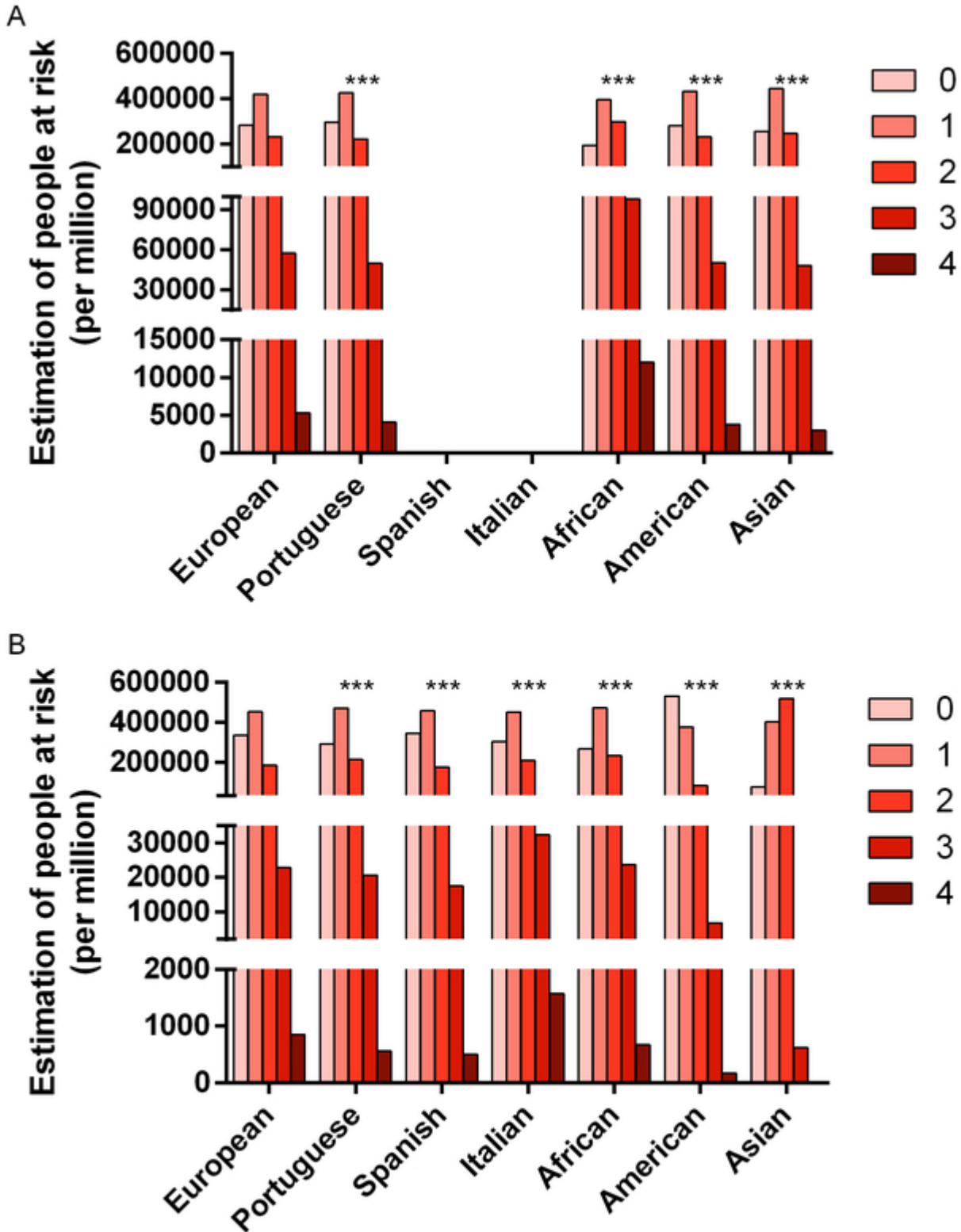


Figure 1 Estimation on the number of people with a cumulative number of risk alleles in the world major populations for A - susceptibility to covid-19 infection (rs286914 + rs12329760) and B – severe covid-19 with respiratory failure (rs657152 + rs11385942). 0 to 4 represents the sum of effect alleles.***: p-value<0.0001. Statistical analyses were performed using European population as reference.

