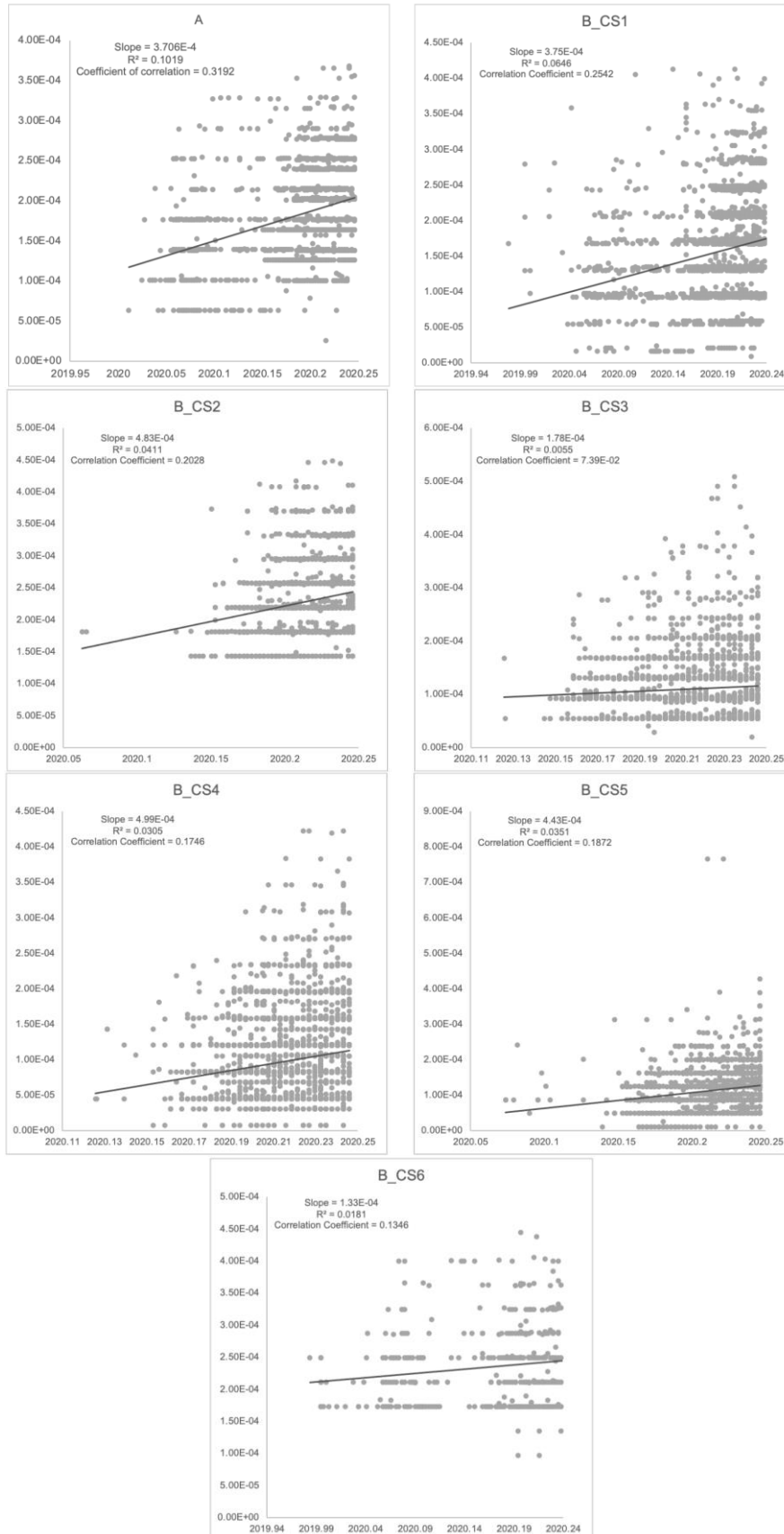
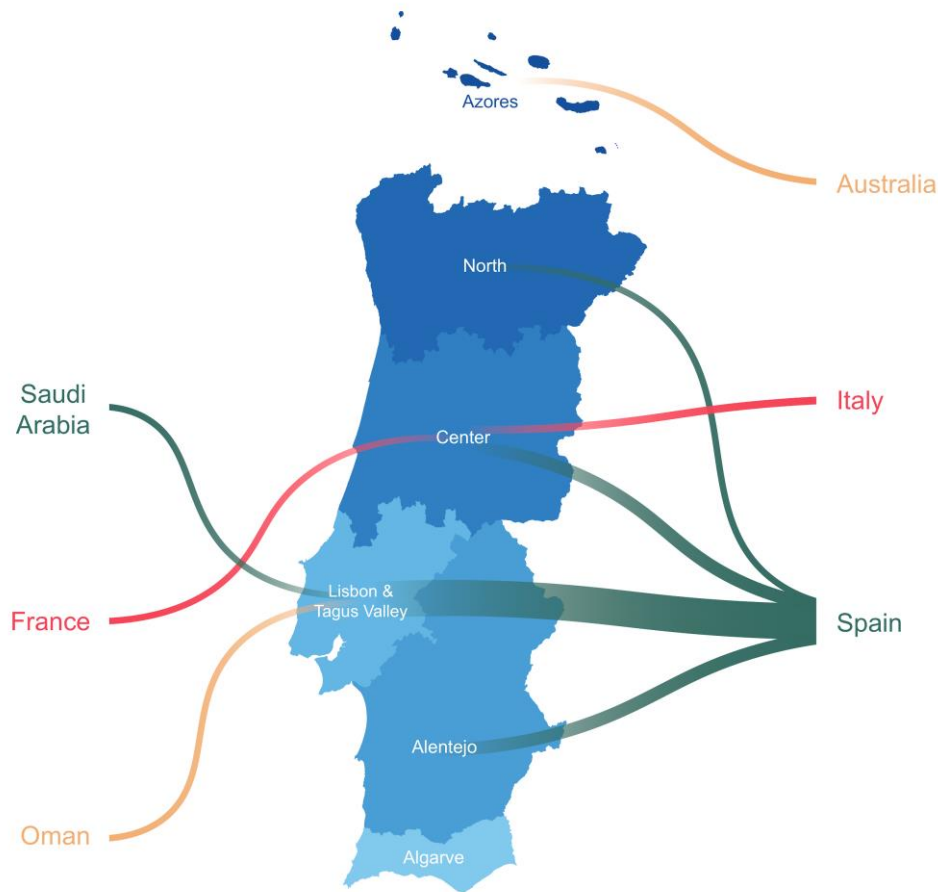


Supplementary Material

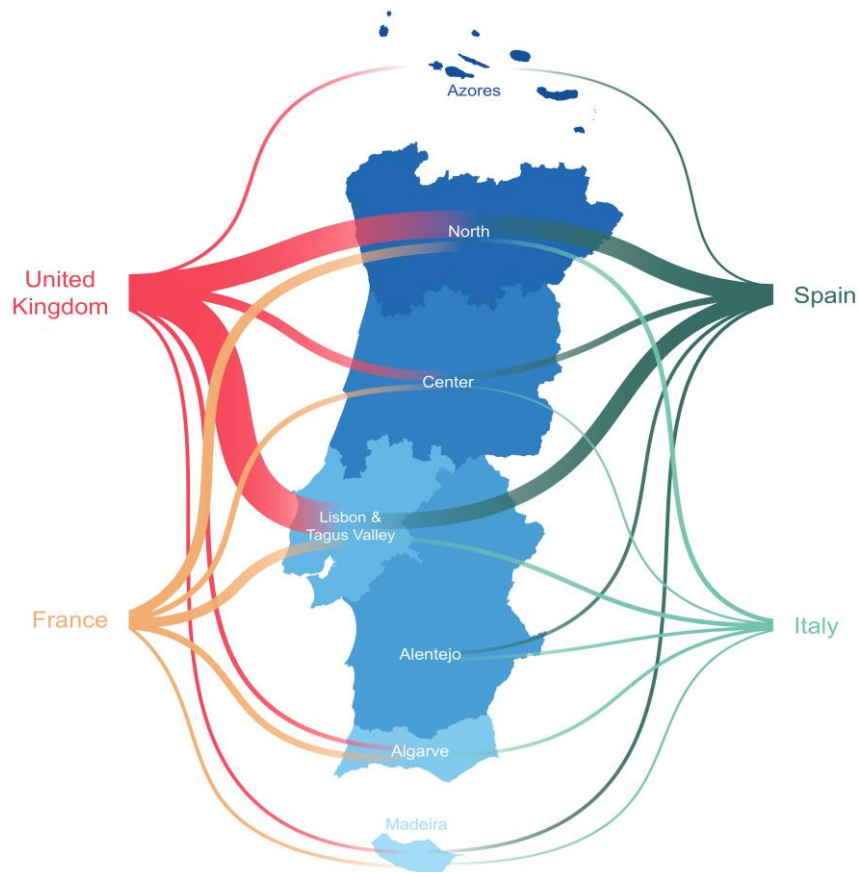
Supplementary Figures



Supplementary Figure 1. Root-to-tip regression analyses. Plots of the root-to-tip genetic distance against sampling time are shown for phylogenies estimated from alignments of datasets A, and BCS_1 to BCS_6.



Supplementary Figure 3. Map summarizing the viral gene flow of Pango lineage A into Portugal Health Administration Regions. The map shows the relative number of transitions between countries of origin and different regions in Portugal. Specifically, the line width represents the relative proportion of viruses seeded into a given Portuguese Health Administration Region by various countries, estimated across phylogenies inferred for Pango lineage A (thin – low proportion of viral introductions attributed to this source; thick – high proportion of viral introductions attributed to this source). We note that there is no temporal order for the transitions involved. For summaries that show all transitions to and from all connected locations for lineage A viruses, we refer to the Supplementary Table 6.



Supplementary Figure 4. Map summarizing the viral gene flow of Pango lineage B into Portugal Health Administration Regions. The map shows the relative number of transitions between countries of origin and different regions in Portugal. Specifically, the line width represents the relative proportion (>0.9%) of viruses seeded into a given Portuguese Health Administration Region by various countries, estimated across phylogenies inferred for Pango lineage B (thin – low proportion of viral introductions attributed to this source; thick – high proportion of viral introductions attributed to this source). We note that there is no temporal order for the transitions involved. For summaries that show all transitions to and from all connected locations for lineage B viruses, we refer to the Supplementary Table 7.