

Figure 1: MST based on all spoligotypes in SITVIT2 (n = 103 856). Separations between the nodes represent the number of different sub-regions shared by a given spoligotype pattern. Please note that the number indicating the size of each phylogenetic lineage should be considered according to the different sub-regions and distinct patterns of spoligotyping. This number does not represent the total number of strains contained in a given lineage.

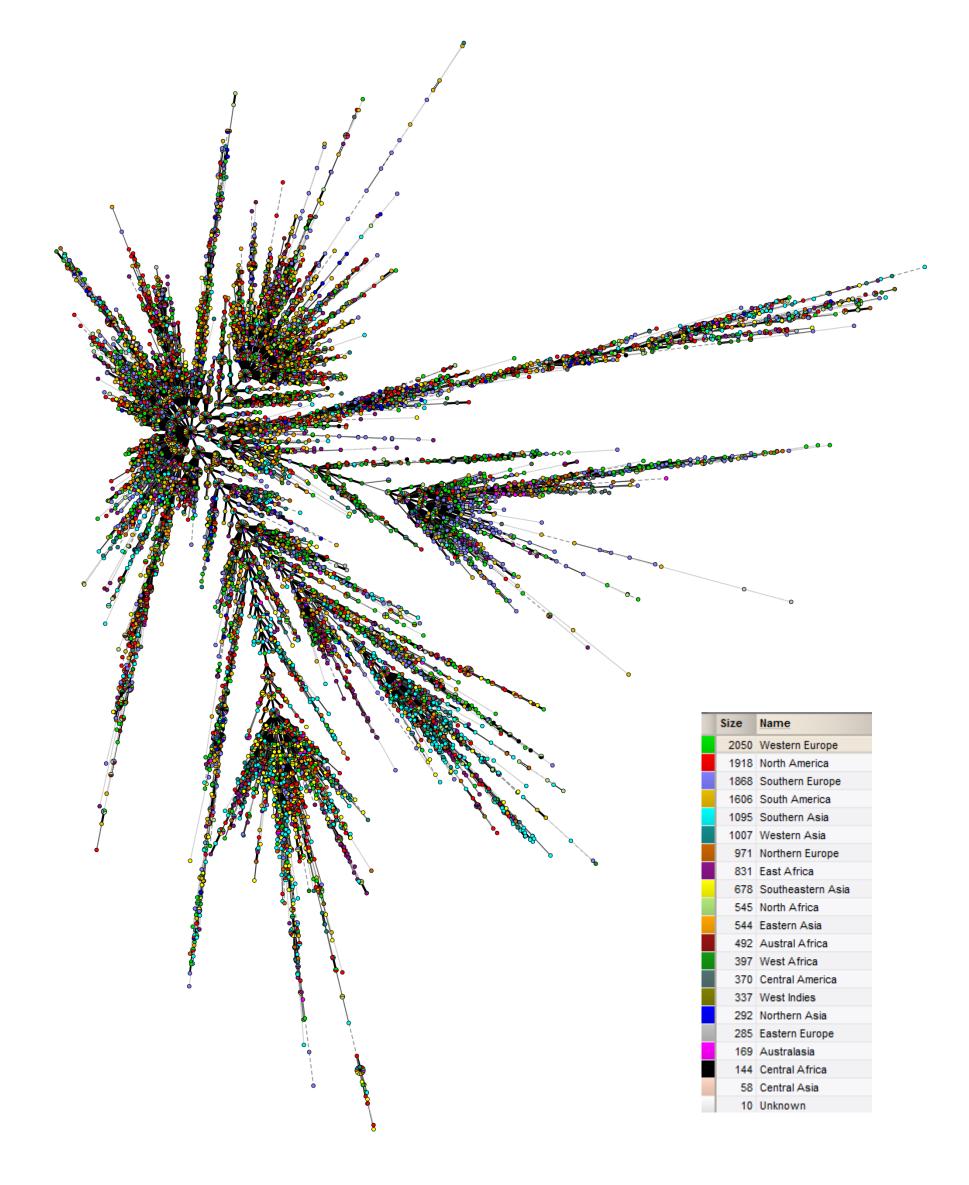


Figure 2: Same MST as in Figure 1, but representing the sub-regions instead of the lineages.