

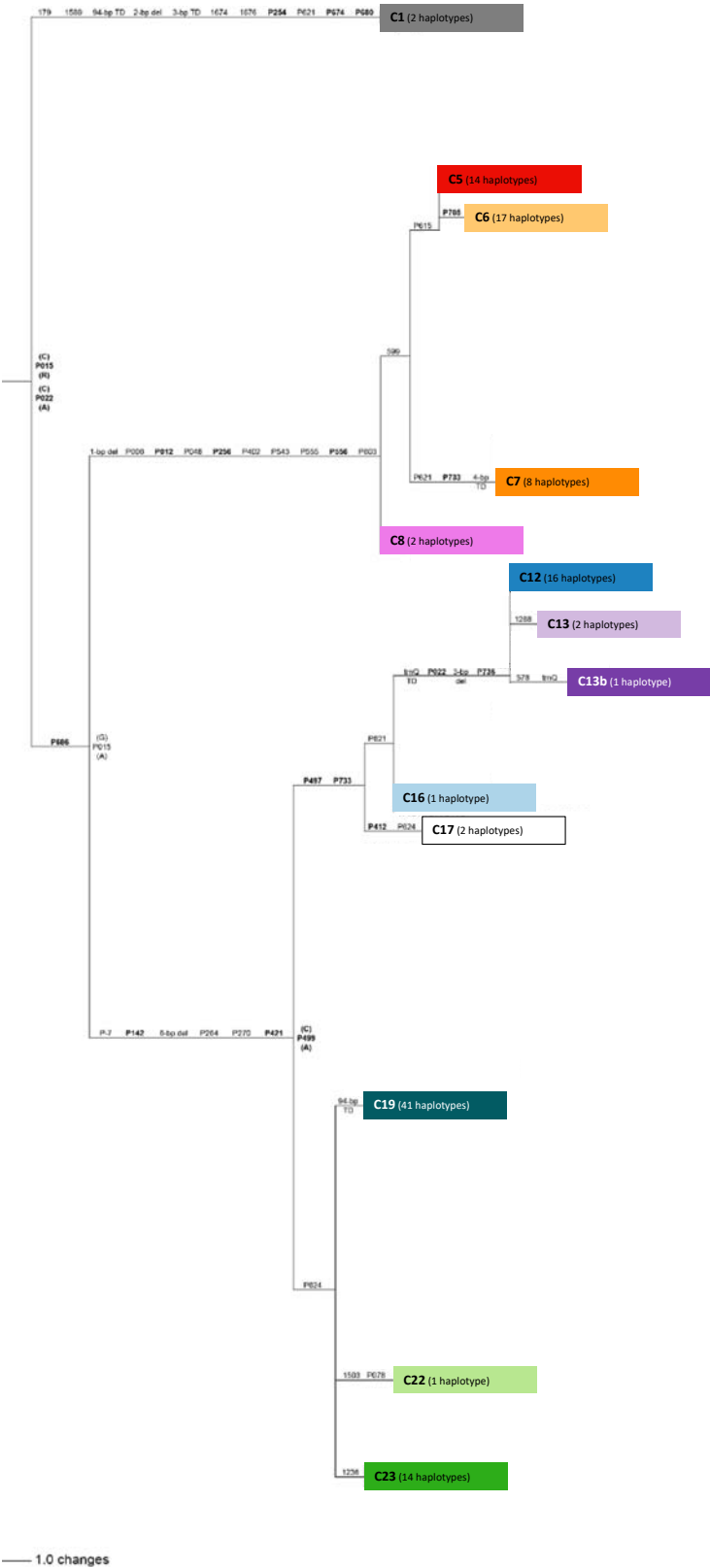


Figure S2. Phylogenetic analysis of all complete haplotypes. Characters represented by numbers indicate the position of point mutations in the multiple sequence alignment. Numbers preceded by a 'P' indicate the position of point mutations in *orf262*. Negative numbers preceded by a 'P' indicate the position of point mutations in positions upstream of *orf262*. Point mutations that cannot be unambiguously polarized with the current data are placed at the respective nodes, with the alternative nucleotide character states in the branches above and below those nodes shown in parentheses. (bp = base-pair; CE = concerted evolution; del = deletion; TD = tandem duplication.)