Phylogenetic distances between HSV1 genomes
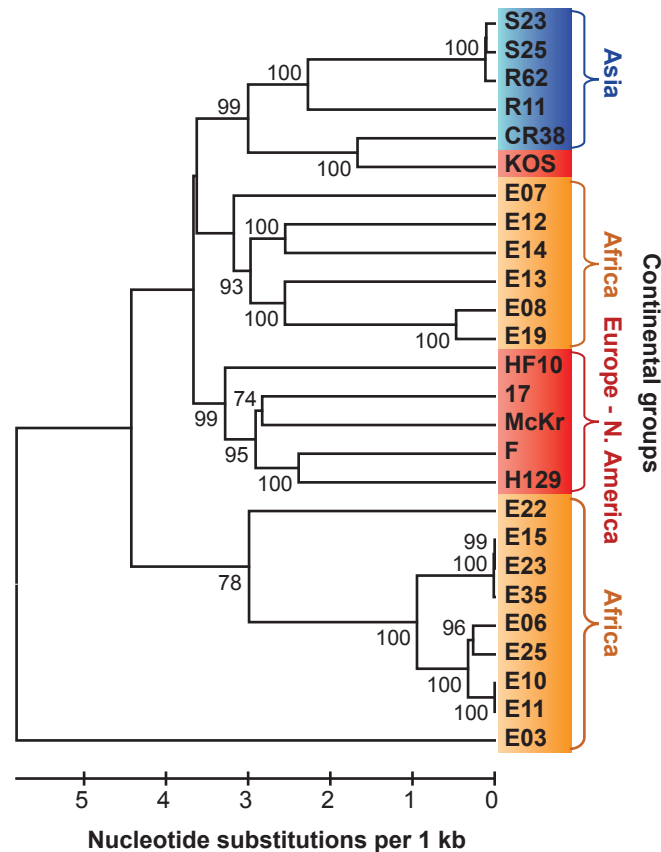
Figure 8. Dendrogram of genetic distances among HSV-1 genomes reveals broad geographic clustering.
The multiple-genome alignment of 26 strains of HSV-1 was used to generate a genetic distance matrix under a Maximum Composite Likelihood substitution model. A dendrogram was then calculated using UPGMA in MEGA, with 1000 bootstrap replicates. The majority of strains cluster into four groupings that reflect their geographic origins, with the large collection of African strains splitting into two groups or potentially three groups (i.e., E03 as a third singleton group).

Szpara *et al.* (2013) JVI. Evolution and diversity in human herpes simplex virus genomes.