



Figure 1. This phylogenetic tree was constructed from the complete Lentivirus genome alignment. Columns in the alignment for which any sequence is represented by a gap were first removed. The tree was constructed using PHYLIP DNADIST with maximum likelihood distance estimation and a transition/transversion ratio of 1.6. The DNADIST output was then used to create a neighbor-joining tree using the WEIGHBOR program (The PHYLIP neighbor program gave similar results). WEIGHBOR is available in UNIX, Mac, and PC at <http://t10.lanl.gov/billb/neighbor/index.html> Some of the genomes are known to represent recombinants or mosaics between two or more different lineages, so this tree should not be assumed to represent the true phylogenetic history of these viruses. For example, the SAB1C genome from the sabaeus subspecies of African green monkeys is recombinant between an African green monkey lentiviral lineage and a Sooty mangabey viral lineage. When the AGM-like regions of its genome are used to build a phylogenetic tree, the SAB1C lineage shares the same major branch with the other AGM lineages. Given these limitations, the tree is still useful for graphically representing the diversity and relationships between these viruses. It is readily apparent that the HIV-2 viruses are related to Sooty mangabey viruses.