

## Construction of the HIV-2/SIV Amino Acid Alignments

### Classification of the sequences

Classification of HIV-2 is straightforward in the sense that the subtype classification of this virus is more or less standardized. SIVs derived from sooty mangabey (SIV-smm), macaques (SIV-mac) and HIV-2s intermingle in phylogenetic trees, however, due to multiple cross-species transmissions (1,2) which complicates the story. Classification of the other SIVs is even more complicated. As the tree in section I of this compendium shows, SIVcpz's are the most related to HIV-1, so included in HIV-1 alignments. The sequences from four subspecies of African Green Monkey, (SIVagm) are included in one alignment due to their distinctive clustering. Included with the SIVagms are representatives of some of the very diverse SIVs, SIVl'hoest, SIVsun, and SIVsykes. The HIV-2/SIVsmm/SIVmac are also included as a separate alignment in this Compendium, as they form their own phylogenetic group. The Drill SIV pol gene sequence was also added to the HIV-2/SIVsmm alignment (3).

In the HIV-2/SIV alignment, the classification of the SIVsmm and SIVmac sequences into SIVmac-SD is probably a simplification. 'SD' stands for 'Simian subtype D'. This classification is based on the fact that they cluster together with the only HIV-2 subtype D isolate known, FO784. Certainly the Env sequence SMI2 and SMI8 cluster far out of the SD cluster, and they probably belong to a different subtype (4); however, since only 2 Env fragments are presently available, no new subtype has been defined yet. For more information on HIV-2 and SIV phylogeny, see (2, 5).

### References

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