

## **Phylogeny and Evolution of Retro-Elements in Primates**

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The possibility that retroviruses and retroposons contribute to genome plasticity and evolution has been widely considered but such elements are numerous and the vast majority must be unrelated to functional genes. We propose a strategy for identifying those elements that might have exerted an influence on the course of human evolution. Between the separation of the hominid and chimpanzee lineages a 4Mb block in Xq21.3 transposed to Yp and was subsequently split by a paracentric inversion. The sequences on the Y are thus human specific and such genes as they may include are subject to new evolutionary pressures, including sexual selection. Within the Xq21.3/Yp region of homology by the use of a PCR-based phylogenetic approach, we have identified two classes of element that are human specific: I) two representatives (HS307 and HS408) of the class of SINE-R elements that have been derived from the HERV-K (human endogenous retrovirus K) genome, and II) two HERV-K LTR sequences that belong to human specific cluster. Each of these classes of element has proliferated since the separation of the chimpanzee and hominid lineages and these particular elements have done so in a region of the genome that has been subjected to discontinuous change within that period of evolutionary time. We also isolated 32 pol gene sequences of HERV-W family in hominoids and Old World monkeys. Phylogenetic analysis indicated close relationships of pol gene sequences across primate species. The analysis indicated that the HERV-W family has evolved independently in different primate species, including man.