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Bioinformatic Analysis of HERV-H Families on Human Sex Chromosomes

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The recent draft of the human genome sequence supports a good opportunity to study the evolutionary history of HERV (Human Endogenous Retroviruses) within the human genome. To gain insight into the duplication events of these retroviruses during hominid evolution, we analyzed sex chromosomes using bioinformatic tools and identified 69 HERV-H families. Chromosomal localization and phylogenetic analysis of the HERV-H families were also analyzed. Fifty one among them showed intact HERV-H sequences (7713bp) on human sex chromosomes. Phylogenetic analysis allowed us to describe the evolutionary history of HERV-H families on sex chromosomes. At least 16 members of the HERV-H families have undergone apparent rearrangements that could have resulted in large-scale duplication. Four members of the HERV-H on Y chromosome seemed to be derived from X chromosome, which are recently proliferated on human sex chromosomes. Compared to HERV-H sequences on X and Y chromosomes, the Y chromosomal sequences showed more diversity than those of the X chromosomes.