Emergence and scattering of multiple neurofibromatosis (NF1)-related sequences during hominoid evolution suggest a process of pericentrometric interchromosomal transposition

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Type 1 neurofibromatosis (*NF1*) gene encodes for a member of the GTPase activating protein family and is considered to be a tumor suppressor gene. Its very high rate of de novo mutation in humans led us to study a specific feature of this gene : the presence of numerous NF1-related sequences. According to our results, the human genome contains at least 11 *NF1*-related sequences, nine of which are scattered near centromeric sequences of seven different chromosomes. These *NF1*-related sequences, whose extent is quite varied according to loci, are unprocessed copies of the NF1 gene, and bear numerous mutations. A phylogenetic analysis of the six largest sequences indicates that they are all derived from a common ancestor, which would have appeared 22-23 million years ago, and was subsequently duplicated several times during hominoid evolution. The most recent duplication and interchromosomal transposition occured in the last million years suggesting that the process could still be ongoing. Intriguing similarities between the evolution of alpha-satellite DNA and *NF1*-related sequences suggest the involvement of a common genetic mechanism for the generation and peripheric spreading of these *NF1* partial copies.