Molecular cytogenetic resources for chromosome 4 and comparative analysis of phylogenetic chromosome IV in great apes

R Marzella ¹, L Viggiano, V Miolla, C T Storlazzi, A Ricco, E Gentile, R Roberto, C Surace, A Fratello, M Mancini, N Archidiacono, M Rocchi

Affiliations + expand

PMID: 10704278 DOI: 10.1006/geno.1999.6092

Abstract

We have generated a panel of 55 somatic cell hybrids retaining fragments of human chromosome 4. Each hybrid has been characterized cytogenetically by FISH and molecularly by 37 STSs, evenly spaced along the chromosome. The panel can be exploited to map subregionally DNA sequences on chromosome 4 and to generate partial chromosome paints useful in the characterization of chromosomal rearrangements involving this chromosome. Furthermore, a panel of 84 YACs mapping on chromosome 4 has been characterized by FISH. A subset of this panel is recognized by STSs used in the somatic cell hybrid characterization. In this way a correlation between the genetic and the physical maps can be established. These resources have been used to investigate the conservation of the phylogenetic chromosome IV in great apes. The results indicate that all the pericentric inversions that differentiate chromosome IV in these species are distinct and that one of the breakpoints frequently lies very close to the centromere. In 4 instances, the YAC containing the breakpoint was identified. The breakpoint in IVq of PTR and MMU lies in the same YAC, suggesting that this breakpoint has been utilized twice in the evolutionary history of this chromosome.

Copyright 2000 Academic Press.