1425

CHARACTERIZATION OF COMPLEX CHROMOSOME REARRANGEMENTS LEADING TO CHROMOSOME 18 ABNORMALITIES

Rafaella Mergener, Karen Regina Silva de Souza, Júlio César L. Leite, Rafael Fabiano Machado Rosa, Mariluce Riegel. Hospital de Clínicas de Porto Alegre (HCPA)

Chromosome 18 abnormalities are among the most common autosomal anomalies, with deletions of the long arm of chromosome 18 occurring in approximately one in 40,000 live births. In particular, the chromosome 18q-deletion syndrome (OMIM# 601808) is caused by distal 18q deletions and was first described in 1964. Phenotypic variation among patients with distal 18q deletions has been attributed to diversity in the size and position of the deletion. To this end, several studies have evaluated the clinical characteristics of these patients and employed microarray analysis to provide more precise genotype–phenotype correlations. Interstitial deletion of 18q leads to a number of phenotypic features, including multiple types of foot deformities. However, the molecular bases of nonrecurrent interstitial chromosomal deletions have been uncovered only recently. Our aim was to investigate the recombination products for the unusual-sized interstitial deletions on chromosome 18 and to correlate the phenotypic traits. Whole-genome oligonucleotide-based array was applied in each of the patients and control samples and graphical overview were through the Cytogenomics analytics software. We report twelve overlapping interstitial deletions ranged from 7.8 Mb to 26.6 Mb, with distal breakpoints ranging from 18q21.1 to 18q23. Based on the interstitial deletions described in our work and review of other cases in the literature, we confirmed that there is no breakage hotspot involved in the interstitial deletions. In contrast to recurrent common chromosome aberrations, in which the breakpoints are associated with various genomic architectural features such as LCRs, AT-rich palindromes, or fragile sites, the unusual-sized nonrecurrent rearrangements on chromosome 18 were thought to represent random events with different mechanisms of origin leading to a variety of structural rearrangements involving the critical region. The combined literature suggests that a wide phenotypic sprectrum exists among subjects with 18q deletions, specially those with interstitial rearrangements. In order to correlate the phenotypes from the patients with the chromosome 18q abnormalities further assessments by array CGH and FISH validation experiments are needed. Palavra-chave: Array-CGH; chromosome rearrangements; 18q deletions. Projeto GPPG10560