

## Abstract 70

### INVOLVEMENT OF 15q11.2 REARRANGEMENTS IN MENTAL RETARDATION

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Many diagnostic laboratories have implemented the use of MLPA for prenatal and postnatal diagnosis of several genetic diseases. Combined with karyotype and fragile X syndrome analysis, MLPA has become the first-line test in clinical protocols for mental retardation. We have applied MLPA to screen for subtelomeric rearrangements in a series of 222 consecutive mentally retarded patients, 214 with normal karyotype and 8 with abnormal karyotype. MLPA revealed 31 imbalances in 23 patients (10.4%), 13 patients (56.5%) presenting one rearrangement and 10 (43.6%) presenting two rearrangements. Seventeen (54.8%) were deletions and 14 (45.1%) duplications. Twenty six (83.9%) of these rearrangements were *de novo* and 5 (16.1%) were copy number variations inherited from a healthy parent. All but 2 were confirmed by another MLPA kit (P70), familial segregation and/or other molecular techniques such as FISH, aCGH and quantitative PCR. The 2 remaining were false positives. A sequence in the 15q-arm close to the centromere, targeted by the "15p" probe, was the region most frequently involved in rearrangements (25.8%). As this region is deleted or duplicated in some healthy individuals, it has been usually considered a putative polymorphism. Nevertheless, recent reports have implicated copy number variations in this region in some Prader-Willi/Angelman, autistic, schizophrenic and other mentally retarded patients. Due to this fact, rearrangements involving the 15q11.2 region should be molecularly characterized (size, copy number, paternal origin) in order to conclude their real contribution to the phenotype in affected individuals.

Acknowledgements: Fundación Ramón Areces (V-2006-FRARECES) and CIBER de Enfermedades Raras (CIBERER).