Conventional cytogenetics: Gold standard for mapping of large genomic imbalances on chromosome.

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Conventional cytogenetics represents G-banded routine and or high resolution karyotyping of human chromosomes. Recently, FISH and chromosomal microarray analysis (aCGH) techniques aided in the identifi cation of submicroscopic aberrations such as microdeletions and duplications, often undetectable by karyotype studies. We report here three cases with large genomic imbalances identifi ed by chromosomal microarray analysis (CGH + SNP array) but the precise location of the rearrangement sites or the genomic imbalance had to be confi rmed on specifi c chromosome bands by conventional cytogenetics. Methodology: DNA from blood was hybridized to a 400K oligonucleotide array, with probes at an average of 10.5 kb throughout the genome and at 5 kb on the X chromosome. Copy losses or gains are detected in comparison with a control DNA sample. Routine karyotype on G-banded cells is performed and reported. Results: Case 1: aCGH showed pathogenic GAIN of 11.201 Mb at 18p11.32p11.21, which contains 66 genes and a pathogenic LOSS of 7.152 Mb at 18q22.3q23 containing 39 genes . Karyotype analysis revealed additional material at chromosome 18q22.3 [46,XX,add(18)(q22.3)] resulting in the LOSS of terminal 18q and confi rming GAIN of whole 18p (18p11.32p11.21) at the distal end of 18q which may be a result of a meiotic recombination of a pericentric inversion in a carrier parent. Case 2: aCGH showed pathogenic LOSS of 3.8 Mb at 14q32.32q32.33 that includes 67 genes, LOSS of 10.5 Mb at 15q11.1q13.2 with 223 genes including SNRPN and UBE3A and LOSS of 0.67 Mb at 15q13.3 with two genes, respectively. Karyotype analysis revealed an unbalanced translocation between chromosome 14q32.3 and chromosome 15q12, resulting in the loss of distal 14q and the proximal15[45,XX,der(14) t(14;15)(q32.3;q12)], confi rming the structural location of genomic imbalance on the derivative chromosome. Case 3: aCGH showed pathogenic GAIN of 26.11 Mb that contains 190 genes at Yp11.31q11.23, most likely representing an additional whole Y chromosome. Karyotype analysis revealed an additional Y chromosome with a pericentric inversion involving Yp and Yq [47,XY, inv(Y) (p11.3q11.23], confi rming the chromosomal location of genomic imbalance. Conclusion: These are few examples of the many reported in the literature that clearly support the notion that karyotyping studies are essential and complement the microarray results when large genomic imbalances are seen.