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Microarray application in prenatal diagnosis: a position statement from the cytogenetics working group of the Italian Society of Human Genetics (SIGU), November 2011

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ABSTRACT

A precise guideline establishing chromosomal microarray analysis (CMA) applications and platforms in the prenatal setting does not exist. The controversial question is whether CMA technologies can or should soon replace standard karyotyping in prenatal diagnostic practice. A review of the recent literature and survey of the knowledge and experience of all members of the Italian Society of Human Genetics (SIGU) Committee were carried out in order to propose recommendations for the use of CMA in prenatal testing. The analysis of datasets reported in the medical literature showed a considerable 6.4% incidence of pathogenic copy number variations (CNVs) in the group of pregnancies with sonographically detected fetal abnormalities and normal karyotype. The reported CNVs are likely to have a relevant role in terms of nosology for the fetus and in the assessment of reproductive risk for the couple. Estimation of the frequency of copy number variations of uncertain significance (VOUS) varied depending on the different CMA platforms used, ranging from 0–4%, obtained using targeted arrays, to 9–12%, obtained using high-resolution whole genome single nucleotide polymorphism (SNP) arrays. CMA analysis can be considered a second-tier diagnostic test to be used after standard karyotyping in selected groups of pregnancies, namely those with single (apparently isolated) or multiple ultrasound fetal abnormalities, those with de novo *chromosomal rearrangements, even if apparently balanced, and those with supernumerary marker chromosomes. Copyright © 2012 ISUOG. Published by John Wiley & Sons, Ltd.*

BACKGROUND

In the last few years chromosomal microarray analysis (CMA) technology (array comparative genomic hybridization, aCGH; single nucleotide polymorphism array, SNP array) has acquired increasing relevance, becoming a fundamental diagnostic tool in medical genetics. In fact, technological evolution and experimental optimization have resulted in a notable simplification of analytic protocols, leading to a decrease in costs and enabling the progressive spread of this technology in many laboratories all over the world. Encouraging results, in terms of detection rate, were obtained in patients affected by unexplained developmental delay/intellectual disability (DD/ID), autism spectrum disorders (ASD) or multiple congenital anomalies (MCA), in whom

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