Outros

(21482) - PRENATAL DIAGNOSIS STUDY USING ARRAY COMPARATIVE GENOMIC HYBRIDIZATION FOR GENOTYPE-PHENOTYPE CORRELATION IN A COHORT OF 772 FETUSES

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Introdução

Currently, microarray-based comparative genomic hybridization (aCGH) is at the forefront of prenatal genetic diagnosis. The indications for performing genetic studies are variable and it is important to correlate the clinical findings with the genetic alteration.

Objectivos

The aim was to evaluate the main indications for prenatal diagnosis, the prevalence of abnormal copy number variations (CNV) in prenatal samples and correlate pathological CNV with clinical findings, the prevalence of VUS, report the rare variants found and additionally highlight the clinical importance of aCGH in prenatal diagnosis.

Metodologia

Using aCGH, we performed a retrospective study of 772 fetuses with indication for genetic study in two tertiary hospitals, between March 2013 and June 2022. Cases were sorted into groups according indication to perform invasive test.

Resultados e Conclusões

Our results demonstrated 8.3% (6.4-10.5%, 95% confidence interval (CI)) detection rate of pathogenic CNV. Within this group, the main indication was structural malformations (57%) mainly involving CNS, musculoskeletal and cardiac systems. Pathogenic results in cases with multiple malformations was statistically higher than in cases with isolated anatomical system malformations ($p<0.001$). The second most frequent indication was increased nuchal translucency (5-6.4mm).

However, the rate of pathogenic CNV did not show significant differences between structural and non-structural malformations ($p>0.001$), highlighting the relevance of genetic study by aCGH in all cases.

A total of 217 fetuses with CNV classified as VUS were identified, mainly involving chromosomes X, 1 and 16.

Our findings demonstrate 4.9% (4.2-5.6%, 95% CI) increased in the diagnostic yield using aCGH compared to the use of conventional karyotype alone, confirming that the aCGH can improve the accuracy of prenatal diagnosis.

Our survey provides a full genotype-phenotype analysis that can be clinically useful for the classification of variants and for the understanding of phenotypes so that the diagnostic result is increasingly reliable and clear.

Palavras-chave : Copy number variations, prenatal diagnosis, aCGH, structural malformations, non-structural abnormalities