Detection of DiGeorge and Cri du Chat Syndrome Deletions from Maternal Plasma by Deep Sequencing Cell Free DNA (cfDNA)

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OBJECTIVE

The objective of this retrospective study was to examine the potential of massively parallel sequencing (MPS) of cell-free DNA (cfDNA) for noninvasive detection of sub-chromosomal abnormalities that may cause fetal abnormalities.

RESULTS

Seven cases with fetal ultrasonography anomalies and confirmed cytogenetic abnormalities (5 22p- and 2 5p-) and seven gestational age-matched controls with normal karyotypes were studied. MPS detected 4/5 cases with Di George syndrome (22q-) and 2/3 with Cri du Chat (5p-) (See Table).

CONCLUSIONS

NPT can detect sub-chromosomal deletions associated with clinically relevant syndromes as 4/5 samples with DiGeorge syndrome and both cases of Cri du Chat syndrome were detected.

Failure to detect a 22p- deletion, which was confirmed using a 100k FISH probe, indicates a possible size resolution limitation using current MPS methods.

No false positive results were seen in this small cohort. Further studies using larger numbers of samples are required to understand limits of sensitivity and specificity before introduction into clinical practice.

References

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