Noninvasive twin zygosity assessment and aneuploidy detection by maternal plasma DNA sequencing

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Objective

This study aimed to provide an individualized assessment of fetal trisomy 21 and trisomy 18 status for twin pregnancies by maternal plasma DNA sequencing.

Methods

Massively parallel sequencing was performed on the plasma/serum DNA libraries of eight twin pregnancies and 11 singleton pregnancies. The apparent fractional fetal DNA concentrations between genomic regions were assessed to determine the zygosities of the twin pregnancies and to calculate the fetal DNA concentrations of each individual member of dizygotic twin pairs. Z-scores were determined for the detection of trisomy 18 and trisomy 21.

Results

Circulating DNA sequencing showed elevated chromosome 21 representation in one set of twins and elevated chromosome 18 representation in another pair of twins. Apparent fractional fetal DNA concentration analysis revealed both sets of twins to be dizygotic. The fractional fetal DNA concentrations for each individual fetus of the dizygotic twin pregnancies were determined. Incorporating the information about the fetal DNA fraction, we ascertained that each fetus contributed adequate amounts of DNA into the maternal circulation for the aneuploidy test result to be interpreted with confidence.

Conclusion

Noninvasive prenatal assessment of fetal chromosomal aneuploidy for twin pregnancies can be achieved with the use of massively parallel sequencing of cell-free DNA in maternal blood.