Topic: Non-invasive Prenatal Testing

FETAL FRACTION ESTIMATION FOR NONINVASIVE PRENATAL SCREENING (NIPS)

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Objectives: Fetal fraction (FF) is a crucial parameter for noninvasive prenatal testing. Low fetal fraction can cause false negative test calls and results in lower sensitivity of NIPS. Estimation of fetal fraction is simple for male fetuses but female ones cause problems.

Methods: The aim of the study was to develop SNP-based method for fetal fraction estimation. FF is estimated using targeted next generation sequencing in loci were mother has homozygous genotype and fetus heterozygous by counting minor allele coverage. The highest probability to get such combination arises in case of 50% heterozigosity of polymorphism in population. Selection of appropriate loci was based on genotype frequency information from Hapmap study for European, African, Asian and Japanese population. Genotype frequency for Russian population was validated using pooled (NGS) sequencing for about 1000 individuals. To evaluate the efficacy of the approach we compared fetal fraction values obtained by SNP-based and Y chromosome based methods for 50 samples with male fetuses.

Results: 80 loci were selected from hapmap database. After validation of genotype frequency and PCR performance 54 polymorphic loci left. We observed 0,8 correlation between FF estimations by Y chromosome and SNP-based methods.

Conclusions: In this study we developed SNP-based method for fetal fraction estimation. It showed good correlation with Y chromosome-based fetal fraction estimation and can be used for both male and female fetuses. Using targeted NGS sequencing allows to get data for aneuploidy analysis and FF estimation in the same chip.