Clinical Experience Utilizing Single-Nucleotide Polymorphism Data Captured by FAST-SeqS to Reduce the Transfer of Polyploid Embryos

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BACKGROUND

Our FAST-SeqS NGS aneuploidy screening (PGT-A) platform analyzes single-nucleotide polymorphisms (SNPs) in addition to long interspersed nucleotide elements (LINE-1s).

The SNP enhancement permits the detection of all forms of trio (e.g., 69,XXX), other forms of polyploid (e.g., 92,XXXX), haploidy/whole genome uniparental isodisomy (WG-UPiD), and many instances of single-chromosome UPiD, in addition to whole-chromosome and segmental aneuploidy.

These FAST-SeqS enhancements allow for correct classification of abnormalities potentially misclassified previously, which is essential for decreasing molar pregnancy and miscarriage rates.

Here, we report our clinical experience with polyploidy and miscarriage rates.

METHODS

Trophoectoderm biopsies from >67,000 embryos were analyzed using our refined PGT-A pipeline. FAST-SeqS, an NGS platform, has been validated to detect whole-chromosome and segmental aneuploidies (~10 MB) and more recently, to analyze data from ~10,000 polymorphic sites to accurately identify WG-UPiD, all forms of triplody, and many instances of single-chromosome UPiD.1,4

For this study, ploidy and UPiD results were stratified by oocyte age, clinical indication, and fertilization type.

RESULTS

Over a 14 month period, 67,847 embryos were analyzed. We identified 1,090 polyploid and haploid/WG-UPiD embryos (1.6%) across all age groups (20-48 years old) and clinical indications. Table 1 shows the ploidy types.

Of those cases where fertilization method was indicated, intracytoplasmic sperm injection (ICSI) was performed at a similar rate (90%) in both the polyploid and non-polyploid groups.

In this dataset, 22 single-chromosome UPiD abnormalities were detected involving chromosomes 1,3,4,8,10,11,14,15,16,18 & X, with UPiD 15 being the most frequent (n=6). Figure 2 illustrates an example of whole chromosome UPiD 10 (in addition to trisomy 9).

Figure 2: Example of whole chromosome UPiD detected by SNP data

CONCLUSIONS

In 14 months, this SNP enhancement has identified 570 embryos that otherwise may have been incorrectly classified as euploid or mosaic using traditional NGS data/allele ratios.

Preventing transfer of chromosomally abnormal embryos is essential to improving PGT-derived pregnancy outcomes.

REFERENCES