EXPLORING THE CONCORDANCE BETWEEN TWO TROPHECTODERM (TE) BIOPSIES IN PREIMPLANTATION GENETIC TESTING FOR ANEUPLOIDY (PGT-A) WITH DIFFERENT NEXT GENERATION SEQUENCING (NGS) PLATFORMS

Ee-Leen Lim, Ying-Chen Soo, Chee-San Heong, Sze-Tian Tee

TMC Fertility, Thomson Hospital Kota Damansara, Malaysia

INTRODUCTION

In preimplantation genetic testing for aneuploidy (PGT-A) with next generation sequencing (NGS), euploidy and whole chromosome aneuploidy are generally consistent across multiple samples of same embryo, but mosaic and segmental aneuploidy have lower reproducibility [1][2]. Two of the major NGS platforms are IonTorrent and Illumina [3]. It is intriguing to explore the concordance between initial and retesting trophectoderm (TE) biopsy results using different platforms.

MATERIALS AND METHODS

Fifteen aneuploid/mosaic blastocysts were reanalyzed. In the first phase, 5-10 cells were biopsied from the trophectoderm of day 5/6 blastocysts. Biopsied blastocysts were then vitrified. PGT-A was conducted using IonTorrent PGM. Aneuploidy was interpreted automatically by Ion Reporter Software. In the second phase, selected blastocysts were thawed and second biopsies were performed from trophectoderm again. PGT-A was conducted using Illumina Miseq. Aneuploidy was interpreted manually by observing profile generated on BlueFuse Multi software. All sequencing data met the quality control metrics established by respective manufacturers. Ploidy was classified as euploid (<25% aneuploidy), mosaic (25-75% aneuploidy), and aneuploid (>75% aneuploidy).

RESULTS

Concordance was analysed by concordance per embryo's ploidy and concordance per chromosome pair. The concordance of embryo's ploidy was 93.3% (14/15). Among the 15 blastocysts, 11 blastocysts were aneuploid and 3 blastocysts were mosaic on both platforms. Concordance of embryo's ploidy between two platforms was 93.3% (14/15). The discordant sample involved detection/non-detection of segmental gain. A total of 345 chromosome pairs were assessed for concordance per chromosome pair. Chromosome pairs were grouped as diploid, mosaic, whole chromosome aneuploid or segmental aneuploid. The concordance per chromosome pair was 92.5% (319/345). Among the concordant pairs, 304 pairs were diploid. Concordances of each category were 7.7% for mosaic (2/26), 92.3% for whole chromosome aneuploid (12/13), and 50% for segmental aneuploid (1/2).

Category	No. of chromosome pair			Concordance of each category
	Concordant	Discordant	Total	
Diploid	304	n/a	304	n/a
Mosaic	2	24	26	7.7%
Whole chromosome aneuploid	12	1	13	92.3%
Segmental aneuploid	1	1	2	50.0%
Total	319	26	345	92.5%

Table 1: Concordance analysis per chromosome pair.

CONCLUSIONS

Though sample size is small, our result accords with previous literatures. Compared to whole chromosome aneuploidy, mosaicism and segmental aneuploidy are less concordant. Possible reasons include their mitotic nature, and higher risk of misinterpretation, especially when tested using different platforms. Caution should be exercised when deselecting embryos classified under these two categories from transfer.

REFERENCES

1. Navratil, R., Horak, J., Hornak, M., Kubicek, D., Balcova, M., Tauwinklova, G., ... & Vesela, K. (2020). Concordance of various chromosomal errors among different parts of the embryo and the value of re-biopsy in embryos with segmental aneuploidies. *Molecular Human Reproduction*, 26(4), 269-276.
2. Marin, D., Xu, J., & Treff, N. R. (2021). Preimplantation genetic testing for aneuploidy: a review of published blastocyst reanalysis concordance data. *Prenatal Diagnosis*, 41(5), 545-553.
3. Chuang, T. H., Wu, Z. H., Kuan, C. S., Lee, M. J., Hsieh, C. L., Wang, H. L., ... & Chen, S. U. (2021). High concordance in preimplantation genetic testing for aneuploidy between automatic identification via Ion S5 and manual identification via Miseq. *Scientific Reports*, *11*(1), 1-9.

CONTACT

eeleen.lim@tmclife.com