Karyomapping: A Rapid PGT-M Solution for Single-Gene Disorders

In PGT-M, embryos are assessed for a specific genetic condition before transfer into the uterus. The goal of PGT-M is to prevent couples with a known risk of transmitting an inherited genetic disorder of having children affected with that disorder. PGT-M relies on the use of genetic markers within the genome to assess the likelihood of an embryo carrying a mutated version of the gene involved in a severe single-gene disorder. Karyomapping[1], uses linkage-based genome-wide mapping to provide a high-density view of chromosomes and insight into their parental origin. Karyomapping creates a complete map of the chromosomes inherited by the embryo for accurate assessment of the presence of severe single-gene disorders from a single embryonic cell and can be performed with a 24-hour protocol. Illumina technology provides the accuracy, reliability, and ease of use required for karyomapping. The HumanKaryomap-12 BeadChip targets the most informative markers in the genome for efficient genome-wide coverage. The result is the single most informative assay available at the single-cell level, providing insight into the inheritance of single-gene defects, genome-wide.

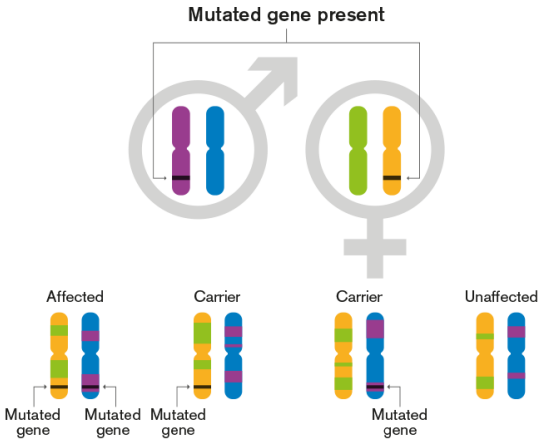
PGT-M

PGT-M, with karyomapping, identifies genetic loci on the inherited chromosomal segments to assess the genetic status of each embryo. These methods require genetic information from the parents, and a "reference", which is a close relative of known disease status. The determination of the disease status of the embryo works by establishing whether the embryos have inherited the same chromosome segments from the parents as the reference or not.

Karyomapping

Karyomapping analysis uses genome-wide linkage to reveal the inheritance of genetic disease loci present in one or both parents. Karyomapping uses single nucleotide polymorphisms (SNPs). A SNP is a DNA sequence variation occurring when a single nucleotide in the genome differs between individuals. They are easily identified using existing genome-wide SNP technologies. Karyomapping compares SNPs from an embryo to those of a reference to establish the likelihood of the embryo having inherited the mutated gene.

Karyomapping uses SNP genotyping data from the parents and reference to create a comprehensive map of the parental origin of chromosome segments inherited by the embryo. These chromosome segments are called haploblocks By establishing the inheritance of haploblocks surrounding the region of interest, it is possible to infer the disease status of each embryo—affected, carrier, or unaffected by comparing it to the disease status of a reference.



Reference

1. Handyside AH, Harton GL, Mariani B, Thornhill AR, Affara N, et al. (2010) Karyomapping: A universal method for genome wide analysis of genetic disease based on mapping crossovers between parental haplotypes. J Med Genet. 47: 651–658.