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Correction Factor Reveals Uniform Levels of Mitochondrial DNA in Human Blastocysts Irrespective of Ploidy, Age, or Implantation Potential

Manuel Viotti*, Andrea Victor, Alan Brake, Christo Zouves, and Frank Barnes

The human genome in its complete form is composed of nuclear DNA (nDNA) and mitochondrial (mtDNA). Recent studies report a correlation between elevated mtDNA levels and embryos that are aneuploid, that are derived from older patients, or that fail to implant upon transfer. Consequently, mtDNA content has been proposed as a biomarker for embryo viability in IVF.
We developed a mathematical formula resulting in the accurate calculation of mtDNA levels as established by next generation sequencing (NGS) or quantitative polymerase chain reaction (qPCR). Here, we demonstrate the rationale behind our calculation method, and go on to analyze mtDNA levels in our in-house IVF embryos.

Precise determination of mtDNA levels must take the nuclear genetic makeup of the tested embryo into account, and adjusting for gender and/or ploidy can significantly affect the results. All laboratories quantifying mtDNA content by NGS or qPCR should use the proposed correction factor. When applied to our in-house data, accurate determination of mtDNA levels show no statistically significant difference when blastocysts are grouped by ploidy, maternal age at oocyte retrieval, or implantation potential, in stark contrast with previous reports.