Mosaic human preimplantation embryos and their developmental potential in a prospective, non-selection clinical trial

Antonio Capalbo,¹,² Maurizio Poli,¹ Laura Rienzi,² Laura Girardi,¹ Cristina Patassini,¹ Marco Fabiani,¹ Danilo Cimadomo,² Francesca Benini,³ Alessio Farcomeni,⁴ Juliana Cuzzi,⁵ Carmen Rubio,⁶,⁷ Elena Albani,⁸ Laura Sacchi,⁸ Alberto Vaiarelli,² Matteo Figliuzzi,¹ Necati Findikli,¹ Onder Coban,¹¹ Fazilet K. Boyukalin,¹² Ivan Vogel,¹³ Eva Hoffmann,¹³ Claudia Livi,³ Paolo E. Levi-Setti,⁸ Filippo M. Ubaldi,² and Carlos Simón⁶,⁷,¹⁴,¹⁵

Summary

Chromosome imbalance (aneuploidy) is the major cause of pregnancy loss and congenital disorders in humans. Analyses of small biopsies from human embryos suggest that aneuploidy commonly originates during early divisions, resulting in mosaicism. However, the developmental potential of mosaic embryos remains unclear. We followed the distribution of aneuploid chromosomes across 73 unselected preimplantation embryos and 365 biopsies, sampled from four multifocal trophectoderm (TE) samples and the inner cell mass (ICM). When mosaicism impacted fewer than 50% of cells in one TE biopsy (low-medium mosaicism), only 1% of aneuploidies affected other portions of the embryo. A double-blinded prospective non-selection trial (NCT03673592) showed equivalent live-birth rates and miscarriage rates across 484 euploid, 282 low-grade mosaic, and 131 medium-grade mosaic embryos. No instances of mosaicism or uniparental disomy were detected in the ensuing pregnancies or newborns, and obstetrical and neonatal outcomes were similar between the study groups. Thus, low-medium mosaicism in the trophectoderm mostly arises after TE and ICM differentiation, and such embryos have equivalent developmental potential as fully euploid ones.

Introduction

Aneuploidy in human conceptions is the leading cause of embryo implantation failure, pregnancy loss, and congenital disorders in live-born infants. Although chromosome segregation errors in oocytes are its major cause,¹ recent observations suggest that aneuploidy can also arise significantly during preimplantation embryonic divisions.² Aneuploidies due to mitotic errors are present uniformly throughout the embryo, whereas those with a mitotic origin (i.e., post-fertilization) give rise to cell lineages with different chromosomal content (embryonic mosaicism). Understanding the incidence of mosaicism and the distribution of aneuploid cells throughout the embryo is important because genetic testing of preimplantation embryos and prenatal fetuses is carried out, respectively, on a trophectoderm biopsy or samples of placental tissue originated from it, rather than the cell lineage programmed to form the embryo proper (i.e., inner cell mass (ICM), ICM).

With the introduction of high-resolution next-generation sequencing (NGS) protocols, chromosomal mosaicism has been reported in up to 20% of clinical trophectoderm (TE) biopsies³ (Figure 1A), which consist of a sample of 3 to 10 cells. Recent large genome-wide non-invasive prenatal screening (NIPS) studies performed at 12 weeks of gestation have shown that the presence of confined placental mosaicism (CPM) explains a significant fraction of false-positive cases of rare autosomal trisomies (RATs).⁴ Yet, the prevalence of chromosomal mosaicism in human pregnancies is reported in fewer than 0.3% of prenatal tests (e.g., by amniocentesis or by NIPS).⁵ On the basis of experiments in murine models, the sharp drop in mosaicism between pre- and post-implantation stages has been explained by the selective elimination of aneuploid cells through competitive growth of euploid cells or apoptosis of the abnormal cellular clones.⁶,⁷ In humans, the prevalence and developmental potential of mosaic embryos consisting of both diploid and aneuploid cells remain the subject of intense debate.⁹ This is largely due to a paucity of studies that have assessed mosaicism across the whole embryo; as a result, our understanding of the distribution of aneuploid cells is limited. One major clinical impact of this shortcoming has been that fewer than 3% of mosaic embryos are being used in in babies born after in vitro

¹Igenomix, Reproductive Genetics, Marostica 36063, Italy; ²Clinica Valle Giulia, GeneraLife IVF, Rome 00197, Italy; ³DEMETRA, GeneraLife IVF, Florence 50141, Italy; ⁴Department of Economics and Finance, University of Rome “Tor Vergata,” Rome 00133, Italy; ⁵Igenomix US & Canada, Miami, FL 33126, USA; ⁶Igenomix, Valencia 46980, Spain; ⁷Igenomix Foundation, Reproductive Genetics, Valencia 46980, Spain; ⁸Istituto di Ricovero e Cura a Carattere Scientifico, Humanitas Research Hospital, Division of Gynecology and Reproductive Medicine, Fertility Center, Rozzano (Milan) 20089, Italy; ⁹Bahceci Fulya IVF Centre, Embryology Laboratory, Istanbul 34394, Turkey; ¹⁰Department of Biomedical Engineering, Beykent University, Istanbul 34498, Turkey; ¹¹British Cyprus IVF Hospital, Nicosia 2681, Cyprus; ¹²Bahceci Fulya IVF Centre, Infertility Clinic, Istanbul 34394, Turkey; ¹³Danish National Research Foundation Center for Chromosome Stability, Department of Cellular and Molecular Medicine, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen 2200, Denmark; ¹⁴Valencia University and INCLIVA, Department of Obstetrics and Gynecology, Valencia, 46010, Spain; ¹⁵School of Medicine, Department of Obstetrics and Gynecology, Harvard University, Cambridge, MA 02115, USA

*Correspondence: antonio.capalbo@igenomix.com

https://doi.org/10.1016/j.ajhg.2021.11.002.

© 2021 The Author(s). This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).
Figure 1. Aneuploidy incidence in clinical trophectoderm biopsies and embryonic concordance study

(A) The pie chart represents the distribution of aneuploidy categories observed in 6,766 clinical trophectoderm (TE) biopsies analyzed in our PGT-A diagnostic setting (classified according to the most severe abnormality across all chromosomes). The stacked bar chart represents the incidence of each aneuploidy category at the chromosome level.

(B) Top left: 73 human blastocysts were disaggregated into five portions: four TE biopsies and the inner cell mass (ICM) biopsy. Top right: examples of PGT-A plots displaying a low mosaic configuration confined to TE1 and a uniform aneuploidy detected in all portions. Bottom: this heatmap shows diagnostic concordance rates per chromosome on the basis of 73 embryos with five biopsies each (365 embryo biopsies), leading to 6,424 comparisons (73 embryos × 22 autosomal chromosomes × 4 permutations of reference biopsy). One of the four TE biopsies is considered as a reference, whereas the remaining biopsies (three TE + ICM) are used for verifying the outcome of the reference. Based on its copy-number result, each autosomal chromosome within the reference biopsy is classified into one of five categories.

(legend continued on next page)
fertilization (IVF) treatment\textsuperscript{10–12} as a result of concerns that the aneuploidy detected in the TE might affect the ICM and, therefore, potentially the baby. However, mosaicism is not generally detected at increased rates IVF treatment,\textsuperscript{13–15} suggesting that aneuploid cells in mosaic preimplantation embryos do not contribute toward the genetic make-up of live-born infants. Consistent with this hypothesis, a small study of mosaic embryos showed they are capable of giving rise to healthy live births.\textsuperscript{16}

Larger, retrospective studies have concluded that mosaic embryos have a lowered reproductive potential.\textsuperscript{10,17} Such retrospective data, however, are affected by a strong selection bias. In particular, retrospective analyses do not take into account the fact that mosaic embryos are transferred as a last option and, consequently, that their reproductive performance is often measured on a highly selected subpopulation of women who had previous failed implantsations with euploid embryos. Mosaic embryos are also transferred in those individuals producing only aneuploid embryos, introducing again a strong selection bias toward a poor-prognosis population. For example, in the largest retrospective study published to date where the reproductive competence of putative mosaic embryos was assessed, 94.6\% of cases involving mosaic-embryo transfer were included because no uniformly euploid embryos were available.\textsuperscript{17} Accordingly, the reproductive potential of mosaic embryos remains to be tested in a robust, well-powered prospective, non-selection clinical trial.

Here, we have first investigated the prevalence and distribution of aneuploid cells in the largest dataset of disaggregated human blastocysts currently available. Our findings show that in the majority of cases where mosaicism is detected in TE biopsies, this is due to a few aneuploid cells that originate from the trophectoderm tissue and give rise to a low- to medium-grade mosaicism configuration. To provide exhaustive evidence on the effects that highly localized aneuploid cells have on a mosaic embryo’s clinical performance, we carried out a prospective non-selection study allowing an unbiased comparison between uniformly euploid and mosaic embryos in terms of reproductive potential and chromosomal normalcy between uniformly euploid and mosaic embryos, providing exhaustive evidence related to their clinical performance and the ensuing offspring. We report that putative mosaic embryos show clinical outcomes similar to those of uniformly euploid embryos and that there are not any significant implications for pregnancy and live-birth outcomes or the offspring’s health. The clinical data generated from this trial will clearly resolve major concerns related to the management of mosaicism findings in preimplantation genetic testing for aneuploidies (PGT-A) and will be of fundamental importance for helping many infertile individuals to make more informed reproductive decisions.

Materials and methods

Assessment of mosaicism incidence and prevalence in human blastocysts

Data from clinical cases, consisting of 6,766 clinical TE biopsies performed in 2020 and 2021, were recovered so that the incidence of different aneuploidy categories observed in the diagnostic setting of PGT-A could be computed. A total of 91 blastocyst-stage human embryos were donated to research at the British Cyprus IVF Hospital under ethical-committee approval obtained from the institutional review board at Near East University (project number YDU/2018/64-685). Approved informed-consent forms were signed by all the individuals donating their embryos to this study. Embryos were warmed, and ICM biopsies were isolated by a previously validated mechanical method.\textsuperscript{18} The TE was then disaggregated in four equally sized portions. Blinded NGS analysis was performed on all re-biopsies, and results were analyzed so that the prevalence and distribution of abnormal cells in the remaining embryonic sections could be assessed according to the original estimated mosaicism rate in the reference TE biopsy (see supplemental methods).

Clinical trial design and participants

We conducted a multicenter, double-blinded, non-selection trial (trial registration NCT03673592) involving consecutive IVF with blastocyst-stage PGT-A treatments followed by frozen euploid, low-grade, or medium-grade mosaic single-embryo transfer (SET). Women eligible for participation were below the age of 45, had autologous oocytes, were undergoing intra-cytoplasmic sperm injection (ICSI) for all oocytes, and had at least one transferable embryo available (euploid or low- to moderate-grade mosaic). Treatment cycles were excluded from the study if the embryo to be transferred showed the worst morphological grade according to an adaptation of Gardner’s criteria\textsuperscript{19} or if the female partner had a chronic medical condition associated with adverse pregnancy outcomes. The purpose this criterion was to mitigate an intrinsic bias; euploid blastocysts of very poor morphological grade were shown to result in lower live-birth and higher miscarriage rates than embryos with better morphology.\textsuperscript{20} IVF procedures were carried out according to standard practices employed at each clinic (supplemental methods).

The trial was conducted in compliance with the International Conference on Harmonisation and the Declaration of Helsinki. The protocol was approved by the institutional review board of Clinica Valle Giulia, Rome (September 3, 2018) and the Humanitas...
Intervention
After TE biopsy and NGS-based chromosomal analysis, a diagnostic report on embryos’ chromosomal status was sent to the clinical sites (supplemental methods). Embryos showing a low or moderate degree of chromosomal mosaicism were blindly reported as euploid without distinction from uniformly euploid embryos. Among those reported as euploid, embryos were selected for SET on the basis of standard morphological features, providing a blinded allocation of the participants into the three main categories “euploid” (group A), “low-grade mosaic” (group B; 20–30% aneuploid cells), and “medium-grade mosaic” (group C; 30–50% aneuploid cells). Cases were followed up on during the post-transfer, gestational, and postnatal periods. The chromosomal status of 38 newborns derived from the transfer of putative mosaic embryos was investigated via single-nucleotide polymorphism arrays (SNPa genotyping) on saliva samples collected from the newborns and their parents. Genotyping data of the trios were used for investigating any potential instance of mosaicism or uniparental disomies (UPDs) in the offspring. Details of the genotyping protocol are reported in the supplemental methods.

Outcomes
The primary outcome measure was sustained implantation rate (the probability that any transferred embryo will implant and progress to delivery), defined as live-birth rate (LBR) per transferred embryo according to the World Health Organization and International Committee for Monitoring Assisted Reproductive Technologies International Glossary on Infertility and Fertility Care. The LBR was calculated as the number of newborns delivered on or after 22 weeks of gestation over the number of embryos replaced. In the event of a SET, as occurred in this study for all cases, the metric is identical to delivery rate per transfer. The secondary outcome was miscarriage rate, defined as the spontaneous loss of an intra-uterine pregnancy prior to 20 completed weeks of gestational age. This included the evaluation of pregnancy rate (PR) and biochemical pregnancy (BP). Mean gestational age at birth and birth weight were collected as neonatal outcomes. Adverse outcomes were determined by the detection of chromosomal abnormalities, including uniparental disomy, in the miscarried product of conception (POM) during prenatal diagnosis (PND; amniocentesis/chorionic villi sampling CVS) and/or at birth.

The implication of excluding putative mosaic embryos from clinical use has been evaluated in consideration of the potential loss of live births in a given IVF treatment cycle (cumulative LBR, CLBR per cycle) by two different methods: (1) using actual data from embryo transfer in the study period but excluding live births achieved from low- and moderate-mosaic embryos and (2) by modeling the optimistic scenario where all transferable embryos are replaced. A complete description of the outcome of these analyses is reported in the supplemental methods.

Statistical analysis
The primary endpoint for this analysis was the non-inferiority of LBR when euploid and mosaic embryos were compared. Assuming an LBR of 45% for uniformly euploid embryos versus 42.5% for low- or moderate-degree mosaics, a 1:1 sampling ratio for the two groups, and a planning non-inferiority margin of 7.5% [23,24], we calculated that 421 embryos per group would guarantee the power of at least 90% for a significance level set at 5%. The same sample size was sufficient for targeting non-inferiority claims in the miscarriage rate. Assuming a 10% miscarriage rate for uniformly euploid embryos and 15% for moderate to low mosaics, and setting a significance level at 5%, we also found the sample size had >90% power to assess non-inferiority in the miscarriage rate between control and test groups; the non-inferiority margin was 2%.

Data are expressed as mean ± standard deviation or percentages as appropriate. Proportions were compared via the chi-square test or Fisher exact test for 2 × 2 contingency tables. The non-inferiority endpoint was set as the 95% CI for difference in proportions lying below the planned margin. In addition to computing confidence intervals and p values for the difference in proportions, we computed the odds ratios (ORs) and adjusted odds ratios (AORs) of miscarriage for LBR, PR, IR, MC, and BP through logistic regression models. In multivariate analyses, ORs were adjusted for female age, male age, center, morphology of the blastocyst, day of the biopsy, number of previous implantation failures, previous miscarriages, previous live birth, infertility indication, and sperm origin (ejaculated versus surgical). All other tests were two tailed. Data had no missing values for variables involved in the primary analysis. A complete case approach was used for secondary analyses. All analyses were conducted with SPSS v. 21 and R v. 3.5.1.

Results
Incidence and prevalence of chromosomal mosaicism on blastocyst-stage human embryos
To shed light on the incidence and prevalence of chromosomal mosaicism in human preimplantation embryos, we first analyzed a large historical dataset of 6,766 embryos, where a clinical trophectoderm (cTE) biopsy had been processed with NGS technology. This approach could detect a mosaicism rate as low as 20% in cell line mixture models. This clinical dataset of cTE biopsies (n = 6,766; mean maternal age n = 38.06; SD 3.65) revealed an incidence of diploid-aneuploid mosaicism of 18.7%; smaller chromosomes were more frequently represented than others (Figure 1A).

Next, we investigated the prevalence of mosaicism and its clonal distribution in 91 unselected human blastocysts that were donated for research. We divided the trophectoderm into four biopsies and isolated the ICM by using a validated mechanical method able to retrieve ICM specimens free of TE contamination (Figure 1B). The collection of all five samples from the same blastocyst was successful for 75 out of 91 embryos. Blinded NGS analysis generated an informative result for all five samples in 73 embryos, allowing robust diagnosis for each of the four TE biopsies and the ICM. Chromosomal mosaicism rates were calculated for each of the five blastocyst biopsies,
and the concordance rate between the reference TE biopsy and the remaining four embryonic portions (including the ICM) was assessed on the basis of permutation analysis (Figure 1B). Using one TE biopsy as a reference, we found that chromosomal abnormalities in the ICM were extremely rare and not statistically different irrespective of whether the reference biopsy had been classified as euploid or low- to medium-grade mosaic (p = 0.14). In these cases, segregation patterns were confined to a single portion of the TE and rarely affected the ICM (Figure 1B). In contrast, high-grade mosaicism (50–70%) in a single TE sample was commonly associated with uniform aneuploidy throughout the embryo (including the ICM) in 65% of cases (13 out of 20 embryos; 95% CI = 43–82%; Figure 1B). We conclude that, in the vast majority of cases, the detection of low- to medium-grade mosaicism in one TE biopsy reflects a status of highly confined aneuploidy rather than its random distribution throughout the embryo.

**Prospective non-selection clinical-trial results**

Our data suggest that low- to medium-grade mosaic embryos might have developmental potential similar to that of euploid ones. So far, clinical outcomes of mosaic embryos have only been compared retrospectively in selected subpopulations of individuals who failed to get pregnant with previous transfers of euploid embryos or who only had one putative mosaic embryo available and were therefore of poor prognosis.\(^7,10–12\) To produce unbiased effects of treatments on those participants’ IVF cycles were included in the primary analysis, which was powered for the LBR as a primary outcome. LBRs of uniformly euploid embryos and low- and moderate-grade mosaic embryos were 43.4% (95% CI = 38.9–47.9%), 42.9% (95% CI = 37.1–48.9%), and 42% (95% CI = 33.4–50.9%), respectively (Table 1). The fact that the confidence interval for the difference fell below the planned 7.5% margin (95% CI = −5.7–7.3%) shows that the non-inferiority endpoint for the primary outcome measure was met, suggesting similar reproductive outcomes for euploid and low- and moderate-grade mosaic embryos. No difference was observed in miscarriage rates (OR = 0.89; 95% CI = 0.50–1.55; p = 0.69), providing additional support for chromosomal normalcy of pregnancies from low- and medium-grade mosaic embryos (Table 1). Additionally, the number of chromosomes showing a mosaic configuration (commonly referred as complex mosaic) was also not associated with any of the outcomes investigated (see Table S2). At a multivariate-analysis level, an effect on LBR was observed for poor-quality blastocyst morphology (adjusted odds ratio (AOR) = 0.56 compared to the top-quality category, 95% CI = 0.35–0.89; p = 0.0146), day of biopsy (e.g., day 5 versus day 6) (AOR = 0.68 per day, 95% CI = 0.51–0.90, p = 0.008), and surgical origin of sperm (AOR = 0.158, 95% CI = 0.04–0.75, p = 0.020).

Although our study was not powered to detect mosaicism in pregnancies, we nevertheless investigated potential mosaicism by conducting follow-up analysis of all the available products of conceptions (POCs) after spontaneous miscarriages and elective prenatal diagnosis procedures. Miscarriage rates were similar in the three groups (Table 1). Four of the 52 miscarriage cases were analyzed by standard cytogenetics, all of which were euploid. Twenty-six sustained pregnancies (26 out of 388, 6.7%) underwent prenatal diagnosis by amniocentesis (group A = 15; group B = 6; group C = 3) or by chorionic villi sampling (group A = 2). These numbers were small because the reduction in the use of invasive prenatal diagnosis is one of the aims of PGT-A. All prenatal diagnoses showed euploid karyotype except in one pregnancy from group A (uniformly euploid), where confined placental mosaicism for trisomy 22 (20% abnormal cells) was detected at chorionic villi sampling analysis. However, subsequent follow-up amniocentesis displayed a normal euploid cytogenetic result.

At birth, obstetric and neonatal outcomes were similar between mosaic and euploid embryos (Table 1). One developmental abnormality was observed among the moderate-grade mosaicism cases (group C), where a baby was born with a diagnosis of Beckwith-Wiedemann Syndrome caused by hypomethylation in the region KvDMR/IC2.\(^26\) This condition is not a diagnostic target of PGT-A nor...
due to chromosomal mosaicism. To further investigate any potential persistence of the abnormal cell line after mosaic embryo transfer, we carried out postnatal genotyping of newborns on a subset of 38 families willing to participate (9.8% of all newborns derived from the study; Figure 3). At genome-wide resolution, all genotyping tests showed
fully normal karyotypes and the absence of uniparental di- 
type configuration in the cohort of babies born from 
mosaic-embryo transfer (Figure 3 and Figure S2).

to determine the clinical impact of not transferring low-
and medium-grade mosaic embryos, we developed a theo-
retical model of cumulative treatment outcomes on the 
basis of the incidence of mosaicism and clinical outcomes 
from this trial (~43% LBR). If we model a scenario that 
considers the embryos transferred in the trial, an overall 
reduction of 24 and 7% in LBR would be expected if low-
and medium-grade mosaic embryos or if medium-grade 
embryos only were removed, respectively (Figure S3 A). 
If we consider an optimistic scenario that assumes all 
potentially available embryos are transferred for a given IVF 
treatment cycle, not transferring group B and C or group 
C alone would have resulted in an overall reduction in cu-
mulative LBR of 36 and 11%, respectively (Figure S3 B; 
source data from Tables S3 and S4).

**Discussion**

Since the introduction of NGS in preimplantation genetic 
testing for aneuploidy (PGT-A), there has been substantial 
debate over the incidence and the distribution of aneu-
plloid cells throughout human preimplantation embryos 
and how this might affect developmental potential. In 
this study, we combined the assessment of both the dis-
tribution of aneuploid cells throughout human blastocysts 
and their impact on the embryo's reproductive potential. 
The latter parameter was investigated in a prospective 
multicenter, double-blind, non-selection trial aimed at 
assessing the clinical performance and safety of low- 
and medium-degree mosaic embryos by minimizing biases 
deriving from skewed populations' prognoses and em-
broyo-prioritization strategies.

First, we assessed the distribution of aneuploid cells 
throughout blastocyst embryos by analyzing aneuploidy 
in 365 biopsies derived from 73 unselected blastocyst em-
broys. Our data support a model in which aneuploidy is 
focused to a small cluster of cells in the peripheral 
placental lineages (i.e., TE) at the peri- and early post-im-
plantation stages. This results in low- and medium-grade 
mosaic embryos when a single cTE biopsy is taken and 
the signal from aneuploid cells is “averaged” over 3–10 
cells. In effect, our disaggregation experiments suggest 
that once the aneuploid cells have been removed, the re-
aining embryo consists of euploid cells.

The subsequent prospective, non-selection clinical trial 
found no evidence of inferior performance of low- 
and medium-grade mosaic embryos with regards to preg-
nancy outcomes, including LBR, pregnancy loss, or chro-
mosomal abnormalities in the pregnancy and in children 
(Table 1, Figure 3). In fact, on the basis of the transfer of 
thousands of mosaic embryos carried out to date, the 
positive predictive value of a mosaic finding in blastocyst 
embryos by PGT-A has been confirmed in only a single 
case. Accordingly, the evidence from our trial does 
not support the cascade of procedures commonly trig-
gered by the reporting of mosaicism in PGT-A testing 
cases, including additional genetic counseling sessions, 
instituted anxiety and distress in treated individuals, 
higher costs, increased adoption of invasive prenatal 
diagnosis, and its associated risk of iatrogenic abort-
on (0.3%).

Whereas low- and medium-grade mosaicism do not 
appear to affect live birth, the outcome of high-grade 
mosaic embryos is clearly a different matter given that 
65% of high-grade mosaic embryos were extensively 
affected, including in the inner cell mass (Figure 1B). In 
this study it was impossible to investigate the reproductive 
outcomes of high-grade mosaic embryos because it would 
be unethical to do so given the disproportionate impact on 
women, who would most likely be aggrieved by the 
transfer of fully aneuploid embryos (e.g., by miscarriage). 
However, this lack of information is not expected to

### Table 1. Reproductive outcomes of euploid and mosaic embryos

|                         | Group A: Euploid (20–30% variation) | Group B: Low-grade mosaic (95% CI; p value) | Group C: Medium-grade mosaic (30–50% variation) | Adjusted OR (95% CI, p value) |
|-------------------------|-------------------------------------|---------------------------------------------|---------------------------------------------|------------------------------|
| Test sets, n            | 484                                 | 282                                         | 131                                         | -                           |
| Positive pregnancy test, % (n) | 55.8% (270/484)                       | 55.0% (155/282)                             | 55.7% (73/131)                             | 0.98 (0.75–1.27; 0.86) |
| Biochemical pregnancy loss, % (n) | 10.7% (29/270)                        | 12.3% (19/155)                             | 13.7% (10/73)                              | 1.18 (0.69–2.02; 0.53)|
| Miscarriage, % (n)      | 12.0% (29/241)                        | 11.0% (15/136)                             | 12.7% (8/63)                               | 0.89 (0.50–1.55; 0.69) |
| Live birth, % (n)       | 43.4% (210/484)                       | 42.9% (121/282)                            | 42.0% (55/131)                             | 0.97 (0.74–1.26; 0.82) |
| Monochorial twins delivery, n | 1                                   | 1                                           | 1                                           | -                           |
| Gestational age, mean (95% CI) | 38.4 (38.0–38.7)                      | 38.2 (37.9–38.6)                           | 38.1 (38.0–38.5)                           | -                           |
| Birth weight, mean (95% CI) | 3,286 (3,200–3,371)                  | 3,174 (3,080–3,267)                        | 3,130 (2,950–3,310)                        | -                           |

Biochemical pregnancy is defined by a positive pregnancy test. Implantation rate is defined as the number of gestational sacs observed by vaginal ultrasound at the fifth gestational week divided by the number of embryos transferred. Multiple pregnancy is defined by any scan with more than one heartbeat or gestational sac at the stage of clinical pregnancy (approximately 6 weeks). Miscarriage is defined as the loss of a clinical pregnancy, excluding ectopic pregnancies, before 20 weeks of gestation. A live birth is defined as a delivery that resulted in at least one live birth after 22 weeks of gestation. CI denotes confidence interval. "-" indicates not applicable.
significantly impact the effectiveness of PGT-A cycles because high-grade mosaicism was detected in only 1.6% of embryos analyzed (Figure 1A). It should be noted that the results reported in this study were obtained through the analysis of raw NGS data independent from any proprietary diagnostic algorithm or chromosome-specific consideration commonly used by PGT-A laboratories. Accordingly, our approach provides all PGT laboratories with common ground that is highly reproducible and independent of specific individual settings. Nevertheless, it is important that each laboratory tests and validates its specific algorithms in prospective non-selection studies like the one presented here. Furthermore, these findings concern whole-chromosome mosaic aneuploidies only and cannot be extended to segmental mosaic configuration, which might follow different trajectories. Using a similar embryo-disaggregation design, we have recently demonstrated that most segmental unbalances detected in human blastocysts are indeed in a mosaic state, in opposition to what is observed for whole-chromosome aneuploidies, which mostly originate after meiotic segregation errors.1,30 Future non-selection studies are needed for the investigation of the clinical predictive values of mosaic segmental abnormalities detected in TE biopsies.

Although it remains unclear whether aneuploid cells arrest, become senescent or apoptotic, or are precursors of placental mosaicism,13 our data also support the existence of early developmental bottleneck events able to normalize mosaic-initiating post-zygotic aneuploidies in human embryos. As shown here, low- and medium-grade mosaic embryos have similar reproductive potential as uniformly euploid embryos and, according to our modeling, deselecting them from clinical treatment10 would have resulted in a reduction of LBRs of up to 36% in IVF/PGT-A cycles. Considering that in the US alone, more than 50,000 PGT-A cycles are performed every year, the inclusion of putative mosaic embryos in transfer selection would rescue a remarkable number of embryos and live births. In light of this experience, we encourage the preliminary use of data from non-selection trials before being incorporating new

**Figure 3.** Euploid biparental inheritance in children born from “mosaic” embryo transfer
(A) Illustration of a mosaic paternal monosomy inferred from the trophectoderm biopsy. The fetal tissues derive from the inner cell mass, which might contain biparental or uniparental chromosomes or a mixture of them. Supporting SNPs where the maternal and paternal genotypes are homozygous but carry opposite alleles (AA and BB or vice versa) can be used for determining the presence or absence of parental chromosomes.
(B) LogR and B allele frequencies for chromosome 6 from a child born from group C.
(C) Cumulative AB genotypes in the child of supporting SNPs across chromosome 6.
(D) Number (No.) of children investigated with postnatal SNP testing. Total number of samples showing euploid or mosaic karyotype (“ploidy”) or containing both parental chromosomes (biparental disomy, BPD) or two homologous chromosomes from the same parent (UPD).
PGT-A algorithms and aneuploidy classification criteria in routine practice.

Data and code availability

All necessary data are available in the main text or supplemental material. For Figure S3, all data points are provided in the supplemental information. The complete dataset of anonymized clinical records is available upon request. The code for SNP-array-based UPD and mosaicism analysis of trios is publicly available at the following link: https://github.com/Meiomap/TrioAnalysis.

Supplemental information

Supplemental information can be found online at https://doi.org/10.1016/j.ajhg.2021.11.002.

Acknowledgments

The study was supported by Igenomix. The authors also acknowledge the support of a European Research Council consolidator grant (724718-ReCAP), the Novo Nordisk Foundation Young Investigator Award (NNF15OC0016662), ReproUnion, and the Danish National Research Foundation (center grant 6110-00344B). Furthermore, the authors would like to thank all colleagues and collaborators who have contributed to this study and to acknowledge their work in data collection and treatment monitoring across all the participating sites and institutions. A special acknowledgment is given to the following individuals for their contributions: Carlos Gomez De La Cruz and Emilio de la Fuente Lucena from Igenomix; Cinzia Gentile from Genera Veneto, GeneraLife IVF; Erminia Alviggi from Ruesch Clinic, GeneraLife IVF; Antonella Smeraldi and Amalia Cesana from Humanitas; and Valentina Zicaro from Demetra.

Declaration of interests

A.C., M.P., L.G., C.P., M.F., M.F., J.C., and C.R. are full-time employees of Igenomix.

L.R. is the Scientific Director of GeneraLife IVF. She is editor of reproductive biomedicine online and has been associate editor of human reproduction update. She has been the principal investigator of a study sponsored by Merck KGaA. She has received honoraria and consultation fees from Merck, MSD, Ferring, Ibsa, Cooper Surgical, Cook, Nterilizer, Fujifilm-Irvine Scientific, Medea, and Universal Clinics. She is a partner/shareholder of Global Investment Clinics, Genera Health Care, and Nterilizer, and has been of Flam.

C.S. is the head of the scientific advisory board of Igenomix. The other authors declare no competing interests.

Received: September 15, 2021
Accepted: October 29, 2021
Published: November 18, 2021

References

1. Gruhn, J.R., Zielinska, A.P., Shukla, V., Blanshard, R., Capalbo, A., Cimadomo, D., Nikiforov, D., Chan, A.C.H., Newnham, L.J., Vogel, I., et al. (2019). Chromosome errors in human eggs shape natural fertility over reproductive life span. Science 365, 1466–1469.
2. Popovic, M., Dhaenens, L., Boel, A., Menten, B., and Heindryckx, B. (2020). Chromosomal mosaicism in human blastocysts: the ultimate diagnostic dilemma. Hum. Reprod. Update 26, 313–334.
3. van Echten-Arends, J., Mastenbroek, S., Sikkema-Raddatz, B., Korevaar, J.C., Heineman, M.J., van der Veen, F., and Repping, S. (2011). Chromosomal mosaicism in human preimplantation embryos: a systematic review. Hum. Reprod. Update 17, 620–627.
4. van der Meij, K.R.M., Sistermans, E.A., Macville, M.V.E., Stevens, S.J.C., Bax, C.J., Bekker, M.N., Bilardo, C.M., Boon, E.M.J., Boter, M., Diderich, K.E.M., et al.; Dutch NIPT Consortium (2019). TRIDENT-2: National Implementation of Genome-wide Non-invasive Prenatal Testing as a First-Tier Screening Test in the Netherlands. Am. J. Hum. Genet. 105, 1091–1101.
5. Van Den Bogaert, K., Lannooy, L., Brison, N., Gatinos, V., Baetens, M., Blaumpeiser, B., Boemer, F., Bourlard, L., Bours, V., De Leener, A., et al. (2021). Outcome of publicly funded nationwide first-tier noninvasive prenatal screening. Genet. Med. 23, 1137–1142.
6. Hsu, L.Y.F., Yu, M.T., Richkind, K.E., Van Dyke, D.L., Crandall, B.F., Saxe, D.E., Khodr, G.S., Mennuti, M., Stetten, G., Miller, W.A., and Priest, J.H. (1996). Incidence and significance of chromosome mosaicism involving an autosomal structural abnormality diagnosed prenatally through amniocentesis: a collaborative study. Prenat. Diagn. 16, 1–28.
7. Singla, S., IWamoto-Stohl, L.K., Zhu, M., and Zernicka-Goetz, M. (2020). Autophagy-mediated apoptosis eliminates
aneuploid cells in a mouse model of chromosome mosaicism. Nat. Commun. 11, 2958.
8. Bolton, H., Graham, S.J.L., Van der Aa, N., Kumar, P., Theunis, K., Fernandez Gallardo, E., Voet, T., and Zernicka-Goetz, M. (2016). Mouse model of chromosome mosaicism reveals lineage-specific depletion of aneuploid cells and normal developmental potential. Nat. Commun. 7, 11165.
9. Capalbo, A., Hoffmann, E.R., Camiadomo, D., Ubaldi, F.M., and Rienzi, L. (2017). Human female meiosis revised: new insights into the mechanisms of chromosome segregation and aneuploidies from advanced genomics and time-lapse imaging. Hum. Reprod. Update 23, 706–722.
10. Munne, S., Blazek, J., Large, M., Martinez-Ortiz, P.A., Nisson, H., Liu, E., Tarozzi, N., Borini, A., Becker, A., Zhang, J., et al. (2017). Detailed investigation into the cytogenetic constitution and pregnancy outcome of replacing mosaic blastocysts detected with the use of high-resolution next-generation sequencing. Fertil. Steril. 108, 62–71.e8.
11. Cram, D.S., Leigh, D., Handyside, A., Handyside, A., Xu, K., Harrington, L., Tan, G., Grifo, J., Rubio, C., Fragouli, E., Kahraman, S., et al. (2019). PGDS position statement on the transfer of mosaic embryos 2019. Reprod. Biomed. Online 39 (Suppl 1), e1–e4.
12. Practice Committee and Genetic Counseling Professional Group (GCPG) of the American Society for Reproductive Medicine. Electronic address: asm@asrm.org (2020). Clinical management of mosaic results from preimplantation genetic testing for aneuploidy (PGT-A) of blastocysts: a committee opinion. Fertil. Steril. 114, 246–254.
13. Zamani Esteki, M., Viltrop, T., Tsuiko, O., Tiirats, A., Koel, M., Nõuks, M., Zilina, O., Teearu, K., Marjonen, H., Kahila, H., et al. (2019). In vitro fertilization does not increase the incidence of de novo copy number alterations in fetal and placental lineages. Nat. Med. 25, 1699–1705.
14. Huang, A., Adusumalli, J., Patel, S., Liem, J., Williams, J., 3rd, and Pisarska, M.D. (2021). Lack of evidence to support recommendation for prenatal uniparental disomy (UPD) testing for aneuploidy (PGT-A) and imbalances in PGT-SR. Genes (Basel) 11, 724.
15. García-Pascual, C.M., Navarro-Sánchez, L., Navarro, R., Martínez, L., Jiménez, J., Rodrigo, L., Simón, C., and Rubio, C. (2020). Optimized NGS approach for detection of aneuploidies and mosaicism in PGT-A and imbalances in PGT-SR. Genes (Basel) 11, 724.
16. Girardi, L., Serdarogullari, M., Patassini, C., Poli, M., Fabiani, M., Caroselli, S., Coban, O., Findikli, N., Boynukalin, F.K., Bahceci, M., et al. (2020). Incidence, Origin, and Predictive Model for the Detection and Clinical Management of Segmental Aneuploidies in Human Embryos. Am. J. Hum. Genet. 106, 525–534.
17. Coorens, T.H.H., Oliver, T.R.W., Sanghvi, R., Sovio, U., Cook, E., Vento-Tormo, R., Haniffa, M., Young, M.D., Rahbari, R., Sebire, N., et al. (2021). Inherent mosaicism and extensive mutation of human placenta. Nature 592, 80–85.