

# Segmental aneuploid embryos and management strategies for transfer

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- 2. Frequency at different developmental stages >
- 3. Nature and origin of segmental aneuploidies detected in PGT >
- 4. Transfer outcomes of segmental aneuploidies >
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- >

# **Background and definitions**

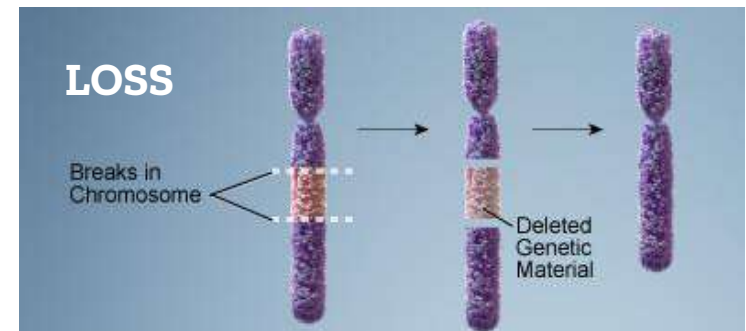
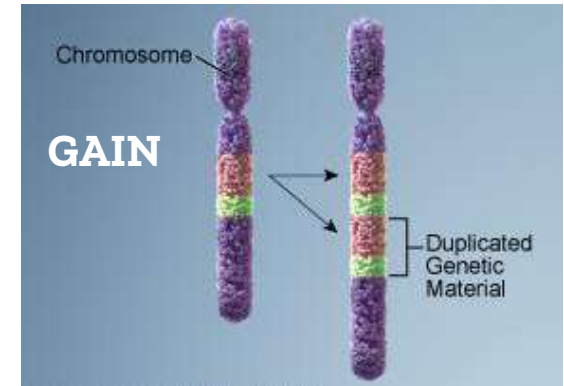
# Background

## SEGMENTAL ANEUPLOIDIES in PGT

Sub-chromosomal copy number changes involving the gain or loss of a portion of the chromosome

- No clear embryologic phenotype
- The majority occur de novo in the embryo, involving any of the 24 chromosomes

5-10Mb  
Resolution in  
PGT



Inherited from parents with abnormal karyotype

Mis-segregation of translocations/inversions

Expected fragments involved

The diagram shows two chromosomes, labeled "Chromosome A" and "Chromosome B", on the left. An arrow points to a second set of chromosomes on the right, which are labeled "Balanced Translocation". The chromosomes in the second set are rearranged, showing segments from both Chromosome A and Chromosome B. The text "U.S. National Library of Medicine" is visible in the bottom left corner of the diagram.

# **Frequency of segmental aneuploidies in oocytes and preimplantation embryos**

# Incidence of segmental aneuploidies in oocytes, cleavage and blastocyst stage embryos

Human Reproduction, Vol.32, No.12 pp. 2549-2560, 2017  
Advanced Access publication on November 8, 2017 doi:10.1093/humrep/dex324

human  
reproduction

ORIGINAL ARTICLE Reproductive genetics

## The incidence and origin of segmental aneuploidy in human oocytes and preimplantation embryos

D. Babariya<sup>1,2,\*</sup>, E. Fragouli<sup>1,2</sup>, S. Alfarawati<sup>1</sup>, K. Spath<sup>1,2</sup>, and D. Wells<sup>1,2</sup>

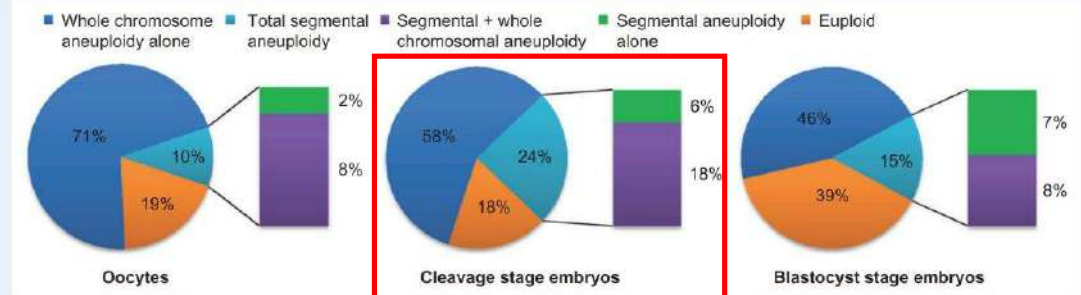
The prevalence of SA decreases as the embryo progresses through its developmental stages

The rates of segmental aneuploidies peak in early mitotic divisions

Table III Prevalence of oocytes/embryos affected by segmental abnormality.

| Stage analysis performed | Number of oocytes/embryos with a segmental aneuploidy | Ratio of loss:gain of material |
|--------------------------|---|--------------------------------|
| Oocyte                   | 47 (10.39%) <sup>a,b</sup>                            | 0.5 (30/60)                    |
| Cleavage stage           | 428 (24.29%) <sup>a,c</sup>                           | 1.38 (324/234)                 |
| Blastocyst               | 207 (15.59%) <sup>b,c</sup>                           | 1.57 (168/107)                 |

Statistical comparisons, using Fisher's exact test: (a)  $P < 0.0001$ ; (b)  $P = 0.0207$ ; (c)  $P < 0.0001$ .



**Figure 3** The frequency of segmental aneuploidy increased significantly from oocytes to the cleavage stage embryos but decreased from cleavage to blastocyst stages. Most of the segmental imbalances occurred along with other whole chromosomal aneuploidies with 8.4% (38/452) in oocytes, 18.4% (352/1762) in cleavage stage embryos and 8.1% (108/1327) at blastocyst stage. It was rare to see segmental aneuploidies occurring alone in oocytes (9/452; 1.99%) however, this was seen significantly more often at the cleavage (103/1762; 5.85%;  $P = 0.013$ ) and blastocyst stages (99/1327; 7.46%;  $P < 0.0001$ ). No significant difference was observed in the occurrence of segmental aneuploidy alone between cleavage and blastocyst stage embryos.



# Incidence and features of de novo segmental aneuploidies detected in preimplantation embryos

Incidence of segmental aneuploidy in blastocyst-stage preimplantation embryos.

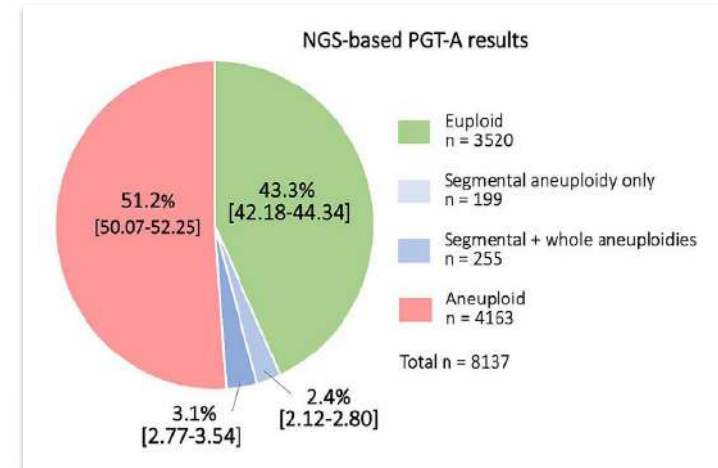
| Incidence of SA in blastocyst-stage embryos |                          |                         |                 |              |
|---|--------------------------|-------------------------|-----------------|--------------|
| Reference                                   | Total no. of blastocysts | SA-positive blastocysts | Incidence of SA | Platform     |
| McCarthy et al., 2022 (27)                  | 89,226                   | 2,766                   | 3.10%           | NGS          |
| Babariya et al., 2017 (28)                  | 1,327                    | 207                     | 15.60%          | aCGH         |
| Tiegs et al., 2021 (18)                     | 2,110                    | 186                     | 8.82%           | tNGS         |
| Escribà et al., 2019 (26)                   | 3,565                    | 299                     | 8.39%           | NGS          |
| Zore et al., 2019 (30)                      | 377                      | 20                      | 5.31%           | aCGH         |
| Kubicek et al., 2019 (17)                   | 967                      | 54                      | 5.58%           | Karyomapping |
| Rechitsky et al., 2020 (35)                 | 14,992                   | 2,099                   | 14.00%          | NGS          |
| Girardi et al., 2020 (24)                   | 8,137                    | 653                     | 8.03%           | NGS          |
| Zuffardi et al., 2022 (31)                  | 1,501                    | 79                      | 5.26%           | NGS          |
| Vialard et al., 2022 (32)                   | 182,827                  | 20,557                  | 11.24%          | FAST-SeqS    |
| Robberecht et al., 2021 (33)                | 1,708                    | 97                      | 5.68%           | NGS          |
| Zhou et al., 2018 (25)                      | 2,095                    | 206                     | 9.83%           | NGS          |
| Xie et al., 2022 (21)                       | 15,411                   | 2,273                   | 14.75%          | NGS          |
| Dviri et al., 2020 (34)                     | 3,118                    | 104                     | 3.34%           | NGS          |
| Insua et al., 2018 (29)                     | 3,628                    | 314                     | 8.65%           | NGS          |
| Mean incidence of SA                        | -                        | -                       | 8.51%           | -            |

Picchetta et al. F&S Science, 2023

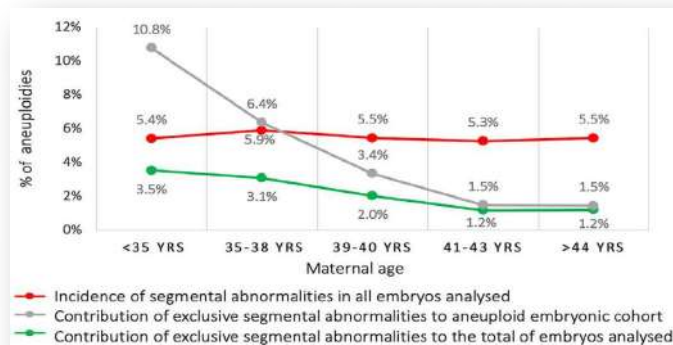
Mean incidence of SA 8.5%

15%

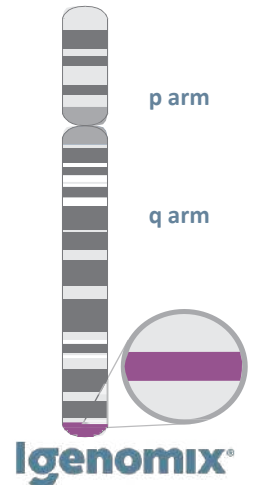
3%



Girardi et al, AJHG 2020



- SA's incidence does not increase with maternal age
- SA appear to be more frequent in the q arm
- SA are more frequently telomeric than interstitial



# Impact of segmental aneuploidies in later stages of development

- In PRENATAL DIAGNOSIS

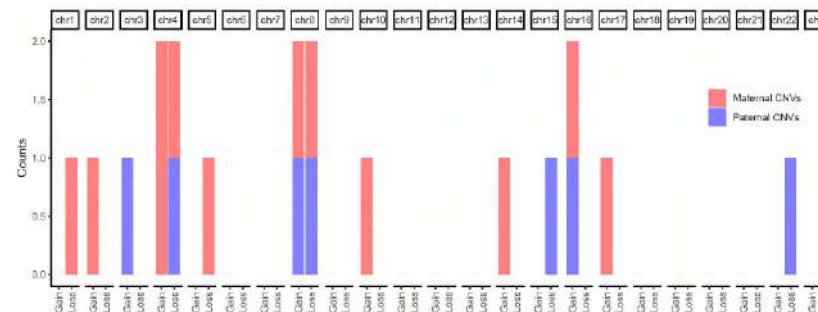
Mean incidence  
3.5%

| Reference                  | Analyzed samples | Prenatal incidence of SA |                 | Platform       |
|----------------------------|------------------|--------------------------|-----------------|----------------|
|                            |                  | SA-positive samples      | Incidence of SA |                |
| Breman et al., 2012 (65)   | 1,115            | 43                       | 3.80%           | CMA            |
| Farcas et al., 2013 (66)   | 528              | 12                       | 2.27%           | Karyotype/FISH |
| Levy et al., 2014 (67)     | 1,861            | 43                       | 2.30%           | SNP array      |
| Shen et al., 2016 (68)     | 436              | 23                       | 5.30%           | aCGH and NGS   |
| Sahoo et al., 2017 (69)    | 7,396            | 181                      | 2.40%           | SNP array/aCGH |
| Wang et al., 2018 (16)     | 3,398            | 41                       | 1.20%           | CNV-Seq        |
| Peng et al., 2019 (70)     | 836              | 40                       | 4.80%           | aCGH           |
| Lini et al., 2020 (71)     | 10,377           | 223                      | 2.10%           | SNP array      |
| Kowalczyk et al., 2022(72) | 7,400            | 579                      | 7.80%           | aCGH           |
| Mean incidence of SA       | -                | -                        | 3.55%           | -              |

Picchetta et al. F&S Science, 2023

- In PREGNANCY LOSS  
Size: 200kb-100Mb

1.3%



Arnadottir, G.A., Jonsson, H., Hartwig, T.S. et al. Sequence diversity lost in early pregnancy. Nature (2025).

- In the FETUS:

0.45%\*

Schlaikjær Hartwig, 2023, Lancet

- At BIRTH:

0.015%\*

Extrapolated from UK Biobank

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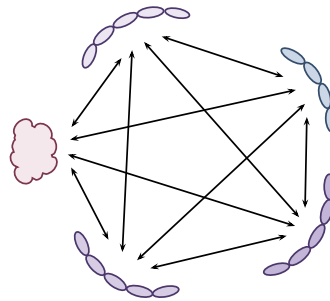
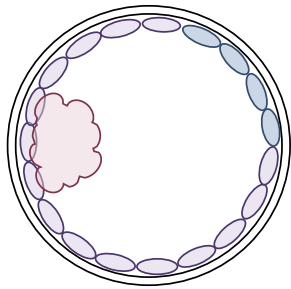
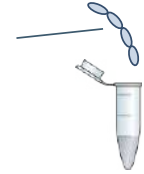


# Nature and origin of segmental aneuploidies in PGT

# cell divisions origin of aneuploidies: multifocal biopsies in the research setting

**Design: embryo disaggregation  
models and NGS-based PGT-A analysis**

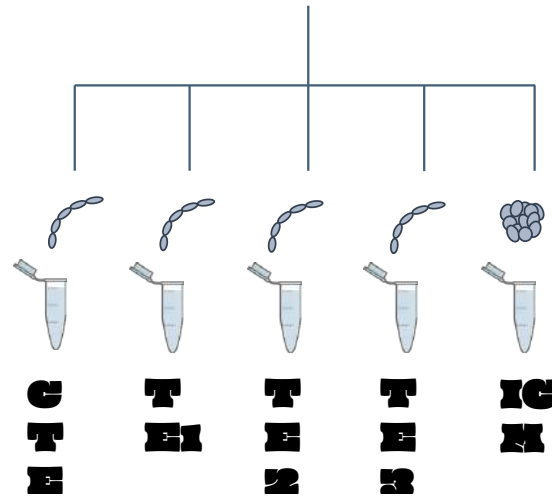
**Initial PGT-A  
result:  
segmental  
aneuploidy**



**CLINICAL  
TROPHOBLASTIC  
BIOPSY (TE)  
MULTIFOCAL  
BIOPSIES (TE  
1,2,3)**

**embryos  
donated for  
research**

**multifocal  
biopsies**



# Cell divisions origin of aneuploidies: multifocal biopsies in the research setting

Concordance rate of SA findings in PGT-A.

| Reference                  | Concordance rate of SA in PGT-A |                  |                  |                 |
|----------------------------|---------------------------------|------------------|------------------|-----------------|
|                            | Platform                        | Embryo stage     | Concordance rate | Absolute values |
| Chuang et al., 2018 (47)   | NGS                             | Blastocyst       | 55.50%           | 5/9             |
| Popovic et al., 2019 (48)  | NGS                             | Outgrowth 12 dpf | 38.46%           | 5/21            |
| Victor et al., 2019 (49)   | NGS                             | Blastocyst       | 44.40%           | 4/9             |
| Lawrenz et al., 2019 (50)  | NGS                             | Blastocyst       | 16.70%           | 1/6             |
| Navratil et al., 2020 (46) | NGS                             | Blastocyst       | 36.80%           | 14/38           |
| Girardi et al., 2020 (24)  | NGS                             | Blastocyst       | 32.10%           | 17/53           |
| Sachdev et al., 2020 (51)  | NGS                             | Blastocyst       | 0                | 0/12            |
| Kim et al., 2021 (11)      | NGS                             | Blastocyst       | 21.30%           | 36/196          |
| Mean concordance rate      | -                               | -                | 30.66%           | -               |

Picchetta et al. F&S Science, 2023

Mean concordance rates  
~30%

## SEGMENTAL ANEUPLOIDIES CONFIGURATIONS

### Uniform concordance



32.1%  
[19.92-46.32]

Meiotic  
32.1%

### Partial concordance

4/7, 1 discordant sample  
2/7, 2 discordant samples  
1/7, 3 discordant samples



13.2%  
[5.48-25.34]

Mitotic/  
mosaic  
67.9%

### Reciprocal segmental



5.7%  
[1.18-15.66]

### Confined to TE

2/5, 4 TE segmental  
3/5, 3 TE segmental



9.4%  
[3.13-20.66]

### Low grade mosaic or artefact



39.6%  
[26.45-54.00]

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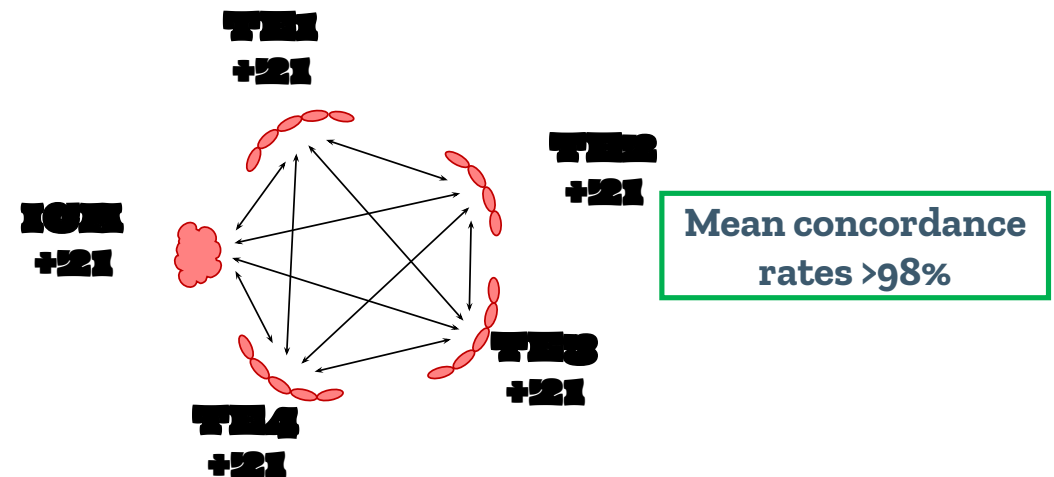
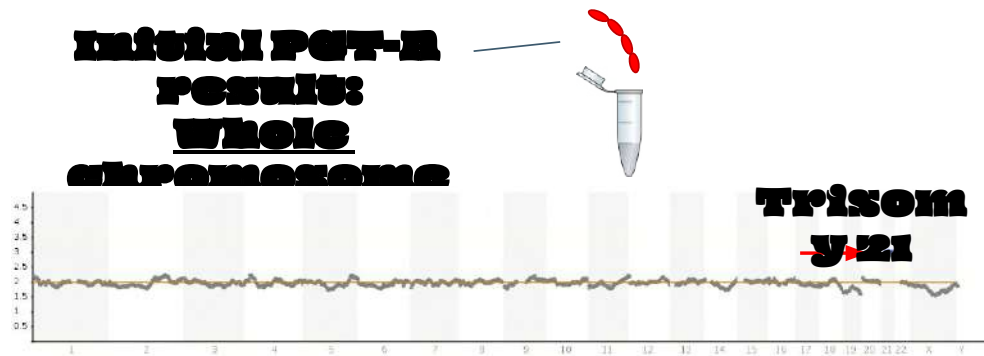
Girardi et al 2020. American Journal of Human Genetics

### Legend



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# Cell divisions origin of whole chromosome aneuploidies



1

Concordance rates of SA between multiple TE biopsies as well as vs ICM are significantly reduced compared to whole chromosome aneuploidies

2

Different etiology for subchromosomal alterations: more frequently mitotic in nature, arising during the first embryonic cell divisions. Mosaic in preimplantation embryos

# How to move to the clinical setting: additional parameters to better classify SA

Clinical application of a risk stratification model

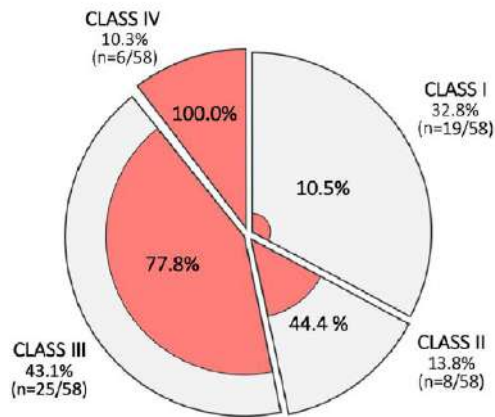
Re-biopsy, euploid transfer and pregnancy follow-up

(WGA)-based NGS  
PGT-A

**Length of the region involved**

**Re-biopsy result**

Correlation between cTE/scTE confirmation status, segmental size and ICM concordance



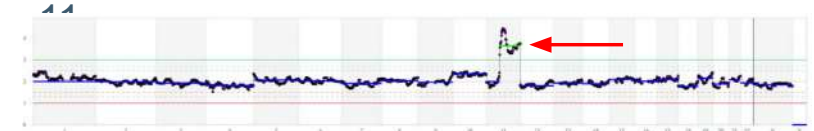
Likelihood of ICM involvement

| CLASS | DETAILS  |
|-------|--|
| I     | <ul style="list-style-type: none"><li>NOT confirmed in scTE</li><li>Length ≤80.0 Mb</li></ul>    |
| II    | <ul style="list-style-type: none"><li>NOT confirmed in scTE</li><li>Length &gt;80.0 Mb</li></ul> |
| III   | <ul style="list-style-type: none"><li>Confirmed in scTE</li><li>Length ≤80.0 Mb</li></ul>        |
| IV    | <ul style="list-style-type: none"><li>Confirmed in scTE</li><li>Length &gt;80.0 Mb</li></ul>     |

**Girardi et al, BJOG 2020**

Re-biopsying the embryo can be an option for obtaining a more reliable clinical diagnosis if a SA is detected in PGT

1<sup>st</sup> Biopsy: 82.5 Mb duplication on chr 14



**Viotti et al, JNRC 2025**

2<sup>nd</sup> Biopsy: Euploid

Genetic counselling + specialized informed consent outlining the associated risks

**Embryo transfer**

At week 13, amniocentesis was performed

Cytogenetic  
**46,XX**

SNP microarray  
**arr(X,1-22) × 2**

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# How to move to the clinical setting: additional parameters to better classify SA

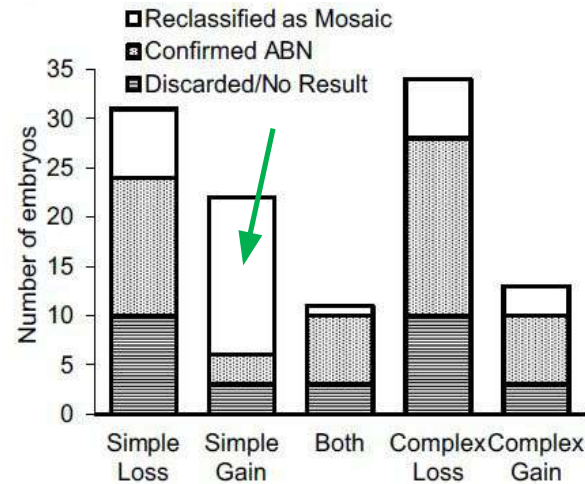
## Clinical re-biopsy and type of alteration: gains vs losses

Journal of Assisted Reproduction and Genetics (2022) 39:1313–1322  
https://doi.org/10.1007/s10815-022-02487-z

### GENETICS

#### Clinical re-biopsy of segmental gains—the primary source of preimplantation genetic testing false positives

Steve Grkovic<sup>1</sup> · Maria V. Traversa<sup>1</sup> · Mark Livingstone<sup>1</sup> · Steven J. McArthur<sup>1</sup>



72.7% simple **segmental gains** were reclassified as mosaic (vs 22.6% of single loss)

### ARTICLE

#### Incidence, Origin, and Predictive Model for the Detection and Clinical Management of Segmental Aneuploidies in Human Embryos

Laura Girardi,<sup>1</sup> Muneevver Serdarogullari,<sup>2</sup> Cristina Patassini,<sup>1</sup> Maurizio Poli,<sup>1</sup> Marco Fabiani,<sup>1</sup> Silvia Caroselli,<sup>1</sup> Onder Coban,<sup>2</sup> Necati Findikli,<sup>3,4</sup> Fazilet Kubra Boynukalin,<sup>5</sup> Mustafa Bahceci,<sup>5</sup> Rupali Chopra,<sup>6</sup> Rita Canipari,<sup>7</sup> Danilo Cimadomo,<sup>8</sup> Laura Rienzi,<sup>6</sup> Filippo Ubaldo,<sup>9</sup> Eva Hoffmann,<sup>9</sup> Carmen Rubio,<sup>10</sup> Carlos Simon,<sup>10,11,12,13</sup> and Antonio Capalbo<sup>1,7,10\*</sup>

**Reclassification of 88% segmental gains vs 37% losses**

**ICM involvement : 27% segmental gains vs 74% segmental losses**

**SEGMENTAL MONOSOMIES**  
are more likely to be confirmed in a 2<sup>nd</sup> biopsy and in the ICM



# Transfer outcomes of non-mosaic segmental aneuploid embryos

# Transfer outcomes of non-mosaic segmental aneuploidies

A multicenter, prospective, blinded, nonselection study evaluating the predictive value of an aneuploid diagnosis using a targeted next-generation sequencing–based preimplantation genetic testing for aneuploidy assay and impact of biopsy

Adley W. Tiegs, M.D.,<sup>a,b</sup> Xin Tao, Ph.D.,<sup>c</sup> Yiping Zhan, Ph.D.,<sup>c</sup> Christine Whitelwood, R.N.,<sup>c</sup> Julia Kim, M.D.,<sup>a,b</sup> Brent Hanson, M.D.,<sup>a,b</sup> Emily Osman, M.D.,<sup>a,b</sup> Thomas J. Kim, M.D.,<sup>a</sup> George Patounakis, M.D., Ph.D.,<sup>a</sup> Jacqueline Guzmán, M.D.,<sup>a</sup> Arthur Castelbaum, M.D.,<sup>a</sup> Emre Seli, M.D.,<sup>a,c</sup> Chaim Jales,<sup>a</sup> and Richard T. Scott Jr., M.D.<sup>a,b</sup>

**Design : Non-selection study**

**PGT-A platform/technology: target NGS**

**Number of embryos transfer: 39  
embryos with uniform segmental aneuploidies**

**Sustained implantation rate : 30.8%  
(n=12/39)**

**Design : Retrospective**

**Follow-up: no  
PGT-A platform/technology: NGS,  
SNP array, Array CGH**

**Number of embryos transfer: 25  
embryos with non-mosaic  
segmental aneuploidies**

**Live birth rate : 24.0% (n=6/25)**

**Prenatal testing : 4/6 live birth  
tested and normal (CVS, Amnio or  
cDNA)**

Journal of Assisted Reproduction and Genetics  
<https://doi.org/10.1007/s10815-024-03282-8>

ASSISTED REPRODUCTION TECHNOLOGIES

Healthy live births achieved from embryos diagnosed as non-mosaic segmental aneuploid

Andria Besser<sup>1</sup> · Emily Weidenbaum<sup>2</sup> · Julia Buldo-Licciardi<sup>2</sup> · Caroline McCaffrey<sup>1</sup> · James Grifo<sup>1</sup> · Jennifer Blakemore<sup>1</sup>

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# What do we know about transfer outcomes of uniform whole chromosome aneuploidies

**Table 1. Published non-selection and cohort study outcome data involving transfer of full aneuploid embryos for whole chromosomes**

| Study                   | Design    | Transfers of uniformly aneuploid embryos n <sup>a</sup> | Miscarriage rate % (n, 95% CI)           | Lethality rate % (n, 95% CI)     |
|-------------------------|-----------|---|--|----------------------------------|
| Scott et al., 2012 (45) | blinded   | 95  | 33.3% (2/6)<br>(4.3%–77.7%) <sup>b</sup> | 95.8% (91/95)<br>(84.5%–99.4%)   |
| Tiegs et al., 2021 (40) | blinded   | 102   | 100% (24/24)<br>(85.8%–100%)             | 100% (102/102)<br>(96.5%–100%)   |
| Wang et al., 2021 (41)  | blinded   | 44  | 75.0% (6/8)<br>(34.9%–96.8%)             | 95.5% (42/44)<br>(84.5%–99.4%)   |
| Yang et al., 2022 (44)  | blinded   | 6   | 100% (6/6)<br>(54.1%–100%)               | 100% (6/6)<br>(54.1%–100%)       |
| Barad et al., 2022 (46) | unblinded | 106   | 85.7% (6/7)<br>(42.1%–99.6%)             | 99.1% (105/106)<br>(94.9%–99.9%) |
| Total                   | N/A       | 353   | 86.3% (44/51)<br>(73.7%–94.3%)           | 98.0% (346/353)<br>(96.0%–99.2%) |

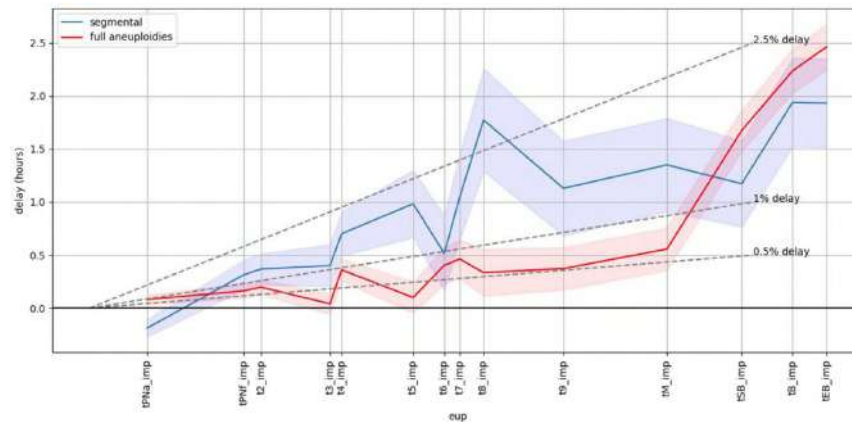
<sup>a</sup>Embryos with at least one whole-chromosome aneuploidy in the uniform range (non-mosaic).

<sup>b</sup>Post-transfer polar body analysis revealed likely mitotic (mosaic) origin of the aneuploidy detected through PGT-A.

**Lethality rate:  
98%**

# Research and future perspectives

## Adding time-lapse and morphokinetic analysis to predict segmental aneuploid embryos



Figliuzzi et.al, Fertil Steril  
2025

Blastocysts with SA and WCA exhibit a delay in reaching the expanded blastocyst-stage compared with euploid.

SA embryos have a distinct morphokinetic signature

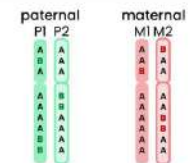
Segmental score: specificity 92.5% sensitivity 20.0%

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## Adding genotyping data and parental DNA analysis in PGT to better predict the origin of aneuploidy

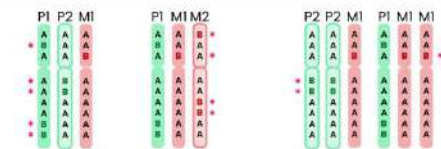
### Cell Division Origin of Aneuploidy

1. Identify informative SNPs where there is a unique allele (i.e., 1 b-allele and 3 a-alleles)

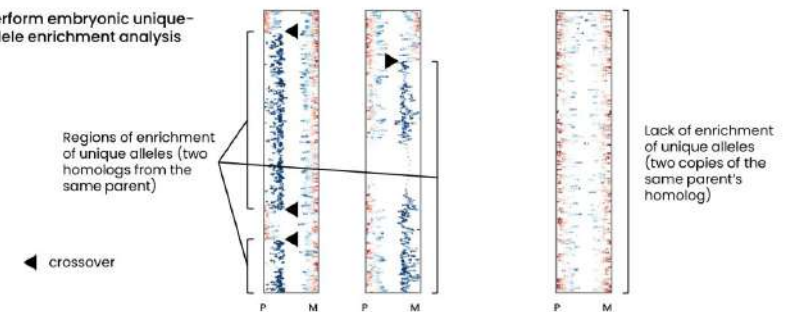


2. Consider possible trisomy chromosome inheritance outcomes

\* unique allele present



3. Perform embryonic unique-allele enrichment analysis



4. Predict cell division origin of aneuploidy

Paternal Meiotic Trisomy  
Maternal Meiotic Trisomy  
Paternal Mitotic (Embryonic) Trisomy  
Maternal Mitotic (Embryonic) Trisomy

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# conclusions and management strategies for transfer

# Conclusions and management strategies for transfer

Historically, embryos diagnosed as segmental aneuploid have been categorized alongside whole chromosome aneuploid embryos and considered unsuitable for transfer.

→ SA should be considered as a separate category compared to WCA and should be subjected to different interpretation and ad-hoc management strategies.

## MANAGEMENT STRATEGIES FOR UNIFORM SEGMENTAL ANEUPLOIDIES

- Deletions/duplications can be associated with a wide range of phenotypes: genetic syndromes, embryonic lethality, miscarriage, no clinical consequences
- Transfer outcomes of uniform segmental aneuploidies are limited but...transfer “**may be considered**” as 25-30% success rate is significantly different from <1% of uniform WCA
- The assessment of a **second TE biopsy** can enhance predictivity on ICM constitution and empowering the decision-making process
- Risks associated with double round of re-biopsy and vitrification should be considered and commented



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**THANKS FOR  
YOUR  
ATTENTION**