

Preimplantation genetic diagnosis for couples at high risk of Down syndrome pregnancy owing to parental translocation or mosaicism

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Abstract

The population risk for trisomy 21 is 1 in 700 births but some couples are at a much higher risk owing to parental translocation or mosaicism. We report on the first attempt to carry out preimplantation genetic diagnosis for two such couples using cleavage stage embryo biopsy and dual colour FISH analysis. Each couple underwent two treatment cycles. Couple 1 (suspected gonadal mosaicism for trisomy 21) had two embryos normal for chromosome 21 transferred, but no pregnancy resulted; 64% (7/11) unfertilised oocytes/embryos showed chromosome 21 aneuploidy. Couple 2 (46,XX,t(6;21)(q13;q22.3)) had a single embryo transferred resulting in a biochemical pregnancy; 91% (10/11) oocytes/embryos showed chromosome 21 imbalance, most resulting from 3:1 segregation of this translocation at gametogenesis. The opportunity to test embryos before implantation enables the outcome of female meiosis to be studied for the first time and the recurrence risk for a Down syndrome pregnancy to be assessed.

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The recurrence risk of a Down syndrome pregnancy after the birth of an affected child is approximately 1-2%¹ and studies have shown that while the majority of second trisomy 21 pregnancies may be the result of chance alone,² cytogenetic analysis is necessary to exclude parental translocation or mosaicism. In cases where such predisposing factors are present, parents can usually achieve a normal pregnancy with the help of prenatal diagnosis. However, a minority suffer repeated pregnancy termination following trisomy 21 conception and these couples are coming forward for genetic diagnosis before implantation to avoid later abortion.

Preimplantation genetic diagnosis (PGD) involves the screening of in vitro fertilisation (IVF) generated embryos by the genetic analysis of one or two biopsied blastomeres. Following the transfer of only those embryos that are diagnosed as unaffected, couples at high risk of transmitting single gene defects or chromosomal abnormalities can begin a pregnancy in the knowledge that it is not affected by the familial disorder.³ Fluorescent in situ hybridisation (FISH) is now the technique of choice

for detecting the chromosome status in single cells for PGD and has been used successfully both for sexing embryos to avoid X linked disease⁴⁻⁵ and to screen embryos for age related aneuploidy for older women undergoing IVF.⁶⁻⁸ In contrast, the aim of the treatment cycles presented here was to screen for specific imbalance of chromosome 21 from abnormal segregation of translocation chromosomes or mosaicism for individual patients. Although a wider selection of commercial probes is now becoming available, the development of suitable probe combinations is expensive and labour intensive. This means that, particularly for reciprocal translocation carriers, each case prepared for PGD requires individual research time dedicated to it. These factors probably account for the limited number of cycles which have been carried out to date, including those reported for carriers of Robertsonian translocations⁹⁻¹⁰ and chromosomal inversions.¹¹

Fluorochrome labelled α satellite probes give intense FISH signals and allow the use of a rapid two hour technique for PGD.¹² Unfortunately, the lack of specific repeat probes for chromosomes 13, 14, 21, and 22, because of centromeric sequence homology, means that locus specific probes remain the only choice for accurately detecting the acrocentric chromosomes in interphase nuclei. For this reason, we have evaluated combinations of two differentially labelled YAC and cosmid probes specific for chromosome 21 in somatic cells and in spare IVF embryos donated for research. As has been shown in previous studies detecting trisomy 21 in uncultured amniocytes, this dual labelling of a single chromosome greatly increases the accuracy of diagnosis¹³⁻¹⁴ and this is a particularly important consideration for PGD based only on one or two biopsied cells.

We present data on FISH analysis of chromosome 21 status in preimplantation embryos from four IVF cycles for two couples at high risk of a Down syndrome pregnancy owing to a balanced reciprocal translocation in one case and suspected gonadal mosaicism for trisomy 21 in the other.

Subjects, materials, and methods

ETHICAL APPROVAL

The preliminary study on surplus untransferred embryos and the clinical application of PGD were approved by the Human Fertilisation and Embryology Authority and the Research Ethics Committee of the Royal Postgraduate Medical School, Hammersmith Hospital. Informed written consent was obtained

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Table 1 Probe details

Probe	Type	Insert size	Location	Source
y940	YAC	1150 kb	21q22.2	HGMP
yGART2	YAC	600 kb	21q22.1	Gnirke <i>et al</i> ²⁰
cCMP 21.a	Cosmid contig	55 kb	21q22.3	Zheng <i>et al</i> ²¹
c242c	Cosmid contig	80 kb	21q22.3	Davies <i>et al</i> ¹³
cCMP 9.27	Cosmid	—	9qh	N Carter
D6Z1	Plasmid	—	6 centromere	Oncor

HGMP = Human Genome Mapping Project Resource Centre, Hinxton Hall, Cambridge, UK. N Carter, University of Cambridge, Cambridge, UK.

from patients for surplus embryos to be used for research purposes.

SPARE IVF EMBRYOS

Eighteen day 3 post-insemination embryos, surplus to IVF requirements and donated for research, were used in the preliminary work. All were normally fertilised (presence of two pronuclei 18 hours post-insemination) and scored as of good morphology (less than 25% blastomere fragmentation).

PATIENTS

Two couples at high risk of a Down syndrome pregnancy underwent a total of four PGD cycles (two standard IVF cycles and two intracytoplasmic sperm injection (ICSI) cycles). Both couples were counselled about the PGD procedure and the need to confirm diagnosis with prenatal diagnosis.

Couple 1

Although couple 1 have one normal child, they were referred for PGD after three trisomy 21 conceptions (two terminations of pregnancy and a Down syndrome child). DNA polymorphism analysis proved maternal origin of the extra chromosome in two cases and was compatible with maternal gonadal mosaicism. However, this could not be proven by somatic studies since the mosaicism appeared to have a mitotic origin (P Farndon, personal communication). FISH analysis did not detect a second trisomic cell line in lymphocytes of either partner. Maternal age was 36 years.

Couple 2

Couple 2 were referred for PGD owing to maternal balanced reciprocal translocation 46,XX,t(6;21)(q13;q22.3) detected after four early spontaneous abortions and the birth of a Down syndrome daughter (karyotype: 47,XX,t(6;21)(q13;q22.3),+21). Maternal age was 32 years.

PREIMPLANTATION GENETIC DIAGNOSIS (PGD)

Couples underwent routine IVF¹⁵ or ICSI¹⁶ and PGD was carried out as we have described previously.⁴ Briefly, patients underwent superovulation and oocyte retrieval was carried out by vaginal ultrasound guided aspiration. Oocytes were inseminated with a prepared sample of partner's sperm or subjected to ICSI and assessed for normal fertilisation after 15 to 18 hours (day 1). Embryos were cultured in vitro until day 3 post-insemination when the majority had reached the 6-10 cell stage. At this time embryo biopsy was performed by gentle aspiration of one or two blastomeres through a

hole made in the zona pellucida as described by Handyside.¹⁷ Two blastomeres were only removed from embryos of six cells or more. After biopsy, embryos were immediately returned to normal culture conditions.

SLIDE PREPARATION

Biopsied blastomeres for PGD and whole day 3 post-insemination embryos for the preliminary work were spread using the same method described in detail previously.^{12,18} In brief, cells were transferred to poly-L-lysine slides in spreading solution (0.01 N HCl, 0.1% Tween 20) which was gently agitated until lysis occurred and all nuclei were clear of cytoplasm.

Unfertilised oocytes were analysed 48 hours after insemination and spread using the air drying method of Tarkowski.¹⁹

Control slides of metaphase and interphase nuclei were prepared from phytohaemagglutinin stimulated human peripheral lymphocytes using standard cytogenetic techniques.

DNA PROBES

Probes used in this study are listed in table 1. YAC probes were obtained from total genomic yeast DNA amplified by Alu-PCR as described by Lengauer *et al*.²² Cosmid probes were isolated from bacterial strains using a commercial maxiprep protocol (Wizard, Promega, USA). All probes were labelled via nick translation with biotin-14-dATP (Bionick labelling system, BRL, UK) or digoxigenin-11-dUTP (Nick translation system, Boehringer Mannheim, Germany) or both. Working concentrations of probe DNA were YACS 20 ng/μl and cosmids 15 ng/μl.

FLUORESCENT IN SITU HYBRIDISATION (FISH)

The FISH technique was carried out as we have previously described.¹⁰ Briefly, slides were pretreated by incubation in 100 μg/ml pepsin in 0.01 N HCl at 37°C for 20 minutes and fixation in 1% paraformaldehyde in PBS at 4°C for 10 minutes. Combinations of probes were applied to dehydrated slides in a final 10 μl volume under a coverslip, sealed with rubber cement, denatured simultaneously with nuclear DNA at 75°C for five minutes, and allowed to hybridise overnight (approximately 16 hours) at 37°C. Post-hybridisation washes were carried out at 45°C in 50% formamide/2 × SSC followed by 2 × SSC (3 × 3 minutes each). Signal detection and amplification were carried out via three sequential incubations: biotin labelled probes detected with FITC-avidin/biotinylated anti-avidin/FITC-avidin and digoxigenin labelled probes detected with mouse-anti-digoxin/TRITC-rabbit-anti-mouse/TRITC-goat-anti-rabbit IgG. Slides were then mounted in antifade medium (Vector Laboratories, USA) containing 1.25 μg/ml 4',6-diamidino 2 phenylindole (Sigma, UK) counterstain.

DIAGNOSIS

FISH signals were scored according to the criteria of Hopman *et al*²³ using a Reichert Jung Polyvar fluorescence microscope. Image capture was carried out using a Zeiss Axioskop 20

Table 2 Dual colour FISH analysis of chromosome 21 in spare IVF embryos for preliminary work

Probes tested	Uniformly normal	Diploid mosaic	Aneuploid mosaic	Chaotic
Chr 21 YACS	8	2	0	0
Chr 21 cosmids	5	1	1	1
Total 18 (100%)	13 (72%)	3 (17%)	1 (5.5%)	1 (5.5%)

microscope equipped with a cooled CCD camera controlled by Smartcapture software (Vysis, UK). Only embryos from which two biopsied blastomeres were diagnosed as normal for chromosome 21 were recommended as suitable for transfer on day 4 post-insemination. Remaining untransferred embryos were spread (day 4) and analysed to assess levels of mosaicism. Embryos were categorised after Delhanty *et al*⁷ as: normal (uniformly normal), diploid mosaic (majority of cells normal but one or a few cells differ), aneuploid (uniformly aneuploid), aneuploid mosaic (majority aneuploid but one or a few cells differ), or chaotic (chromosome constitution varies randomly from cell to cell and status of original zygote cannot usually be determined).

REPROBING OF UNTRANSFERRED EMBRYOS

Untransferred embryos and biopsied cells were reanalysed after the initial FISH analysis for PGD by reprobng with a chromosome 9 or chromosome 6 specific probe to provide more information on ploidy status. Coverslips and mounting medium were removed from slides by 2 × 5 minute washes in 10 mmol/l Tris, 0.15 mol/l NaCl, pH 8, + 0.05% Tween 20 (TNT) before passing through an ethanol series and air drying. No additional slide pretreatment was carried out before the new probe was applied to the slide for denaturation which was reduced to four minutes, after which the remaining steps were as for the first FISH analysis.

Results

RESULTS OF PRELIMINARY WORK

Two combinations of two differentially labelled probes (one labelled with biotin and the other digoxigenin) were evaluated to detect chromosome 21 in interphase nuclei, one YAC probe combination (y940 and yGART2) and one cosmid contig probe combination (cCMP21.a and c242c) (table 1). Following this dual labelling strategy, normal nuclei exhibit four signals, two red and two green. Lymphocyte controls showed that both combinations gave strong discrete signals in interphase nuclei showing

Table 3 Couple 1. Gonadal mosaic for trisomy 21: FISH analysis of embryos from two PGD cycles

Embryo	Biopsied cells	Cells in remainder of embryo
Cycle 1		
1	2 trisomy 21	7 trisomy 21: 2 disomy 21
2	2 trisomy 21	3 trisomy 21: 1 tetrasomy 21
Cycle 2		
3	2 normal	Transferred
4	2 normal	Transferred
5	2 trisomy 21	3 trisomy 21: 1 disomy 21: 1 monosomy 21
6	Not biopsied	5 trisomy 21
7	Not biopsied	2 tetraploid (arrested)

the expected number of four signals in 92% nuclei (n=100) for the two YAC probes and 88% nuclei (n=100) for the two cosmid probes. The slightly lower efficiency of the cosmid probes reflects the smaller signal size compared to the large YAC probe signals.

These two probe pair combinations were then applied to 18 normally fertilised spare embryos (118 blastomeres) of good morphology at the 6-9 cell stage on day 3 post-insemination. Ten embryos were hybridised with the YAC probe combination and eight embryos with the cosmid contig combination. Of these, 13 (72%) embryos were uniformly normal for chromosome 21 with each cell showing two signals per probe. Four embryos were mosaic with one or two cells differing from the remainder of the embryo and one was highly mosaic and scored as chaotic (table 2). Embryonic nuclei spread in this study by the HCl/Tween method are smaller and more compact than those spread with conventional methanol/acetic acid as a hypotonic stage is avoided. For this reason, these cells show highly discrete FISH probe signals (compared to lymphocyte nuclei) and this was found to be advantageous for diagnostic purposes where split signals from locus specific probes can lead to inaccuracies.

RESULTS OF PGD CYCLES

Couple 1. Suspected maternal gonadal mosaicism for trisomy 21

Two PGD cycles were carried out to exclude trisomic embryos using dual colour FISH with the two chromosome 21 specific YACS (y940 and yGART2). The fertilisation rate was particularly low in the first standard IVF cycle with just 31% (4/13) oocytes fertilised; this increased to 50% (9/18) fertilised in the second cycle from ICSI. In total, 31 oocytes were collected, 13 fertilised, five embryos were biopsied, and one double embryo transfer was carried out (cycle 2), but no pregnancy resulted. Two embryos (embryos 6 and 7) had fewer than six cells on day 3 post-insemination and so were not biopsied.

Five untransferred embryos were analysed; of these four showed trisomy 21 and one was tetraploid but arrested at the 2 cell stage. Only embryo 6 was completely trisomic for chromosome 21; the remaining three embryos were mosaic (the majority of cells trisomy 21 but one or two cells differing). All embryos were later reprobbed for chromosome 9 to check ploidy and all cells were diploid except the one tetraploid embryo (embryo 7) (table 3). Of four unfertilised oocytes analysed, three were hyperhaploid for chromosome 21 and only one was normal haploid. In total, 7/11 (64%) oocytes/embryos analysed showed chromosome 21 aneuploidy (fig 1A-C).

Couple 2. Reciprocal translocation carrier 46,XX,t(6;21)(q13;q22.3)

Two PGD cycles were carried out to exclude chromosome 21 imbalance (and also any chromosome 6 imbalance associated with derivative chromosomes) using dual colour FISH with the two chromosome 21 specific probes (y940

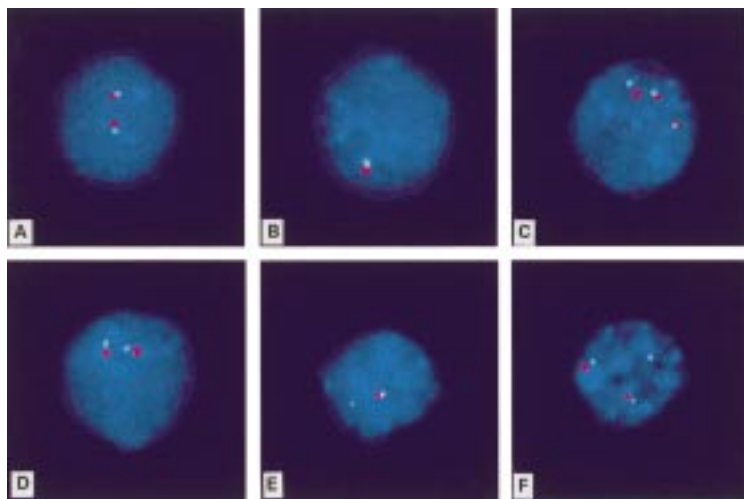


Figure 1 Dual colour FISH analysis of blastomere nuclei from day 3 post-insemination embryos using chromosome 21 specific probes for preimplantation genetic diagnosis of Down syndrome. Couple 1 (gonadal mosaicism for trisomy 21): (A) normal for chromosome 21 (two red, two green), (B) monosomy 21 (one red, one green), (C) trisomy 21 (three red, three green). Couple 2 (46,XX,t(6;21)(q13;q22.3)): (D) normal for chromosome 21 (two red, two green), (E) monosomy 21pter→q22.3 (one red, two green, orange shown where red and green overlap), (F) trisomy 21q22.3→qter (two red, three green).

and c242c) which flank the breakpoint on chromosome 21 (21q22.3): y940 (21q22.2) mapping to the derivative chromosome 21 and c242c (21q22.3) mapping to the derivative chromosome 6. As these two differentially labelled chromosome 21 probes map closely on 21q, they occasionally appear as an overlapping orange signal when combined in interphase nuclei. For this reason the chromosome 6 α satellite probe (also detected as an orange signal) was excluded from the diagnosis to avoid ambiguous results but was used for reprobing after the diagnosis to provide more information on the segregation of the derivative chromosomes at maternal gametogenesis. Standard IVF was carried out for the first treatment cycle with a fertilisation rate of 47%. ICSI was used for the second cycle but only 2/13 (15%) oocytes fertilised and both resulting embryos were retarded on day 3 and so were not biopsied for diagnosis but spread whole for analysis. In total, 32 oocytes were collected, 11 fertilised, four embryos were biopsied, and one embryo scored as normal for chromosome 21 was transferred resulting in a biochemical pregnancy as judged by a transient increase in serum hCG levels. Three embryos had fewer

than six cells on day 3 and so were not biopsied.

Of the eight untransferred embryos analysed, one showed complete trisomy 21 and six were unbalanced for the region distal and one for the region proximal to the breakpoint on chromosome 21 (table 4). Embryos and biopsied cells from both cycles were later reprobbed with the chromosome 6 α satellite probe, allowing the most likely mode of segregation of the maternal translocation chromosomes to be predicted. These segregations (listed in table 4 for each embryo) were based on the simplest outcome assuming a normal paternal gamete contribution, with minor cell lines treated as of postzygotic origin. Reprobing of the biopsied cells for embryo 1 (which was transferred to the mother) showed that while one cell was unavailable for reanalysis, the second cell showed monosomy for chromosome 6. If the embryo were monosomic throughout, this would provide an explanation for the biochemical pregnancy. The two arrested embryos from the second cycle (embryos 8 and 9) were highly mosaic and the original zygote chromosome constitution was difficult to determine. Of the nine embryos, three showed chromosome constitutions compatible with 2:2 segregation and six with 3:1 segregation. None were in fact balanced although the transferred embryo from the first cycle was normal for chromosome 21. Two unfertilised oocytes were available for analysis and both showed an unbalanced chromosome complement: oocyte 1 with a normal chromosome 21 and a derivative chromosome 6 from adjacent 1 segregation and oocyte 2 with a derivative chromosome 6 only from 3:1 segregation. In total, 10/11 (91%) oocytes/embryos analysed showed chromosome 21 aneuploidy (fig 1D-F) and of these 7/11 (64%) resulted from 3:1 segregation at gametogenesis.

Discussion

Four PGD cycles were carried out for two couples at high risk of a Down syndrome pregnancy with the aim of selectively transferring only embryos which were normal for chromosome 21. All cycles resulted in very few day 3 embryos at the 6-10 cell stage suitable for biopsy of two cells (five embryos for couple 1 and two embryos for couple 2). Although severe chromosomal imbalance may have com-

Table 4 Couple 2. 46,XX,t(6;21)(q13;q22.3): FISH analysis of embryos from two PGD cycles

Embryo	Biopsied cells	Remainder of embryo	Probable segregation (maternal contribution for translocation chromosomes)*
Cycle 1			
1	2 Normal for chr 21	Transferred	3:1 interchange aneuploidy † (21)
2	2 Trisomy 21q22.3→qter	Trisomy 21q22.3→qter (mosaic)	Adjacent 1 (der 6; 21) ‡
3	1 Monosomy 21q22.3→qter	Monosomy 21q22.3→qter (mosaic)	3:1 tertiary aneuploidy (der 21)
4	1 Trisomy 21q22.3→qter	Trisomy 21q22.3→qter	Adjacent 1 (der 6; 21)
5	Not biopsied	Monosomy 21pter→q22.3	Adjacent 2 (6; der 6)
6	Not biopsied	Normal/trisomy 21q22.3→qter	3:1 tertiary aneuploidy (6; der 6; 21)
7	Not biopsied	Trisomy 21	3:1 interchange aneuploidy (der 6; 21; der 21)
Cycle 2			
8	Not biopsied	Trisomy 21q22.3→qter/monosomy 21pter→q22.3	3:1 tertiary aneuploidy (6; der 6; 21)
9	Not biopsied	Trisomy 21q22.3→qter/monosomy 21q22.3→qter	3:1 interchange aneuploidy (der 6; 21; der 21)

*Most likely segregation to produce embryo outcome deduced from PGD results and reprobbing data using chromosome 6 α satellite probe.

†Based on reprobbing data from one biopsied cell.

‡der = derivative chromosome.

Table 5 Summary. Analysis of chromosome 21 in preimplantation embryos from two couples at high risk of Down syndrome pregnancy undergoing PGD

Parental karyotype	Normal*	Diploid mosaic	Aneuploid/ mosaic
(1) Gonadal mosaic for trisomy 21			
Cycle 1	0	0	2
Cycle 2	2	0	3
(2) 46,XX,t(6;21)(q13;q22.3)			
Cycle 1	1	1	5
Cycle 2	0	0	2
Combined totals 16 (100%)	3 (19%)	1 (6%)	12 (75%)

*Normal for chromosome 21.

promised embryo development, there is no obvious explanation for the rather low fertilisation rate since it is not thought to be affected by the chromosome constitution.²⁴ In both cases the majority of embryos analysed were abnormal for chromosome 21, categorised as aneuploid or aneuploid mosaic. In total, of 16 embryos analysed for both couples, only three were normal for chromosome 21 and transferred, but no clinical pregnancies were achieved (table 5).

Low level mosaicism was seen frequently in untransferred embryos on day 4 from both couples with 61% (8/13) embryos showing one or two cells differing from the remainder of the embryo. The use of two differentially labelled probes to detect a single chromosome was seen greatly to increase the accuracy of detection by reducing scoring errors and has confirmed that the mosaicism observed in previous preimplantation diagnosis cycles is not a FISH artefact owing to hybridisation failure or overlapping signals, even when just one cell differs and no cell resulting from a reciprocal non-disjunction event is found. As PGD for specific chromosome abnormalities is still at the research stage, it is important to document such levels of mosaicism found in these cases. This was the first occasion that we have observed two disomic cells in an otherwise trisomy 21 embryo (couple 1, embryo 1), posing a risk of misdiagnosis by inadvertent sampling of the minor cell line only. However, it must be emphasised that while biopsy and diagnosis takes place on day 3, the remainder of untransferred embryos are analysed on day 4 (after embryo transfer), hence further cell division has occurred and so mosaicism levels could be higher. Also it would be unlikely that both normal cells were biopsied in a trisomic mosaic embryo and it seems reasonable to continue with transfer on the basis of two independently biopsied cells, diagnosed normal for the tested chromosome, as long as the risk of non-representative biopsy is acknowledged. Mosaicism has been well documented in human preimplantation embryos both from routine IVF and PGD cycles.^{5, 6, 25-28} While embryos showing highly abnormal chromosome constitutions (chaotic embryos) are unlikely to develop further, it is unclear how the low level mosaicism observed here would affect further development, as selective mechanisms to rescue less abnormal embryos may operate. It is possible that the presence of even a few chromosomally normal cells at such early cleavage stages may give rise to a normal fetus. This may follow either preferential distribu-

tion of aneuploid/polyploid cells to extraembryonic tissues, as seen in 2n/4n chimaeric mouse embryos,²⁹ or somatic loss of supernumerary chromosomes, as seen in the majority of disomy/trisomy mosaics and uniparental disomy cases which originate as trisomic fertilisations.³⁰

Although interphase FISH analysis of sperm allows segregation patterns to be followed in male translocation carriers,³¹ results from couple 2 represent the first observations of reciprocal translocation segregation in preimplantation embryos from a female carrier. Interestingly, a variety of combinations of maternal chromosomes were observed, showing that translocation heterozygotes may often produce gametes from most of the possible chromosome segregations, although the vast majority will not be viable. The most common segregation patterns of the 46,XX t(6;21) observed were 3:1 with tertiary aneuploidy (three embryos) and 3:1 with interchange aneuploidy (three embryos). Following Jalbert *et al*,³² the quadrivalent formed at pachytene of meiosis I is asymmetrical with the large chromosome 6 and small chromosome 21 translocated segments and predicts, of 16 theoretical segregations, 3:1 segregation as the most likely mode of segregation. In total, 64% embryos/oocytes analysed resulted from 3:1 segregation of this translocation at gametogenesis.

Analysis of unfertilised oocytes was carried out to complement the findings of the embryo analysis. All oocytes are retained for as long as possible to allow for late fertilisation, particularly when few embryos are available for diagnosis, and this is reflected in the small numbers of analysable oocyte metaphases that were available. For couple 1, four of five untransferred embryos showed trisomy 21 in the majority of cells and, although these results are compatible with maternal gonadal mosaicism, analysis of hyperhaploid unfertilised oocytes was needed to prove this diagnosis, by showing the existence of trisomic primary oocytes in this patient (J Cozzi, unpublished observations). Both oocytes analysed from couple 2 were unbalanced for the translocation chromosomes and if fertilised would have given rise to embryos with chromosome constitutions monosomy 6q13→qter/trisomy 21q22.3→qter (as in embryos 2 and 4) and monosomy 6q13→qter/monosomy 21pter→q22.3.

Although two IVF cycles have been carried out for both couples, each had only one cycle which resulted in embryo transfer, and given the low numbers of embryos available for diagnosis it is likely that multiple treatment cycles would be necessary to increase the chance of obtaining a normal pregnancy. However, our results show that 64% of oocytes/embryos for couple 1 and 91% oocytes/embryos for couple 2 were aneuploid for chromosome 21. This would predict a very high recurrence risk of a Down syndrome conception in both cases, as the majority of gametes produced must be chromosomally unbalanced. These results highlight how genetic analysis of embryos for

PGD enables the levels of normal gametes produced by individual patients to be assessed. This information not only allows couples to make an informed decision on their options concerning future assisted reproduction, but is also of value to investigate patterns of meiotic segregation.

In conclusion, although standard prenatal diagnosis remains the method of choice for age related aneuploidy, PGD may offer an alternative treatment option for translocation carriers and gonadal mosaics experiencing repeated chromosomally abnormal pregnancies, as testified by the increasing number of referrals at our Centre. However, although large numbers of embryos can be screened simultaneously using this approach, where the majority of embryos are chromosomally abnormal, as found in both patients' cycles detailed here, the chances of a continuing pregnancy will still be low.

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- 1 Mikkelsen M, Stene J. Genetic counselling in Down's syndrome. *Hum Hered* 1970;20:457-64.
- 2 Pangalos CG, Talbot CC, Lewis JG, et al. DNA polymorphism analysis in families with recurrence of free trisomy 21. *Am J Hum Genet* 1992;51:1015-27.
- 3 Delhanty JDA, Wells D, Harper JC. Genetic diagnosis before implantation. *BMJ* 1997;315:828-9.
- 4 Griffin D, Handyside AH, Harper JC, et al. Clinical experience with preimplantation diagnosis of sex by dual fluorescent in situ hybridisation. *J Assist Reprod Genet* 1994;11:132-43.
- 5 Delhanty JDA, Harper JC, Ao A, Handyside AH, Winston RML. Multicolour FISH detects frequent chromosomal mosaicism and chaotic division in normal preimplantation embryos from fertile patients. *Hum Genet* 1997;99:755-60.
- 6 Munné S, Lee A, Rosenwaks Z, Grifo J, Cohen J. Diagnosis of major aneuploidies in human preimplantation embryos. *Hum Reprod* 1993;8:2185-91.
- 7 Munné S, Weier HUG. Simultaneous enumeration of chromosomes 13, 18, 21, X and Y in interphase cells for preimplantation genetic diagnosis of aneuploidy. *Cytogenet Cell Genet* 1996;75:263-70.
- 8 Verlinsky Y, Cieslak J, Freidline M, et al. Polar body diagnosis of common aneuploidies by FISH. *J Assist Reprod Genet* 1996;13:157-62.
- 9 Munné S, Scott R, Berg P, Cohen J. First pregnancies after polar body biopsy for testing of chromosome translocations. *Fertil Steril Suppl* 1996;1:0-001.
- 10 Conn CM, Harper JC, Winston RML, Delhanty JDA. Infertile couples with Robertsonian translocations: preimplantation genetic analysis of embryos reveals chaotic cleavage divisions. *Hum Genet* 1998;102:117-23.
- 11 Cassel MJ, Munné S, Fung J, Weier HUG. Carrier-specific breakpoint-spanning DNA probes: an approach to preimplantation genetic diagnosis in interphase cells. *Hum Reprod* 1997;12:2019-27.
- 12 Harper JC, Coonen E, Raemakers FCS, et al. Identification of the sex of human preimplantation embryos in two hours using an improved spreading method and fluorescent in-situ hybridisation (FISH) using directly labelled probes. *Hum Reprod* 1994;9:721-4.
- 13 Davies AF, Barber L, Murer-Orlando M, Bobrow M, Adinolfi M. FISH detection of trisomy 21 by the simultaneous use of two differentially labelled cosmid contigs. *J Med Genet* 1994;31:679-85.
- 14 Soloviev I, Yurov YB, Vorsanova G, Fayet F, Roizes G, Malet P. Prenatal diagnosis of trisomy 21 using interphase fluorescence *in situ* hybridisation of post-replicated cells with site-specific cosmid and cosmid contig probes. *Prenat Diagn* 1995;15:237-48.
- 15 Hillier SG, Afnan AMM, Margara RA, Winston RML. Superovulation strategy before in vitro fertilisation. *Clin Obstet Gynaecol* 1985;12:687-723.
- 16 Van Steirteghem A, Nagy Z, Joris H, et al. High fertilisation and implantation rates after intracytoplasmic sperm injection. *Hum Reprod* 1993;8:1061-6.
- 17 Handyside AH. Biopsy of human cleavage stage embryos and sexing by DNA amplification. In: Verlinsky Y, Strom C, eds. *Proceedings of the first symposium on preimplantation genetics*. New York: Plenum, 1991:75-83.
- 18 Harper JC, Delhanty JDA. FISH in preimplantation diagnosis. In: Walker J, ed. *Methods in molecular biology: molecular diagnosis of genetic disease*. New York: Humana, 1996:259-68.
- 19 Tarkowski AK. An air drying method for chromosome preparations from mouse eggs. *Cytogenetics* 1966;5:394-400.
- 20 Gnirke A, Barnes TS, Patterson D, Schild D, Featherstone T, Olson M. Cloning and in vivo expression of the human GART gene using yeast artificial chromosomes. *EMBO J* 1991;10:1629-34.
- 21 Zheng YL, Ferguson-Smith MA, Warner JP, Ferguson-Smith ME, Sargent CA, Carter NP. Analysis of chromosome 21 copy number in uncultured amniocytes by fluorescence *in situ* hybridisation using a cosmid contig. *Prenat Diagn* 1992;12:931-43.
- 22 Lengauer C, Green ED, Cremer T. Fluorescence *in situ* hybridisation of YAC clones after Alu-PCR amplification. *Genomics* 1992;13:826-8.
- 23 Hopman AHN, Raemakers FCS, Raap AK, et al. In-situ hybridisation as a tool to study numerical chromosome aberrations in solid bladder tumours. *Histochemistry* 1988;89:307-16.
- 24 Almeida PA, Bolton VN. The relationship between chromosomal abnormalities in the human oocyte and fertilisation *in vitro*. *Hum Reprod* 1994;9:343-6.
- 25 Benkhalifa M, Janny L, Vye P, Malet P, Boucher D, Menezo Y. Assessment of polyploidy in human morulae and blastocysts using co-culture and fluorescent *in situ* hybridisation. *Hum Reprod* 1993;8:895-902.
- 26 Delhanty JDA, Griffin DK, Handyside AH, et al. Detection of aneuploidy and chromosomal mosaicism in human embryos during preimplantation sex determination by fluorescent *in situ* hybridisation. *Hum Mol Genet* 1993;2:1183-5.
- 27 Harper JC, Coonen E, Handyside AH, Winston RML, Hopman AHN, Delhanty JDA. Mosaicism of autosomes and sex chromosomes in morphologically normal monospermic preimplantation human embryos. *Prenat Diagn* 1995;15:41-9.
- 28 Laverge H, De Sutter P, Verschraegen MR, De Paep A, Dhont M. Triple colour fluorescent *in situ* hybridisation for chromosomes X, Y and 1 on spare human embryos. *Hum Reprod* 1997;12:809-14.
- 29 James RM, Klerkx AHEM, Keighren M, Flockhart JH, West JD. Restricted distribution of tetraploid cells in mouse tetraploid->diploid chimaeras. *Dev Biol* 1995;167:213-26.
- 30 Robinson WP, Binkert F, Bernasconi F, Lorda-Sanchez I, Werder EA, Schinzel AA. Molecular studies of chromosomal mosaicism: relative frequency of chromosomal gain or loss and possible role of cell selection. *Am J Hum Genet* 1995;56:444-51.
- 31 Van Hummelen P, Manchester D, Lowe X, Wyrobek J. Meiotic segregation, recombination and gamete aneuploidy assessed in a t(1;10)(p22.1;q22.3) reciprocal translocation carrier by three and four-probe multicolor FISH in sperm. *Am J Hum Genet* 1997;61:651-9.
- 32 Jalbert P, Sele B, Jalbert H. Reciprocal translocations: a way to predict the mode of imbalanced segregation by pachytene diagram drawing. A study of 151 human translocations. *Hum Genet* 1980;55:209-22.