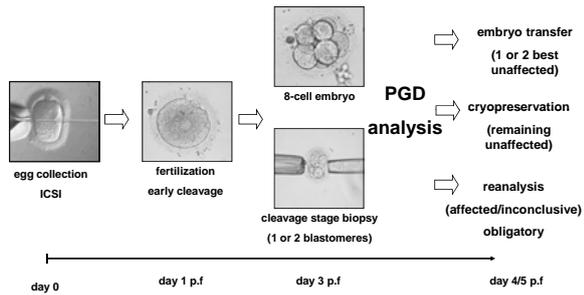


Quality control by means of spare embryo re-analysis

Dreesen et al., 2008
Validation of Preimplantation Genetic Diagnosis by PCR analysis:
genotype comparison of the blastomere and corresponding embryo, implications for clinical practice.
Mol Hum Reprod. Sep. [Epub]



PGD - PCR routine



PGD - PCR protocol



embryo biopsy
one/two blastomeres
↓
alkaline lyses step
↓
PCR with fluorescently labelled primer (40-50 cycles)
↓
mutation detection / genotyping
↓
analyses on ABI 3100/3730 capillary automatic sequencer with laser detection

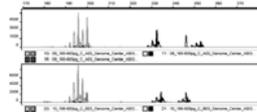
PGD-PCR protocols

Monogenic disorders

Spinal Muscular Atrophy
 Cystic fibrosis
 Myotonic Dystrophy
 Fragile-X syndrome
 Huntingtons disease
 Spinocerebellar Ataxia 3
 Marfan syndrome
 AR Polycystic kidney disease
 Adrenogenital syndrome
 Phenylketonuria
 Incontinentia pigmenti
 Pelizaeus Merzbacher

Fanconi Anemia
 Congenital Deafness
 Familial Adenomatous polyposis coli
 Tyrosine hydroxylase deficiency
 enzyme complex I deficiency
 Ehlers-Danlos syndrome
 Hypochondroplasia
 Achondroplasia
 Metachromatic Leukodystrophy
 Citrullinaemia
 Tuberos Sclerosis type 1
 Tuberos Sclerosis type 2
 Krabbe disease
 CADASIL
 Familial Atypical Mole-Malignant Melanoma Syndrome
 Holoprosencephaly
 Nail Patella syndrome
 Mucopolidosis type 2

Mitochondrial disorders
 NARP/Leigh syndrome (T8993C/G mutation)
 Leigh syndrome (T9176C mutation)
 MELAS (A3243G mutation)



CUMULATIVE PGD-PCR DATA until 2007

No. of patients	No. of cycles	No. cancelled	No. of OR	No. of embryos diagnosed	No. of cycles to ET	No. of HCG positive	No. of FHB positive	Clinical pregnancy rate		No. children Born
								FHB/OR	FHB/ET	
115	257	52	205	1241	182	52	45	22,0%	24,7%	53

Frozen cycles not included

ESHRE PGD consortium data collection I-VII 20% FHB/OR, 26% FHB/ET

How valid is PGD-PCR diagnosis ?

Validation of PGD may be performed by:

- follow up of children born after PGD
- reanalysis of spare embryos after PGD

aims of the study

- validate PGD-PCR analysis through a diagnostic-test analysis
- to determine the diagnostic value

validation PGD-PCR analysis

422/1241 embryos with initial genotype based on biopsied blastomere were reanalyzed

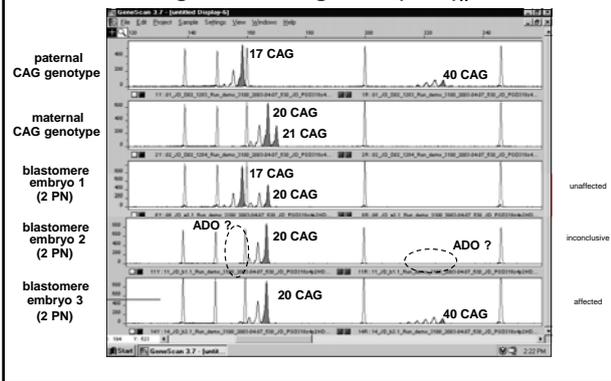
- removal of the zona
- several washing steps
- embryo reanalysis by single cell PCR, using same initial strategy

initial biopsied blastomere genotype was compared to reanalyzed embryo genotype

distribution of blastomere/embryo comparison results over the different genotype outcome groups

different genotype outcome groups	no. blastomeres / embryos compared
	n
blastomere genotype confirmed by embryo genotype (allele match)	367
ADO in blastomere genotype confirmed by embryo genotype	32
blastomere genotype not confirmed by embryo genotype due to contamination	4
blastomere genotype not confirmed by embryo genotype	19
total	422

Huntington PGD single cell (CAG)_n



distribution of blastomere/embryo comparison results
over the different genotype outcome groups

different genotype outcome groups	no. blastomeres / embryos compared
	n
blastomere genotype confirmed by embryo genotype (allele match)	367
ADO in blastomere genotype confirmed by embryo genotype	32
blastomere genotype not confirmed by embryo genotype due to contamination	4
blastomere genotype not confirmed by embryo genotype (mainly additional maternal allele)	19
total	422

diagnostic test analysis

- genotype outcome was converted to diagnostic outcome
- embryos diagnosed by PGD as unaffected; test negative (T-)
 - embryos diagnosed by PGD as affected or aberrant; test positive (T+)
 - embryos reanalyzed after PGD as unaffected; disease negative (D-)
 - embryos reanalyzed after PGD as affected or aberrant; disease positive (D+)
- compare diagnostic outcome of blastomere to reanalyzed embryo
- reanalyzed embryo was used as golden standard
- diagnostic-test analysis performed on diagnostic outcome

Conversion of genotype outcome to diagnostic outcome for the different blastomere/embryo genotypes outcome groups

different genotype outcome groups	blastomeres / embryos compared	different diagnostic outcome groups			
		n	T-D-	T-D+	T+D+ T+D-
blastomere genotype confirmed by embryo genotype	367	167	0	200	0
ADO in blastomere genotype confirmed by embryo genotype	32	5	0	8	19
blastomere genotype not confirmed by embryo genotype due to contamination blastomere	4	0	0	3	1
blastomere genotype not confirmed by embryo genotype	19	2	7	7	3
total	422	174	7	218	23

Conversion of genotype outcome to diagnostic outcome for the different blastomere/embryo genotypes outcome groups

different genotype outcome groups	blastomeres / embryos compared	different diagnostic outcome groups			
		n	T-D-	T-D+	T+D+ T+D-
blastomere genotype confirmed by embryo genotype	367	167	0	200	0
ADO in blastomere genotype confirmed by embryo genotype	32	5	0	8	19
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		n	T-D-	T-D+	T+D+ T+D-
blastomere genotype confirmed by embryo genotype	367	167	0	200	0
ADO in blastomere genotype confirmed by embryo genotype	32	5	0	8	19
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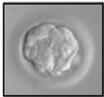
Embryo Quality

- embryo morphology

morphology grading systems used for



cleavage stage



morulae



blastocysts

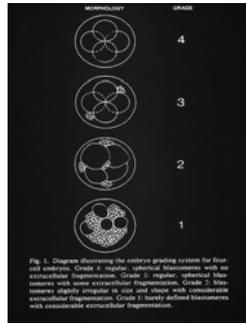
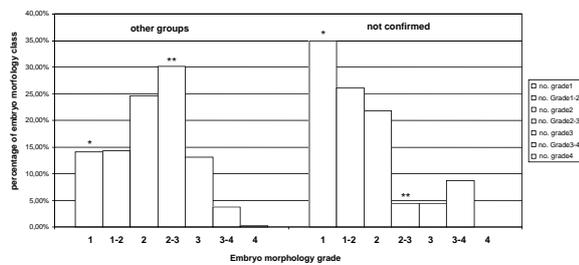


Fig. 1. Diagram illustrating the embryo grading system for four-cell embryos. Grade 4: regular spherical blastomeres, with no cytoplasmic fragmentation. Grade 3: regular spherical blastomeres with some cytoplasmic fragmentation. Grade 2: blastomeres slightly irregular, cytoplasmic fragmentation. Grade 1: irregularly shaped blastomeres with extensive cytoplasmic fragmentation.
Bolton et al., J IVF ET 6: 30 (1989)

Conversion of genotype outcome to diagnostic outcome for the different blastomere/embryo genotypes outcome groups

different genotype outcome groups	blastomeres / embryos compared	different diagnostic outcome groups				
		n	T-D-	T-D+	T+D+	T+D-
blastomere genotype confirmed by embryo genotype		367	167	0	200	0
ADO in blastomere genotype confirmed by embryo genotype		32	5	0	8	19
blastomere genotype not confirmed by embryo genotype due to contamination blastomere		4	0	0	3	1
blastomere genotype not confirmed by embryo genotype		19	2	7	7	3
total		422	174	7	218	23

distribution of embryo morphology on day 4 p.f in different genotype outcome groups



* And ** significantly different; p<0,01

re-validation of PGD-PCR analysis

Validation of the PGD-PCR analysis

- total group reanalyzed embryos
- embryo group grade 1 day 4 p.f
- grade 1 day 4 p.f embryo group only

Validation of PGD-PCR analysis by calculating sensitivity, specificity, accuracy and Likelihood Ratio

Establish the diagnostic value by calculating Positive- and Negative Predictive Value

**diagnostic-test analysis
total group**

		affected/aberrant embryos at reanalysis (D+)	unaffected embryos at reanalysis (D-)	total
affected/aberrant embryos at PGD	(T+)	218	23	241
unaffected embryos at PGD	(T-)	7	174	181
total		225	197	422

Sensitivity; the proportion of affected/aberrant embryos (D+) correctly diagnosed by PGD (T+), (218/225)

Specificity; the proportion of unaffected embryos (D-) correctly diagnosed by PGD (T-), (174/197)

PPV; the proportion of PGD analysis predicted correctly as affected/aberrant (218/241).

NPV; the proportion of PGD analysis predicted correctly as unaffected (174/181).

**diagnostic-test analysis
total group**

		affected/aberrant embryos at reanalysis (D+)	unaffected embryos at reanalysis (D-)	total
affected/aberrant embryos at PGD	(T+)	218	23	241
unaffected embryos at PGD	(T-)	7	174	181
total		225	197	422

Sensitivity; the proportion of affected/aberrant embryos correctly diagnosed by PGD (218/225).

Specificity; the proportion of unaffected embryos correctly diagnosed by PGD (174/197).

PPV; the proportion of PGD analyses correctly predicting embryos to be affected/aberrant (218/241)

NPV; the proportion of PGD analyses correctly predicting embryos to be unaffected (174/181)

total group

Validity of the PGD-PCR analysis	
Total group	
Sensitivity	96,9 % (218/225)
False Negative	3,1 % (7/225)
Specificity (low due to ADO)	88,3 % (174/197)
False Positive	11,7 % (23/197)

Diagnostic value of the PGD-PCR analysis	
Total group	
Negative predictive value	96,1 % (174/181)
Positive predictive value	90,5 % (218/241)

Validity of the PGD-PCR analysis

	Grade 1 (day 4 p.f)	Grade 1 (day 4 p.f) excluded
Sensitivity	82,9 % (29/35)*	99,5 % (189/190)*
False Negative	17,1 % (6/35)*	0,5 % (1/190)*
Specificity	93,1 % (27/29)	87,5 % (147/168)
False Positive	6,9 % (2/29)	12,5 % (21/168)

*significant; p<0,001

Diagnostic value of the PGD-PCR analysis

	Grade 1 (day 4 PF)	Grade 1 (day 4 PF) excluded
Negative predictive value	81,8 % (27/33)*	99,3 % (147/148)*
Positive predictive value	93,6 % (29/31)	90,0 % (189/210)

*significant; p<0,001

summary validation (1)

ADO is the major cause of false positives, no false negatives were obtained due to the fact that ADO is taking into account in developing PGD-PCR protocols

Grade 1 embryos on day 4 p.f are overrepresented in the group in which the blastomere genotype is not confirmed by the embryo genotype.

If grade1 embryos are excluded from transfer in a PGD-PCR procedure, sensitivity increases from 96.6% up to 99.5%

summary validation (2)

We would unnecessarily discard 27(unaffected)/422 embryos by excluding grade 1 embryos from transfer

We would prevent transfer of 6 affected/aberrant embryos and increase the negative predictive value from 96.1% to 99.3%.

Conclusions

The PGD-PCR method is validated as a diagnostically valid method with a good diagnostic value for selecting unaffected embryos for transfer

By not accepting grade1 embryos on day 4 p.f for transfer, the negative predictive value will increase from 96.1 to 99.3% at the cost of unnecessarily excluding 6.4% unaffected grade 1 embryos

Implication

In PGD-PCR, we do no longer consider embryos grade 1 on day 4 p.f. transferable

THANK YOU

Distribution of embryo morphology on day 3 post OR in different genotype outcome groups.

