

PRE-CONGRESS COURSE 6

Organised by the Special Interest Group Reproductive Genetics

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PRE-CONGRESS COURSE 6 - PROGRAM

Latest developments in preimplantation genetic diagnosis

Organised by the Special Interest Group Reproductive Genetics

Course co-ordinators: Karen Sermon (Belgium), Stephane Viville (France), Sjoerd Repping (The Netherlands), Filipa Carvalho (Portugal)

Course description: This course aims to bring the latest developments in preimplantation genetic diagnosis primarily in the technical field, but also in the field of patient follow-up and ethics. For the technical aspects, an update will be given on the latest efforts to improve efficiency and accuracy for PGD in monogenic disease and chromosomal abnormalities. The technology behind and the first clinical results on microarray-CGH will be presented and discussed. The organisation of a PGD centre, as well as the long term follow-up of children born after PGD will also be discussed

Target audience: Scientists and clinicians with an interest in PGD: those who already provide PGD to their patients and wish to expand their experience as well as those who have followed the developments in PGD through literature Participants are expected to have a minimal background on basic techniques used in PGD (ICSI, embryo culture, biopsy, FISH, PCR)

09:00 - 09:30	Set-up a PGD lab and clinic: guidelines, QA and accreditation - <i>Alan Thornhill (United Kingdom)</i>
09:30 - 09:45	Discussion
09:45 - 10:15	One vs two cell biopsy - the same answer for monogenic and chromosomal abnormalities? - <i>Catherine Combelles (USA)</i>
10:15 - 10:30	Discussion
10:30 - 11:00	Coffee break
11:00 - 11:30	Optimizing PGD for monogenic diseases: minimal requirements in

multiplex PCR and MDA - Céline Moutou (France)

11:30 - 11:45	Discussion
11:45 - 12:15	Chromosomal abnormalities: development of generic tests – Catherine Staessen (Belgium)
12:15 - 12:30	Discussion
12:30 - 13:30	Lunch
13:30 - 14:00	Studying all chromosomes: is more better? - <i>Evelien Vanneste</i> (<i>Belgium</i>)
14:00 - 14:15	Discussion
14:15 - 14:45	PGS: the final settlement - Sebastiaan Mastenbroek (The Netherlands)
14:45 - 15:00	Discussion
15:00 - 15:30	Coffee break
15:30 - 16:00	Long-term children follow-up - Alison Lashwood (United Kingdom)
16:00 - 16:15	Discussion
16:15 - 16:45	What have we learned from 10 years of the PGD Consortium? – Peter Braude (United Kingdom)
16:45 - 17:00	Discussion

Setting up a PGD lab and clinic: Guidelines, QA and accreditation

Latest developments in preimplantation genetic diagnosis

ESHRE SIG: Reproductive Genetics, 2009

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Director, Bridge Genoma

Disclosure: I have no commercial relationships, nor am I engaged in other activities that might be perceived as a potential conflict of interest

Learning Objectives

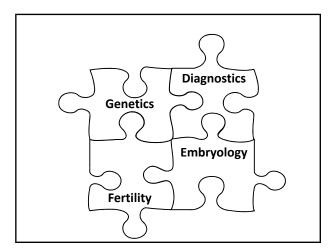
- Understand what is required to provide PGD treatment
- Describe activities required to perform PGD according to specific guidelines and general laboratory accreditation standards
- Identify the differences between transport, satellite and in-house PGD
- Discriminate between satisfactory and excellent quality PGD treatment
- Identify future improvements in PGD services

Organisation of a PGD centre

- What is required to perform PGD?
- Building the PGD puzzle
- Patient vs centre experience of PGD
- Satellite/transport PGD Pros and Cons
- What makes an excellent PGD centre?
- Impact of future developments on PGD
- Bibliography

What is required to perform PGD?

- Building the PGD puzzle
- 4355 4355 2375
- Appropriate testing (genetic counselling/testing)
- In Vitro Fertilization
- Embryo biopsy
- Diagnostic test on biopsied blastomere
- Reporting and explaining results
- Transfer of selected embryos to the uterus
- Follow-up of pregnancy and resulting child



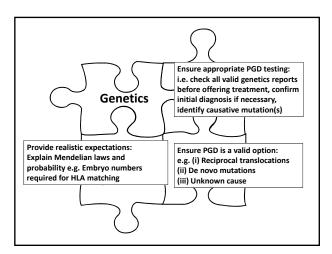
Genetics

- Full family and medical history
- Assess severity of condition
- Estimate genetic risk
- Provide realistic expectations
- Explain PGD process, disorder and tests
- Ensure appropriate tests offered
- Discuss options (risk/benefit)
- Obtain informed consent

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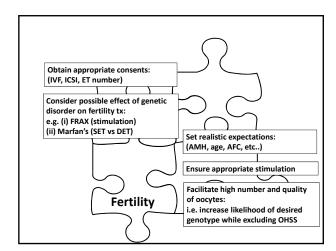
Options for potential 'PGD' patients

- Contraception
- Childlessness
- Prenatal testing (± pregnancy termination)
- Donation (egg, sperm, embryo)
- Adoption
- Reproductive roulette (emotional, physicial & financial cost of affected child?)



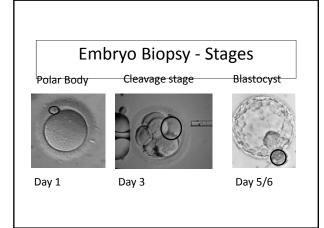
Fertility

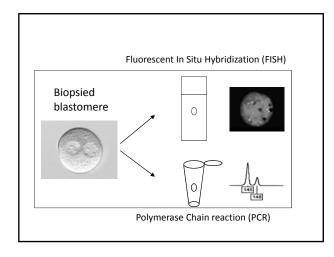
- Full reproductive and medical history
- Provide realistic expectations
- Explain IVF process and tests
- Discuss options (risk/benefit)
- Obtain informed consent
- Prescribe IVF medication
- Perform IVF procedures (EC and ET)

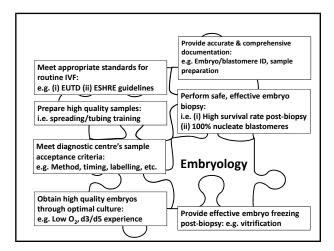


Embryology

- Prepare and introduce gametes in vitro
- Culture embryos
- Biopsy (method, equipment, competency)
- Prepare diagnostic sample (single cells)
- Culture biopsied embryos (label, d3-d5)
- Select embryo(s) for transfer (based on genetic result and morphology)
- Surplus embryos (freeze, QC/QA, research)







Embryology - EUTD/Guidelines

General examples (standards)

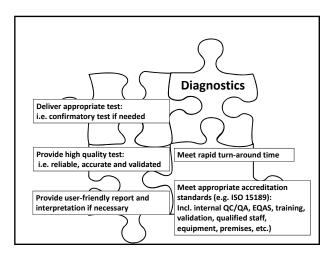
- Presence of QMS
- Air Quality
- Trained, competent staff
- Labelling and traceability

Specific examples (guidelines)

- Biopsy efficiency >95%
- ICSI for PCR based cases
- Biopsy embryos with >6 cells?
- 1 cell biopsy wherever possible

Diagnostics

- Develop and validate single cell test
- Receive and accession sample
- Perform test
- Analyse and Report results
- Provide interpretation



Diagnostics - ISO 15189/Guidelines

Examples

- Internal QC/QA (controls, int. Standards, confirmation of diagnosis, TAT, failure rates)
- EQAS (pilots for FISH and PCR)
- Validation (new specific test vs generic test, precycle polymorphism check)
- Qualified staff (for testing and sign-off, training plan, ongoing competency assessments)
- Labelling (from pencil to barcodes)
- Premises and equipment (single cell diagnostics, 'clean room', FISH microscope)

Patient experience of PGD

- Comprehensive information
- Calm
- Communication
- Control
- Consent
- Clear instructions



IVF centre experience of PGD

- Confusing
- Complex
- Control (lack of)
- Clear instructions (Ts and Cs)
- Communication
 - Smart NOT necessarily more!

Satellite/transport PGD - Pros and Cons Pros - Improved patient access and convenience - Lower costs - Experienced reference diagnostics lab - Centres of excellence model Cons - Quality of sample preparation - Transportation risks and timings - Inadequate counselling/pre-cycle screening - Negligible follow-up /responsibilities Impact of future developments on PGD More.... Satellite and transport PGD Quality control/quality assurance (reliability/accuracy) • PGD laboratories accredited • Test methods (whole genome amplification/microarray – cost?) • Types of screening test (mutation analysis, linkage, haplotyping, aneuploidy, gene expression, protein) • Patient access (funding for PGD, shorter wait times) • Information for patients (report/interpretation complexity) Time for diagnosis (vitrification of biopsied embryos) What makes an excellent PGD centre? Genetic Evaluation and Counselling - Best performed by genetics professionals, support throughout • IVF Platform Routine IVF results must be good • Diagnostics Laboratory - Accreditation, experience, reputation · Patient experience - Manage expectations (wait time, cost, success, misdiagnosis) • Integration of Services No blame culture, smart communication, follow rules

Quality Control/Quality Assurance

Comprehensive Ethical Review

Req. in accredited labs, Best test = best chance, follow-up

Relevant bibliography Kullev A, Verlinsky, Y. (2004) Thirteen years' experience of preimplantation diagnosis: report of the fifth International Symposium on Preimplantation Genetics. Reprod Blomed Online. 8(3):229-35. ESHR FGD Convortium Seering Committee (2001) Eshrift Preimplantation Genetic Diagnosis Consortium: data collection in (Mey 2001). Hum Reprod. 17(1):233-46. Off Centres: Prenat Diagn. 21(2):1368-92. Solini et al. (2006) The Interface between assisted reproductive technologies and genetics: technical, social, ethical and legal issues. Eur J Hum Genet. 14(5):585-645. Thomhill et al. despines, 5 (2006) Julie Vocation and Cally Assurance: in Preimplantation Genetic Diagnosis (PDD) and preimplantation genetic screening (PGS). Hum Reprod. 20(1):33-48. Thomhill et al. despines, 5 (2006) Julied Vocation and Cally Assurance: in Preimplantation Genetic Diagnosis in Consortium data collection (Vill: cycles from annuary to December 2005 with pregnancy follow-up to October 2006. Hum Reprod. 23(12):256-94. Generades et al (2001) Preimplantation genetic diagnosis (PGD): a collaborative activity of clinical genetic departments and IVC centres. Prenat Diagn. 21(12):1086-92. Preimplantation Genetic Diagnosis international Society (2001) The Preimplantation Genetic Diagnosis in Europe. Eur J Hum Genet. Vecinically et al. (2004) Over a decade of experience with preimplantation genetic diagnosis in Europe. Eur J Hum Genet. Vecinically et al. (2004) Over a decade of experience with preimplantation genetic diagnosis: a multicenter report. Fertil Servil. 22(2):299-4.

One *vs.* two cell biopsy the same answer for monogenic and chromosomal abnormalities?

Catherine Combelles, Ph.D. Faculty, Biology Department Middlebury College Middlebury, Vermont U.S.A

Learning objectives

- \blacksquare To appreciate the differences in clinical practices with respect to one vs. two cell biopsy
- To evaluate the current data on the efficiency, accuracy, outcomes of one *vs.* two cell biopsy
- \blacksquare To compare and contrast diagnostic parameters based on the type of analysis
- To relate clinical findings to our current understanding of early human embryogenesis

The biopsy of one vs. two cells FISH: 10.75% PCR: -20.30% Uncertain Affected Unaffected Unaffected Embryo transfer

Potential trade-offs in the biopsy of one vs. two cells Reasons to biopsy two cells: $\blacksquare \uparrow$ diagnostic efficiency: human, embryo errors; technical limitations ■ ↑ diagnostic accuracy ■ Detection of discordant genetic make-ups: mosaicism • Performed during an already invasive procedure Reasons NOT to biopsy two cells: ■ Developmental handicap(s): ↑ cell loss ■ ↑ workload The biopsy of one vs. two cells: who does what? • No comprehensive data on how PGD is performed ullet In the U.S., 1/4 of PGD clinics report on the biopsy of two cells (Baruch et al., 2006) ■ PGD labs with a chosen biopsy protocol except: Suboptimal embryo quality on day 3Issues with first removed cell • PGD/PGS studies are based on one or two cells, or both. Practice guidelines from PGDIS, ESHRE, and ASRM The biopsy of one vs. two cells: why under scrutiny? Different lab procedures 'good' ? 'harm' $\angle o$ Argued benefits of PGS Arguments based Direct comparisons Embryo quality bias Sample sizes on modeling and assumptions Retrospective designs Cryopreservation, error rates

\underline{Some} of the key diagnostic measures based on number of cells and type of analysis

Diagnostic	1-cell		1- and 2-cell	
measures (%)	PCR	FISH	PCR	FISH
Efficiency	795-896	95-981	855-883	952-963
Accuracy (false- positive)	144-165	7-151	115-124	82

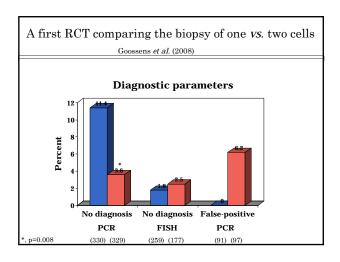
 $^1{\rm Li}$ et al. (2005); $^2{\rm Staessen}$ et al. (2004); $^3{\rm ESHRE}$ PGD data collection VIII for 2005; $^4{\rm Dreesen}$ et al. (2008); $^3{\rm Ray}$ et al. (1998); $^6{\rm Goossens}$ et al. (2008)

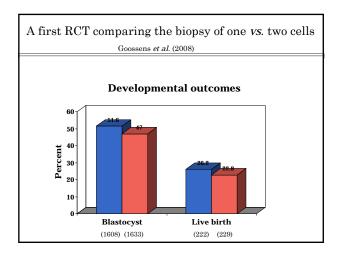
Direct comparisons of one vs. two cell biopsy

	1-cell	2-cell	Analysis	Study design	Ref.
Diagnostic	70% (23)	78% (41)	FISH	retrospective 3 probes	Emiliani et al. '04
efficiency (embryos)	95.9% (413) p = 0.	98.2% (1366)	FISH	not randomized 2-c if ≥6 c	Michiels et al. '06
False-	12.6%	6%	FISH	modeling assumptions	Los et al. '04
positives (embryos)	25.6% (39)	13.6% (66)	FISH	$\begin{array}{c} not\ randomized \\ 2\text{-}c\ if \geq 6\ c \end{array}$	Michiels et al. '06
	42% (29)	43% (54) 18% if con (11)	FISH	not randomized levels of mosaicism	Baart et al. '06

Some further insights into one vs. two cell biopsy

	1-cell	2-cell	Analysis	Study design	Ref.
Unaffected embryos transferred	69% 47%	88% 85%	PCR- rec. - dom.	modeling assumptions	Lewis et al. '01
False- positives (embryos)	14.3% (98)	9.1% (99)	PCR	retrospective 2-c if ≥ 8 c	Dreesen et al. '08
Cycle outcomes:					
Preg. Impl. Birth (transfers)	21.4% 20.0% 20.0% (14)	29.1% 18.6% 17.0% (117)	PCR + FISH	retrospective 2-c if ≥7 c	van de Velde <i>et al.</i> '01





Rates of unacceptable misdiagnosis: false-negatives

- Anecdotal cases in published studies
- \blacksquare Reported rates from ESHRE PGD Consortium data collection: 0.16% misdiagnosis (FISH + PCR; 1-cell + 2-cell)
- Limitations in data collection
- \blacksquare Preliminary results from one vs. two cell re-analyses:

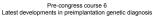
1-cell	2-cell	Analysis	Ref.
1/12	0/24	FISH	Emiliani et al. '04
0/114	0/267	FISH	Michiels et al. '06
2/78	5/147	PCR	Dreesen et al. '08
0/54	0/57	PCR	Goossens et al. '08

So how many cells to biopsy?	
It depends on:	
the methodology for genetic analysisthe disease screened	
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A further understanding of human embryogenesis awaits	
Are cleavage-stage blastomeres totipotent?	
How much pre-patterning is in place?	
Which cell or two cells to biopsy?	
Is early embryogenesis regulative in human?	
How much & how well can an embryo adapt post-biopsy?	
	1
Additional questions that remain unanswered	
☐ What to do with the current evidence on mosaic embryos?	
☐ Can, and how much can, the embryo 'self-correct'?	
☐ How 'normal' do embryos have to be?	
☐ Are any detrimental effects due to the loss of cell(s) <i>per se</i> or the biopsy itself?	
☐ How may changes in lab practices and techniques influence the relative risks and benefits of 1 or 2 cell biopsy?	

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ESHRE Annual Meeting 2009 AMSTERSDAM





Optimizing PGD for monogenic diseases: minimal requirements in multiplex PCR and MDA

Dr. Céline MOUTOU, PhD Hôpitaux Universitaires de Strasbourg Université de Strasbourg **FRANCE**

Objectives

- describe the different approaches in PCR PGD
- explain why multiplex PCR is the standard for PGD for monogenic diseases
- describe the minimum requirements to set up a multiplex protocole
- explain the principle of multiplex PCR and MDA
- give tools to optimize protocols
- describe the advantages and disavantages of both methods
- help to choose the best approach for a specific indication

Requirements for PGD protocols

• Fast (transfer day 3-5)



• Sensitive : single cell PCR



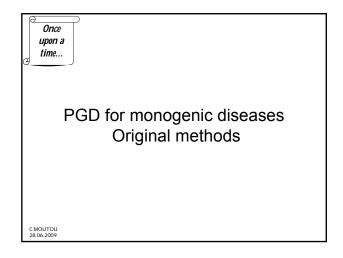
• Powerful :

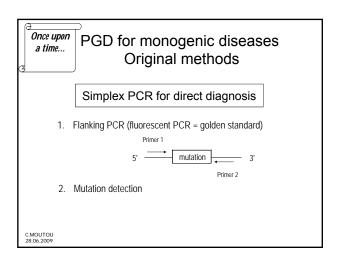


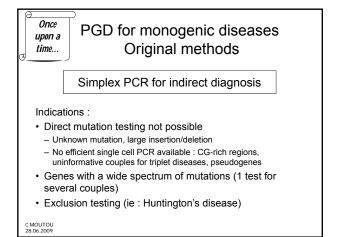


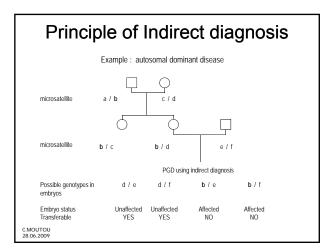
• Distinguish affected / unaffected embryos

Never transfer an affected embryo









BUT... Pitfalls in single cell PCR Simplex PCR may lead to misdiagnosis PCR problem Observation Adverse misdiagnosis Amplification failure autosomal dominant diseases Allele drop-out (ADO) autosomal dominant diseases Contamination recessive diseases ∫ b meiosis Recombination during Dominant and recessive diseases meiosis (indirect diagnosis) C.MOUTOU 28.06.2009

Conclusion: simplex PCR · Not safe enough for PGD of monogenic disease Misdiagnosis risk: « benign misdiagnosis » (no transfer of unaffected embryos or transfer of carrier embryos thought to be free of the mutation) « adverse misdiagnosis »: transfer of affected embryos thought to be unaffected (TOP or birth of an affected child) · Golden standard : Multiplex PCR - mutation detection and linkage - or linkage with several markers Multiplex PCR for linkage analysis in PGD Multiplex PCR for PDG · Several tests in the same cell : increased reliability • 1 universal test for 1 disease (for familial cases) · Valid for combined indications • Possible detection of problems : - PCR level : contamination, ADO, AOF

– Embryo/blastomere level : recombination event, blastomere quality
 ➤ Avoidance of misdiagnosis leading to affected embryo

transfer

Disavantages:

PCR setup more difficultFamily study needed

• SNP : Single nucleous confidencer • VNTR : variable number of tandem repeats : minisatellites • STR : Short tandem repeats : microsatellites • High heterozygousity rate • Abundant and spanning the whole genome • Polymorphic in the general population • Stable during transmission • Short fragments compatible with single cell PCR and multiplexing STR : Marker of choice for PGD

How to choose a Microsatellite Number of Repetitions: from 2 to 5 nucleotides Dinucleotide repeats: (CA)n, (GT)n, (TA)n. - the most common - characteristic stutters (training needed for interpretation) Trinucleotide repeats: (CAG)n (few stutters) Tetranucleotide repeats: (GATA)n (no stutters) Pentanucleotide repeats: (AAAAT)n (rare)

How to choose a Microsatellite Human genome database: www.genome.ucsc.edu Known markers (AFM or others) Intragenic; flanking (proximal AND distal) to reduce the risk of recombination events max Het >70% (better if >80%) If flanking: close to the gene (<1MB) + search repeat: | Microsate | Time | - 0 | - - - - | - - - | - - | - | - - | - | - | - | - | - | - | | - | - | - | - | - | | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - | - |

How many markers? Depending of the test Minimum N° of markers Information (full informative) detection of contamination only 1, linked or not Mutation + contamination detection Mutation + linkage 1 linked (intragenic) 2 flanking if semi-Confirmation of embryo informative status + Linkage 2 flanking the mutation Detection of contamination, ADO, recombination event HLA typing 4-5 within HLA region

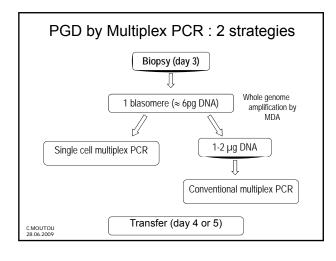
Family study

Familial case: at least 2 affected (mutation carrier) needed in 2 generations.

De novo mutation:

 Mutation + markers : phase can be deduced during PGD or using single sperm or polar body

C.MOUTOU 28.06.2009



Principle of single cell multiplex PCR • All primer sets in the PCR mastermix • Amplification: • single round PCR • or split after a few cycles to run each part with opimized conditions

HD: D4S1614 + D4S127 + Intron1 + D4S3034 + D4S3038 + D4S412

C.MOUTOU 28.06.2009

Optimization

Preliminary work:

— map the region and find STRs (5-6)
— primer design: similarTm, no stable dimer, same expected annealing T° for PCR
— (informativity testing for the couple)
— heterozygousity estimation for new markers
— marker choice
— PCR set up and validation

Single cell multiplex PCR

Optimization

- primer : test different ratios for primer set concentration
- mastermix : [MgCl2], modified dNTPs (CG-rich regions), polymerases, activators (glycerol, DMSO)
- try different amplification conditions (step duration, annealing $T^{\circ})$
- or use commercial kits dedicated to multiplex PCR
 Validation on heterozygous cells (≥50)

C.MOUTOL

Single cell multiplex PCR

Warning ...

N° of loci /

ADO rate per locus /
Complete genotyping per cell \
Contamination by carry-over /

- Validation should be done per locus but also per cell
- · Evaluation : haplotypes rather than genotypes
- Lower contamination rate when small series during validation.

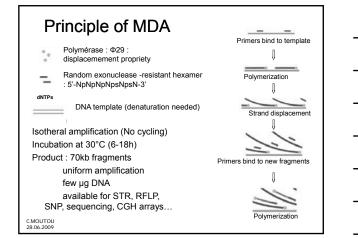
C.MOUTOU

MDA: Multiple displacement Amplification

- For limited DNA sample size : forensic, paleonthology, precious samples, single cell
- · Idea:
 - whole genome amplification \Rightarrow sufficient amount of DNA.
 - · conventional molecular testing
- Requirement for PGD
 - high fidelity (not sufficient using DOP-PCR or PEP-PCR)
 - compatible with the timing between biopsy and transfer

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26	of	104	



MDA: Multiple displacement Amplification

Optimization

- Single cell optimization :
 - MDA : YES
 - post MDA steps: NO
- cell storing before MDA (freezing / fresh cells)
- lysis buffer / time / temperature
- denaturation
- amplification time : initial protocols 16 hours, PGD protocols 1.5 to 2 hours
- Validation on single cells (>50 cells)

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C.MOUTOU 28.06.2009

Single cell multiplex PCR Warning ...Major drawback: MDA increases ADO and preferential amplification (PA) • ≈ 30% ADO (versus ≈ 10% for multiplex single cell PCR) More loci needed for linkage analysis Evaluation: haplotypes rather than genotypes PGH: preimplantation genetic haplotyping

Single cell Multiplex / MDA Single cell Multiplex single cell setup Foreach mutliplex For MDA only Time for setup A few weeks to months Nb of loci Limited Unlimited but Higher number needed (ADO) ADO rate ≈ 10% (5-6 loci) ≈ 30% PGD Application Linkage (± mutation) Linkage Haplotyping (few loci) Haplotyping (HLA) Yes (single sperm, De novo mutation polar body) How to choose a strategy? Type of lab Genetic unit performing DNA test, PND, PGD: · MDA: avoid to develop new tests •PGD lab only: if no test for the disease, setup needed • balance time for setup and number of loci needed C.MOUTOU 28.06.2009 How to choose a strategy? Indication • Common disease, 1 major mutation • multiplex PCR (mutation + linkage) · Common disease, no major mutation • multiplex PCR (linkage) or MDA • Rare disease : « private disease/mutation » • multiplex PCR (mutation + linkage or linkage) or MDA •HLA •MDA

• Combined indications • MDA

• MDA ?

• GC-rich region + linkage

How to choose a strategy ?	
Family history	
affected relatives available multiplex PCR (mutation + linkage or linkage) or MDA	
de novo mutation (or no relative available) multiplex PCR (mutation + linkage)	
gs,	
C.MOUTOU 28.06.2009	
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Conclusion	
Single cell multiplex PCR and MDA followed	
by multiplex can both be used in PGD.Single cell multiplex PCR : mutation detection	
+ linkage	
MDA : more complex indications (HLA, combined indications) + other possibilities	
than monogenic (aneuploidy, chromosome rearrangements	
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28.06.2009	<u> </u>
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Renwick et al Proof of principle and first cases using preimplantation genetic haplotyping—a paradigm shift for embryo diagnosis. Reprod Biomed Online. 2006 Jul;13(1):110-9. Shifts et al. Onlimization and evaluation of single-cell whole-genome.	
Spits et al. Optimization and evaluation of single-cell whole-genome multiple displacement amplification. Hum Mutat. 2006 May;27(5):496-503. Thombill et al. ESHRE PGD Consortium Best practice guidelines for	
clinical preimplantation genetic diagnosis (PGD) and preimplantation genetic screening (PGS). Hum Reprod. 2005 Jan;20(1):35-48. • Wilton et al. The causes of misdiagnosis and adverse outcomes in	
PGD. Hum Reprod. 2009 May;24(5):1221-8. Epub 2009 Jan 20.	

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Chromosomal abnormalities: development of generic tests

Staessen Catherine

CENTRE FOR MEDICAL GENETICS
CENTRE FOR REPRODUCTIVE MEDICINE



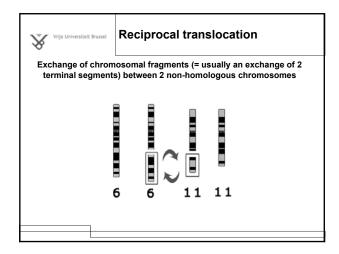
Learning objectives

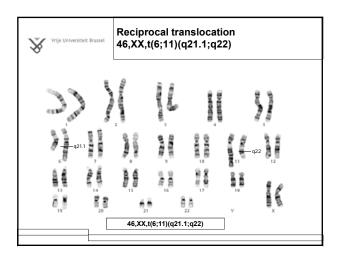
- List the basic categories of chromosomal abnormalities
- Describe the various strategies used clinically in PGD for chromosomal abnormalities
- Results obtained with clinical application of PGD for structural chromosomal abnormalities
- Describe research for implementation of microarray as a generic test for PGD for chromosomal abnormalities

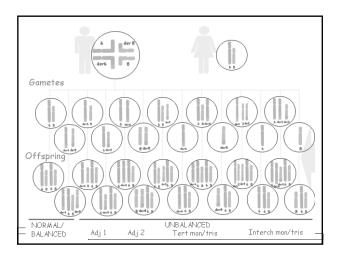


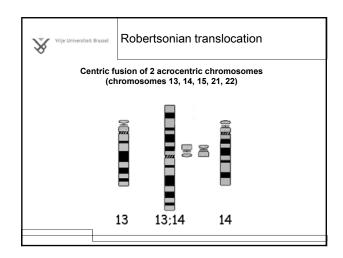
Types of chromosomal abnormalities

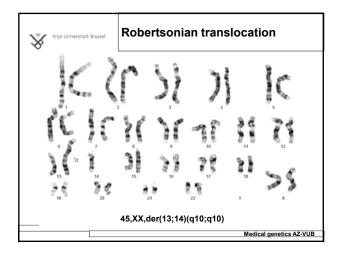
- · Numerical abnormalities: aneuploidy
 - One chromosome too many or too few: monosomy - trisomy - tetrasomy
 - One or more sets of chromosomes too many: triploidy - tetraploidy - polyploidy
- Structural abnormalities: balanced or unbalanced
 - Translocations (reciprocal; Robertsonian)
 - Inversions (paracentric; pericentric)
 - Deleties (interstitial; terminal)

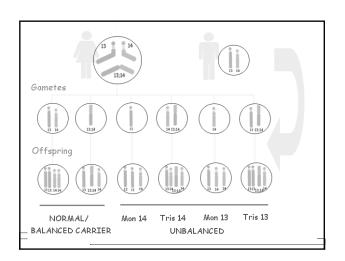














Indications for prenatal diagnosis for chromosomal abnormalities

- Presence of balanced structural chromosome abnormality in one of the parents
- Previous child with de novo chromosomal aneuploidy
- Advanced maternal age



For carriers of balanced translocations

PGD

- · As an alternative for prenatal diagnosis
- Associated infertility and in need of ART:
 - high incidence of unbalanced embryos
 - limited number of embryos transferred
 - selection of normal/balanced embryos for transfer: a necessity to obtain the highest chance for the delivery of a healthy child

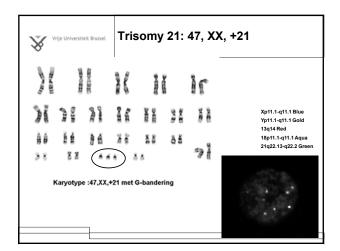
Chromosome abnormalities in oligozoospermic and NOA males 16,0 14,0 12,0 10,0 38 8,0 4,0 2,0 0,0 0 oligozoospermic azoospermic Total of 1701 oligospermic males investigated (5 studies) Total of 1151 non-obstructive azoospermic males investigated (6 studies) Van Assche et al., Hum Reprod, Vol 11, suppl 4, 1996

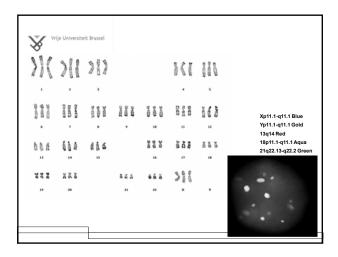


Approaches to PGD of aneuploidy

- polar bodies
- cleavage stage embryos

Detection of aneuploidy by FISH







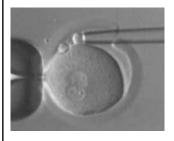
Different approaches to PGD of translocations

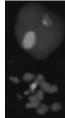
- · Metaphase analysis from
 - first polar bodies



Metaphase analysis from first polar bodies

Munne S et al., J Assist Reprod Genet, 15(5):290-296, 1998







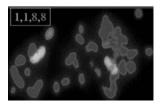
- Metaphase analysis from
 - first polar bodies
 - single blastomeres or second polar bodies by oocyte fusion



Metaphase analysis from single blastomeres by oocyte fusion

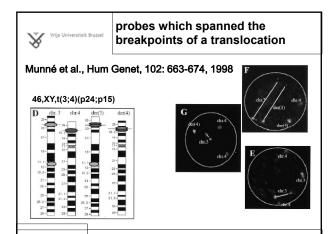
Day-3 blastomere nuclear conversion and metaphase FISH (fusion with murine or bovine zygotes)

Verlinsky Y et al., Reprod Biomed Online, 5(3):300-305, 2002



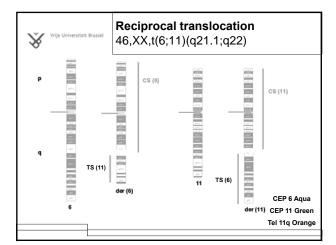


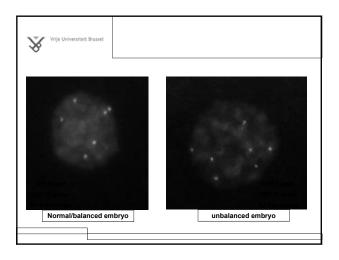
- · Metaphase analysis from
 - first polar bodies
 - single blastomeres or second polar bodies by oocyte fusion
- Interphase FISH on blastomeres
 - for reciprocal translocations: breakpoint spanning probes





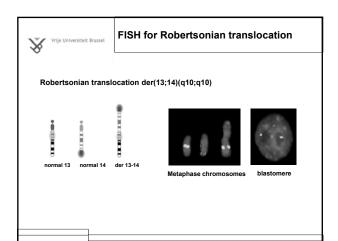
- Metaphase analysis from
 - first polar bodies
 - single blastomeres or second polar bodies by oocyte fusion
- Interphase FISH on blastomeres
 - for reciprocal translocations: breakpoint spanning probes
 - for reciprocal translocations combination of centromeric and telomere probes or probes distal to the breakpoints (Scriven et al., 1998)

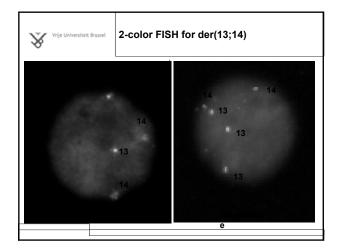






- · Metaphase analysis from
 - first polar bodies
 - single blastomeres or second polar bodies by oocyte fusion
- Interphase FISH on blastomeres
 - for reciprocal translocations: breakpoint spanning probes
 - for reciprocal translocations: combination of centromeric and telomere probes or probes distal to the breakpoints
 - for Robertsonian translocations: combination of alpha satellite/locus specific probes







UZBrussel experience: PGD for structural abnormalities

- From 2001 \rightarrow 2007: 558 cycles (with biopsy) performed (285 patients)
 - 167: Robertsonian translocations (103 patients)
 - 337: Reciprocal translocations (162 patients)
 - 14: Pericentric inversion (6 patients)
 - 3: Paracentric inversion (1 patient)
 - 18: Deletion: 22q11; del (X); ... (6 patients)
 - 19: Various: + marker, both parents rec translocation, (7 patients)



UZ-Brussel experience

	Robertsonian	Reciprocal
No. of OPU (patients)	181 (103)	366 (162)
Mean age	33.0 ± 4.8	33.2 ± 4.3
No. of oocytes	13.6 ± 6.9	12.9 ± 5.5
Fertilization (%)	73.7%	65.6 %
Cycles to biopsy	167 (92.3%)	337 (92.1%)



UZ-Brussel experience

	Robertsonian	Reciproca
Mean n° biopsied	5.5 ± 4.1	5.5 ± 3.7
Number of embryos for biopsy	926	1844
Diagnosed embryos	92.1%	94.3%
% normal embryos	50.4	19.2
Cycles to ET (%)	113 (67.7)	159 (43.4)

Vrije Universiteit Brusse	M	Male versus female carriers			
	rob	rob 🛉	rcp	rcp	
Mean N° biopsied	5.3 ± 3.9	6.1 ± 4.6	5.7 ± 3.8	5.3 ± 3.7	
% normal embryos	49.3	52.4	19.8	18.6	
Cycles to ET	75 (66.4%)	38 (70.4%)	77 (43.1%)	82 (44.2%)	
Mean N° transferred	1.7 ± 0.7	1.6 ± 0.6	1.5 ± 0.7	1.3 ± 0.5	

Vrije Universiteit Brussel	UZ-Brussel experience		
	Robertsonian	Reciprocal	
Mean N° transferred	1.6 ± 0.7	1.4 ± 0.6	
No. of transfers	113	159	
N° +HCG	57	63	
%/OR	34.1%	17.2%	
%/ET	50.4%	39.6%	
N° +FHB	45 (+1 no info)	44 (+2 no info)	
%/OR	26.9%	13.1%	
%/ET	38.7%	27.7%	

Vrije Universiteit Brussel	Outcome pi	regnancies
	Robertsonian	Reciprocal
No. of pos. HCG	57	63
Lost of follow up	1 (1.8%)	2 (3.2%)
Preclin misc	11 (19.3%)	17 (27.0%)
Clinical misc singleton twin triplet Ongoing/delivered singleton twin triplet	3 (5.3%) 1 2 0 42 (73.7%) 25 16 1	2 (3.2%) 1 1 0 42 (66.6%) 31 11 0



ESHRE PGD consortium data I-VIII: Chromosome abnormalities

- 2712 to oocyte retrieval; 2514 to biopsy
- % infertile (63%)
- Majority cleavage stage aspiration (93%)
- 1788 cycles to embryo transfer (71%)
- 332 clinical pregnancies (16% per OR, 24% per ET)
- No male/female differences.
- Robertsonian higher pregnancy rate than reciprocal

Goossens et al., Hum. Reprod., 2008



ESHRE consortium data Misdiagnoses in PGD with FISH

3 misdiagnosis for translocations on 2514 cycles = 0.12%

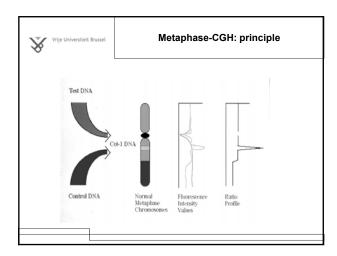
Diagnosis	Outcome
Miscarried	Miscarried
PND	ТОР
PND	TOP
	Miscarried PND

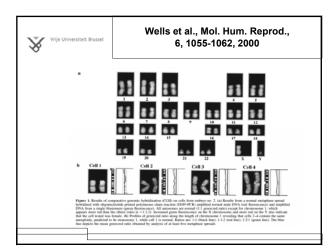
Wilton et al., 2009



Single-cell Comparative Genomic Hybridization

- Whole genome amplification:
 - degenerate Oligonucleotide Primed Polymerase Chain Reaction (DOP-PCR)
 - multiple displacement amplification (MDA)
- Comparative Genomic Hybridization (CGH)
 - metaphase CGH
 - array CGH



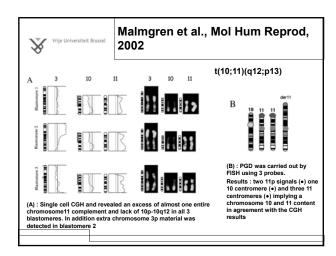


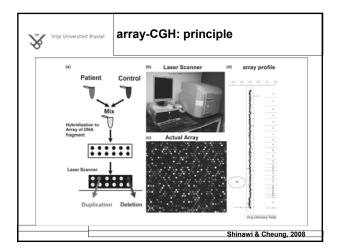


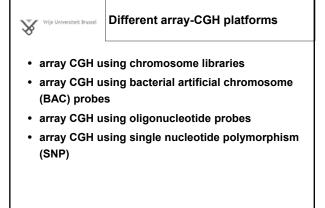
Malmgren et al., Mol Hum Reprod, 2002

Individual blastomeres from translocation carriers: analysed by CGH

- single cell CGH analysis reveals a high degree of mosaicism in human embryos from translocation carriers
- found a resolution limit of 10-20Mb for CGH
- small deletions or amplifications of the telomeric regions were difficult to interpret
- all protocols have a time requirement that is impossible to fit into the PGD situation with day 4-5 transfer









array CGH using chromosome libraries

- Arrays utilizing DOP-PCR products from chromosomespecific DNA libraries, depleted of repetitive sequences, as probes
- Hu DG et al. (2004): detecting of chromosomal copy-number variation from single lymphoblasts and fibroblasts
- No robust results were obtained since incorrect ratios were sometimes observed for chromosomes 2, 4, 9, 11, 17, 22, X and Y.
- · Disadvantage: inability to detect deletions and duplications
- Advantage: it takes only 30 h to perform

Hu et al., Mol. Hum. Reprod., 2004



array CGH using BAC probes

- Arrays consisting of a thousand of individual probes (BAC clones)
- Le Caignec et al., 2006:

Method accurately detects chromosomal imbalances from a single lymphoblast, fibroblast and blastomere within a single day following MDA

 Demonstrate the accurate detection of the del(4q) and the unbalanced translocation t(X;14) with deletion sizes of 34 and 58 Mb, respectively and a duplication of 47Mb in the fibroblasts.



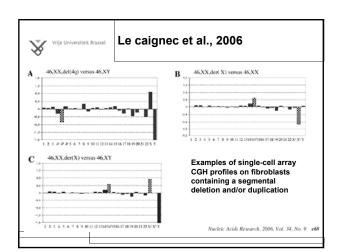
Vrije Universiteit Brussel

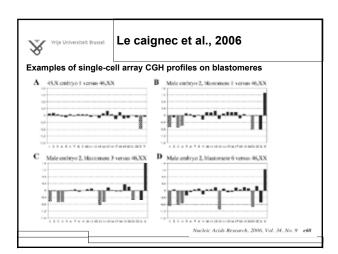
Nucleic Acids Research, 2006, Vol. 34, No. 9 e6 doi:10.1093/nar/gkl33

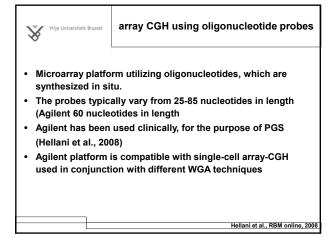
Single-cell chromosomal imbalances detection by array CGH

Cedric Le Caignec^{1,2}, Claudia Spits², Karen Sermon², Martine De Rycke², Bernard Thienpont¹, Sophie Debrock¹, Catherine Staessen², Yves Moreau², Jean-Pierre Fryns¹, Andre Van Steirteghem², Inge Liebaers² and Joris R. Vermeesch^{1,*}

¹Center for Human Genetics, University Hospital Gasthuisberg, Leuven, Belgium, ²Research Centre Reproduction and Genetics, University Hospital and Medical School, Vrije Universited Brussel, Brussels, Belgium ³ESAT-SISTA, K.U. Leuven, Leuven, Belgium and ⁴Leuven University Fertility Center, University Hospital Gasthuisberg, Leuven, Belgium





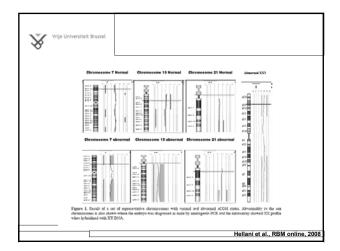




RBMOnline Vol 17 No 6. 2008 841-847

- Successful pregnancies after application of arraycomparative genomic hybridization in PGSaneuploidy screening
 - aneuploidy screening

 Dr Ali Hellani Laboratory, Saad Specialist Hospital Kingdom of Saudi Arabia
- Preimplantation genetic screening (PGS) using multiple displacement amplifications (MDA) and array comparative genomic hybridization (aCGH) was successfully performed on eight patients with a minimum of seven recurrent IVF failures with the aim of detecting aneuploidy and ameliorating pregnancy rate.





Array CGH using single nucleotide polymorphism

- An oligonucleotide array based upon the analysis of single nucleotide polymorphisms (SNPs): common polymorphic DNA sequences throughout the genome.
- The amplified material from the test sample is hybridized separately, with reference DNA samples assessed in parallel.
- A significant advantage of SNP micro-arrays is that the probes used provide genotype data in addition to chromosome copy number information. The simultaneous analysis of thousands of polymorphisms scattered throughout the genome produces a unique DNA fingerprint for each embryo tested.



Conclusions

- · Array CGH on single blastomeres:
 - determination of the copy number of all chromosomes
 - enabled the detection of imbalance of chromosomal segments, providing a universal platform, whereas different FISH probes have to be optimized for each specific translocation
- Array CGH requires further development and investigation before general clinical application can be considered: still clinical research
- Array CGH: still too expensive for clinical application

×	Vrije	Universiteit	Brussel

References

- Goossens V, Harton G, Moutou C, Scriven PN, Traeger-Synodinos J, Sermon K, Harper JC, ESHRE PGD Consortium data collection VIII: cycles from January to December 2005 with pregnancy follow-up to October 2006. European Society of Human Reportation and Embryology PGD Consortium. Hum Report. 2006. 23, 2629-2645.
 Helitan A, Abu-Amero K, Azouri J, Et-Akcoum S, Successful pregnancies after application of array-comparative genomic Helitan A, Abu-Amero K, Azouri J, Et-Akcoum S, Successful pregnancies after application of array-comparative genomic Human Control (1998). 2004. (1998). 2004. (1998). 2004. (1998). (2004)

- Le Caigne C. Spots C. Semon K. De Kycze M. Thereport B. Debrock S. Staessen C. Moreau Y. Fryns J. P. van Steintgem Adjöyse B. Membersch JR. Single-ein d'invensional ministence detection by sarry Ceth Nuclèer Audis Res. 2008. Malarigner H. Sahlen S. Incuraza J. Aho M. Resenland B. Fridatrion. Howatta O. Ahrtund-Richter, Nordenskyld N and Beternov E. Single call COH analysis ervokas a flight design of mosalisation in human embryos from pasteris with balanced Murné S. Fung J. Cassel JM. Marquez C., Weier H. U.G. Preimplantation genetic analysis of translocations: case-specific probes for interplace cell analysis. Hum Genet 1998. 102 Cell-658-674. D. Grundfeld L. Schoolcraft B. Scott R. Cohen J. Marquez C. Weier J. Barlog M. Sable D. Grundfeld L. Schoolcraft B. Scott R. Cohen J. Schoolcraft B. Schoolcraft B. Schoolcraft B. Schoolcraft B. Schoolcraft



Studying all chromosomes: is more better?

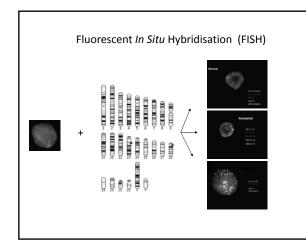
Evelyne Vanneste PhD student

Center for Human Genetics & University Fertility Center Leuven Belgium

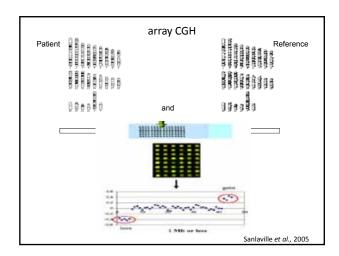
PCC ESHRE, Amsterdam, 28-6-200

Overview

- Introduction
 - From FISH to arrays
 - Amplifications of single cells
 - Basic analysis of single cell array results
- Copy number variation detection in single cells
 - Advanced analysis of single cell array results
 - BAC array
 SNP array
- · Clinical implementation
 - Array screening results of GQE from young fertile patients
- · Biological implications
 - Consequences of array technique for PGD and PGS

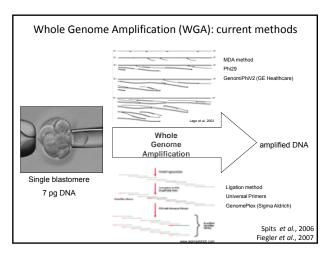


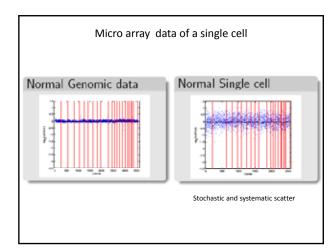
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Overview

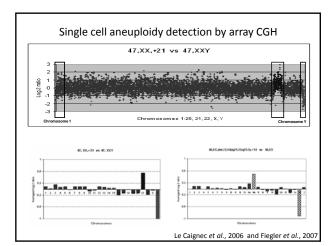
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Overview

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Conclusion introduction Array of single cells : amplification needed Advantages single cell array Screen complete genome at once Detection of whole chromosome aberrations - Detection of a priori known partial chromosome imbalances Disadvantages single cell array :

Overview

Studying all chromosomes: is more better?

Introduction

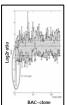
Array > FISH Accuracy

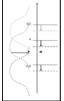
– Threshold?

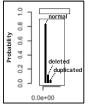
- Non a priori known aberrations ? • Replace FISH by array CGH for PGD and PGS ??

- From FISH to arrays
- Amplifications of single cells
- Basic analysis of single cell array results
- Copy number variation detection in single cells
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A novel statistical method that calculates likelyhood estimates on imbalances detected with SC BAC-arrayCGH

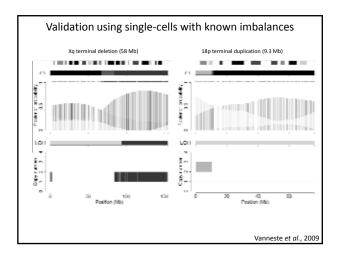


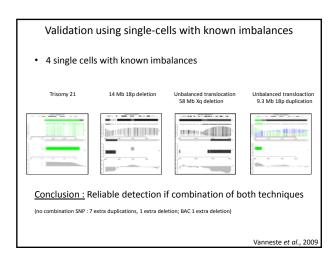




Clone specific variability
Clone specific correction
Clone specific likelyhood estimate

Ampe et al., 2009





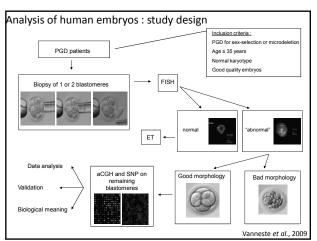
Genome-wide equal probabilities for all copy numbers states Origin :High SD between intensity ratios of consecutive BAC-clones? Technical or biological? Hypothesis : relation with cell cycle - S-phase : more scatter - M-phase : chromosomes highly condensed Consequence: cell type specific reference set

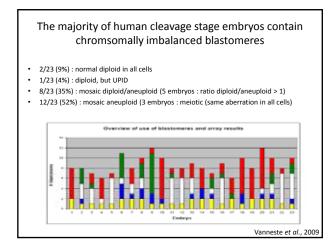
Conclusion CNV detection in single cells

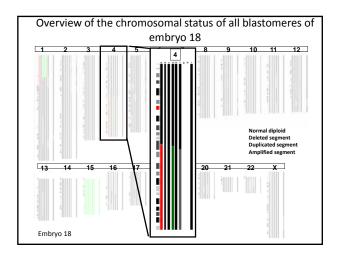
- Combination of BAC and SNP : reliable detection of aberrations
 - Advantages of BAC-model
 - Correction for systematic biases
 - Posterior probabilities for deletions, duplications and diploidy
 - Quality of SC array data (equal probabilities = not informative)
 - Advantages of SNP-model
 - CN + LOH
 - Detection of nullisomy and amplifications
 - Detection of uniparental disomy
- High 'drop out' due to high SD
- Cell type specific

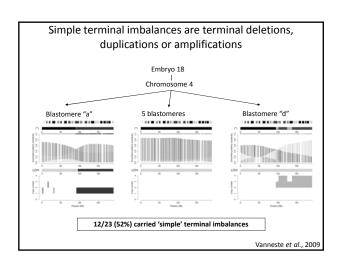
Overview

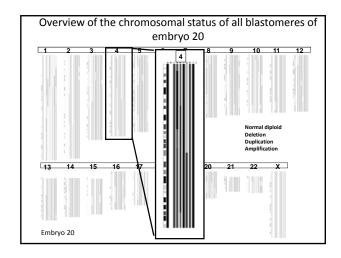
- Introduction
 - From FISH to arrays
 - Amplifications of single cells
 - Basic analysis of single cell array results
- · Copy number variation detection in single cells
 - Advanced analysis of single cell array results
 - BAC array
 SNP array
- Clinical implementation
 - Array screening results of GQE from young fertile patients
- Biological implications
 - Consequences of array technique for PGD and PGS

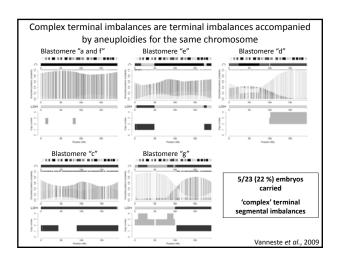












Conclusion clinical implementation Chromosomal aberrations (> 9 Mb) can be accurately detected in single cells by microarrays Questions to solve before clinical implementation: Combination of array results in practice ('no golden standard') Duration of protocols Resolution Quality criteria

Overview

Studying all chromosomes: is more better?

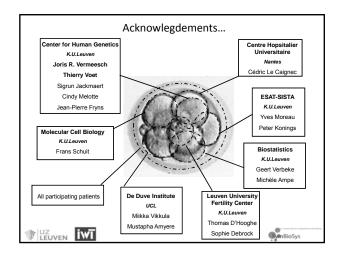
- Introduction
 - From FISH to arrays
 - Amplifications of single cells
 - Basic analysis of single cell array results
- Copy number variation detection in single cells
 - Advanced analysis of single cell array results
 - BAC array
 SNP array
- Clinical implementation
 - Array screening results of GQE from young fertile patients
- Biological implications
 - Consequences of array technique for PGD and PGS

Studying all chromosomes: is more better? CHROMOSOME INSTABILITY = common to human IVF embryogenesis 91% of early human IVF embryos are chromosomally abnormal FISH not appropriate to detect segmental aberrations Not confined to aneuploidy risk couples IVF/ICSI success rate > normal diploidy rate Self correction and/or self selection mechanisms Explanation for low human fecundity Biological basis for failure of preimplantation genetic screening (PGS) in improving baby take home rates

NO, it isn't !!! YES, is it Better insight in early embryogenesis Not in preimplantation context

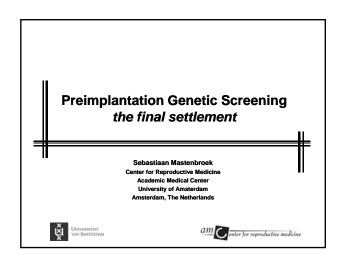
Near Future

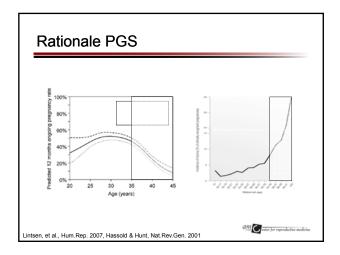
- Arrays for PGD
 - Translocations
 - · Which chromosomes?
 - De novo events (Kasakyan et al., 2008)
- More studies using high resolution arrays: confirmation of
 - Percentage of normal diploid embryos
 - Segmental aberrations
 - UPD
- Segmental aberrations
 - Origin

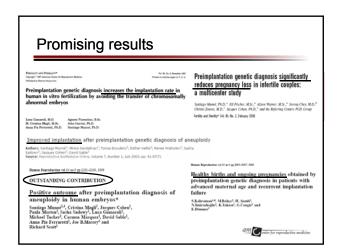


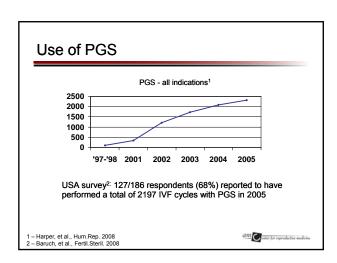
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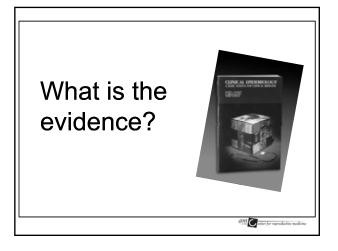
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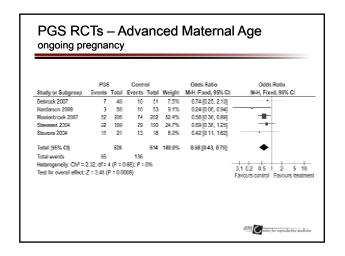


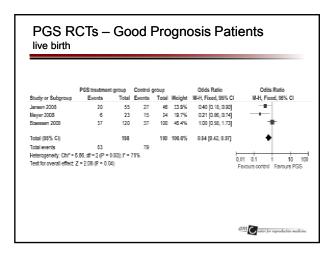


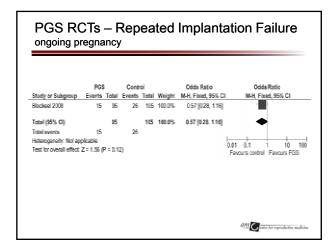


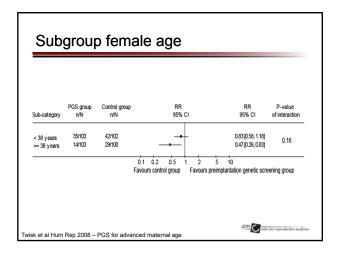


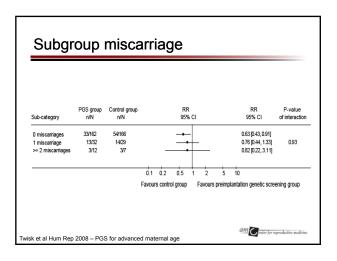


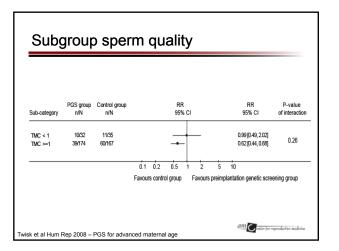


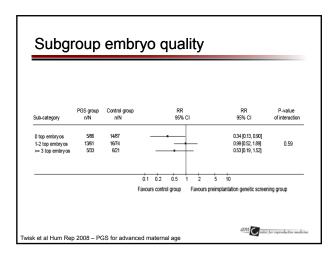












Preimplantation genetic testing: a Practice Committee opinion The Practice Committee of the Society for Assisted Reproductive Technology and the Practice Committee of American Society for Reproductive Medicine Available solvence does not upport the use of PGS as currently performed to improve the best rates in pacients with aburdent internal separation failure, decisions concerning future reasonest should not be based on the results of PGS in our errors better seament should not be based on the results of PGS in our errors better and the seament should not be based on the results of PGS in our errors better in tracts in pacients with recurrent pregnancy loss related to amerginally. Available evidence does not support the use of PGS as courrently performed in improve first in rates in pacients with recurrent pregnancy loss related to amenginally. Available evidence does not support the use of PGS as coursely performed to reader inscringer seaso in pacients with recurrent pregnancy loss related to amenginally. Available evidence does not support the use of PGS as coursely performed to reader inscringer seaso in pacients with recurrent pregnancy loss related to amenginally.

Recommendations | Pritish Fertility Society | Concerns | Concerns

Recommendations

ACOG COMMITTEE OPINION

Preimplantation Genetic Screening for Aneuploidy



Why doesn't it work?





Technical aspects

failure rate

	AMC/UMCG1	VUB ²	ESHRE PGD consortium ³	Saint Barnabas ⁴
biopsy (embryos)	2.8%	5.8%	1.3%	
fixation (blastomeres)	10.9%	6.4%	12.5%	
FISH (blastomeres)	6.7%	7.1%		
Total unknown	20.1%	2.4%*	13.7%	4.4%**

- 2-cell biopsy
 Transferpolicy: ET of abnormal embryos allowed, but excluded from analysis. No definition of abnormal.
- 1 Mastenbroek, et al., NEJM (2007), 2 Michiels, et al., Hum.Rep. (2006) 3 Sermon, et al., Hum.Rep. (2007), 4 Munne, et al., RBMO (2003)

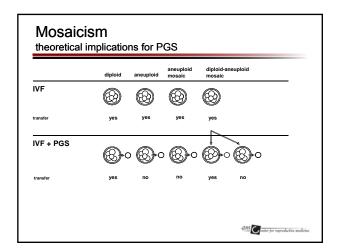
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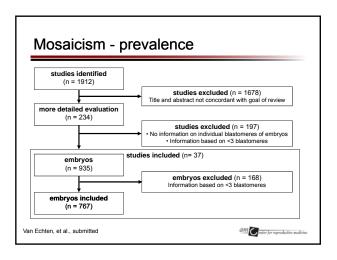
Technical aspects

- · Biopsy possibly more harmful than previously thought
 - the effect of biopsy alone on pregnancy rates has never been studied¹
- · FISH is not 100% accurate
 - Estimated accuracy in lymphocytes 92-99%
 - Not determined for PGS probe set on human blastomeres
 - Estimated FISH error rate
 - 0.928 → 49% error
 - 0.948 → 39% error
 - 0.968 → 28% error
 - 0.988 → 15% error





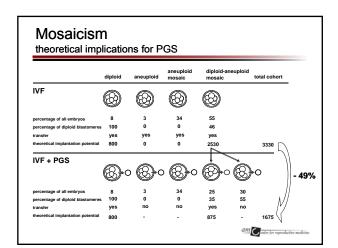


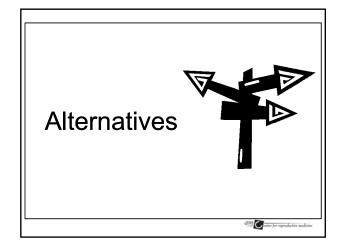


	(n=767) <i>all</i>		(n=260) cleavage stage >5 chromosomes		(n=360)	
Diploid	168	22%	39	15%	29	8%
Aneuploid	36	5%	36	5%	11	3%
haploid	2	0%	0	0%	1	0%
polyploid	4	0%	1	0%	0	0%
aneuploid	17	2%	10	4%	6	2%
complex abnormal	13	2%	11	4%	4	1%
Mosaic	563	73%	199	76%	320	89%
aneuploid-mosaic	108	14%	47	18%	122	34%
diploid-aneuploid mosaic diploid blastomeres	455	59% 72%	152	58% 61%		55% 46%

Van Echten, et al., submitted Mastenbroek, et al., submitted







New or improved forms of PGS

- · Developmental stage at which biopsy is performed
 - polar body
 - blastocyst
- Methods of analysis¹
 - CGH arrays
 - SNP arrays
- · First experiences
- · Development stage or pilot-study stage
 - too premature for routine clinical application



New or improved forms of PGS

ESHRE PGS Task Force

- · No need for further RCT using cleavage stage biopsy
- · Polar-body biopsy and 24-chromosome analysis in theory best alternative
- · Stepwise approach
 - 1. Preclinical study / method assessment
 - 2. Pilot study
 - 3. Randomised clinical trial
 - → currently phase1

edts Focus on Reproduction January 2009



Non-invasive selection

- ≠ Preimplantation Genetic Screening
- Examples¹
 - metabolomic profiling
 - spectrophotometric analysis of metabolomic changes in culture medium
 - amino acid profiling
 - assessment of amino acid depletion and production by embryo in culture medium
 - respiration-rate measurement
 - · respiration-rate of embryos is assessed
 - birefringence imaging
 - polarization light microscopy is used to assess meiotic spindle or zona pellucida
- Development stage or pilot-study stage
 - too premature for routine clinical application

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Summary

- · All clinical evidence shows that PGS does not work
 - Harmful
- · Reason for inefficacy
 - Technical aspects
 - Failure of biopsy / fixation / FISH
 - · Biopsy harmful
 - FISH not 100% accurate
 - Mosaicism
 - Half of all embryos are diploid-aneuploid mosaic
 - Half of all blastomeres are diploid
 - · Discarding of potentially viable embryos



Future

- Further development and evaluation of new or improved forms of PGS
 - Polar body biopsy, blastocyst biopsy
 - CGH arrays, SNP arrays
- · Alternative selection methods (non-invasive)
- · Preimplantation embryology
 - Origin of diploid-aneuploid mosaic embryos
 - · Physiological? Pathological?
 - · Induced through hyperstimulation and/or in vitro culture?
 - Fate of diploid-aneuploid mosaic embryos
 - Rescue mechanisms?



PGS: the final settlement?

- PGS with the use of current techniques
 - cleavage stage biopsy and FISH
- Routine clinical application not justified





PGS: the final settlement?

- New or improved forms of PGS
 - Polar body biopsy, blastocyst biopsy
 - CGH arrays, SNP arrays, etc
- Method assessment, pilot studies and subsequent RCTs needed
- · We should learn from the past
 - No routine clinical application before efficacy is proven
 - Harm of biopsy, accuracy of analysis, mosaicism





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ESHRE Pre course congress Latest developments in preimplantation genetic diagnosis Long-term children follow up

Alison Lashwood (MSc. RGN, RSCN, DipHV) Consultant Nurse Centre for PGD, Guy's Hospital, London

Objectives

- To be aware of the data available to date and convey this to couples requesting treatment for PGD.
- To be aware of on going studies and the importance of these.
- To understand the difficulties inherent in long term follow up

Recommendations for paediatric follow up

- PGDIS- guidelines for good practice in PGD (PGDIS- 2008)
- ESHRE- best practice guidelines for clinical PGD
- Human Genetics Commission- UK (Making babies 2006)
- Huge variation in practise across the EU- impact on follow up (Lawford Davies 2007)
- In 1996 Simpson and Leibaers recommended a standardized approach to collating data at birth on PGD babies

Paediatric outcome after PGD Reports on outcome at birth: Case controlled study 2007 (Brussels) 563 babies- increased NND and SB rate, but major abnormality 2.9% less than ICSI (personal communication 2008) • ESHRE (Goossens 2009)-indicated abnormality rate at birth • 109 babies from polar body biopsy- no increase in abnormality rate (Strom 2000) 24 babies over 5 years PGD for CF- no increase in major abnormalities (Keymolen 2007) Paediatric outcome after PGD Long term follow up: • Little long term data on PGD babies - 3 papers have reported longer term case controlled outcomes Mental & psychomotor development at 2 yrs-70 children (Nekkebroeck 2008) Auxological & medical follow up at 2 yrs-70 children (Desmyttere 2009) • General health at 2 yrs- 49 children (Banerjee 2008) All report developmental parameters same as control groups What are the abnormalities?

Malformations in context-back ground risks

Major malformation

"major structural anomalies have medical and social consequences"

(Stevenson & Hall- Human malformations & related anomalies)

- 2-3% at birth
- 5% at 5 years

Minor malformations

"minor anomalies are relatively frequent structural alterations that pose no significant health or social burden" (occur in <4% of population)

• 15% at birth

Range of major abnormalities

(ESHRE 2009)

- Aorta coarction
 Absence of corpus callosum
 Absence of corpus callosum,
 Absence of corpus callosum,
 Absence of corpus callosum, kidney
 dilatation, growth
 Retardation
 Absence of ductus venosus
 Bilateral clubfoot
 Cataract
 Choanal artresia
 Cleft lip unilateral
 Cleft lip and palate
 Congenital inhi juxation
 Congenital inhi juxation
 Congenital inhyosiform erythrodermia
 Fryns syndrome, neonatal death
 Hemangioma

 Hydrocephaly

 Large cavernous haemangioma

 Laryngomalacia, receding chin,
 strawbery naevus

 Pes equinovarus
 Phocomelia and pulmonary deficiency
 Right ear- external meatus obstruction
 Sacrate dimple without intestinal
 connections

 Pulmonary stenosis
 I achycardia of Cournel
 I etratogy of Fallot
 Unilateral cryptorchidia
 Unilateral intrauterine torsio testis
 Ventricular septum defect
 Ventricular septum defect
 Ventricular septum defect, retrognatia

-			

Range of minor abnormalities (ESHRE 2009) Bilateral hydrocoele Microcephaly Mongolean spot Capillary haemangioma Cardiac septum defect Positional talipes Cerebral calcifications + Pre-auricular tags limb malformation Pyelourethral junctional Congenital hip luxation stenosis Pyelo-caliectasy bilateral Cryptorchidy Sacral dimple Heart murmur Heart problems + 1 testicle + mental retardation Syndactyly digit iv-v Syndrome of Rubinstein-Taybe Hypospadias Kidney and bladder problems, mental Uniumbilical artery What can we learn from ART (1) In developed countries ART babies represent 1-4% of babies There is a need to compare singleton pregnancies to control for confounding multiple birth factors It is difficult to assess whether the underlying cause of subfertility or ART is responsible • 3 meta-analyses (Hansen 2005, Lie 2005 & Rimm 2004) and a controlled study of nearly 3000 infants (Bonduelle 2002) confirmed relative risk of major abnormality of 1.24 in ART babies

 Longer term studies on ICSI/IVF babies show a relative increase risk of abnormality- ICSI (2.77) and

Beckwith Wiedemann, Angelman and retinoblastoma (Sutcliffe 2006, Maher 2003, Moll 2003)

· Possible increase risk of imprinting disorders such as

IVF (1.8) (2005 Bonduelle)

What can we learn from ART (2) "Time to pregnancy" (with & without fertility treatment) is implicated in: • maternal health factors e.g. pre-eclampsia • birthweight- 2 fold increase in low or very low BW • Perinatal/neonatal death and SCBU admission odds ratio 2.9. Review ESHRE 2008 data (Goossens et al 2009 in press) ESHRE data collection from January 1997 to December 2006 (& subsequent pregnancies) • Data available on 3303/3841 babies • No data available on 538/3841 babies (14%) • Multiple birth rate 23% (ESHRE 2009) • Malformations reported in 132/3303 babies Overall malformation rate = 3.99% Major malformations= 68 Minor malfomration= 65 (1 baby had more than 1 malformation) Difficulties with PGD paediatric collection? Numbers per centre are small- 700 children needed for power to detect major abnormalities (Desmyttere 2008) • Easy to lose contact with families and fail to collect complete data • Funding of paediatric follow up Distance to travel to PGD Centre & secrecy of PGD Ascertainment bias, requires control population

Number of variables to control for: • 1 versus 2 cell biopsy • Singletons versus multiples • PGD vs PGS as background reason for treatment is different • Fresh vs cryopreserved embryos GSTT paediatric follow up • Introduced at the beginning of the PGD service- (1997) • Encouraged all couples to participate • Committed paediatrician as part of the PGD team Follow up process • Discussed with couples at the outset of treatment • Pregnancies managed by local obstetric teams. Multiple pregnancies referred to Fetal Medicine Unit for chorionicity scan. • Birth outcome questionnaire sent to couple at 30/40 • Follow up appointments arranged at 1 and 2 years of age

Birth outcomes 1997-September 2007

Total babies born = 126 Total deliveries = 93

- 63 singletons-
- 51 twins (26 x 2)- 1 IUD @ 29/40
- 12 triplets (4 x 3)

Singletons	at	birth
63		

- 62/63- reviewed (1 no details)
- 49/62- no problems reported (79%)
- 5 neonatal complications

Major abnormalities

- 1 hypothyroidism
- 1 hydronephrosis

Minor abnormalities

- 2 positional talipes (resolved)
- 1 undescended testes (resolved)
- 1 laryngomalacia (resolved)
- 1 microcephaly & meconium aspiration
- 1 cardiac murmur

-			 	

Singletons at 1 year 42

29/42 reviewed 21/29- no problems reported (72.4%)

New problems

• 1 capillary haemangioma (27/40)

- 1 congenital hip dysplasia
- 1 convergent squint
- 1 lactose intolerance
- 1 LF hearing loss (+++URTI)
- 1 torticolis

Continuing problems

- 1 hypothyroid-treatment in progress
- 1 pyeloplasty for hydronephrosis

Singletons at 2 years 31

12/31 reviewed 9/12 no problems reported

New problems

Continuing problems

- 1 Congenital hip dysplasia
- 1 Squint
- 1 Congenital hip dysplasia

Twins at birth 51 (26 x 2)

- 51/51 reviewed (1- IUD @ 29/40)
- Zygosity
 - DZ 18 (sets)
 - MZ 1
- unknown 7 (all 2ET)
- 43/51 no problems reported (84%)
- 1 minor abnormality- hydrops (resolved)
- 7 neonatal complications

Twins at 1 year 40

- 30/40 reviewed
- 22/30 no problems reported

New problems- minor abnormalities

- 1 motor delay
- 1 motor delay
 1 floppy larynx
 2 squints 1 microcephaly
 1 2/3 syndactyly
 1 skin tag
 1 microcephaly
 1 hearing deficit

Twins at 2 years 22

- 16/22 reviewed
- 14/16 normal

Abnormalities- no new abnormalities

- 1 motor delay (as before)
- 1 floppy larynx (as before)

Triplets 12 (4 x 3)

- 12/12 reviewed
 MZ twins 2 sets
 8/12 no problems reported
 1 minor abn- undescended testes
 3 neonatal complications

- 7/12 reviewed
 3/7 no problems reported
 4 abnormal
 1 deceased SID cardiac
 abnormality (29/40)
 2 patent foramen ovale (29/40)
 1 multiple abns. including NEC (30/40)

- 6/9 reviewed5/6 normal1 dev delay & behavioural problems (new)

Summary of GSTT data Major abnormalities (3.9%) • 2 major at birth • 3 more by 2 years Minor abnormalities (15.8%) • 8 at birth (most in singletons, 1 preterm) • 12 more by 2 years Neonatal complications • 15 - 11/15 preterm - 2/15 maternal pre eclampsia **New studies** EU 8th Framework PGD study Multi faceted study. The main goals of the study are: to facilitate the collection of data relating to the use of reproductive technologies and their outcomes in EU member states through the use of common terminologies and data registers (the 'technical strand') to facilitate the referral of patients from one centre to another, particularly for patients at risk of rare monogenic diseases (the "clinical strand")

to enable the efficient follow-up of patients and their off-spring so as to monitor safety and efficacy through data collection and a data register (the 'monitoring strand')

 to examine the relevant requirements of the EU Human Tissue and Cells Directive (2004/23/EC) and other relevant legal requirements at EU and member state level, and to address related ethical issues (the 'legal and ethical strand').

The history ESHRE steering committee committed to retrospective data collection. 2005- 2006 questionnaires sent to centres asking their views and willingness to participate in study. 2006- Responses indicated that in first instance at least a retrospective follow up study could be done. Centres were invited to participate if they met study criteria which were: - must have 10 or more live births - patients must be able to read and write 1 of 6 languages, English, German, Flemish, French, Spanish, Czech - Babies born up to and including 30/10/07 Study size

- 16 centres agreed to participate
- Approximately 2000 babies
- May be able to increase numbers if database allows

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Study process • Parental questionnaire based study. • Non case controlled, one time period study Managed centrally by CI Alison Lashwood • Local centre collaborator to administer questionnaires. • Returned to CI with unique identifier Data management Data to be stored on a new paediatric web based database created as part of the EU project (Consortium Database Working Group) • This database will form a prototype for possible future PGD data collection. • Database still being created therefore data will be entered centrally. **Ethics**

- UK centres require ethics approval-complex process- granted in September 2008
- All centres asked about local requirements for ethical approval- many centres indicated this was not required.

Current progress · Participating centres in process of despatching questionnaires • Data entry hopefully will start in 2-3 months • First reports due by October 2009 Summary • Short and long term data on PGD babies is limited. · At present the overall abnormality rate at birth appears to be no higher than abnormality rates for other ART procedures • In future studies a number of variables will need to be considered and controlled for. · A large collaborative, prospective case controlled study is required. Such a study is complicated by multicentre participation (in multiple countries), language, standardisation of terminology and paediatric review.

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What have we learned from 10 years of the **ESHRE PGD Consortium**

Peter Braude MB BCh PhD FRCOG FMedSci Head of Department of Womens Health, Kings College London, and Centre for Premiplantation Genetic Diagnosis, Guy's Hospital, London

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- Why collect data?
- What has the data revealed?
- Is there still a need to continue collecting the same data?
- Should the reporting emphasis of reporting change?
- What has the consortium achieved?



Who wants the data

- Involved Profession:
- Is PGD effective and how are they doing in comparison?
- Who is offering PGD?
- What new diseases are being tested?
- What are the trends in disease diagnosis technologies?
- Is the procedure safe?
- What are the risks?
- Media and patients
 - Information who needs PGD and how its done?
 Does it work for my disease?

 - What is on offer and where?
 - Is it safe?
 - What's new?



Aims of the ESHRE PGD Consortium

- To survey the availability of PGD
- To collect prospectively and retrospectively data on the accuracy, reliability and effectiveness of PGD
- To initiate follow-up studies of pregnancies and children born
- To produce guidelines and recommended PGD protocols
- To formulate a consensus on the use of PGD



Different parts to the collection and reports

- Referrals why are patients being referred?
- Cycles- how many, how and for what?
- Pregnancies how many, outcome?
- Children outcome and early health long term health



In the beginning - Data collection I Jan 97- Sept 98

- Joep Geraedts
- Alan Handyside
- Joyce Harper
- Inge Liebaers
- Karen Sermon
- Catherine Staessen
- Alan Thornhill
- Anna VanderfaeillieStephan Viville





PGD Data collections I-IX

- Series I Jan 1997-Sept 1998 [16 centres] (120 OR; 82 Children)
- Series II Oct 1998 May 2000 + from 1993 [26 centres]
 (196 OR;162 children)
- Series III May 2000-May 2001 + any from before [25 centres] (426 OR; 279 Children) Social sexing included
- Series IV May 2001 Dec 2001 [36 centres] (1819 OR; 243 babies) Major increase PGS
- Series V Jan 2002 Dec 2002 (children to Oct 2003) [43/66 centres]
 2219 cycles; 485 pregnancies; 382 babies



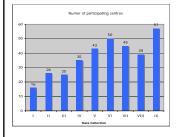
PGD Data collections V-IX

Links babies to the cycles

- Series V Jan 2002 Dec 2002 (children to Oct 2003) [43/66 centres] 2219 cycles; 485 pregnancies; 382 babies
- Series VI Jan 2003 Dec 2003 (children to Oct 2004) [50 centres] 2984 cycles; 501 pregnancies; 373 babies
- Series VII Jan 2004 Dec 2004 (children to Oct 2005) [45 centres] 3358 cycles; 679 pregnancies; 528 babies
- Series VIII Jan 2005 Dec 2005 (children to Oct 2006) [39 centres]
 3488 cycles; 845 pregnancies; 670 babies
- Series IX Jan 2006 Dec 2006 (children to Oct 2007) [57 centres] 5858 cycles; 1437 pregnancies; 1206 babies



Effectiveness of PGD - trends in use Centres participating in data collection

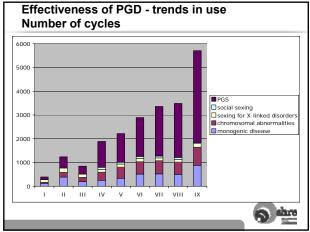


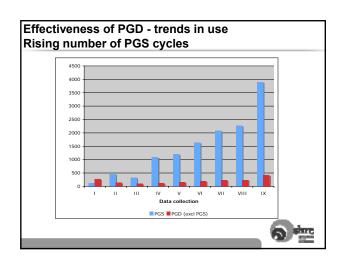
- Steady increase in number of centres participating
- Not all registered centres send in data; varies year on year
- Number of centres limiteddoes not include some of the busiest USA centres

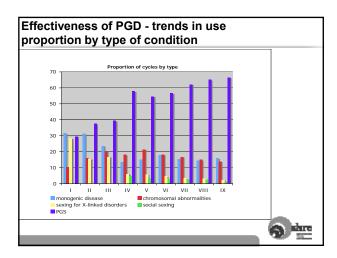


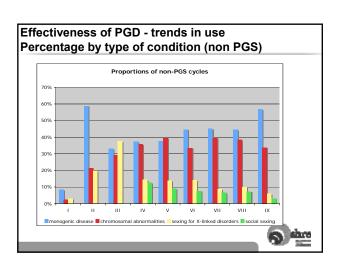
93 Members by country I-IX (full + associate) Argentina: Australia: Brazil Netherlands: Poland: Portugal: Belgium: Bulgaria: Czech Republic: Russia: Serbia: Singapore: South Africa: Denmark: 1 11 2 2 1 3 Egypt: Spain: Germany: Japan: Finland Thailand: Taiwan: Turkey: France: Greece: India: UK: Ukraine: United Arab Emirates: USA: Israel: Italy: Korea:

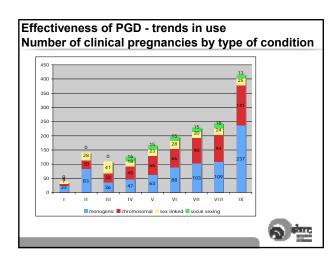
Full Send in full data Associate Send in summary data All receive / share communication Newsletters Surveys Meetings Information on web site











Effectiveness of PGD - outcome I-IX percentage by type of condition

	Cycles to OR	No. embryos biopsied	Embryos transferred	Transfer procedures	Pregnancy rate (per OR / per ET)
Monogenics	3481	19988	5296	2730	21% per OR
(Rec, Dom)					27% per ET
Chromosome	3476	22878	4045	2254	16% per OR
Rearrangements					25% per ET
Sexing X linked	1072	6691	1458	798	19% per OR
					26% per ET
Social sexing	542	3317	815	395	21% per OR
					29% per ET
Aneuploidy	13020	71119	16897	9394	18% per OR
PGS					25% per ET

Headline data not useful information for patients



Cumulative data I-IX: PGS

- Almost all patients infertile -13020 to OR
- 12597 cycles to biopsy, Majority cleavage stage aspiration + PB biopsy
- 9394 cycles to ET (72%)
- 2390 clinical pregnancies (18% per OR, 25% per ET)

Differences from PGD:

- Not about recurrent genetic disease appropriate comparator IVF/ICSI
- Indications variable and often unclear
- High proportion go ahead with 1 embryo
- Although gives additional information about safety of biopsy and early outcome of children, provides little helpful information about usefulness
- To date no account has been taken of lack of efficacy shown in randomised trials



PGD for Monogenic Disease

- Recessive
 - β-thalassaemia
 Cystic Fibrosis
- Spinal muscular atrophy
 Sickle cell disease

- Dominant Huntington's disease
 Myotonic dystrophy
 Charcot-Marie-Tooth disease
- Sex linked (specific diagnosis)
 Duchenne muscular dystrophy
 Haemophilia
 X-linked mental retardation



Headline rates unhelpful as disguise true information based on type of inheritance

Collection IX

PGD for Monogenic Disease

Collection I-VIII

Dominant conditions : Outcome I-IX

MD	HD		MD	HD
294/393	252/326	Reaching	80/98	72/98
74%	77%	ET	81%	73%
Clinical	pregnancy		Delivery	rate
21%/ET	23%/ET		26%/ET	34%/ET
16%/OR	18%/OR		19%/OR	27%/OR



PGD Chromosome rearrangements: Outcome I-VIII

Robertsonian translocations Reciprocal translocations

Male	Female		Male	Female	
331/450	234/315	Reaching	430/737	470/768	
73%	74%	ET	58%	61%	

CPR/ET 22% CPR/ET 28% CPR /OR 13% CPR /OR 21%



PGD Chromosome rearrangements:

Outcome: Collection IX

Robertsonian translocations Reciprocal translocations

Male	Female		Male	Female	
116/161	54/83	Reaching	112/208	139/260	
72%	65%	ET	53%	53%	
33%/ET	18%/ET	Delivery rate	26%/ET	28%/ET	
24%/OR	12%/OR		14%/OR	15%/OR	



Sexing for X-linked disease Cumulative data I-IX:

- 1072 cycles to OR
- 1060 to biopsy most cleavage/aspiration
- 798 cycles to ET
- 204 clinical pregnancies (19% per OR, 26% per ET)

Findings

- Similar results to recessive conditions
- More cases now being done by molecular means to allow unaffected males to be diagnosed.



Social sexing: Cumulative data I-IX

- 542 cycles to OR 43 were infertile
- 526 cycles to biopsy
- 3317 biopsied, 99% successful
- 395 cycles to ET, 72%
- 116 clinical pregnancies (21% per OR, 29% per ET)

indings

- Similar results to monogenic disease and PGS as proportion to ET similar
- Relatively few cases proportionally 3% (USA not reported)
- What does this add to knowledge of PGD/PGS safety?

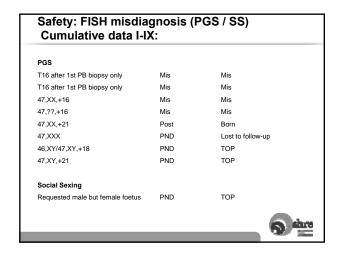


Outcome: Pregnancies Cumulative data I-IX: • 3703 clinical pregnancies • 2726 singletons • 858 twins (23%) 90 triplets (2.4%)6 quads • 23 unknown • 482 losses 1st trimester: 355 miscarriage, 37 ectopic, 8 TOP, 3 unknown 2nd trimester: 60 miscarriage, 19 TOP Early collections do not take account of these losses inflating success of PGD?PGS Safety: Deliveries and complications Cumulative data I-IX: • 3075 deliveries: • 2351 singletons • 697 twins (22%) • 27 triplets (0.9%) 47 % C-section (40 % singletons, 67 % twins, 74 % triplets) 28 % pre-term (mainly twins and triplets) • 511 pregnancies with complications Minor (emesis): Major (abruptio placentae) • More frequent in twins (17%) and triplets (20%) than in singletons (12 %) Safety: Malformations Cumulative data I-IX: 133/3240 malformations (4%) Minor malformations: 61 cases (1.8%) Major malformations: 69 cases (2.1%) • Impairing normal function or necessitating surgery • From haemangioma to serious heart defects • Unknown malformations: 3 cases

Safety

Safety: PCR misdiagnosis Cumulative data I-IX Myotonic dystrophy type 1 PND TOP SMA Post Born TOP ß-thalassemia PND ß-thalassemia PND TOP Familial amyloid polyneuropathy PND Born Cystic fibrosis PND Born Cystic fibrosis (1 of twins) Post Born CMT1A PND Born CMT1A (twins) TOP of both twins PND PND Fragile X Born Sexing for X-linked disease 46,XY in retinitis pigmentosa PND Born TOP of one twin 46,XY in Duchenne muscular dystrophy twin PND

Sexing for X linked disease		
45,XO Haemophilia A	PND	TOP
46,XY Haemophilia A	Post	Born
46,XY Retinitis Pigmentosa (twins)	Post	Born
Translocations		
T13 after 45,XY,der(13;14)(q10;q10)	Mis	Mis
47,XX,+der(22)t(11;22)(q23.3;q11.2)	PND	TOP
46,XY,der(15)t(13;15)(q25.1;q26.3)pat	PND	TOP



Conclusions and comments

Consortium and its publications have served a useful purpose

- Answered some of the proposed questions about use, types of conditions referred, types of conditions undertaken.
- Preliminary answers to early outcome
 - High incidence of multiple pregnancy and expected complications
 - No obvious concern about biopsy (large numbers)
- Brought together many unit with similar intentions to share data and ideas
- Significant moves to standardise methods and improve safety by running training courses, EQA measures, and reporting misdiagnoses



Conclusions and comments

Achieved by highly motivated [and often the same] group of individuals who have believed in its usefulness and purpose



Steering Committee 2007

Chair, Joyce Harper,
Past Chair, Karen Sermon,
Deputy Chair Alan Thornhill.
Joep Geraedts, Netherlands,
Stephane Viville, France,
Christine deDie, Netherlands,
Leeanda Wilton, Australia,
Paul. Scriven, UK,
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Celine Moutou, France,
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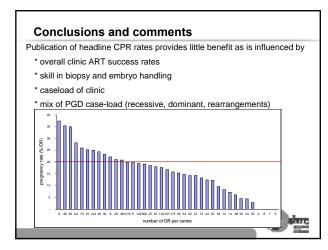


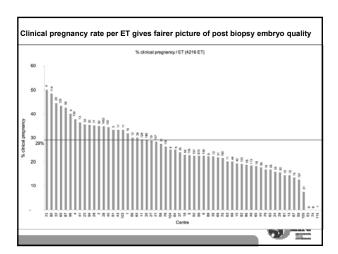
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Conclusions and comments

The recording and reporting of PGS success rates with the recurrent genetic disease (PGD) figures is unhelpful, since PGS is generally offered to patients without genetic disease, and failed or compromised IVF/ICSI cycles. They should be recorded with the overall figures for ART procedures as that is what they seek to improve.

Most useful PGD outcome data will be LBR per disease type which will give patients and clinician a fair idea of how PGD can benefit them (or not)

Early outcome safety of biopsy (whatever the reasons for its undertaking) has largely been shown

The most important safety data still to be collected are

- long term health of children
- accurate figures for misdiagnosis and ways to avoid them



Data Collection - 10 years

www.eshre.com/ESHRE/English/SIG/Reproductive-Genetics/PGD-Consortium/page.aspx/201

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