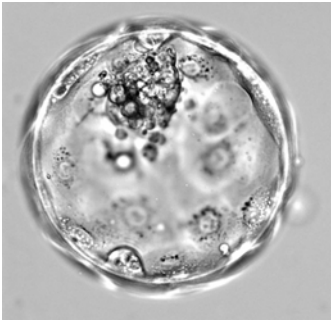


Working with Single Human Preimplantation Embryos



Human Blastocyst

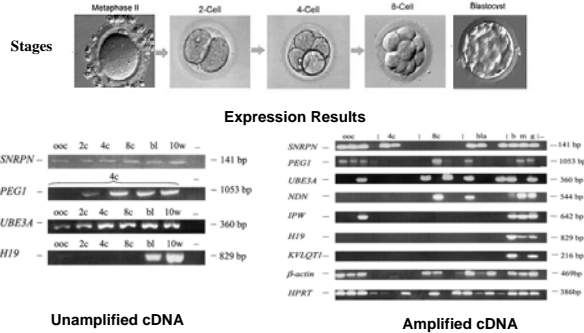
Challenges and Restrictions

- Ethical
- Consent from patient for research use
- Quality of samples
- Sample Numbers low
- Small amount of mRNA , DNA
- Little/no functional work can be done

From Single Embryo Can Analyse:

1. Genotype
2. Methylation
3. Gene expression
4. Secretome +uptake from media

Earlier Work: Human Imprinted Gene Expression From Oocyte to Blastocyst



Salpekar A, Huntriss J, Bolton V, Monk 2001
 The use of amplified cDNA to investigate the expression of seven imprinted genes in human oocytes and preimplantation embryos. Mol Hum Reprod. 7(9):839-44.

Limitations of Analysis in Human Oocytes Preimplantation Embryos

- **Limitations of non-array methods for expression**
- Non-array methods allow analysis of only ~4 genes per embryo/oocyte
- Hard to control across individual experiments
- Replicate experiments?

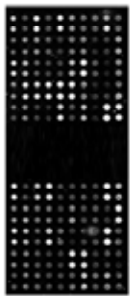
Focused Microarray Analysis of Imprinted Gene Expression
in Human Preimplantation Embryos

- 1. To design, develop & validate a bespoke gene expression microarray containing all human IGs
- 2. To develop gene expression microarray technology to single oocyte/embryo level to detect potential disruption of IG expression in human blastocysts.
- 3. Use to map IG expression in *in vitro* derived embryos
- 4. To use this system to test the 'safety' of existing and emerging human ART procedures including IVF, ICSI and oocyte IVM (*in vitro* maturation).

Justification of a Focused Gene Expression Approach to Assessing
Epigenetic Disruption in Human Embryos and ES cells.

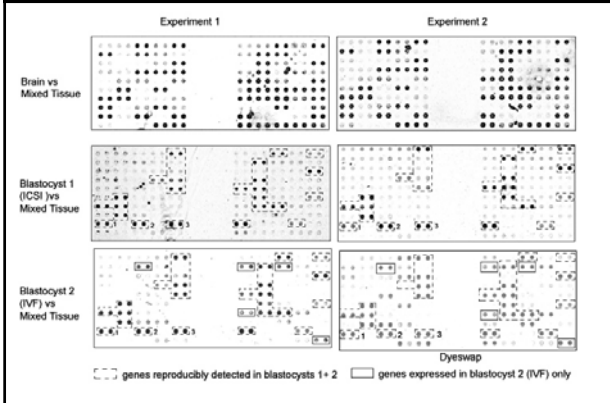
- Imprinted Genes are susceptible to disruption during *in vitro* culture
- Use Imprinted Genes themselves as **Biomarkers**
- Focused array-based methods allows analysis of all known imprinted genes (n=70) per single embryo/oocyte
- Can repeat experiments from each embryo, pool or use individually
- Gives a 'Global' idea of epigenetic disruption for imprinted genes across all chromosomes
- In contrast, alternative such as bisulphite genomic sequencing analysis limited to one gene/region.
- Controls included (sample 'quality', sexing)
- Limitation to 100 genes (total) reduces complexity of bioinformatics

Focused Human Imprinted Gene Array Design Features

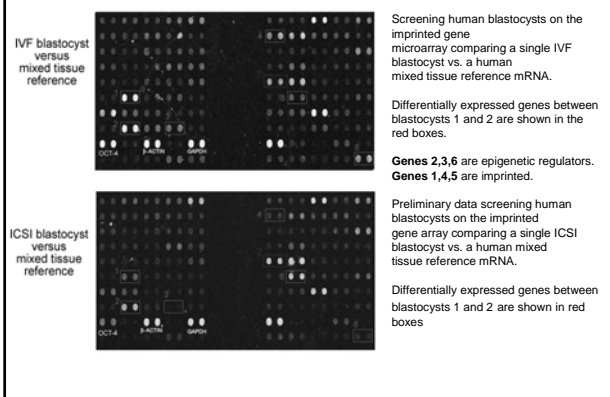


Chromosome 1 imprinted genes: ARH1,NDY2, TP73
 Chromosome 6 imprinted genes: PLAGL1, HYMAI, IGF2R,SLC22A2, SLC22A3
 Chromosome 7 imprinted genes: GRB10, PEG10, ASB4,SOXE, DLX5, catur, Nurbin / PPP1R3A, MEST/PEG11, PEG1-AS (MESTIT1), COPG2,CPH4, Cntn4,SPIN4, ADG2
 Chromosome 11 imprinted genes: WT1, AWT1, WT1-AS, H19, IGF2, IGF2AS, PIG-Hes6n, ASCL3,FAH2H, PHEM3, CD11, TSC2L, TRPM2, PCN2196, D17, KCNE1D17, D17, PEGD17-AS, PEGMRL1, KCAC1,ICUBSWT1, CDKN1C,CDKN2C, SLC22A1L,IMP1T, BSM1A,OCATL,DHMT2,CCSMET, SLC22A1L,SOX12,AS, PHELDAT7,CC139P,EMWTC, NAP1L4,UBPHYD,SSPL3, ZNF215,SDHD, Control:AP2A2
 Chromosome 12 imprinted genes: AT3,SLC35A4, DCN
 Chromosome 13 imprinted genes: H192A
 Chromosome 14 imprinted genes: MEG3, GTL2, DLX1, PEG9, DIO3
 Chromosome 15 imprinted genes: SPON3,SNF127, ZNF127AS, MAGEL2, XCV, CDAR1, PAB1,SN, RAS1, SNRPB, IPW, RAN1, UBE3A, EGAP, ATP10A, GABRB3, GABRB4, GABRG3, OCA2, RAB39PT, Control: Fbeta, beta-actin
 Chromosome 18 imprinted genes: TCEB3C, IMPACT
 Chromosome 19 imprinted genes: ZIM2, PEG3, LSP29, ZIMS, ZNF264
 Chromosome 20 imprinted genes: NNAT1,IMB1L, GNAS-AS (SANG), NESP55, XAlpha s, GNAS, G5a (zeon 1)
 Epigenetic Regulators: DNMT1, DNMT3A, DNMT3B, DNMT3C, DNMT3L, DNMT3H
 Cell Sexing controls: ZFY, SRY, AFK, XIST
 Blastocyst Marker Genes: OCT4, TERF1, DAB2, KRT18

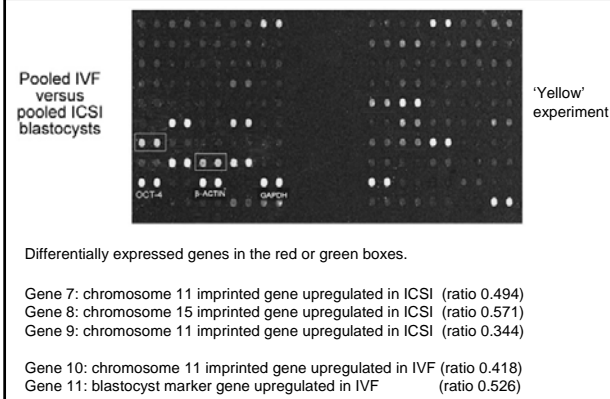
Replicate Array Experiments: Somatic Tissues and Single Blastocysts



Preliminary Microarray Data :
Clinical Samples: IVF Derived Embryos vs ICSI Embryos



Pooled IVF blastocyst cDNA versus stage & grade matched pooled ICSI blastocyst cDNA.



Retained DNA from embryo can be used for methylation analysis or genotyping

Methylation, Genotype, Imprinting and Array Analysis from Single Human Preimplantation Embryos

- Is differential IG expression between embryos or ART treatments (array) associated with methylation differences?
- Use embryonic DNA & methylation analysis to investigate further.
- Use DNA for genotyping
- Use cDNA for imprinting analysis
- Use cDNA for array work
- Confirm array with Real Time PCR

The flowchart illustrates the workflow starting from an oocyte or embryo. It involves adding oligo dT and Dynabeads for mRNA extraction, followed by cDNA generation. Simultaneously, DNA is extracted and treated with MethylAmp for methylation analysis. The resulting DNA and cDNA are used for genotyping and expression analysis, respectively. The final analyses include Methylation (Nested PCR for PEG1, DMF), Genotype (Nested genomic PCR for PEG1), and Expression (RT-PCR for PEG1 transcript, Imprinted Gene Array).

**Allelic Expression of Human Imprinted Genes
When Do Genes Become Imprinted?**

SNRPN Imprinting in Human Preimplantation Embryos

a) •PCR around a *BstU1* polymorphism
•2 heterozygous 4-cell embryos identified

b) •Embryos were genotyped with DNA from parental samples
•*SNRPN* expression monoallelic in both embryos
•Huntriss et al., 1998 Am J Hum Genet. 63(4):1009-14.

**Allelic Expression of Human Imprinted Genes
H19 Gene**

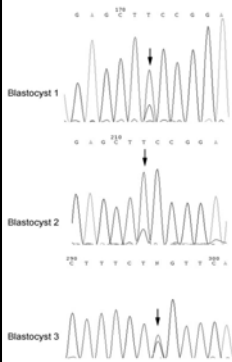
***H19* Genotyping for *RsaI* polymorphism and Allelic Expression Analysis from Single Human Preimplantation Embryos**

PCR scheme:

Blastocysts: •Genomic DNA + amplified cDNA obtained from same embryo
•2 heterozygous blastocysts identified

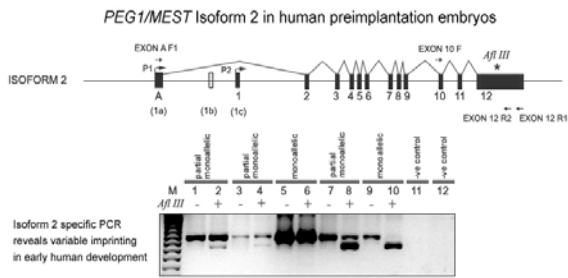
RT-PCR: •In one blastocyst, *H19* expression is strictly monoallelic (lower left)
•In a 2nd blastocyst, expression seen from both alleles, but allelic bias seen (lower right)
•2 other blastocysts with expression from both alleles (not shown)

UBE3A Angelman Syndrome Gene



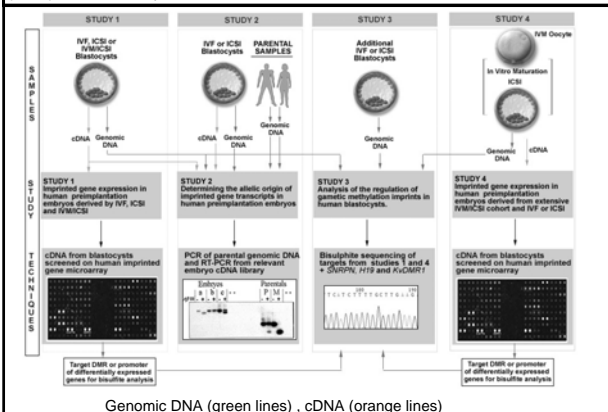
- Angelman syndrome due to lack of maternal *UBE3A* gene expression
- Are genes that are imprinted only in specific adult tissues, imprinted in early development?
- Is *UBE3A* imprinted in preimplantation embryo?
- Have 3 biallelic embryos out of approx. 20
- Studies ongoing

Allelic Origin of *PEG1* Isoform 2 in Human Embryos Variable Imprinting of Isoform 2 in human preimplantation embryos



- 50 embryos tested: variable imprinting of *PEG1/MEST* isoform 2 observed
- Inter-individual variation of isoform 2 imprinting reported in other tissues
- Submitted to ESHRE 2008 (Barcelona)

Experimental strategies for analysing the regulation of imprinting in human oocytes and preimplantation embryos.



Conclusions

- Aim to understand epigenetic biology of human gametogenesis & embryos to assess if/how ART may affect epigenetic regulation.
- Tools & methods described here to assess the effectiveness of using expression of imprinted gene as 'biomarkers' of epigenetic disruption.
- Where expression of IG is affected, follow up by bisulfite methylation analysis of imprinted gene DMRs in the same embryo.
- Tools such the IG array may become useful for the epigenetic safety testing of ART-derived embryos and other *in vitro* cultured cells like human ES cells.
- Allelic expression analysis suggests variable imprinting of *PEG1/MEST* and *H19* between human preimplantation embryos.
- Must establish cause of variability- may be natural inter-individual differences in imprinting or may be induced by ART and embryonic development *in vitro*
- Use this knowledge to adjust ART treatments accordingly

Acknowledgements

This work was supported by BDF NEWLIFE



The UK's leading Child Health and Research Charity.

BDF Direct Help and care for sick and disabled babies, children and families.
