## CHAIRE ÉPIGÉNÉTIQUE ET MÉMOIRE CELLULAIRE

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"L'empreinte parentale, une mémoire de l'origine maternelle
ou paternelle des gènes"
Séminaire
Professor Anne Ferguson-Smith
(Cambridge University, UK)

## Parental origin can matter

Hybrids of different species, but of the same genus, have very different phenotypes depending on parental origin

Male donkey x female horse
Mule

Male tiger x female lion
Tigon

Male horse x female donkey
Hinny

Male lion x female tiger
Liger

## Parent-of-origin phenomena observed in a wide range of phyla from both the plant and animal kingdoms.

1. Paternal chromosome elimination in Sciara (Metz, 1938; Crouse et al., 1960)
2. Inactivation of the paternal genome by heterochromatization in the scale insects (coccids) (Nur, 1990)
3. Parental dominance in hybrid plants (Heslop-Harrison, 1990)
4. Parent-of-origin specific modification of position effect variegation in Drosophila (Spofford, 1976)
5. Phenotypic differences in progeny produced from interspecific crosses in fish (Whitt et al., 1977) and between donkey and horse
6. Preferential inactivation of the paternally derived X chromosome in marsupials and rodent extraembryonic tissues (Cooper et al, 1971; VandeBerg et al., 1987)
7. Parent-of-origin dependent switching of yeast mating types (Klar, 1987)
8. Allelic exclusion of immunoglobulin genes (Holliday, 1990)
9. Gamete-of-origin dependent modifications of transgene methylation and expression in mice (Swain et al., 1987; Reik et al., 1987; Sapienza et al., 1987) and transgenic zebrafish (Martin and McGowan, 1995)
10. Parent-of-origin specific gene expression in plants and mammals

## Genomic Imprinting

- Genomic imprinting results in the expression of genes from only one of the two parental chromosomes - defies Mendel's laws of genetics!
- Brought about by epigenetic instructions - imprints - that are laid down in the parental germ cells.
- Imprinting in mammals is thought to influence the transfer of nutrients to the fetus and the newborn from the mother.
-Imprinted genes often affect growth in the womb and behaviour after birth.
- Aberrant imprinting disturbs development and is the cause of various disease syndromes.


## Evidence for Genomic Imprinting in Humans

Pathologic diagnosis


Pedigree analysis of chromosomes


Normal zygote


Gynogenetic constitution


Androgenetic constitution
"In contrast to androgenetic ova producing only hydropic villi, parthenogenetic oocytes in the ovary produce several mature tissues. Remarkable differences in the end products of both types of conceptuses are of special interest with regard to the possible physiologic difference between maternally and paternally derived genome in the egg cytoplasm, influence of implantation site (ovary versus uterus), and interaction between mother and conceptus in early mammalian embryogenesis."

Wake, Takagi, and Sasaki (1978)


## Evidence for Genomic Imprinting in Mice



Azim Surani Davor Solter

## Nuclear transplantation experiments in mice by Azim Surani and Davor Solter :

- Two male or two female pronuclei are incompatible with normal development
- Formal demonstration of the functional non-equivalence of mammalian parental genomes

Embryon Trophoblaste


BARTON, S. C , SURANI, M. A. AND NORRIS, M. L. (1984). Role of paternal and maternal genomes in mouse development. Nature 311, 374-376.
SURANI, M. A., BARTON, S. C. AND NORRIS, M. L. (1984). Development of reconstituted mouse eggs suggests imprinting of the genome during gametogenesis. Nature 308, 548-550.


Embryon androgénote: Létal


MCGRATH, J. AND SOLTER, D. (1984). Completion of mouse embryogenesis requires both the maternal and paternal genomes. Cell 37, 179-183.

## Evidence for Genomic Imprinting in Mice

Development of chimaeras made with mixtures of normal cells and androgenetic (AG) or gynogenetic (GG) cells on day 13 of gestation.


Reciprocal phenotypes are observed:
gynogenotes are growth retarded while androgenotes show enhanced growth.
Later defects in mesoderm derivatives, skeleton, brain development...
(Barton et al, 1991; Fundele et al, 1990)

## Evidence for Genomic Imprinting in Mice



Bruce Cattanach


Thirteen sub-chromosomal regions exhibiting unipaternal disomy identified:

- Defects in development, behaviour, growth, viability
- Suggesting differential expression from the 2 parental chromosomes homologues
- Requirement for both maternal and paternal alleles for normal development.


## Genomic Imprinting in Humans

First human clinical syndromes recognized to result from imprinted loci were Prader-Willi syndrome and Angelman syndrome (Nicholls et al., 1989).

Identical genetic deletions as well as uniparental disomy for a domain on 15 q result in very different clinical phenotypes depending on the parental origin of the deletion/disomy.
Mild-moderate mental
retardation
Hypotonia
Obesity

| tion Prader-Willi syndrome |
| :---: |
|  |  |
|  |  |



Severe mental retardation
Hypertonia
Happy disposition


## Discovery of Imprinted Genes

Paternal duplication of distal chromosome 7 causes growth enhancement


Courtesy of Azim Surani

In humans, paternal duplication of equivalent region results in Beckwith-Wiedemann


Clinical Features:
Macroglossia; high birth weight; hemihypertrophy; Wilm's tumour

## Genomic Imprinting in Humans



Studies on patients with imprinting disorders:

- Discovery that imprinted gene tend to be in clusters
- Identification of "Imprinting Control Regions"
thanks to analysis of chromosomal microdeletions


## Genomic Imprinting

## Expression of an allele that differs based on the sex of the parent that transmitted the allele

Both alleles of a gene expressed


One allele of a gene expressed


Epialleles:<br>Epigenetic differences<br>Eg X inactivation, imprinting...

## Discovery of Imprinted Genes

## Imprinted (maternally expressed) $\operatorname{Ig} f 2 r$ gene on chromosome 17

Johnson (1974) identified a maternal-effect mutant Tme: maternal but not paternal copy of part of chromosome 17 is essential for embryonic development

Identification of a maternally expressed imprinted gene mapping to Tme locus, Igf2r (insulin-like growth factor type 2 receptor), also known as the cationindependent mannose-6-phosphate receptor - a scavenger receptor for the $I g f 2$ growth hormone.


Barlow DP, Stoger R,Herrmann BG, Saito K, Schweifer N. 1991. The mouse insulin-like growth factor type-2 receptor is imprinted and closely linked to the Tme locus. Nature 349:84-87

## Discovery of Imprinted Genes

## Paternally expressed $\operatorname{Ig} f 2$ and maternally expressed H19: reciprocally imprinted genes on distal chromosome 7

In 1991: Igf2 gene (insulin-like growth factor type 2, which signals through the Igf1 receptor) identified as a paternally expressed imprinted gene (De Chiara et al, 1991, Ferguson Smith et al, 1991).

Discovery of H19 (fetal hepatic cDNA clone 19), a maternally expressed imprinted gene closely linked to $I g f 2$, that produces a non protein-coding RNA (Bartolomei et al, 1991, Zemel et al, 1992).


Crossing different mouse strains that have highly polymorphic genomes, enables distinction of paternal and maternal alleles (at both DNA and RNA levels) using restriction fragment length polymorphisms (RFLPs).
$\Rightarrow$ Determine whether only one (pat or mat) or both alleles are expressed in different tissues of progeny (F1)

Maternal duplication of distal chromosome 7 causes reduced growth, similarly to deletion of paternal Igf2 allele


## Imprinted Genes tend to be Clustered

## Chromosome:


imprinted genes within clusters are in the correct order as far as possible imprinted genes in red are maternally expressed
imprinted genes in blue are paternally expressed
maternally expressed small nucleolar RNAs and microRNA genes
" paternally expressed small nucleolar RNAs and microRNA genes
regions with abnormal imprinting phenotypes with maternal (Mat)
or paternal (Pat) duplication or paternal (Pat) duplication
(?) conflicting data
http://www.har.mrc.ac.uk/research/genomic_imprinting
So far, 16 clusters of imprinted genes identified in mouse and humans as well as some imprinted "loner" genes

Total of 100-140 imprinted genes

## Imprinting Mechanisms

## Imprinting Mechanisms

What are the epigenetic mechanisms allowing parent-of-origin specific information to be passed from parent to embryo and to be maintained in the adult but erased and reset in its germ line?

The underlying marks must:


- control transcription
- be inherited somatically
- be established in the germ line
- be erased in next generation

Imprints can sometimes also be overridden or ignored in certain tissues

## Imprinting Mechanisms

DNA methylation: a strong candidate as it is a stable epigenetic mark, that can be propagated over cell divisions and can influence
transcription (Holliday, Riggs 1975)
CpG islands at imprinted loci are differentially DNA methylated (DMRs)
Differential methylation is found in regions defined genetically as critical for imprinting control (Sutcliffe et al, 1994; Wutz et al, 1997; Thorvaldsen et al, 1993; Smilinich, 1999; Lin et al, 2003; Williamson et al, 2006)


DNA methylation plays a key role in imprinting as imprinted gene expression is disrupted in Dnmtl KO embryos.
Li E, Beard C, Jaenisch R. (1993) Role for DNA methylation in genomic imprinting. Nature, 366, 362-365.
The de novo methyltransferase Dnmt3a and its cofactor Dnmt31 are required for the

## Imprinting Mechanisms

## At least two modes of imprinting control: Insulator mediated and non-coding RNA mediated



ICRs contain Germ-line DMRs
Most are maternal (ie established in the oocyte) but a few are paternal

## Imprinting Mechanisms

1. Insulator mediated control of imprinted gene expression

DMR = Differentially Methylated Region
CTCF $=$ CCCTC-binding factor - can only bind unmethylated DNA


Igf2 H19

S. Tilghman
M. Bartolomei
W. Reik
A. Surani
L. Dandolo

Role of the non-coding H19 RNA?

- No role: decoy for Igf2 enhancer usage?
- Cis- or trans-acting RNA regulator?
- Produces a miRNA
- Most ancestral imprinted ncRNA


## Imprinting Mechanisms

2. Non-coded RNA mediated control of imprinted gene expression


ICR


- Airn transcription, but not its spliced or unspliced lncRNA products, silences the $I g f 2 r$ promoter (Latos et al, 2012, Science 338,1469-1472)
- Airn RNA accumulates and targets histone H3K9 methylation to chromatin in cis, in extraembryonic lineages (Nagano et al, 2008, Science 322, 1717-1720)


## Imprinting Mechanisms

Non-coded RNAs are produced by the ICRs of several imprinted clusters
Transcriptional interference, recruitment of chromatin marks, altered chromosome structure...or simple bystanders? Four of these ncRNAs are linked to ICRs and have been tested for a functional role in imprinting


## Imprinting Mechanisms

- DNA methylation is the instructive mark for germ line imprinting at most loci.
- Non-coding RNAs and other marks also play a role in establishing and maintaining imprinted gene expression at various embryonic stages and in different lineages.


HDACs, HATs, HMTs...
Genes showing imprinted expression only in extra-embryonic tissues may be regulated by different epigenetic mechanisms compared with genes showing imprinted expression in extraembryonic tissues and in embryonic/adult tissues.
E. Heard, February $25^{\text {th }}, 2013$

## Imprinting Mechanisms



Histone modifications (H3K27me3, H3K9me2, H21K119u1) deposited by Polycomb complexes (PRC) and G9a HMTase, are involved in maintaining imprinted gene repression independently of DNA methylation at the Kcnq1 and $I g f 2 r$ clusters in extraembryonic tissues.

Non-coding RNAs (Kcnq1ot1, Airn) are implicated in recruiting these repressive complexes to extraembryonic-specific imprinted genes. The ncRNA forms a cloud that is larger in extraembryonic tissues and often covers the genes that are silenced.
(Lewis et al, 2004; Umlauf et al, 2004; Terranova et al, 2008, Nagano et al, 2008)


## Developmental Dynamics of Imprinting



## Developmental Dynamics of DNA Methylation



The mammalian epigenome shows dynamic changes in DNA methylation during development. How do imprints "resist" this?

How do imprints avoid inappropriate loss of methylation on one allele, or inappropriate gain of methylation on the other?

## Developmental Dynamics of Imprinting



## Imprint Control Regions

Most Germ-line DMRs are Maternal (ie established in the oocyte)
Maternal DMRs are usually in promoters or introns of genes (protein-coding or ncRNAs)
Paternal DMRs are usually intragenic

| Locus (DMR) | Chromosome | DMR methylation | DMR location | Reference |
| :---: | :---: | :---: | :---: | :---: |
| Gnas (Nespas/Gnasxl) | 2 | Maternal | Intron | Coombes et al. 2003 |
| Gnas (1A) | 2 | Maternal | Intron | Liu et al. 2000 |
| Mcts2 | 2 | Maternal | Intron | Wood et al. 2007 |
| Peg10 | 6 | Maternal | Promoter | Ono et al. 2003 |
| Peg1 | 6 | Maternal | Intron ${ }^{\text {a }}$ | Lucifero et al. 2002 |
| Nap115 | 6 | Maternal | Intron | Wood et al. 2007 |
| Peg3 | 7 | Maternal | Intron | Kim et al. 2003 |
| Snrpn | 7 | Maternal | Intron | Mapendano et al. 2006 |
| Kcnq1 (KvDMR) | 7 | Maternal | Intron | Yatsuki et al. 2002 |
| Inpp5f | 7 | Maternal | Intron | Wood et al. 2007 |
| Zac1 | 10 | Maternal | Intron | This study |
| Grb10 | 11 | Maternal | Intron | Arnaud et al. 2003 |
| U2af1-rs1 | 11 | Maternal | Intron | Wood et al. 2007 |
| Peg13 | 15 | Maternal | Intron | Ruf et al. 2007 |
| Slc38a4 |  |  |  |  |
| Igf2r (Air) |  |  |  |  |
| Impact | 18 | Maternal | Intron | Okamura et al. 2000 |
| H19 | 7 | Paternal | Intergenic | Tremblay et al. 1997 |
| Rasgrf1 | 9 | Paternal | Intergenic | Shibata et al. 1998 |
| Dlk1-Gtl2 (IG-DMR) | 12 | Paternal | Intergenic | Takada et al. 2002 |

## Deletion of two paternal DMRs (H19 and Dlkl-Gtl2) is sufficient to allow viable parthenogenesis!

## Imprinting is the only barrier to successful parthenogenetic development in mice



Bi-maternal embryos produced by construction of oocytes from fully grown oocytes and nongrowing oocytes that contain double deletions in the H19 differentially methylated region (DMR) and the Dlk1-Dio3 intergenic germline-derived DMR, efficiently produce viable female mice that can reproduce normally!
$\Rightarrow$ Conclusive evidence that imprinted genes regulated by these two paternally methylated imprinting-control regions are the only paternal barrier that prevents the normal development of bi-maternal mouse fetuses to term.

Nat. Biotechnol. 25, 1045-50.

## Why have Imprinting?

Numerous examples of parthenogenetic amphibians, fish, reptiles and birds exist.


Thus within vertebrates, genomic imprinting seems to be mammal-specific.

How did genomic imprinting arise in mammals, and why was it selected for?
(given the apparent cost: abandoning the advantages of diploidy!)

## WHEN did Imprinting Evolve in Mammals?



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Evolution of eutherian-specific imprinting
E.g. PWS-AS, CLPG, XIC
Lineage-specific imprinting
E.g. loss of IGF2R imprinting in primates,
gain of Frat3 imprinting in mouse
Random X inactivation
Proposed arrival of imprinting
E.g. IFG2, IGF2R, PEG1/MEST and
PEG10 imprinted
Paternal X inactivation
No evidence of imprinting
IGF2, IGR2R and UBE3A are
biallelically expressed
```

Did genomic imprinting evolve just once - with viviparity?
Unlikely - instead imprinting evolution seems to have been a stepwise, adaptive process, with each gene/cluster independently becoming imprinted as the need arose:

- H19-IGF2 is the most "ancient" imprinted locus in therians. Smits et al (2008) Nat Genet. 40, 971-976.
- Other imprinted loci are eutherian-specific, or even rodent ${ }_{\text {COLLège }}$


## HOW did Imprinting Evolve in Mammals?



Allele moves towards extinction
Allele spreads towards fixation

## WHY did Imprinting Evolve in Mammals?

## Imprinted Genes Control:

- Embryonic Growth
- Placenta development
- Transfer of nutrients
- Animal behaviour



## Parental conflict theory?

## Parental conflict theory

Males and females do not have the same interests when they reproduce.

In polyandrous species (where females mate with more than one male), the offspring in a litter do not always have the same father....

The mother's interest is to have multiple equal (smaller) offspring. A father's interest is to have big offspring that can outcompete other males' offspring in the womb.

Genomic imprinting may have evolved from such a inter-parental tug-of-war over the resources allocated to the fetus by the mother during intrauterine gestation in viviparous mammals:

- Paternal epigenotypes drive expression of pro-growth genes
- Maternal epigenotypes suppress growth


## Imprinting and Behaviour

## Postnatal behaviour may be influenced by imprinted genes

- Large number of neurological and psychiatric disorders with parent-of-origin effects: Eg PWS and AS (classical imprinting diseases), as well as in autism, bipolar affective disorder, epilepsy, schizophrenia, Tourette syndrome and Turner syndrome...
- Mice that have paternal disomy for chromosome 2 are hyperkinetic while those with maternal disomy are hypokinetic
- Imprinted Grbl0 gene is important in mouse foetal and brain development and influences adult social behaviour

Garfield et al. (2011). Distinct physiological and behavioural functions for parental alleles of imprinted Grb10.Nature 469, 534.


Opposite imprinting of parental alleles in different locations of the body.
a. maternal Grb10 is expressed in most regions of the body.
b. paternal Grb10 is expressed only in the brain and GE central nervous system

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- Imprinted Grbl0 gene is important in mouse foetal and brain development and influences adult social behaviour
- Knockouts of Grfl and Ube3a (the mouse homologue of the human AS gene) have defects in contextual learning and memory (among others)
- Peg1 and Peg3 have a role in maternal behaviour such that mothers that lack these molecules neglect and do not feed their offspring


## Genomic Imprinting in Plants

Imprinting evolved independently in flowering plants


DNA Methylation and sometimes Polycomb group proteins ensure silencing of the paternal alleles of imprinted genes.
(b) Flowering plants


Imprinted expression


## Genomic Imprinting in Drosophila?

## Gynogenetic and androgenetic D. melanogaster are viable, $\Rightarrow$ imprinting is not essential in this species?

(Fuyama, 1984; Komma and Endow, 1995).
D. melanogaster can form parent-of-origin-specific imprints that affect gene activity, however, the prevalence of imprinted genes in their native genomic context within the D . melanogaster genome remains unclear (Menon and Meller, 2010).


RNA-seq to compare allele-specific expression between pools of 7- to 10-day-old adult female progeny from reciprocal crosses.

- RNA-seq identified 119 potentially imprinted genes in D. melanogaster
- These potentially imprinted genes were significantly clustered in the genome
- Polymorphisms and intrinsic noise caused imprintinglike RNA-seq data
- Conclusion: D. melanogaster genes in their native context are not imprinted

Coolon et al (2012) Genomic Imprinting Absent in Drosophila melanogaster Adult Females. Cell Reports 2 69-75.

## Genomic Imprinting: outstanding questions

- How and when during germline development are old imprints removed and new ones introduced?
- What are the molecular mechanisms (DNA demethylating activities, Dnmts, transcription, DNA binding factors, chromatin factors, RNAi pathways)
- How does epigenetic information spread across imprinting clusters - when? where?
- How are imprints maintained when there is genome-wide active and passive demethylation in the early embryo?
- How is tissue-specific imprinting and cell-type specific "escape" from imprinting achieved?
- How do imprinted genes and imprinting control elements evolve?
- How exactly do imprinted genes affect extraembryonic and embryonic development, and the nutritional exchange with the mother?
- In addition to growth and behaviour, are there other developmental processes and mechanisms in which imprinted genes play a role?

