

Could epigenetics play a role in the developmental origins of health and disease?

Maybe!
A skeptical overview

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Dynamic methylation in development

Global changes

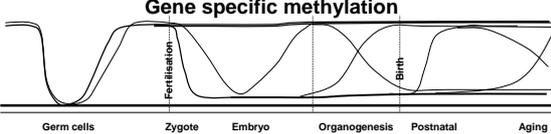


Germ cells Zygote Embryo

Germ cells - active demethylation
Sperm - remethylation
Oocytes - remethylation
Male germline - active demethylation
Female germline - demethylation
Embryo - remethylation

Dynamic methylation in development

Gene specific methylation

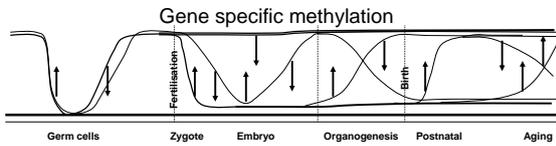


Germ cells Zygote Embryo Organogenesis Postnatal Aging

Normal changes

- Germ cell development and early embryonic development
totipotency; pluripotency
- Cell differentiation - gain and loss of methylation
- Postnatal effects on specific genes
- Aging may be associated with gain and loss of methylation?

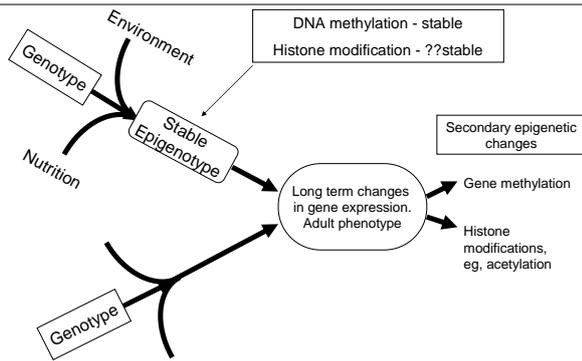
Could epigenetic (methylation) plasticity contribute to variation?



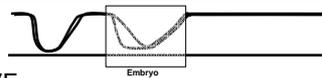
Opportunities for modulation of methylation (normal vs. pathological)

- Germ line (more or less)?
- Less erasure in zygote / over-erasure in zygote?
- Increased methylation in preimplantation embryo?
- Loss of imprinting?
- Altered methylation during organogenesis?
- Altered age related methylation?

Goal - to identify stable epigenetic modifications



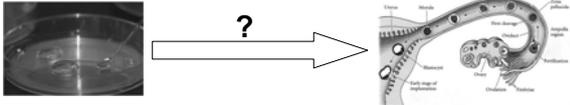
Post-fertilisation - pre-differentiation ART



- Embryo culture and IVF
 - Increase risk of Beckwith Wiedemann syndrome and Angelman syndrome
 - Altered culture media (mice)
 - Manipulation itself alters imprinting
 - Large offspring syndrome (cows/sheep)
- Very important issues for human and animal ART

Post-fertilisation - pre-differentiation ART

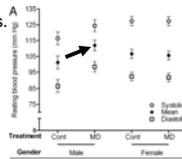
- BUT
 - Can we generalise?
 - Rate of abnormalities in mice ~ 700 fold that of human
 - Large offspring syndrome associated with use of serum
 - Human abnormalities may be related to infertility
 - E.g., Doornbos ME et al Hum Reprod 2007 Rate of BWS/AS same in IVF as in infertile controls.
- AND
 - Even if human IVF does cause methylation abnormalities, **does this imply plasticity in natural conceptions?**



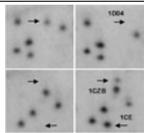
Post-fertilisation - pre-differentiation *In vivo* manipulation - sheep (1)

- "DNA methylation... determined by maternal periconceptional B vitamin and methionine status" Sinclair KD et al PNAS 2007;104:19351
 - 'Methyl deficiency' - dietary deficiency of cobalt and sulphur levels, ↓ capacity of the rumen to synthesize methionine and vitamin B12.
 - 'Deficient' and control day-6 blastocysts were then transferred to normally fed surrogate ewes.
- Offspring heavier, fatter, insulin resistant, higher blood pressure.
- Changes in DNA methylation in 4% of genes.

Males only



Post-fertilisation - pre-differentiation *In vivo* manipulation - sheep (2)



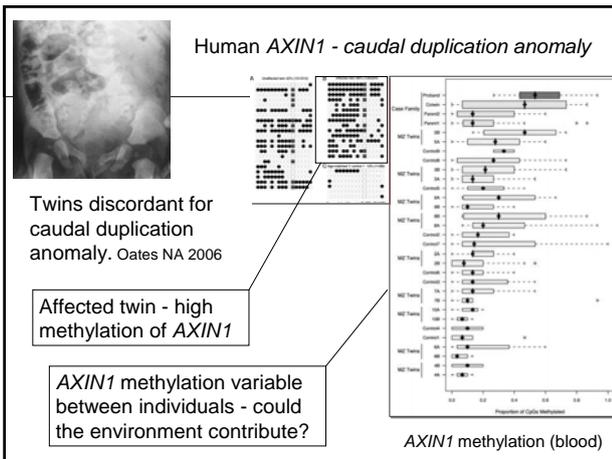
RLGS showed loss (and gain) of methylation in 4% of genes
Binary change ON/OFF!!

A

Allel	Locus	Control	METHYL DEFICIENT GROUP															
			Female offspring					Male offspring										
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
In 6 animals	23k1	M																
In 7 animals	45k1	M																
In 8 animals	18k2	M																
In 10 animals	29k1	V																
In 10 animals	1C11	V																
In 11 animals	45k1	M																

For some genes the changes were very consistent - in males (best examples shown)

Methylated in controls, unmethylated in deficient animals Sinclair KD et al PNAS 2007;104:19351



In vivo manipulation of diet - BUTS

Sheep model is of dietary deficiency of cobalt and sulphur

Are methylation changes the cause or consequence of physiological changes?

Does the altered DNA methylation result from availability of methyl donors?

Mouse model uses "supraphysiologic methyl group supply" (Sinclair 2007)

Genistein, soy-derived phyto-estrogen, has same effect as B12, folate on coat colour.

Bisphenol A (estrogenic compound) has the opposite effect.

- reduces methylation of the *A^{vy}* IAP element.

In vivo manipulation of Agouti^{vy} diet - BUTS

Increasing methylation of IAP

Yellow Brown
Obese Leaner

Prediction: Folate/B12 → leaner animals

BUT: supplementation worsened obesity - opposite

i.e. we don't understand the model - care is needed.

http://hgm2006.hugo-international.org/Presentations/S2/HGM2006_S2_04_Waterland.ppt

Early embryo - summary

- Epigenetic changes will affect all lineages similarly.
- Epigenetic change can be induced, but the mechanism is unclear.
- Focussed studies with specific dietary or drug manipulations are needed.

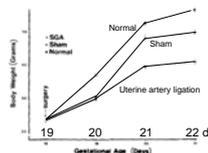
Organogenesis



- Fetal origins of adult disease (Barker hypothesis)
 - Low birth weight - obesity, cardiovascular disease, diabetes, etc
- DNA methylation occurs as tissues differentiate
- Could epigenetic variation/plasticity contribute to:
 - Diabetes?
 - Hypertension?
 - IUGR / metabolic syndrome?
- Much hope - few data

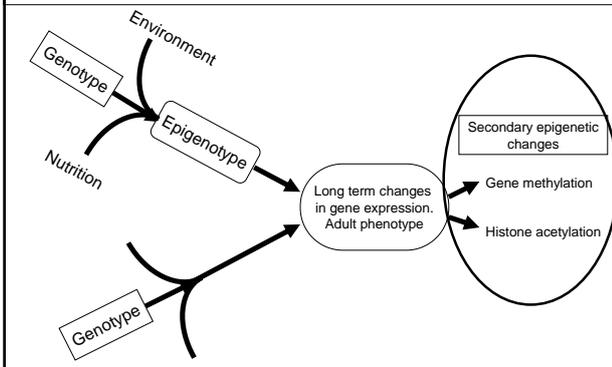
Rat IUGR - diabetes model

- Rat IUGR model
 - reduced pancreatic beta-cell mass
 - reduced insulin secretion
 - insulin resistance
 - type 2 diabetes in adults.
 - bilateral uterine artery ligation 3 days before birth
 - rapidly induces IUGR
- *Pdx1* expression is halved (it regulates pancreatic development)
 - Epigenetic changes at *Pdx1* promoter - histone deacetylation, changes in histone methylation and increasing DNA methylation with age.



Ogata ES Metabolism 1986; Simmons RA Rev Endocr Metab Disord 2007;8:95

Primary or secondary change

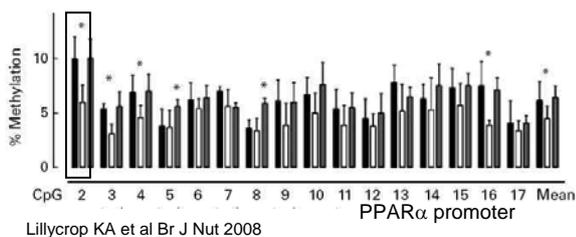


Rat low protein (high carb) model

- Pregnant rats - LP/HC diet during gestation
- Upregulation of glucocorticoid receptor and PPAR α occurs with disturbed metabolic control.
- Many publications - only one useful so far.

Rat low protein (50%) (high carbohydrate) model best results

- Liver - PPAR α promoter methylation (by pyrosequencing)
- Reduction in average methylation from **6.1% to 4.5%** (black bars to white bars) in 34 day offspring.



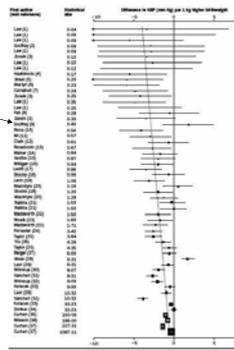
Rat low protein (50%) (high carbohydrate) model



- Is this change physiologically significant?
- Does it explain 10 fold increase in PPAR α expression?
- Could it reflect changes in cellular composition of the liver?

Blood pressure?

- IUGR may cause hypertension
 - Controversial - good studies show very little difference (see Huxley R et al Lancet 2002)
- Hypertension associated with nephron number (Keller G NEJM 2003)
 - Therefore blood pressure may be controlled by anatomic size, not epigenetic memory



Blood pressure?

- Rat low protein model
(Hypertension, upregulated renin angiotensin system)
- Angiotensin II receptor, type 1b
- Reduction in methylation from 22% to 7% in whole adrenals (bisulphite cloning).
- But *Agtr1b* expression predominantly from the adrenal cortex, which constitutes only a small minority of adrenal cells



Bogdarina I et al, Circ Res 2007

Organogenesis summary

- Organ development is an obvious target for epigenetic modulation, but ...
- Published data are poor.
- Need a combination of qualitative (bisulphite sequencing) and quantitative data (pyrosequencing, sequenom, etc) in pure tissues.

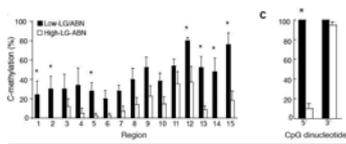
Post-natal



- Behavioural modification changes methylation of offspring
 - Rat model - stressed (low licking and grooming) vs. non-stressed (high LG) mothers.

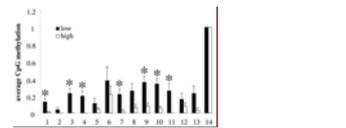
Glucocorticoid receptor promoter 1₇

Weaver I et al Nat Neurosci 2004

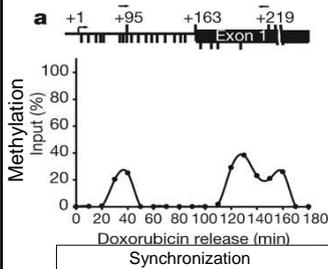


Estrogen receptor- α 1b promoter

Champagne F et al Endo 2006



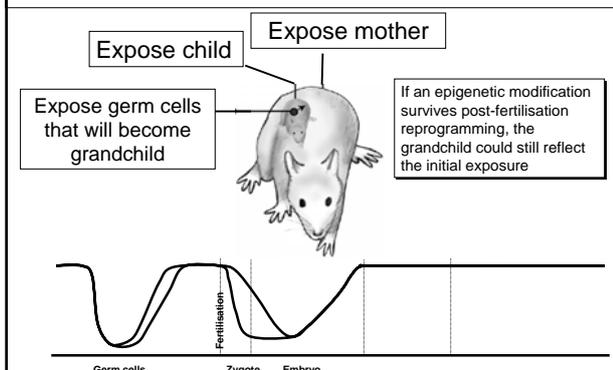
But: Estrogen receptor- α methylation is transient and cyclical



ER- α methylation responds to the endocrine environment. It seems unlikely that methylation provides a longterm signal.

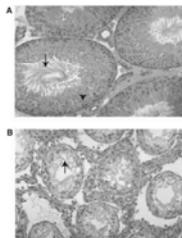
Kangaspeka et al Nature 2008

Transgenerational epigenetic effects



Transgenerational effects

- Best examples: Endocrine disruptors
- E.g., vinclozolin exposure during embryonic gonadal sex determination induces adult onset male fertility and spermatogenic defect for multiple generations (i.e. F1–F4)
- DNA methylation changes in several genes (inconsistent)
- If epigenetic change is primary how is it maintained during reprogramming?



Anway MD et al. Science 2005;308:1466

F3 male

Summary

- Early embryogenesis
 - susceptible to environmentally-induced epigenetic change.
 - Mechanisms need to be clarified.
 - Refined models needed.
- Organogenesis - possible but unproven
- Post-natal - fascinating possibilities
- Transgenerational
 - (more care with nomenclature).
 - Erasure mechanisms suggest that primary epigenetic signals are unlikely.