XV Incontro della Rete Insieme per l'Allatamento « Allatamento fra care e scienza » 30 settembre 2021, Trieste

Epigenetica, Perinatologia... e Allatamento



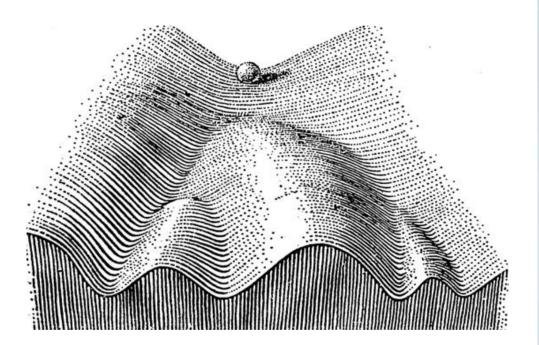
Umberto Simeoni Division of Pediatrics & DOHaD Lab University Hospital of Lausanne, Switzerland

Breastfeeding

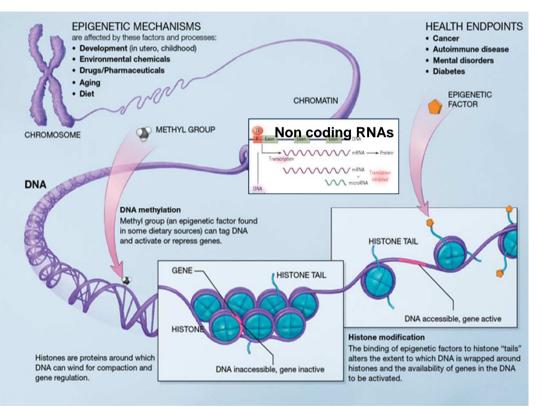
- Optimal nutrition for infants, with unique advantages:
 - Nutrients
 - Functional, bioactive components
 - Dynamic, adaptive composition
 - Mother-infant relationship
- Long term benefits to the infant:

 Cognitive development 	(Victora C.G. et al, 2016)
 Infectious diseases 	(Verduci E. et al, 2014)
 Inflammatory responses 	(McDade T.W. et al 2014)
 Blood pressure 	(Martin R.M. et al 2017)
 Adiposity and obesity 	(Horta B.L. et al, 2014; Martin R.M. et al 2017)

Epigenetic landscape and biological bevelopment: How the environment affects genes regulation and development Epigenetics: a long lasting, heritable molecular translation of early genome-environment interactions, in the absence of gene sequence alteration



C Waddington (1957)

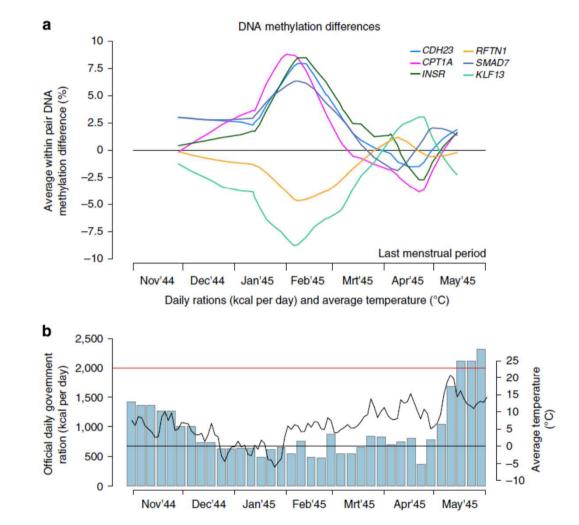


DNA methylation signatures link prenatal famine exposure to growth and metabolism

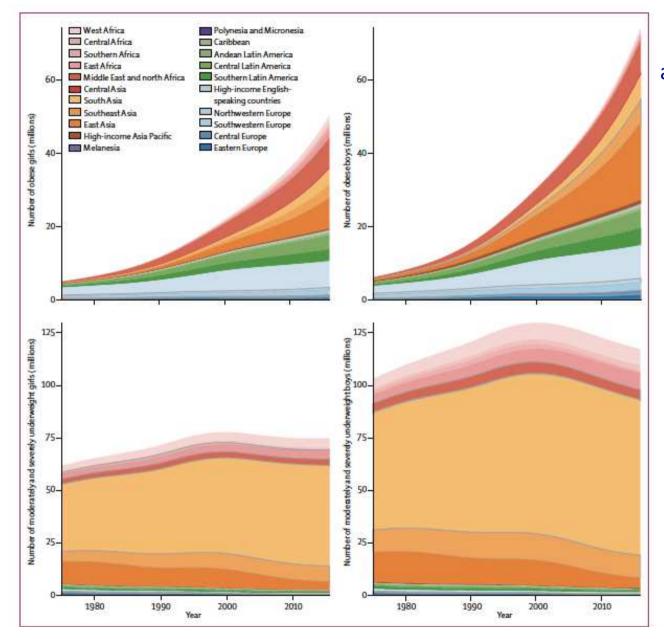


Increased risk in offspring:

- Obesity
- Dyslipemia
- Type 2 Diabetes
- Schizophrenia



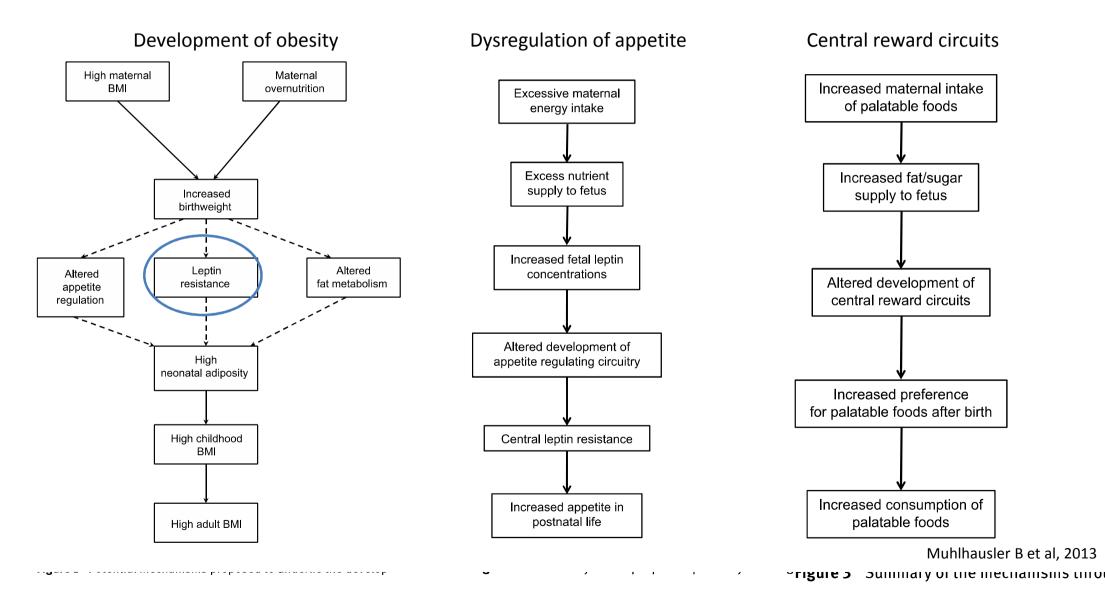
Tobi EW et al, Nature, 2014



Trends in the number of children and adolescents with obesity and with moderate and severe underweight by region

NCD-RisC Lancet 2017

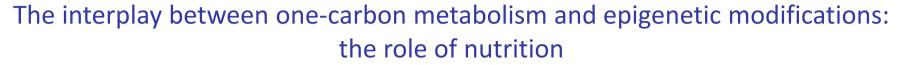
Maternal overnutrition and metabolism programming in the offspring

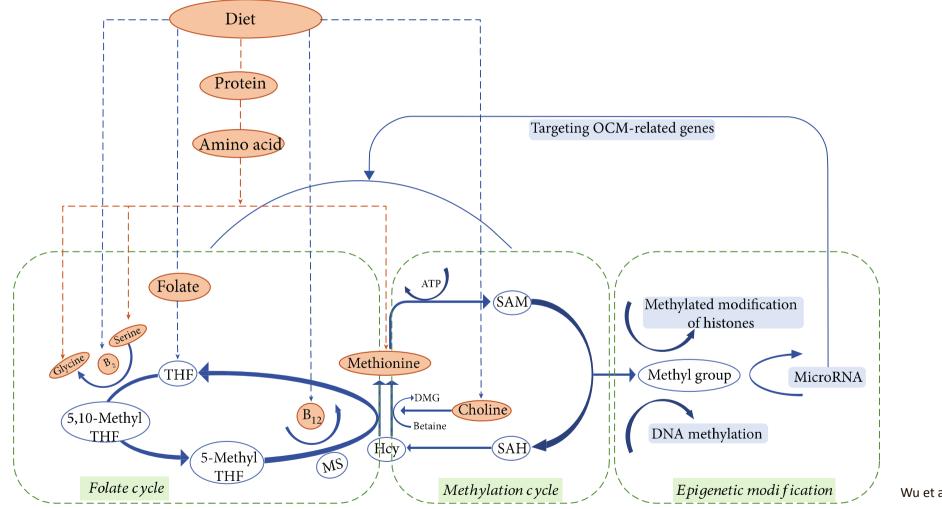


Breastfeeding, early life environment and LEP methylation in 17 month old children Obernann-Borst S et al, 2012

Associations between methylation of *LEP* and several variables

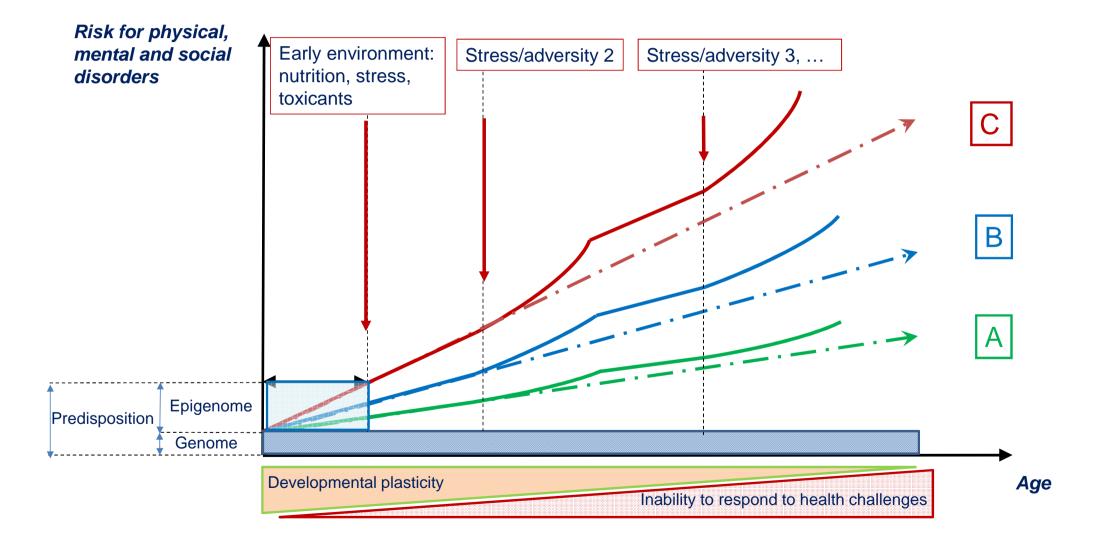
	Model 1			Model 2		
	% Absolute methylation change (SE)ª	% Relative methylation change (SE)	P ^b	% Absolute methylation change (SE) ^a	% Relative methylation change (SE)	Pc
Early environmental factors						
Low education	+2.1 (0.8)	+9.1 (3.5)	0.008	+1.0 (0.8)	+4.2 (3.4)	0.233
No folic acid, periconception	+0.1 (0.8)	+0.0 (0.8)	0.910			—
Smoking, periconception	+1.3 (0.8)	+5.6 (3.4)	0.094	+0.6 (0.8)	+2.5 (3.3)	0.454
Duration of breastfeeding ^d	-0.7 (0.3)	-2.9 (1.2)	0.011	-0.6 (0.3)	-2.5 (1.3)	0.040
Constitutional factors						
Gender, male	-1.8 (0.7)	-7.3 (4.1)	0.010	-2.3 (0.8)	-9.0 (3.9)	0.005
Birth weight ^e	-1.2 (0.4)	-5.0 (1.7)	0.005 ^f	-0.6 (0.5)	-2.5 (2.1)	0.159 ^f
Growth rate ^{e,g}	0.0 (0.4)	0.0 (0.3)	0.985			_
BMI ^e	-0.8 (0.4)	-3.3 (1.7)	0.043	-0.3 (0.4)	-1.2 (1.6)	0.514
Biomarker concentration						
Leptin, serum ^e	-0.4 (0.4)	-1.7 (1.7)	0.035	-1.2 (0.5)	-4.9 (2.0)	0.028



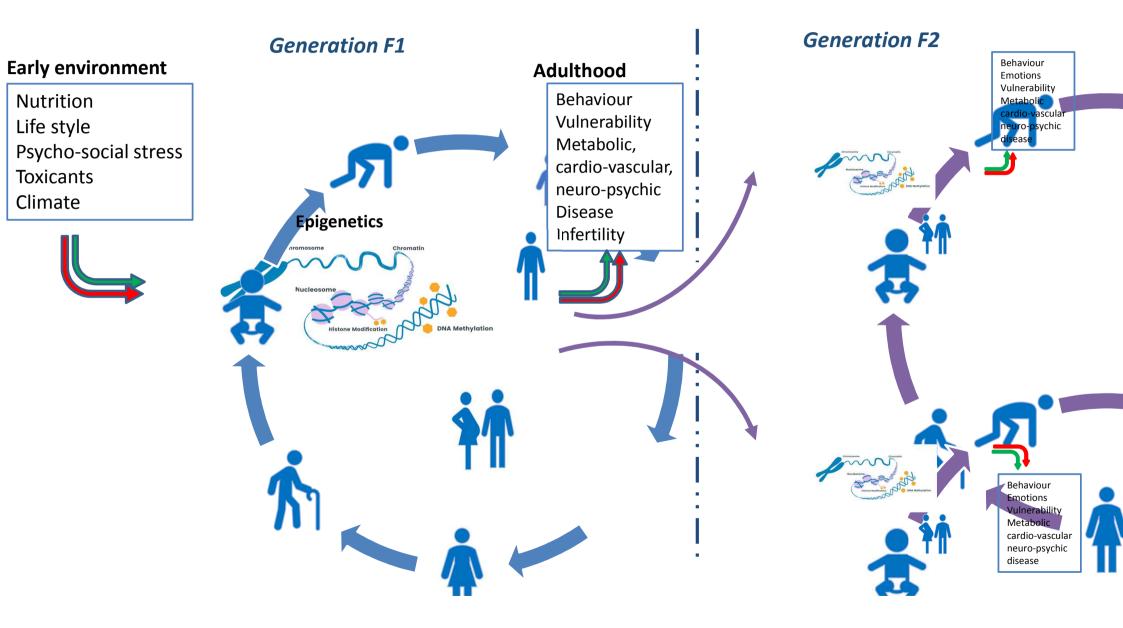


Wu et al, 2019

Developmental Origins of Health and Disease: Predisposition & life trajectories

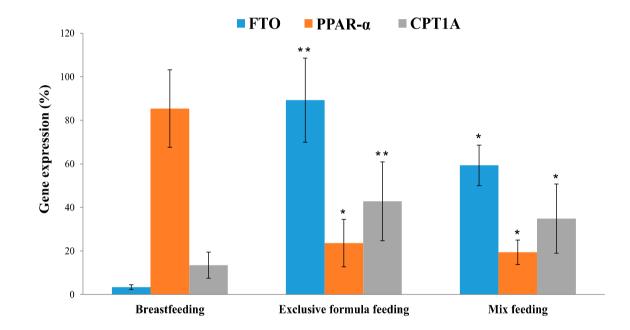


Developmental programming: trans-generational inheritability of acquired epigenetic imprinting



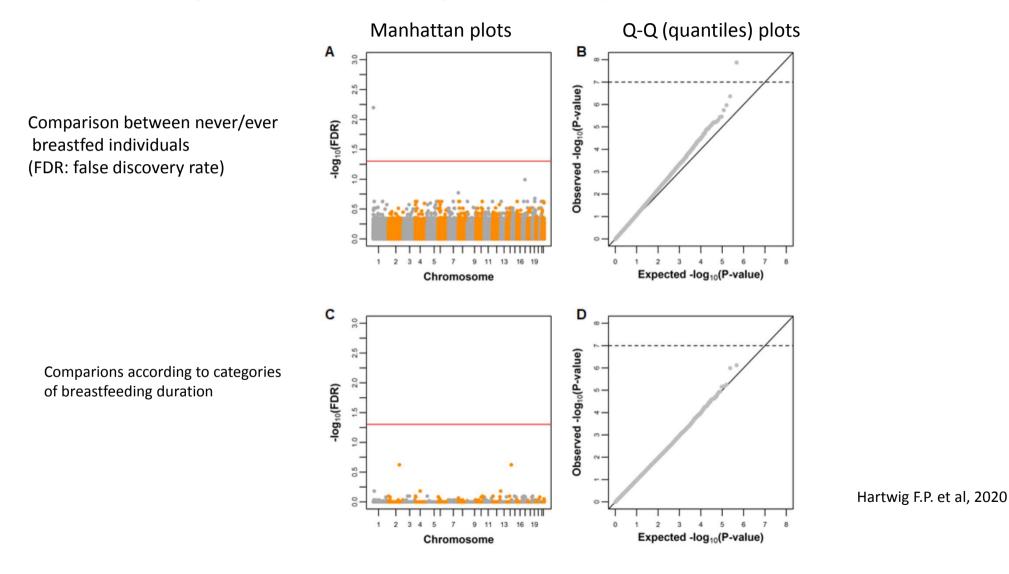
DNA methylation vs breast feeding

Effects of Breastfeeding and Formula Feeding on the Expression Level of FTO, CPT1A and PPAR- α Genes in Healthy Infants



Chesmeh et al, 2020

Association between Breastfeeding and DNA Methylation over the Life Course: Findings from the Avon Longitudinal Study of Parents and Children (ALSPAC)



MicroRNAs associated with offspring overnutrition during lactation

Early, transient overnutrition during lactation alters myocardial function at adulthood and is reversible by late caloric restriction

Left Ventricle Ejection Fraction

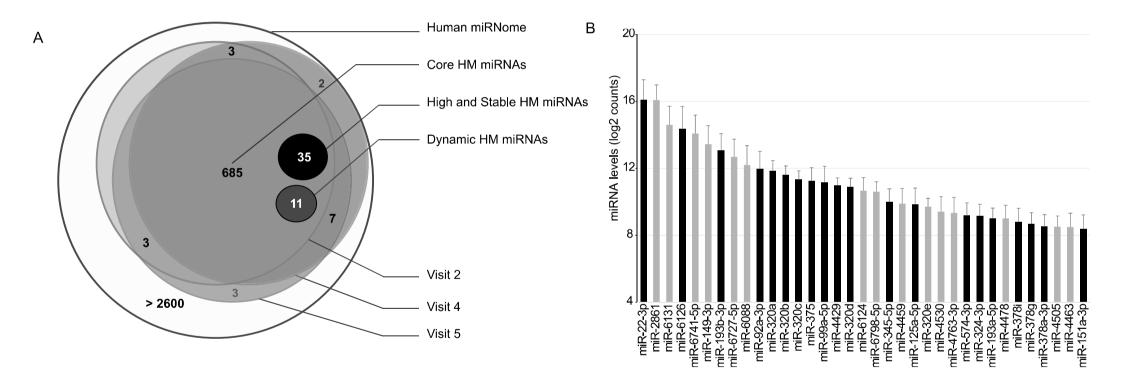
Calorie Restriction in Adulthood

miR- miR-In vitro validation CTRL 193b 65 +15,3% **Tissular measurement** NLRP3 TXNIP miR-193b transfection ETS1 miR-193b 60 PROCASP1 p=0.0194 * p=0.0081 1.5 Cleaved CASP1 miR-193b/miR-16 ratio IL1β NFκB2 p52 55 1.0 - β ACTIN miR- miR-50 CTRL 193b H9C2 cardiomyoblast AKT ser473 total AKT 11.60 0 IRS ser307 NF-CR OF-AL OF-CR NF-AL 45 IRS1 6 months 7 months TNNI3 **β ACTIN Postnatal Overfeeding**

Regulation of inflammasome by miR 193b

Li N et al, Sci Reports 2016 Siddek B et al, Nutr Metab Cardiovasc Dis 2018 Maternal modulation of infant's genes expression and physiology through breat milk miRNAome

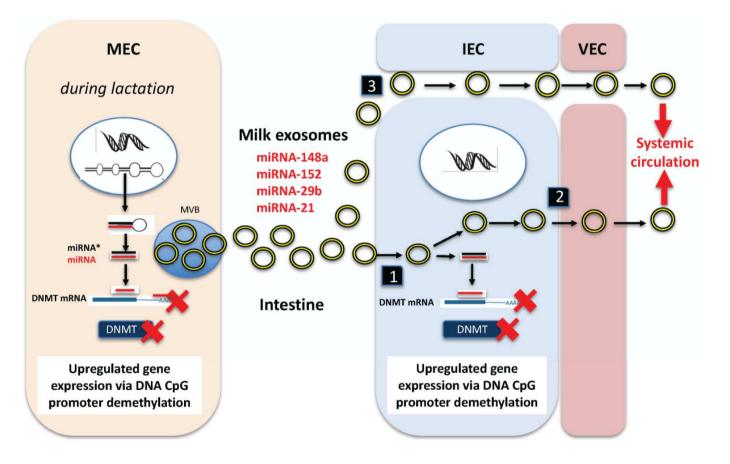
Longitudinal Human Milk miRNA Composition over the First 3 mo of Lactation in a Cohort of Healthy Mothers Delivering Term Infants



Raymond F et al, 2021

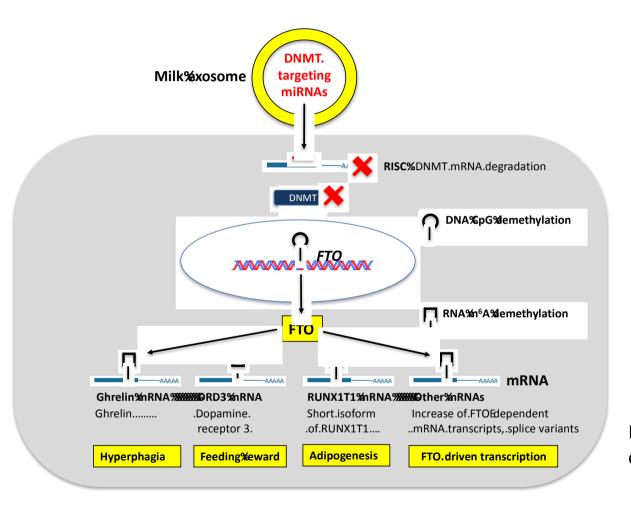
Milk's Role as an Epigenetic Regulator in Health and Disease:

Milk Exosomes: Long-Distance Transmitters of Lactation-Specific miRNAs



Melnik B.C. & Schmitz G., 2017

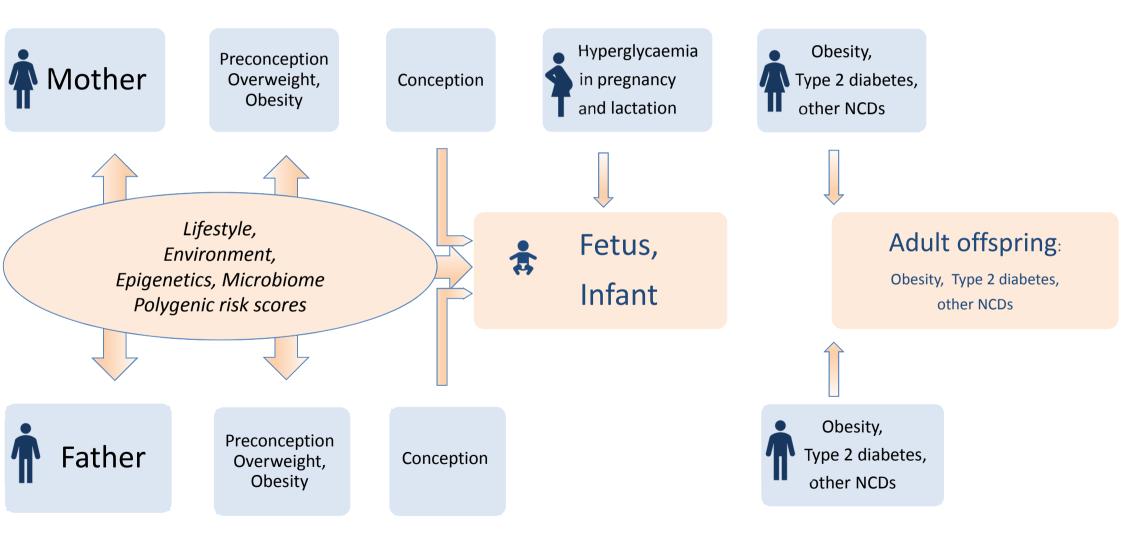
Appetite Control and Feeding Reward



FTO: Fat mass- and obesity-associated protein

Melnik B.C. & Schmitz G., 2017

Maternal, paternal and offspring risk induced by « diabesity »



Conclusion

- As an optimal source of nutrition, protection, and developmental programming for infants, mother milk consists of various bioactive components, including miRNAs.
- Fragmentary information shows associations of epigenetic changes in the expression of genes related to key physiologic and biologic functions with breast feeding. Further studies are necessary to understand the role of epigeneticchanges associated with breastfeeding.
- The concept that human milk miRNAome overall contribution to lactation regulation and/or to infant physiology through horizontal transfer of epigenetic material during breastfeeding is emerging but remains to be demonstrated.

The long term memory of early environmental cues

