CERAD CoE Workshop: Epigenetics
NRPA, 19.08.2013
Program

• 10:00 - 10:15  "Velkommen" Astrid Liland/ Brit Salbu, CERAD/NRPA/UMB

• 10:15 - 10:45  "Novel epigenetic modifications in DNA and RNA"  
Arne Klungland, Oslo Universitetssykehus

• 10:45 - 11:00  Discussion

• 11:00 - 11:30  "CERAD SRA/EU Comet and Figaro",  
Deborah Oughton/Ole Christian Lind, CERAD/UMB

• 11:30 - 12:30  Lunch
After lunch

- 12:30 - 13:30  "Epigentics ved Radiumhospitalet”,
Leonardo Meza-Zepedia og Ola Myklebost,
Oslo Universitetssykehus

- 13:30 - 14:30  "FHI activities”, Gunnar Brunborg,
CERAD/FHI
“Paternal exposure and effects on miRNA
and mRNA expression”,
Nur Duale, FHI

“Proposals for activities related to
epigenetics under CERAD”,
Ann-Karin Olsen (Anka)

- 14:30 - 15:00  Coffee
After coffee

- 15:00 - 15:30 “Epigenetics in aquatic plants, invertebrates and vertebrate models”.
  Knut Erik Tollefsen, CERAD/NIVA

- 15:30 - 16:00 “Correlations between gene expression and epigenetic markers as a result of single and multiple stressor exposure induction, studied in zebrafish founder and offspring generations”,
  Peter Alestrøm, CERAD/NVH

- 16:00 - 16:30 "Epigenetics in human cells and zebrafish embryos",
  Philippe Collas, UiO

- 16:30 – 17:00 Coffee

- 17:00 - 17:30 “NVH Fish'n ChlPs in the lab”,
  Leif Lindeman, Oslo Universitetsykehus

- 17:30 – 18:00 “Reproduction as endpoint”,
  Ian Mayer, NVH

- 18:00 - 18:30 Discussion– veien videre, B. Salbu

- 19:00 Dinner, Haga Golfklubb
Development of an ecosystem based scientific approach to help protect people and the environment from ionizing radiation requires a programme of targeted focused long term research on:

- Source terms and release scenarios,
- Ecosystem transfer,
- Biological responses, and
- Impact and risk assessments

Figure 1. The basic science in RA 1-3 will form the basis of improved impact and risk assessment.
Defining epigenetic epidemiology -
according to Jonathan Mill and Bastiaan T. Heijmans (2013)

We define epigenetic epidemiology as the integration of epigenetic analyses into population-based epidemiological research with the goal of identifying both the causes (that is, environmental, genetic or stochastic) and phenotypic consequences (that is, health and disease) of epigenomic variation.

Other definitions are narrower and have a more direct focus on environmental epigenetics and the specific analysis of transgenerational epigenetic effects
or
the developmental origins of health and disease.

As a fairly immature discipline, epigenetic epidemiology has a lot to learn from the much broader field of classical epidemiology, especially with regard to causal inference and establishing the validity of epigenetic associations
Definitions

- **Chromatin**: The combination of DNA, RNA and protein that constitute the chromosomes in eukaryotic cells. Broadly, heterochromatin is associated with transcriptional repression and euchromatin is associated with transcriptional activity.

- **DNA methylation**: The covalent binding of a methyl group at position 5 of the cytosine pyrimidine ring in CG dinucleotides often associated with the repression of transcription when present at promoters and enhancers.

- **Epigenetic**: Describes mitotically heritable, but reversible, changes in gene expression mediated primarily by modifications to DNA and chromatin structure.

- **Epigenome**: The entirety of epigenetic information in a cell, including DNA methylation, histone modifications, histone variants and non-coding RNAs.
Definitions

- **Epigenome-wide association studies (EWASs):**
  Systematic assessments of a specific epigenetic mark, usually DNA methylation, across the genome in groups of individuals that are different for a given environmental exposure, trait or disease with the goal of identifying differences associated with that exposure or phenotype.

- **Histone:**
  Histone proteins package DNA into structural units called nucleosomes. Covalent post-translational histone modifications include acetylation, methylation, phosphorylation, sumoylation and ubiquitylation; these can influence gene expression through changes in chromatin structure.

- **Methylome:** The entirety of DNA methylation marks across the genome.
### Epigenetics – to be discussed

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**Extrapolation from man to the environment??**
Epigenetics of relevance for the environment – to be discussed

- Why epigenetics? - relevant endpoints for environmental risks?
- What should be studied? – only DNA methylation?
- Where should we look in the genome? – specific genomic regions?
- What kind of samples? Same signals in different tissues/blood?
- Which techniques?
- Additional variables?
- Lab – exp design, to reduce confounding factors
Have a nice day!!!