

**Symposium Mammalian
Tuesday 13 March 2007**



**NucSys
Marie Curie Research Training Network**

NUCLEAR RECEPTOR transcription factor family orchestrate responses to environmental factors by sensing a diverse range of dietary and xenobiotic components.

NUTRIENT – GENE interactions and permit modeling of the impact of diet on health and the development of disease.



NucSys network

1. Kuopio
2. Birmingham
3. Rotterdam
4. Guildford
5. Amsterdam
6. Wageningen
7. Oulu
8. Leuven
9. Bedford
10. Madrid
11. Berlin
12. London
13. Wien
14. Milan

NucSys

- 12 academic and 2 industrial partners is an interdisciplinary co-operative of molecular, cellular and developmental biologists, pharmacologists, physiologists, mathematicians and bio-informaticians
- GOAL: to use systems biology, in order to understand and then predict the actions of the nuclear receptor super-family in cells and disease models.
- The main goal: to define key components of the NUCLEAR RECEPTOR gene regulatory network that facilitate this process and model their impact on the development of **aging-related** syndromes and pathologies, such as **carcinogenesis, metabolic syndromes, osteoporosis** and **skin aging**.

This requires the integration and interpretation of large volumes of data by the application of bioinformatics methods and systems biology mathematical tools.

NEEDED:

Ideal experimental model systems for the disease of interest

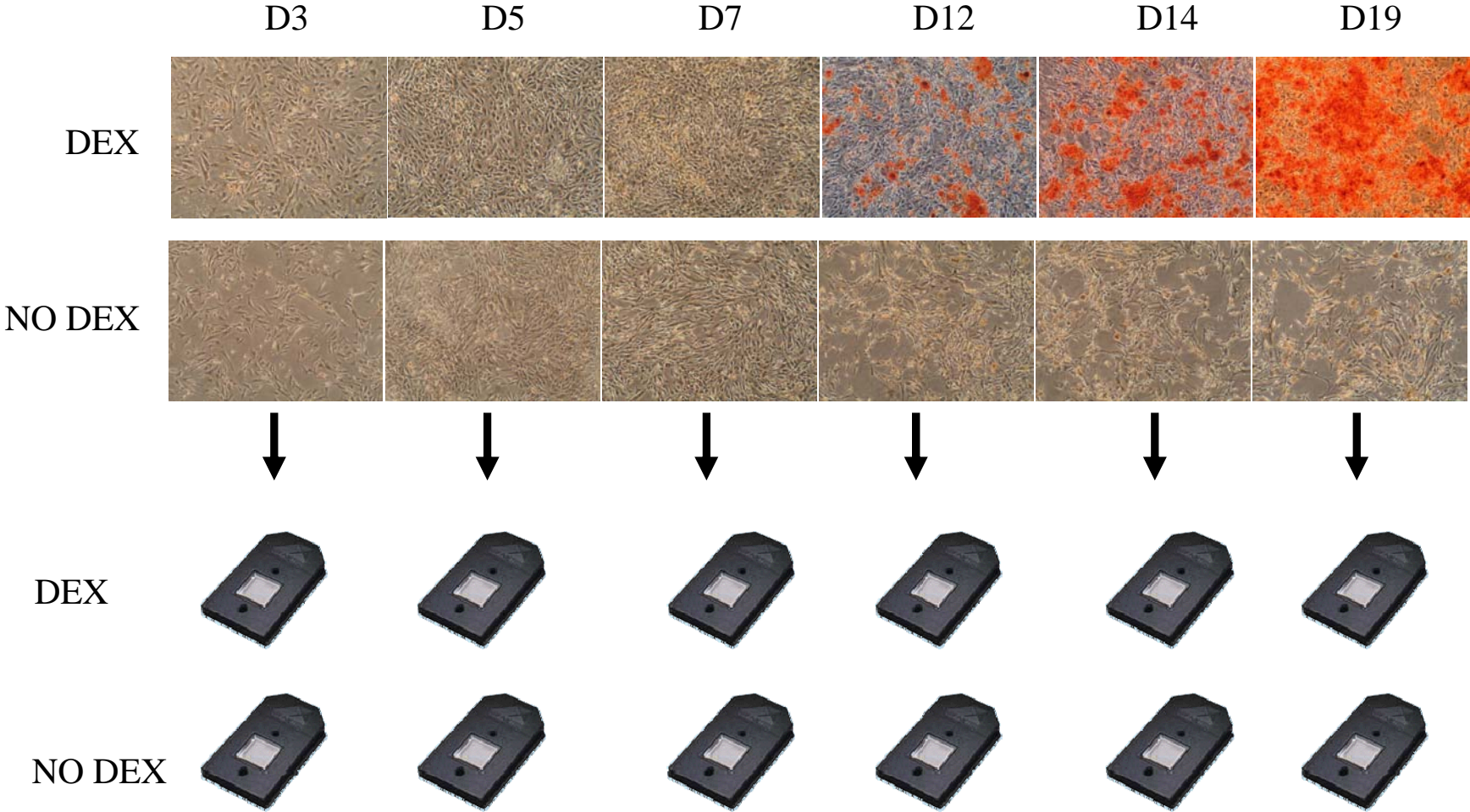
Generation of RNA, PROTEIN, METABOLITE data sets representing specific (disease) phenotypes.

Phenotypic description of the system: Descriptive systems biology

Knowledge for selecting network(s) / signaling pathway(s) for Mathematical description of the phenotype: Modeling

A priori knowledge of important enzymes / proteins: e.g. alkaline phosphatase; 11 β -hydroxysteroid dehydrogenase (11 β -HSD) (for bone cell development)

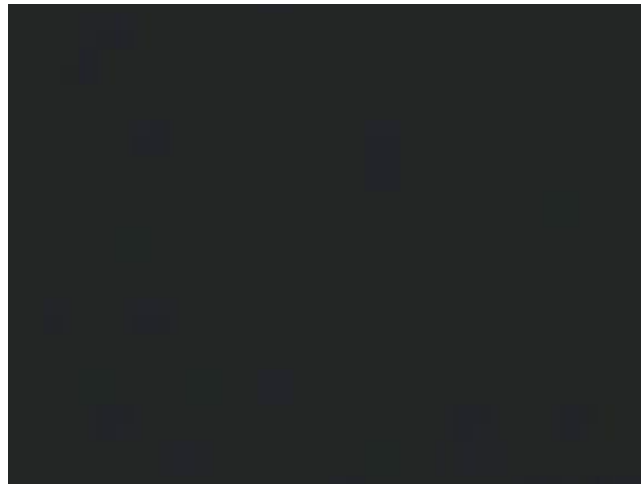
Gene profiling in mineralizing and non-mineralizing cultures



HG-U133Plus2.0

Comparison of nuclear receptor-regulated genes / proteins / metabolites
between different disease models

So that we know which button to push in the
system in case of disease!

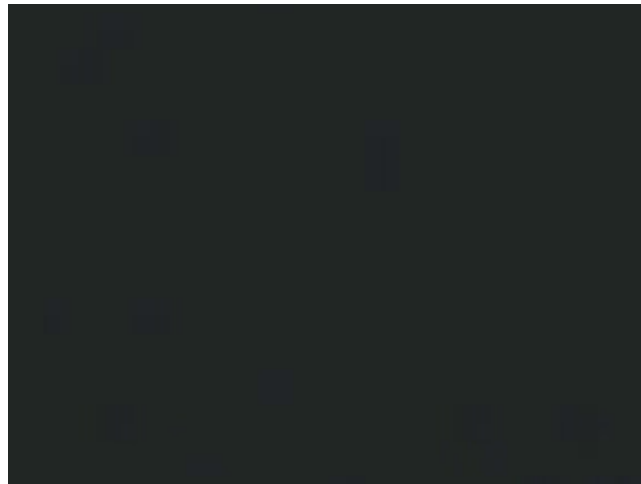


Ursula Klingmüller and Jens Timmer

Bela Novak

Takashi Nakakuki

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