



# Emerging Focus **Nutrigenomics**

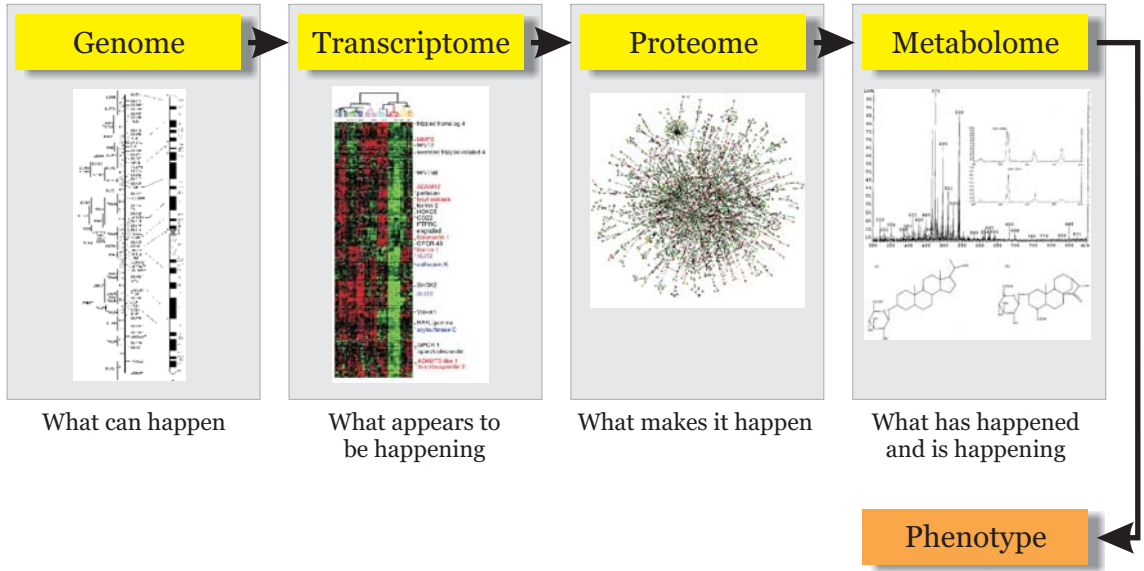
Department of Nutritional Sciences  
Faculty of Life Sciences

# The Emerging Focus Nutrigenomics – *A New Research Group at the Faculty of Life Sciences of the University of Vienna*

## Why Nutrigenomics?

Nutritional sciences have reached a cul-de-sac situation with their approach to develop dietary guidelines for the majority of individuals in the population by ignoring the variation of individual characteristics of influence on nutrient requirements. The new tools now available in the postgenomic era opens a new future for nutritionists being now able for the first time to screen the genetic background, to monitor the transcriptome, proteome and metabolome and to ultimately develop dietary strategies which are targeted to supply the optimum nutrition for single individuals. These tools are the focus of the new emerging field of nutrigenomics.

**Overview**  
Nutrigenomics is the study of the response of humans to food and food components using genomics, proteomics and metabolomics approaches. The goal of nutrigenomics is to develop foods that can be matched to individual human genotype to benefit the health of those individuals and enhance normal physiological processes. Nutrigenomics will lead to the development of new foods for individualised health and nutritional benefit.



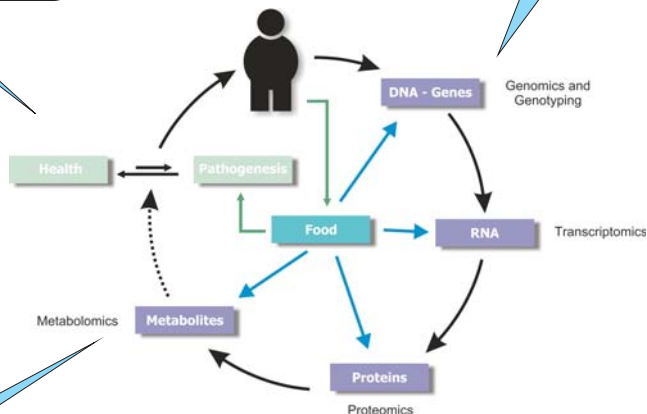
# The Emerging Focus Nutrigenomics

*What we do*

Evaluation of the metabolic profile on possible effects on human health, to ultimately improve human health by nutrition

Intervention studies to test the effects of foods and food components on metabolic changes of the human organism

Genotyping of individuals and population groups on polymorphisms related to nutrition and nutrient metabolism



Metabolic profiling of human samples by LC-MS (QqTOF) in response to nutrition intervention; identification of metabolites and metabolic changes covering known and unknown metabolites and nutrients; identification of molecular and biochemical key pathways of individual health problems (metabolic syndrome, obesity, cardiovascular diseases, aging) and identification of strategies for individual intervention



### Overview

The Emerging Focus Nutrigenomics is formally part of the Department of Nutritional Sciences at the Faculty of Life Sciences. The group is independent in respect to administration, human and capital resources, and research.

## The Emerging Focus Nutrigenomics

### *Who we are*



***Univ.-Prof. Dr. Jürgen König***  
Group leader



***Ulrike Stöger***  
Administrative management



***Sandra Haselmaier***  
Technical Assistance



***Dr. Elisabeth Rudolph***  
Post Doc



***Mag. Doris Ripper***  
PhD student



***Mag. Ulrike Kaindl***  
PhD student

# The Emerging Focus Nutrigenomics

## *How we work*



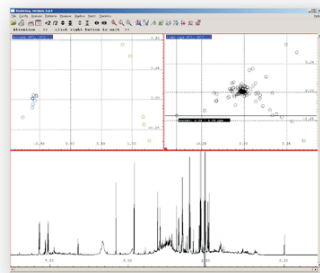
Variations in the human genome are analysed on an Applied Biosystems real time PCR instrument. DNA from buccal swabs or blood samples is extracted and specifically designed primers for the base sequence of interest bind to the corresponding DNA region. Fluorophores added to the primers are used to monitor the binding process.

RT-PCR



A Bruker microOTOF-Q coupled to a Dionex HPG micro HPLC-system provides mass spectra with high mass accuracy for metabolite identification and high sensitivity and dynamic range for metabolite quantification. This technique enables us to assess a wide range of metabolites including unknown compounds which may be affected by the genetic background. This is in contrast to classical LC-MS, which only allows identification of specific metabolites having been identified prior to method development.

QqTOF

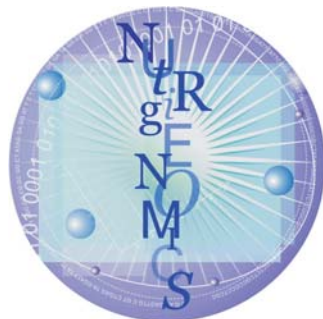


The enormous amount of data generated by LC-MS/MS is processed by metabolic profiler software to allow data clustering and post-run evaluation by principle component analysis. The software is run in close collaboration with Bruker Daltonics. This enables us to identify metabolic variations by combining characteristic modifications and excluding extrinsic influences like diet, physical activity, or any other environmental condition interfering with the interventional parameters.

PCA

# The Emerging Focus Nutrigenomics

## Contact



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# Glossary

## *Some terms explained*

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**SNP** – A Single Nucleotide Polymorphism or SNP (pronounced *snip*) is a DNA sequence variation occurring when a single nucleotide - A, T, C, or G - in the genome (or other shared sequence) differs between members of a species (or between paired chromosomes in an individual). For example, two sequenced DNA fragments from different individuals, AAG**C**CTA to AAG**T**CTA, contain a difference in a single nucleotide. In this case we say that there are two *alleles*: C and T.

**Metabolomics** – is the systematic study of the unique chemical fingerprints that specific cellular processes leave behind - specifically, the study of their small-molecule metabolite profiles. The metabolome represents the collection of all metabolites in a biological organism, which are the end products of its gene expression. Thus, while mRNA gene expression data and proteomic analyses do not tell the whole story of what might be happening in a cell, metabolic profiling can give an instantaneous 'snapshot' of the physiology of that cell. One of the challenges of systems biology is to integrate proteomics, transcriptomics, and metabolomics information to give a more complete picture of living organisms.

**Nutrigenomics** – is the application of the sciences of genomics, transcriptomics, proteomics and metabolomics to human nutrition, especially the relationship between nutrition and health. Nutrition and health research is focused on the

prevention of disease by optimizing and maintaining cellular, tissue, organ and whole-body homeostasis . This requires understanding, and ultimately regulating, a multitude of nutrient-related interactions at the gene, protein and metabolic levels. These new disciplines and their attendant technologies are changing the paradigms of health research.

**Genomics** – is the study of an organism's genome and the use of the genes. It deals with the systematic use of genome information, associated with other data, to provide answers in biology, medicine, and industry.

**Genotyping** – refers to the process of determining the genotype of an individual with a biological assay. Current methods of doing this include PCR, DNA sequencing, and hybridization to DNA chips or beads. The technology is intrinsic for test on father-/motherhood and in clinical research for the investigation of disease-associated genes.

**TOF-MS** – Time of flight mass spectrometry: an ion of known electrical charge and unknown mass enters a mass spectrometer and is accelerated by an electrical field of known strength. The time that it subsequently takes for the particle to reach a detector at a known distance is measured. This time will depend on the mass-to-charge ratio of the particle (heavier particles reach lower speeds). This method of analysis is a powerful tool for finding the mass-to-charge ratio of charged particles, atoms and molecules.



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