

Introduction: Bile acids (BA) are important for many physiological functions including the absorption of lipophilic nutrients. Investigations concerning the pleiotropic roles of BA in human metabolism require a thorough understanding of factors influencing plasma BA concentrations.

Objectives: To investigate whether age, sex, dietary fat intake and markers of lipid metabolism are associated with fasting plasma BA concentrations.

Method / Design: KarMeN (Karlsruhe Metabolomics and Nutrition) is a cross-sectional study performed at the Max Rubner-Institut in Karlsruhe, Germany. Fasted blood samples from 301 healthy male and female participants (age range 18 – 80 years) were collected and triglycerides, LDL, HDL and body fat % were determined. The percentage of energy intake from dietary fat of the day prior to blood sample drawing was assessed. BA were analyzed using an LC-MS stable isotope dilution assay. Subsequent statistical data processing was done by means of a median regression model.

Results: Fasting plasma BA concentrations showed a large inter-individual variation. Overall, median concentrations of the majority of BA were higher in men. Results of the quantile regression revealed significant interactions of selected BA with age and sex. The highest concentrations of these BA were found in young men. Primarily, chenodeoxycholic acid, a primary BA, was affected. Quantile regression accounting for sex and age revealed associations between secondary BA and plasma levels of triglycerides, HDL and body fat. No associations were found for LDL and dietary fat intake.

Conclusions: Fasting plasma concentrations of selected BA are age and sex dependent. Triglycerides, HDL and body fat are associated with secondary BA plasma concentrations whereas no effect of LDL and dietary fat intake was observed. These significant associations have to be taken into account in studies investigating the influence of BA on human metabolism.

Keywords: (maximum 5): bile acids, age, sex, lipid metabolism

149/373. Metabolite patterns characterising age and sex in participants of the “KarMeN”-study

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Introduction: Investigations on the impact of food on the human metabolome requires information on the background variation of the human metabolome.

Objectives: To investigate whether age and sex are associated with metabolite patterns in healthy humans.

Method / Design: KarMeN (Karlsruhe Metabolomics and Nutrition) is a cross-sectional study performed at the Max Rubner-Institut in Karlsruhe, Germany with more than 300 healthy male and female participants (age range 18 – 80 years). Fasted blood and 24h

urine samples were collected and analysed by targeted and untargeted GC×GC-MS, LC-MS and NMR. Predictive modelling was applied using the following machine learning algorithms: SVM, glmnet and PLS.

Results: Based on metabolite profiles from urine and plasma obtained with different analytical platforms, it was possible to identify metabolite patterns which predict age in men with high accuracy. In women, classification according to age groups (based on their menopause status) was possible from both, urine and plasma metabolome data with high accuracy. Besides a number of unknown analytes, some metabolites important for this prediction could be identified, such as glycine and creatinine in urine. Classification of volunteers according to sex was also possible with high accuracy based on urine and plasma metabolite profiles. Plasma metabolites important for correct classification included creatinine and the branched-chain amino acids valine, leucine and isoleucine.

Conclusions: The metabolite profile of human urine and plasma allows prediction of age and sex with high accuracy, which means that age and sex are associated with metabolite patterns of healthy humans. This needs to be considered in studies looking for the effect of food and diets on the human metabolome.

Keywords: (maximum 5): metabolomics, age, sex, predictive modelling

149/376. Effect of caloric restriction on transcriptional response in metabolic challenge tests in PBMCs of humans

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Introduction: Health has recently been redefined as an organism's ability to adapt and to implement own control in light of physical, emotional and social challenges of life. Within the NutriTech project we defined health as 'phenotypic flexibility': the capacity to adapt to the continuously changing environment in time and space. Examples of metabolic challenges to study phenotypic flexibility are the oral glucose tolerance test (OGTT) and the mixed meal test (MMT). Caloric restriction (CR), the consumption of less energy without malnutrition, is hypothesised to increase health and has been used as a model to investigate the response to metabolic challenges in different health-states.

Objectives: We aimed to study phenotypic flexibility by means of whole genome transcriptional response in human peripheral blood mononuclear cells (PBMCs) upon an OGTT and a MMT challenge before and after a CR diet intervention. As CR is expected to result in a healthier state, we expect an improved response to metabolic challenges and a change towards a healthier gene expression profile.

Method / Design: 72 healthy, overweight men and women, aged 50-65, were subjected to an OGTT and a MMT, before and after a 12