Resting energy expenditure is not associated with distinct plasma and urine metabolite profiles in healthy humans

Manuel Armbruster[1], Achim Bub[1], Manuela J. Rist[1], Lara Frommherz[2], Christoph H. Weinert[2], Diana Bunzel[2], Carina Mack[2], Björn Egert[2], Benedikt Merz[1], Alexander Roth[1], Sabine E. Kulling[2], Bernhard Watzl[1]
[1] Department of Physiology and Biochemistry of Nutrition,
[2] Department of Quality and Safety of Fruit and Vegetables,
Max Rubner-Institut, Karlsruhe, Germany

Background
Lean body mass (LBM) substantially impacts human metabolism and is the major determinant of resting energy expenditure (REE). Differences in REE between men and women mainly result from sex related differences in LBM. So far, little is known if REE and LBM are reflected by a distinct human metabolite profile. Therefore, we aimed to identify plasma and urine metabolite patterns that are associated with REE and LBM of healthy men and women.

Methods
We investigated 301 healthy male and female subjects (18 – 80 years) under standardized conditions in the cross-sectional KarMeN study (Karlsruhe Metabolomics and Nutrition). REE was determined by indirect calorimetry and LBM by dual x-ray absorptiometry. Fasted blood and 24h urine samples were analyzed by targeted and untargeted metabolomics methods using GC×GC-MS, GC-MS, LC-MS and NMR. Data were evaluated by predictive modelling of combined data using different machine learning algorithms, namely SVM, glmnet and PLS.

Results
For the participants of the KarMeN study LBM correlates with REE (r = 0.877; linear regression). However, the applied machine learning algorithms did not reveal a metabolite profile predictive for REE or LBM, when analyzing data for men and women, separately. When evaluating data of men and women combined, as it has been described by others, we were able to predict REE and LBM with high accuracy (>90%). This, however, was a clear effect of sex, which is supported by the high degree of overlap in identified important metabolites for LBM, REE and sex, respectively.

Conclusion
We conclude that studies in healthy humans applying metabolomics need to consider sex specific data evaluation.