Association of the metabolome with health parameters and food intake in a prostate cancer cohort; an untargeted metabolomics study

Johnny R Östman,[a] Rui C Pinto,[b] Elin Thysell,[c] Timothy MD Ebbels,[d] Göran Hallmans,[e] and Ali A Moazzami[a]

[a] Dept. of Molecular Sciences, Swed. Univ. of Agricultural Sciences (SLU), Uppsala, Sweden
[b] Dept. of Epidemiology and Biostatistics, Imperial College London, London, United Kingdom
[c] Dept. of Medical Biosciences, Umeå University, Umeå, Sweden
[d] Dept. of Surgery and Cancer, Imperial College London, London, United Kingdom
[e] Dept. of Public Health and Clinical Medicine, Umeå University, Umeå, Sweden

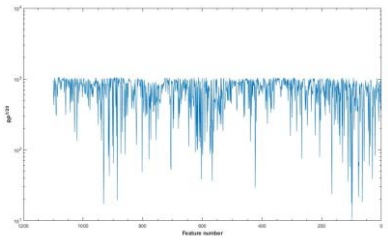

Figure 1. Rank products of 1100 features after multilevel PLSDA

Prostate cancer (PCa) is the most frequently diagnosed cancer and the second most common cause of cancer-related death in men. The associations between PCa risk and pre-diagnostic metabolite levels have been previously investigated, but have yielded inconclusive results.

We used a liquid chromatography-high resolution mass spectrometry untargeted metabolomics approach to look for metabolites associated with the risk of future PCa in fasting plasma using a nested case-control study design of 777 pairs of PCa cases and their matched controls (n = 1554) recruited from Northern Sweden Health and Disease Study Cohort (NSHDS). In order to avoid variation we only included cases with a follow-up of over 5 years. Within this cohort an additional sub-cohort of cases with aggressive PCa was identified (n = 169 pairs). A range of health parameters (*i.a.* body mass index, 2-hour oral glucose tolerance test, food frequency questionnaire answers) was collected for all subjects at baseline.

The untargeted metabolomics approach identified approximately 3000 features, which were further condensed into 1100 features using a novel batch matching algorithm. The associations of the metabolomic features with the health parameters were investigated using conditional logistic regression for both the whole dataset and the aggressive cancer sub-cohort. Indications of associations between hitherto unidentified metabolomic features and health parameters could be shown, shedding light on observable metabolic changes that might manifest as future PCa.