

Human Serum Metabolome

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Abstract

Phenotyping of 1,200 'healthy' adults from the UK has been performed through the investigation of diverse classes of hydrophilic and lipophilic metabolites present in serum by applying a series of chromatography–mass spectrometry platforms. These data were made robust to instrumental drift by numerical correction; this was prerequisite to allow detection of subtle metabolic differences. The variation in observed metabolite relative concentrations between the 1,200 subjects ranged from less than 5 % to more than 200 %. Variations in metabolites could be related to differences in gender, age, BMI, blood pressure, and smoking. Investigations suggest that a sample size of 600 subjects is both necessary and sufficient for robust analysis of these data. Overall, this is a large scale and nontargeted chromatographic MS-based metabolomics study, using samples from over 1,000 individuals, to provide a comprehensive measurement of their serum metabolomes. This work provides an important baseline or reference dataset for understanding the 'normal' relative concentrations and variation in the human serum metabolome. These may be related to our increasing knowledge of the human metabolic network map. Information on the Husermet study is available at <http://www.husermet.org/>. Importantly, all of the data are made freely available at MetaboLights (<http://www.ebi.ac.uk/metabolights/>).

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