

OW4 High throughput online sample cleanup and LC-MS/MS for rapid biomarker discovery

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LC-MS can rapidly provide a plethora of urinary biomarker candidates for further investigation

Metabolomics approaches provide the opportunity to discover novel metabolic effects such as biomarkers of disease, unconstrained by prior conceptions of likely candidate molecules. However this requires the development of fast and reliable unbiased analytical methods that are able to yield qualitative and quantitative data on as many metabolites as possible. High throughput mass spectrometry is one option, providing rapid sample extraction and cleanup can be achieved. Matrices such as urine contain high levels of salts which if not removed can severely affect ionisation and rapidly contaminate the electrospray ion-source.

A fast method was developed for biomarker discovery which utilizes high-throughput online sample cleanup and LC-MS/MS to collect urinary metabolic profiles. We applied this method to a set of urine samples from healthy dairy cows, and cows suffering from facial eczema (FE) (a disease syndrome associated with liver damage caused by the fungal toxin sporidesmin). On analysis of the data by multivariate statistics we could successfully 'classify' the animals into healthy and FE groups as confirmed by elevated concentrations of the enzyme gamma-glutamyltransferase (GGT) in serum from the affected animals. Ions from the MS1 profile with the largest effects on the classification could then be investigated further for characteristic structural information from the MS/MS spectra collected. This method serves as a useful tool for rapidly analysing large sample-sets to search for discriminatory ions which may be potential biomarkers.