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The Metaproteome of "Park Grass" soil - a reference for EU soil science

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Soil metaproteomics, the systemic extraction and identification of proteins from a soil, is key to understanding the biological and physical processes that occur within the soil at a molecular level. Until recently, direct extraction of proteins from complex soils have yielded only dozens of protein identifications due to interfering substances, such as humic acids and clay, which co-extract and/or strongly adsorb protein, often causing problems in downstream processing, e.g. mass spectrometry.

Furthermore, the current most successful, direct, proteomic extraction protocol favours larger molecular weight and/or heat-stable proteins due to its extraction protocol.

We have now developed a novel, faster, direct soil protein extraction protocol which also addressed the problem of interfering substances, while only requiring less than 1 gram of material per extraction. We extracted protein from the ‘Genomic Observatory’ Park Grass at Rothamsted Research (UK), an ideally suited geographic site as it is the longest (>150 years) continually studied experiment on ungrazed permanent grassland in the world, for which a rich history of environmental/ecological data has been collected, including high quality publically available metagenome DNA sequences.

Using this improved methodology, in conjunction with the creation of high quality, curated metagenomic sequence databases, we have been able to significantly improve protein identifications from one soil due to extracting a similar number of proteins that were >90% different when compared to the best current direct protocol. This optimised metaproteomics protocol has now enabled identification of thousands of proteins from one soil, leading therefore to a deeper insight of soil system processes at the molecular scale.