

Roots of decline? Assembly and Function of the Rhizosphere Microbiome in Relation to Yield Decline
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<p>Using established field sites across the UK, rhizosphere samples will be collected from 32 OSR cropping locations. Prokaryotic and eukaryotic microbe community composition will be determined using amplicon sequencing. Communities will be differentiated into core species which are widely distributed and locally abundant, and satellite species which are infrequent and rare. We will elucidate the role of management, environmental variables and distance as drivers of community assembly. Co-occurrence and co-exclusion relationships of rhizosphere taxa will also be determined. We will also focus on understanding those factors which determine distribution and assembly of specific taxa which our earlier work has suggested contribute to OSR yield decline. We will also determine relationships between microbiome composition and yield. Field experiments will be used to investigate changes in microbial community organisation and functioning during the transition from a healthy to a diseased state associated with yield decline. We will use 3 separate locations in order to investigate the extent to which changes in function are conserved across the landscape. Rhizosphere soil metatranscriptomes and root transcriptomes will be sequenced, and in particular, networks associated with microbial pathogenesis, and host defence and nutrition will be characterised. We will investigate the potential to manipulate the assembly of the rhizosphere microbiome through crop genotype and soil management. Four OSR genotypes which we have shown have contrasting root metabolomes will be grown in rotational field experiments and targeted amplicon sequencing used to study community assembly, including pathogens associated with yield decline. We will use a unique field resource at Rothamsted to determine scope for using soil management to influence recruitment of taxa into the root microbiome, including pathogens associated with yield decline.</p>