Identification of fungal ‘endophyte’ populations present in plants on the North Wyke farm platform.

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Consistent yield from agricultural systems are dependent on the management of both abiotic and biotic stresses. Microbes can have a huge negative impact on yield. Fungal pathogens of wheat are estimated to cause losses of up to 29% of the crop (Oerke and Dehne, 2004). Other groups of pathogens along with various abiotic challenges place further pressure on production. Plant-microbe interactions can be complex and transient as they depend on environmental conditions and interaction with contributing organisms within the microbiome present in the plant and the surrounding soil. Generally, they are grouped and studied according to their function, which could fall anywhere between saprophytic (live on dead or decomposing matter) through to symbiotic (or benefit mutually from the interaction). Some microbes can occupy multiple niches within this scale depending on a certain set of conditions. Endophytes are defined as “microbes which occur within plant tissue for at least part of their life cycle without causing disease under any known circumstances” (Le Cocq et al. 2016).

This project set out to isolate and identify fungi residing within plant shoots from the North Wyke farm platform and to compare colonization across treatments and plant species. This resulted in a catalogue of fungi that form part of the microbiome of the plants within the three treatment categories. Figure 1. Describes the experimental outline. Figure 2. describes the methodology employed to isolate the fungi from within the shoots of the plants. Morphological ID and ITS sequencing was used to identify a proportion of the fungi. This revealed that a number of the fungi isolated were significantly related to known fungal pathogens as well as a number of fungi unidentified within the scope of this project.

Figure 1.

Figure 2. Characterization of endophytic fungi

Figure 3. The most popular fungi

Figure 3 demonstrates the differences within fungi collected in each field, highlighting that there are different fugal populations within the three treatment on the North Wyke farm platform. Further analysis demonstrated that the host grass type could be an important factor in this (data not shown). The study concluded that there was a larger range of culturable fungi present in permanent pasture than in the other treatment. This warrants further study as the functional role that these fungi play in the grassland system has yet to be elucidated.

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References
