

100 years of plant breeding – what have we done to the seed microbiome?

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Project Description: Humans have domesticated plants for millennia, with cereals first domesticated in the Fertile Crescent of the Middle East around 9000 BCE. The plant has traditionally been considered as a single entity, with selection based on phenotype resulting in modification of the plant genome, and more latterly, understanding of the genome being used to accelerate selection of key phenotypes. However, with the advent of next generation sequencing technology, there has been greater appreciation of the role of the plant microbiome and its metagenome in plant performance. Seed biobanks are critically important for preserving plant diversity which may be lost in the wild due to habitat loss and the changing environment, but we know nothing about the effect of long-term storage on the microbiome. **We will test the hypothesis that domestication, breeding and storage alter the composition of the plant microbiome, with impacts on plant performance in terms of yield, resilience and quality.** The seed microbiome is the ideal target for this study as this represents the community recruited by the plant and potentially adapted to endophytic existence.

We will analyse the bacterial microbiomes of 3 crops with contrasting histories and agricultural uses:

- ***Avena sativa* (oats):** domesticated as a grain crop for human food during the first millennium BC.
- ***Lolium perenne*:** a forage grass for livestock (meat and milk) production that has been bred for ~100 years.
- ***Miscanthus*:** a tall grass recently selected from the wild as a feedstock for bioenergy and industrial products, as well as nutraceuticals (e.g. prebiotics and sweeteners) and represents a novel domestication in progress.

The seed biobank at AU holds collections, including wild relatives and breeding lines, of all three species, going back approximately 40 years, 100 years, and 15 years respectively.

We are increasingly placing value on seed biobanks to preserve diversity, including for genetic material from which to breed for future climate scenarios. To date there have been no studies on the effect of long-term storage on the microbiome of the stored seeds, despite an increasing body of evidence for the microbiome providing a range of benefits to the plant in terms of performance and resilience to various stresses. Furthermore, very little is known about the impact of domestication and breeding on the plant microbiome and its functionality within the plant. In this project we will use the resources available in the 100 year old collections at Aberystwyth to provide novel evidence on:

1. The impact of storage on the germination and viability of oat, *Lolium* and *Miscanthus* seed.
2. The impact of domestication, breeding and storage on the composition of the plant microbiome: have we selected for the best, or lost functionality due to modern agronomic practices?
3. The impact of diversity loss within the microbiome, and re-application of specific strains, on plant performance in terms of yield, resilience and quality.

The information generated by this project will enable targeted selection of seed for collection/application based on the microbiome (metagenome) as well as the genetic and phenotypic diversity of the plant. It will address the fundamental question of how humans have modified the plant microbiome through selection, and hence how we might optimise it in future, either via application such as biofertilisers or through novel breeding targets. And finally it will provide information on the effect of storage, and hence how we might optimise the preservation of the plant microbiome as well as the plant genome within long-term storage for use by breeders and future generations.

References:

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