

## **Genetic diversity in a crop progenitor *Beta vulgaris* subsp. *maritima***

### **McMullan Group**

Crops are rendered vulnerable to disease because of genetic bottlenecks imposed by domestication and intensive breeding. Therefore, to increase the level of resistance of crops, many breeding programs aim to recruit disease resistance from wild relatives which are genetically diverse. Sugar beet (*Beta vulgaris*) is a recently domesticated crop which can still be crossed with its wild progenitor, sea beet (*Beta vulgaris* subsp. *maritima*). Importantly, sea beet represents a reservoir of genetic diversity and shares pathogens with sugar beet.

This is a self-contained project in which the student will use bioinformatics to identify polymorphic genes within the sugar beet genome, and design primers to PCR amplify and Sanger sequence their marker of choice. The student will then join the lab group to sample wild sea beet along the east coast of the UK and use their marker to describe wild beet genetic diversity using a phylogeny.

Completing this project will give the student an understanding of a miniature phylogenetics project. This project fits within the wider aims of the McMullan group to identify sources of wild beet genetic diversity, and the output of the project will feed directly into a PhD project starting in September. Therefore, this project will give the student an understanding of what a PhD project entails. Due to the nature of the project applicants should be proactive and willing to work independently.