Investigating the genetic control, and environmental impact on the accumulation of beta-glucan in barley

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Introduction & Background

Spring barley is an important and highly economical cereal crop in the UK. Mainly grown for brewing and animal feed, barley offers a potential dietary health benefit, largely due to the presence of **beta-glucan**, a non-starch polysaccharide found in the cell walls of cereal grains. This remains undigested in the small intestine, acting as soluble fibre which confers significant benefits like actively lowering blood cholesterol levels, reducing hypertension, slowing glucose release in the blood and reducing the risks of obesity. It is also low in calories, high in fibre and rich in probiotics, which makes it an ideal food for diabetic patients.

The established UK spring barley varieties are '*hulled*' (presence of a tough, inedible outer hull layer) which requires grains to be further processed, which can also strip away nutrients during the threshing process. '**Naked**' grains (*hull less* barley) thresh free from the husk, offer a more sustainable alternative to this problem. The 'naked' trait is monogenic and is because of loss of function of the *NUD* gene (Yu et al. 2016). While in contrast, the beta glucan trait is under relatively complex control, involving multiple genes (*CslF*, *H* and *J* families) with significant environmental interaction (Burton et al. 2006; Doblin et al. 2009; Dickin et al. 2011). Ideally, it would be sustainable to have consistently high levels of beta-glucan in a naked grain barley to be directly used as a healthy wholegrain functional food.

Project Aims & Objectives

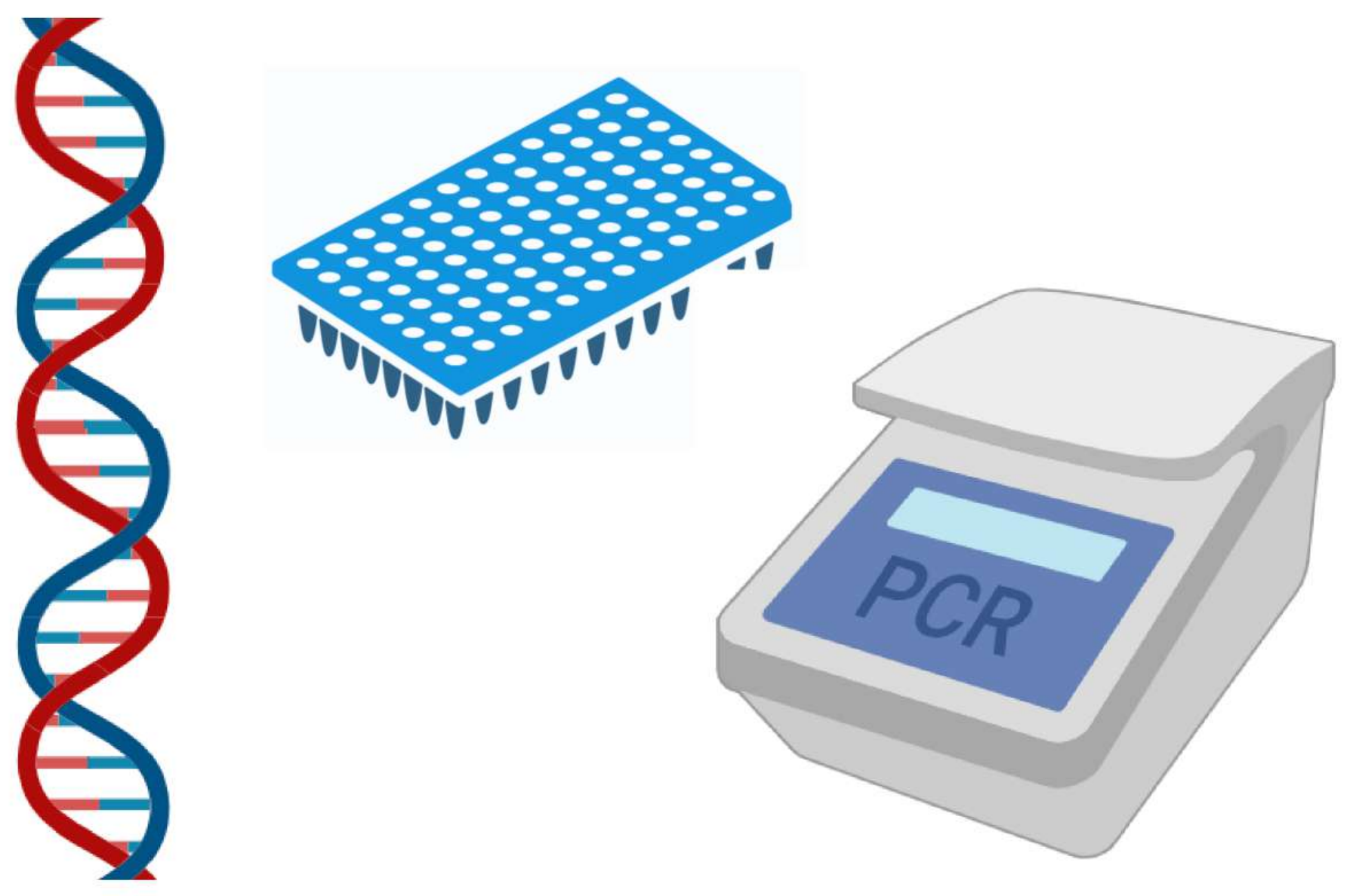
I. Cataloguing, selecting and growing a large barley germplasm (old cultivars, landraces and wild varieties) in fields and glasshouses to identify lines with **higher** and **lower** beta-glucan levels

II. Identifying regulatory genes and QTLs responsible for 'higher and 'lower' beta-glucan levels by **GWAS**

III. Investigating the influence of *genotype by environment* (GxE) and crop management effects of the beta-glucan accumulation in the grain, through multi-location **field trials** in the UK

IV. Understanding the relationship of genetic and molecular players involved in the beta-glucan synthesis and accumulation using **targeted mutagenesis** and molecular genetics

V. Developing biparental and mapping populations with the aim of introgressing high beta-glucan levels into the elite barley cultivars in the UK



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