

PhD School of Agriculture, Environment and Bioenergy (XXXV Cycle)

Project title

“Identification and characterization of the major QTLs for culm diameter in barley”

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ABSTRACT

Barley (*Hordeum vulgare* L.) is one of the most important cereal crops in global agriculture and it has been extensively used as a model for plant genetic analyses and breeding (Stein & Muehlbauer, 2017). Stem lodging in barley can cause a reduction in grain yield and quality. In a climate change scenario, extreme weather events are expected to occur more frequently and threaten barley production by increasing lodging occurrence (Dawson *et al.*, 2015). Barley semi-dwarf varieties have often been associated with lodging resistance, due to the reduced length of their culm. Unfortunately, some of these mutants also show unwanted agronomic traits caused by pleiotropic effects due to alterations in hormonal pathways, such as the gibberellins (GAs) and brassinosteroids (BRs) pathways (Docker & Hansson, 2015). Beside reducing plant height, other strategies could be adopted to reduce the risk of lodging, such as by manipulating traits associated with the physical strength of the culm, which is determined by the morphology and the composition of culm (Hirano *et al.*, 2017). Culm diameter in particular has been associated with lodging resistance in cereals (Kong *et al.*, 2013; Ookawa *et al.*, 2010). In rice, quantitative trait loci (QTLs) controlling culm morphology have been used to develop improved rice varieties which are more resistant to lodging. However, the genetic and molecular bases underlying culm architecture traits are poorly understood in barley. The present PhD project aims to identify new QTLs for culm diameter to improve lodging resistance in barley. We will take advantage of genomic resources available for barley along with accurate phenotyping protocols aiming to dissect the genetic bases of culm diameter. The target QTLs will be characterized through the development of segregating populations to evaluate the allelic effects and estimate the interactions between QTLs. In a parallel approach, we will screen genomic regions previously associated to culm diameter in order to identify and functionally characterize candidate gene(s) for this trait. Mutants in these genes will be identified/created by reverse genetics approaches to evaluate their effects on plant and culm development. This work is expected to provide the basis for the development of lines carrying favorable alleles for culm diameter that could be used as starting material to produce new breeding varieties with an increased lodging resistance.

Literature

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