

PhD School on Agriculture, Environment and Bioenergy

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(XXXVIII cycle, 2022-25)

Project draft

1. Field of interest

Crop genetics, AGR/07

2. Project title

Genetic dissection of plant architecture traits in barley

3. Tutor (membro del Collegio dei Docenti)

Prof. Laura Rossini

<http://orcid.org/0000-0001-6509-9177>

<https://www.unimi.it/it/ugov/person/laura-rossini>

4. Relevance of the topic and state of the art:

Barley (*Hordeum vulgare* L.) is one of the most ancient and important crops and an established model for plant genetics with extensive genomic resources¹. Stem lodging is a major constraint to grain yield and quality and this phenomenon is expected to worsen as a result of extreme weather events associated with climate change, such as thunderstorms and strong winds². In a recent survey on strategies for adaptation to climate change, both farmers and advisors ranked lodging resistance among the top 3 priority traits for cereal cultivar choice³. Albeit useful to reduce plant height, semi-dwarfing genes commonly used in barley breeding have some negative pleiotropic effects (e.g. biomass reduction) [reviewed in^{4,5}]. An attractive route to address this issue is the manipulation of culm architecture traits such as diameter and wall thickness, which have been correlated to lodging resistance in cereals^{6-8,9}. However, lack of knowledge on the genetic determination of these traits has limited their deployment in barley breeding for improved lodging resistance. In order to fill this gap, the host group has developed and applied innovative phenotyping protocols and carried out genome-wide association studies for different culm traits, laying the foundations for genetic dissection and improvement of culm architecture in barley¹⁰.

5. Layout of the project (draft)

The present PhD project will build upon previous work done by the host group to dissect the genetic control of culm architecture to improve lodging resistance and productivity in barley (ClimBar and BARISTA projects). The extensive collaboration network developed by the tutor will provide the PhD student with exposure to world-class scientists with expertise in plant developmental genetics, functional genomics and breeding, opening also opportunities for research visits to international institutes.

5.1. Materials & Methods:

Accurate image analyses-based protocols were developed by the host group and applied to phenotype a European germplasm collection in 7 different environments (site/year combinations), yielding quantitative data for various culm morphology traits, besides plant height and other standard agronomic traits. Genome-wide association studies (GWAS)

uncovered a large number of QTLs¹⁰. Among these, we are focusing on characterization of two QTLs that were shown to have stable effects across environments. To this end, we have developed double haploid (DH) populations segregating for these QTLs. Additionally, a screening of the TILLMore mutagenized population identified a line with increased diameter compared to the wild-type Morex.

The PhD project will take advantage of state-of-the-art genomic resources available for barley¹ and the abovementioned plant materials to precisely map 1-2 loci for barley culm diameter, identify and characterize associated candidate genes. The PhD student will apply accurate phenotyping protocols on a range of materials, develop and characterize segregating populations to carry out a detailed dissection of phenotypic effects and genetic mapping of target loci, identify/generate and characterize mutants in candidate genes.

WP1 – development of segregating progenies for target loci and phenotyping under greenhouse conditions.

WP2 – genetic mapping by appropriate genotyping/sequencing-based strategy.

WP3 – identification/characterization of candidate genes by allelic comparisons, co-segregation analyses, gene-expression analyses, TILLING/genome editing in collaboration with national and international partners.

5.2. Schedule and major steps (3 years):

WP1 – year 1-2. WP2 – year 2. WP3 – year 2-3.

6. Available funds

The present project is connected to National Research Centre for Agricultural Technologies (Agritech) Spoke 1 activities, funded by PNRR

<https://www.mur.gov.it/it/news/mercoledi-15062022/pnrr-nascono-i-5-centri-nazionali-la-ricerca>

7. Literature:

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2. Sowadan, O. *et al.* Mining of favorable alleles for lodging resistance traits in rice (*Oryza sativa*) through association mapping. *Planta* **248**, 155–169 (2018).
3. Macholdt, J. & Honermeier, B. Impact of Climate Change on Cultivar Choice: Adaptation Strategies of Farmers and Advisors in German Cereal Production. *Agronomy* **6**, 40 (2016).
4. Berry, P. M. *et al.* Understanding and Reducing Lodging in Cereals. *Advances in Agronomy* **84**, 217–271 (2004).
5. Dockter, C. & Hansson, M. Improving barley culm robustness for secured crop yield in a changing climate. *J. Exp. Bot.* **66**, 3499–3509 (2015).
6. Chuanren, D., Bochu, W., Pingqing, W., Daohong, W. & Shaoxi, C. Relationship between the minute structure and the lodging resistance of rice stems. *Colloids Surfaces B Biointerfaces* **35**, 155–158 (2004).
7. Berry, P. M., Sterling, M. & Mooney, S. J. Modelling / Site Specific Analysis / Biometrics / Technologies Development of a Model of Lodging for Barley. **158**, 151–158 (2006).
8. Ookawa, T. *et al.* New approach for rice improvement using a pleiotropic QTL gene for lodging resistance and yield. *Nat. Commun.* **1**, 132 (2010).
9. Kong, E. *et al.* Anatomical and chemical characteristics associated with lodging resistance in wheat. *Crop J.* **1**, 43–49 (2013).
10. Bretani, G. *et al.* Multi-environment genome-wide association mapping of culm morphology traits in barley. *bioRxiv* 2022.03.30.486427 (2022).