

Advanced tools for breeding BARley for Intensive and Sustainable Agriculture under climate change scenarios

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INTRODUCTION TO BARISTA

BARISTA is a project dedicated to enhancing genomic knowledge and predictive breeding technologies for barley.

BARISTA delivers new breeding strategies and toolkits for boosting crop improvement, leading to new, high-yielding varieties selected to cope with anticipated future climatic conditions.

BARISTA focuses on the traits relevant for sustainable barley production and resilience under current and future environmental challenges: water use efficiency; response to water scarcity or waterlogging; resistance to biotrophic and necrotrophic pathogens; phenological adaptation and regulation of flowering time; culm architecture and lodging resistance; response to increased atmospheric CO₂, response to reduced nitrogen fertilizer input.

The translation of genomics findings in breeding will be driven by modelling tools including genomic prediction (GP), crop simulation models (CSMs) and integrated GP-CSM strategies through the improvement of current predictive breeding tools for barley, providing breeders with an innovative and efficient toolkit to increase the sustainability and resilience of barley in the face of biotic and abiotic challenges of climate change.

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In this issue the keywords of BARISTA

<http://www.barleyhub.org/projects/barista>

Twitter: BARISTA for sustainable barley

The introduction of predictive technologies in plant breeding might radically innovate and enhance variety development and seed research. **Genomic prediction (GP) combines molecular markers and phenotypic information to create statistical models that aid scientists and breeders to efficiently select plants with superior performance.** The application of GP is gaining momentum in public and private organizations as it is a key predictive tool to quicken breeding operations and optimize the use of resources.

BARISTA is exploiting a collection of 200 spring barley varieties tested in 18 site-by-year combinations to develop GP models for different target populations of environments. Currently, single-environment GP models for grain yield are under development, while more complex GP models to account for marker per environment interactions will be deployed later. Overall, these GP models will be a project legacy for barley breeders and BARISTA's stakeholders to sustain variety development and improve grain yield.

Crop Simulation Models (CSMs) are mathematical representations of the biological and physical interactions and processes occurring in the plant-soil-atmosphere system.

CSMs are developed and evaluated using experimental data and established ecophysiological principles, and embody a deep understanding of crop responses to environment and management variables.

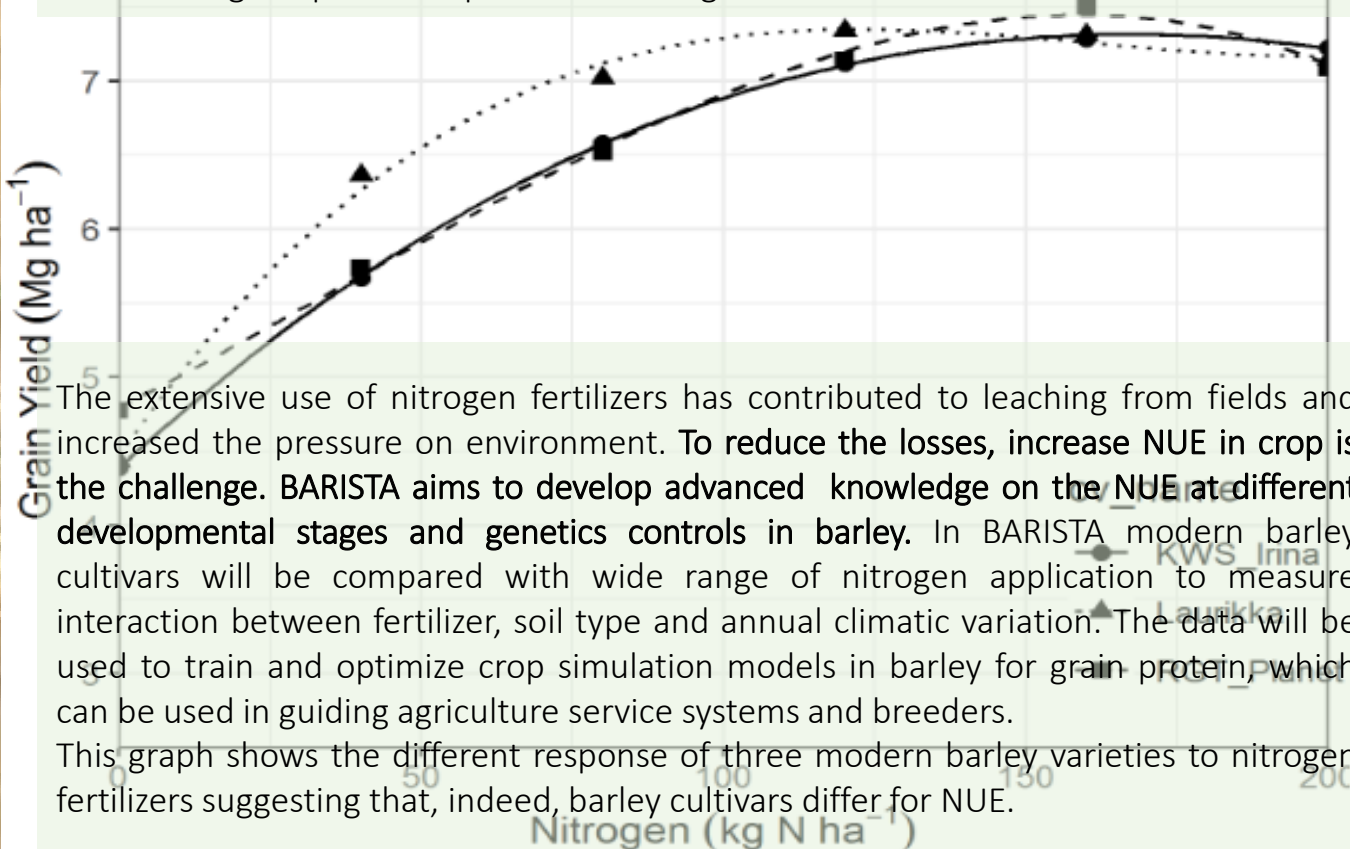
CSMs can aid plant breeding by identifying crop ideotypes, i.e. a set of crop traits (G) that optimize crop performance under given environmental (E) and management (M) conditions.

In BARISTA, we aim at improving and applying Crop Simulation Models for:

- Reproducing barley growth and yield formation in contrasting environments
- Understanding responses of different barley cultivars to drought, stress, elevated CO₂, nitrogen limitation and lodging
- Identifying barley ideotypes for target environments
- Linking genetics and ecophysiological model parameters to improve ideotyping for certain traits /G X E interactions
- Exploring adaptation options (management strategies) for barley to better cope with and perform well under various stresses

Nitrogen Use Efficiency

Nitrogen Use Efficiency (NUE) is defined as the amount of carbon assimilated as biomass or grain produced per unit of nitrogen used.



The extensive use of nitrogen fertilizers has contributed to leaching from fields and increased the pressure on environment. To reduce the losses, increase NUE in crop is the challenge. BARISTA aims to develop advanced knowledge on the NUE at different developmental stages and genetics controls in barley. In BARISTA modern barley cultivars will be compared with wide range of nitrogen application to measure interaction between fertilizer, soil type and annual climatic variation. The data will be used to train and optimize crop simulation models in barley for grain protein, which can be used in guiding agriculture service systems and breeders.

This graph shows the different response of three modern barley varieties to nitrogen fertilizers suggesting that, indeed, barley cultivars differ for NUE.

Adaptation to elevated CO₂

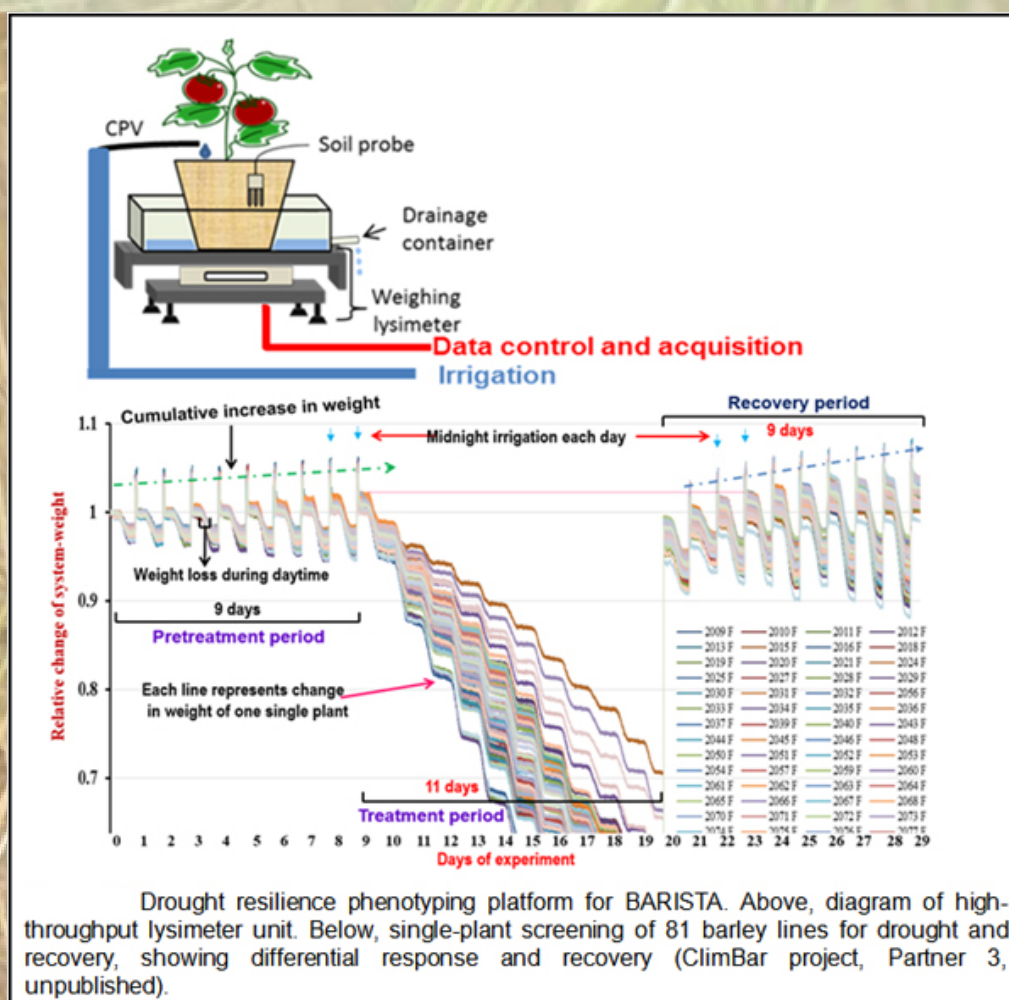
All future scenarios predict a significant increase in atmospheric [CO₂] (approx. 600 ppm in 2050) from the current level above 410 ppm due to anthropogenic activities. It is generally held that an elevated [CO₂] increases plant productivity in C₃ crops, if water is not limited due to increased photosynthesis and decreases grain quality through a reduction in protein and mineral content. Hence, increased [CO₂] may simultaneously drive global warming and increased sensitivity to heat in plants through separate processes. The balance of the counteracting effects of increased [CO₂] regarding yield and stress response may vary with genotype and has not been under selection by breeders.

Investigation of plant response and performance under high [CO₂] in the BARISTA germplasm set is therefore likely to give insight into the underlying control mechanisms and allelic variation, as well as to identify lines useful for breeding abiotic stress resilience under future predicted [CO₂] and climatic conditions.

Water Use Efficiency

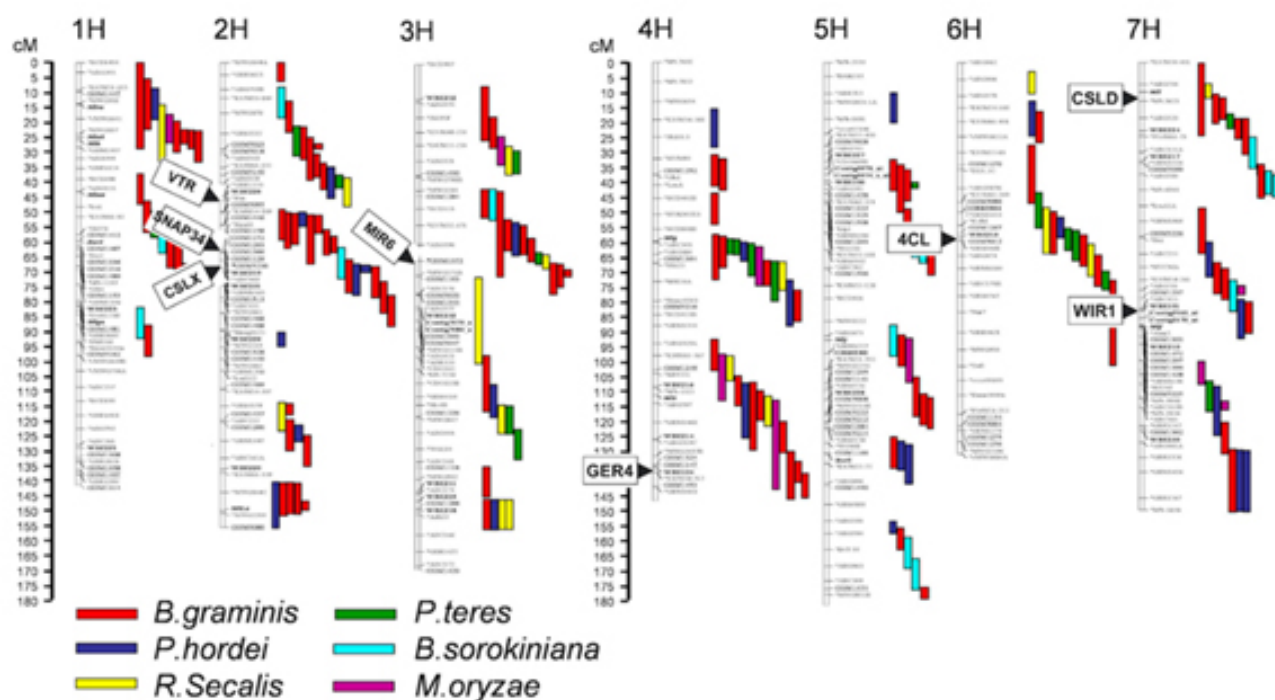
Water Use Efficiency (WUE) is defined as the amount of carbon assimilated as biomass or grain produced per unit of water used. Taking into account that climate change negatively impacts on plant growth and water management mechanisms, **BARISTA** explores the mechanisms of avenues to increase WUE in barley to coping better with limited water supply.

WUE-related traits (net assimilation rate, transpiration, leaf temperature, photosynthesis) as well as transcriptomic response of the selected plant material under different watering regimes will be examined to identify resilient lines and their mechanisms. Barley lines with contrasting WUE, and a set of barley TILLING mutants identified in genes encoding ABA signaling components will be investigated. In plants, ABA is a central phytohormonal regulator of the stress response. ABA-related barley mutants were already described as drought-tolerant at seedling stage, now these mutants together with lines with contrasting WUE will be phenotyped to provide the mechanistic insight for WUE and drought tolerance regulation from pre-flowering to grain filling stage. This work will provide a body of evidence that will support the breeding of varieties with increased WUE.



Quantitative disease resistance

During co-evolution with pathogens plants have evolved a multigenic, broad-acting basal defense system that is triggered by highly conserved pathogen-associated molecular patterns (PAMPs). PAMP-triggered immunity (PTI) is the underlying mechanism of quantitative host- as well as nonhost resistance. Quantitative disease resistance is a promising approach to ensure safe and sustainable crop production, while at the same time reducing pesticide input. Quantitative resistance can act against several pathogens simultaneously and is known to be more durable, because it is less prone to be overcome by a single virulence gene of a pathogen race. **BARISTA aims to use genomics-assisted backcrossing of selected resistance-associated genes to improve quantitative resistance in barley** to pathogens like powdery mildew, leaf rust, scald and net blotch. A set of 160 spring barley single (SSL) and quadruple-stack lines (QSL) containing between one and four selected quantitative resistance candidate genes will be characterized at phenotypic and genetic level and employed to develop improved disease resistance breeding lines.



Meta-QTL analysis of resistance of barley to six fungal pathogens. QTLs for resistance against powdery mildew, leaf rust, scald, net blotch, spot blotch and blast have been placed on a consensus map to indicate hotspots of barley resistance QTL. Potential candidate genes, explaining quantitative resistance are indicated in boxes (modified from Schweizer and Stein 2011).

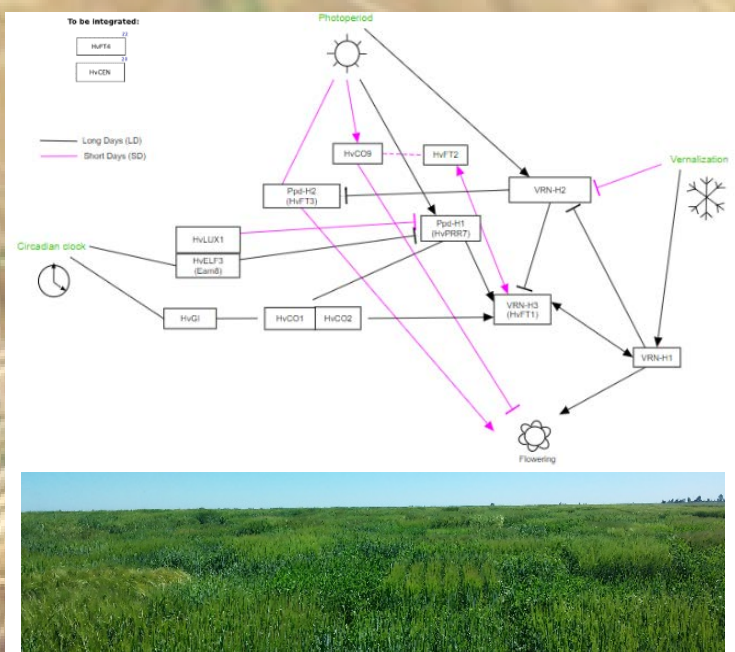
Lodging resistance

Lodging occurs when stems bend or break and plants fall over, causing 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. While barley semi-dwarf varieties have improved lodging resistance, some of these materials exhibit undesirable pleiotropic effects. Alternative strategies to reduce lodging are possible by manipulating traits associated with the physical strength of the culm, as determined by its morphology and composition. Culm diameter in particular has been associated with lodging resistance in cereals. In rice, quantitative trait loci (QTLs) controlling culm morphology have been used to develop improved varieties which are more resistant to lodging. In contrast, the genetic and molecular bases underlying culm architecture traits are poorly understood in barley. BARISTA aims at filling the gap by characterizing 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 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 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 to increase lodging resistance.



Cross section of
a barley stem internode.
Photo credit – Alessandro Vajani.

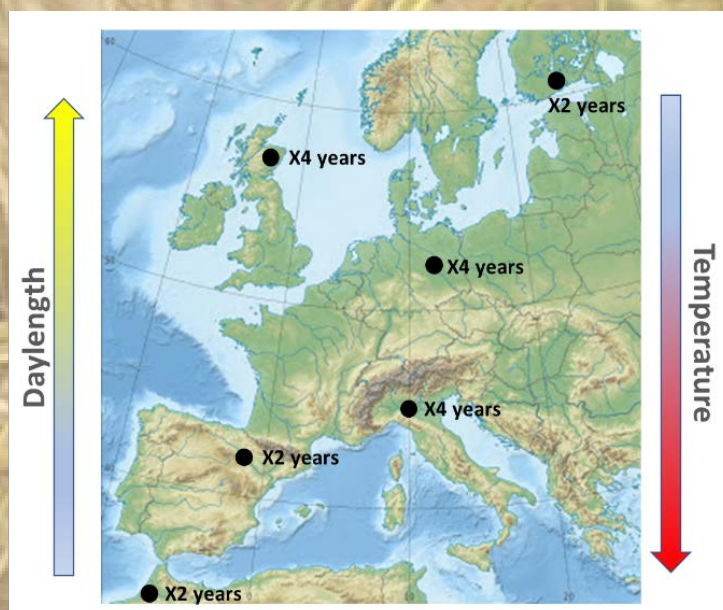
Flowering time



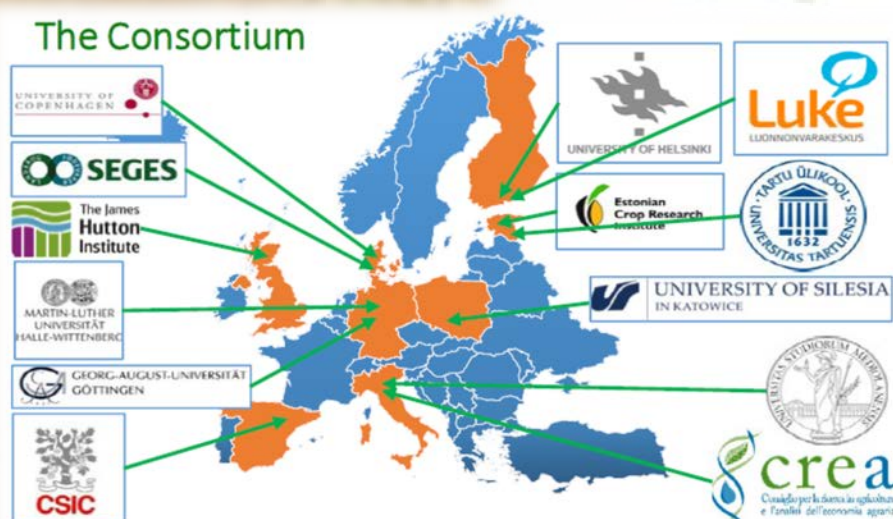
Flowering time is one of the most critical traits for plants' life cycles, since its optimization allows plants to successfully reproduce.

In Europe, barley is cultivated from Iceland to the southern regions of Italy and Spain, and the causal links between the adaptation to such different environments and sequence-level genetic variation is well described (e.g., Comadran et al. 2012). The importance of flowering network genes (top figure, www.wikipathways.org) hinted that combinations of alleles contribute to the overall matching of environment and life history traits. As environments change the optimum combination of alleles will, thus, change.

In BARISTA, phenology and yield-related traits previously collected on the same set of germplasm across the eco-geographical range (bottom figure), are exploited to test their stability and their relationship across contrasting environments. Accessions with different allelic combinations at important flowering time genes have been crossed with the elite barley line RGT Planet to develop populations (by speed breeding), which will be trialled at different sites. In this way, **BARISTA** will exploit new alleles and allele combinations to adapt barley to the expected climatic changes.



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ABLE BARLEY

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