

BARISTA

Advanced tools for breeding **BAR**ley for **I**ntensive and **SusTainable A**griculture under climate change scenarios

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

New breeding strategies:

Breeding today that takes into account future climatic conditions

Toolkits:

- Predictive models capable to predict crop performance under different climatic scenarios
- Novel genes/alleles for sustainable production

Executive Summary

Agriculture will need varieties suited to higher growth temperatures, shifting rain patterns, new disease threats, and reduced inputs. The genes conferring resilience traits for these changes, together with predictive models for the performance they can deliver in combination, are needed for plant breeding to improve crop sustainability and yield potential in the face of these challenges. BARISTA delivered new breeding strategies and toolkits for boosting barley crop improvement, which can lead to new, high-yielding varieties selected to cope with anticipated future climatic conditions. BARISTA has released a barley breeding toolkit made of crop simulation models capable to predict crop performance under different climatic scenario and novel genes/alleles for sustainable production.

Major research findings and outputs:

- Crop Simulation Models (CSMs): a standard Genomic Prediction model produced; a CSM calibrated for barley nitrogen response; new climate scenario data produced from an ensemble of climate models for barley growing season across Europe; evaluation of different CSMs for selected barley genotypes and major traits (lodging, flowering time, nitrogen use efficiency, diseases response).
- New genes and genotypes: Novel loci controlling culm diameter (larger culm contributes to lodging resistance)*; a wide range of flowering-gene haplotypes that allow barley to flower across its eco-geographical range; genotypes with contrasting water conservation behavior* and segregating populations for genetic analysis; barley mutants with increased water use efficiency, affecting response to the plant hormone ABA.

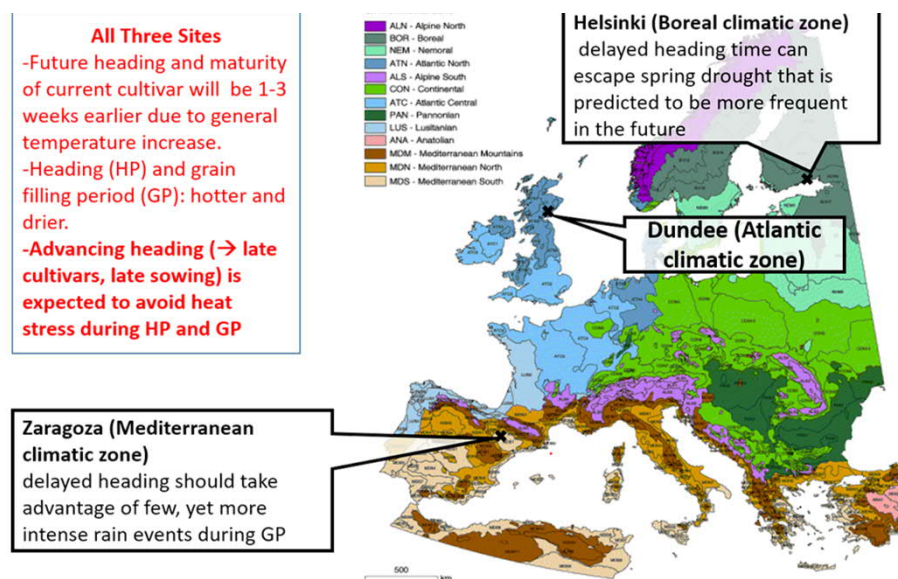
These tools will enable breeding for improved crop sustainability (disease resistance, nitrogen use **efficiency**, water use **efficiency**)

*Output from Finnish partner under MMM funding.

Plant Material: A common set of germplasm across the project, consisting of ~200 barley spring cultivars extensively genotyped and phenotyped in previous projects, together with lines carrying 1 to 4 quantitative resistance loci against the main barley pathogens, and several novel barley ABA-related mutants of candidate genes affecting water use efficiency (WUE) and drought tolerance. BARISTA was built on extensive phenotypic and genotypic data generated in previous projects and on current understanding of the genetics of ideotype traits for biotic and abiotic stress resilience.

Major research findings and outputs

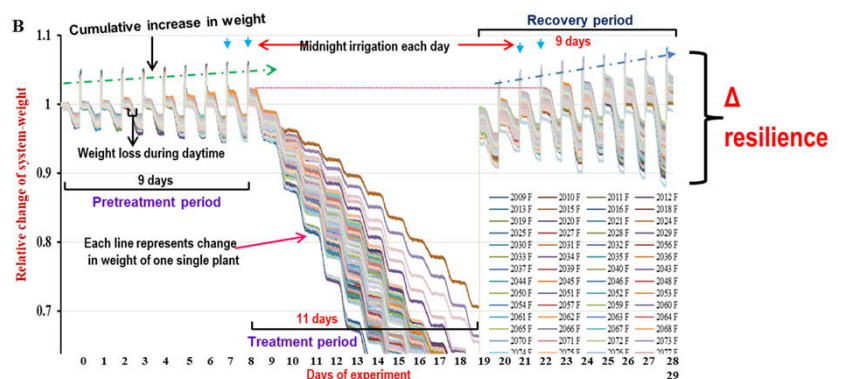
Projected impacts of sowing date and cultivar choice on the timing of heat and drought stress in spring barley grown along a European transect



Genotypes with contrasting water conservation behavior suited for spring (Nordic) vs terminal (Mediterranean) droughts

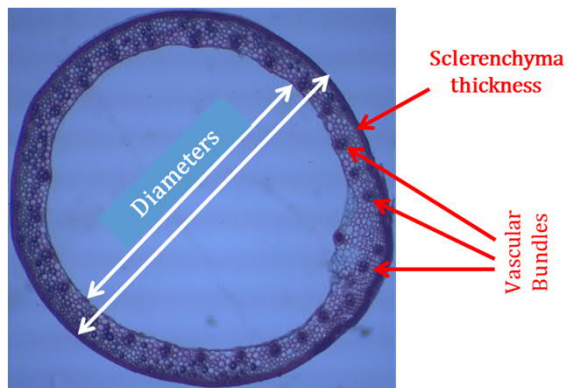


Precision phenotyping lysimeter platform (iCORE), HUJI, Rehovot, IL.



Differential drought response and resilience Drought response and resilience of 81 barley lines on iCORE lysimeter platform

Genotypes with improved resistance to lodging from storms, via increased culm diameter. Diversity for culm diameter within elite germplasm was used to identify two loci (chr. 1H, 4H) and corresponding candidate genes (TILLING mutants are available)



Light microscopy of culm structure.



Diversity in culm diameter and wall thickness

Conclusions and Recommendations

BARISTA has developed the know-how for a predictive barley breeding (Breed today for the climate of tomorrow).

Work by the Finnish partner has clarified that future heading and maturity of current cultivars will be 1-3 weeks earlier due to general temperature increase. Simultaneously, early-season drought will be increasingly problematic. This suggests that delayed heading time, but not delayed maturity, would be a useful breeding goal: hence, accelerated grain filling. This will also require appropriate stomatal response to soil water content. Identified genotypes (and alleles) in the germplasm diversity set can be exploited for spring drought tolerance followed by resilient and robust later growth. Identified loci and alleles for culm strength will be of use for lodging resistance to the stormier conditions associated with a warming climate.

What results can be put into practice? New loci for water use efficiency, flowering time, culm diameter, disease resistance; new crop and genomic selection models.

What stakeholders can use these results? Plant breeders, passing them on to the farmers.

How can stakeholders use the results for their innovations? Marker Assisted Selection, Genomic Prediction and Crop Simulation Models within breeding programs. Germplasm accessions identified with specific traits can be used in introgressions.

Publications, Finnish partner

<https://www.suscrop.eu/projects-first-call/barista>

1. Mercy Appiah, Gennady Bracho-Mujica, Nicole C.R. Ferreira, Alan H. Schulman, Reimund P. Rötter. 2023. Projected impacts of sowing date and cultivar choice on the timing of heat and drought stress in spring barley grown along a European transect. *Field Crops Res* 291: 108768 online 05.12.2022, DOI: 10.1016/j.fcr.2022.108768
2. Gianluca Bretani, Salar Shaaf, Alessandro Tondelli, Luigi Cattivelli, Stefano Delbono, Robbie Waugh, William Thomas, Joanne Russell, Hazel Bull, Ernesto Igartua, Ana Maria Casas, Pilar Gracia, Roberta Rossi, Alan H. Schulman, and Laura Rossini. 2022. Multi-environment genome-wide association mapping of culm morphology traits in barley. *Frontiers in Plant Science* 13:926277. DOI: 10.3389/fpls.2022.926277
3. Maitry Paul, Jaakko Tanskanen, Marko Jääskeläinen, Wei Chang, Ahan Dalal, Menachem Moshelion, Alan H. Schulman. Drought and recovery in barley: key gene networks and retrotransposon response. <https://biorxiv.org/cgi/content/short/2023.03.05.531133v1>