



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

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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.

#### ANNOUNCEMENT

The BARISTA consortium in collaboration with Mediterranean Agronomic Institute of Zaragoza organizes the Advanced Course on: PREDICTIVE BREEDING TOOLS FOR INTENSIVE AND SUSTAINABLE PRODUCTION UNDER CLIMATE CHANGE SCENARIOS

#### Zaragoza (Spain), 17-21 January 2022

A course for the integration of conventional breeding with high-precision phenotyping, genetic modelling and crop growth simulation methods to deliver new strategies and toolkits for the selection of high-yielding varieties adapted to future climatic conditions.

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# Climate change will challenge barley production in Europe

The Figure illustrates projected changes in air temperature (°C) and precipitation (mm) for the March to August period, between the baseline period (Historical = 1981-2010) and two future time slices (2020-50 and 2051-2080). Air temperatures will rise markedly, more in the North and continental East than in the Atlantic West. Precipitation patterns also change considerably. Especially the West and Mediterranean regions become drier while northern Europe becomes wetter, and this is not only due to the reduced precipitation but also due to higher evapotranspiration rates as a result of warming. Differences shown in the figure were calculated between the baseline and future projections for a high emissions scenario (SSP5-8.5) using BIAS-adjusted data from the latest CMIP6/ISIMIP.



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In BARISTA, climate change scenario data are further processed into agroclimatic indicators (e.g. drought indices) to highlight climate risks in time and space. The data are then used as input for crop simulation models to project the impact of climate change on future barley production across Europe. Combining climate modelling with crop modelling can generate the base information required for designing region-specific adaptation and mitigation measures for future barley cultivation.



## Barley varieties differ for response to Nitrogen

Some spring barley varieties have a better nitrogen use efficiency and higher grain yield under fertilizer limitation. Crop production is challenged by drought in recent years. This calls for improved use of water and nitrogen fertilizer by crops, which besides securing grain yield, also will lead to reduced nitrogen leaching. This was tested for three modern spring barley varieties Laurikka, KWS Irina and RGT Planet, in 2019 and 2020 in several locations in Denmark. Six levels of nitrogen fertilizers ranging from 0 to 200 kg N per ha were compared.

There was no drought stress in sandy soils in 2020 due to irrigation, and Laurikka had the highest grain yield at all nitrogen levels (Figure 1). This is in agreement with a high harvest index of Laurikka. Contrary to this, in the clay soil with more water available in the deeper soil layers and potential for deeper root growth, Laurikka had the highest grain yield and grain nitrogen content in the range 40-120 kg fertilizer N per ha, where nitrogen limits yield.

It is speculated that the difference in root system development between the varieties could explain the observed differences since previous studies have shown a reduced ability for Laurikka to develop a deep root system (Svane 2019).





### Improving culm strength to contribute to lodging resistance



Figure Comparison for culm diameter, section modulus and lodging means values between the small culm parent and the large culm parent selected for 3 different crosses. The error bars represent the 95% confidence intervals. Different letters indicate significant differences (p-value= 0.05).

Despite the introduction of semi-dwarfing reduce culm length, lodging genes to resistance is still a problem in barley. Traits associated with culm morphology and composition could be manipulated to reduce the risk of lodging. BARISTA is studying the genetic architecture of culm morphology features and their relationships with plant height and lodging. Phenotypic data from a diverse panel of European barleys were collected through a newly developed imageanalysis based protocol and multienvironment association mapping analyses allowed to identify several Quantitative Trait Loci (QTLs), including loci with stable effects across different environments. Interestingly, some of these alleles associated with an increased culm diameter and/or section modulus also showed negative impact on lodging without affecting plant height. Based on these results we selected large and small culm lines carrying contrasting alleles at key markers, but similar for plant height, and crossed them to develop segregating populations. The goal is to obtain lines carrying different allelic combinations for the target QTLs to further characterize their effects and interactions

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## High-throughput field gas exchange measurements

Plant gas exchange measurements enable to monitor plants' basic traits, CO<sub>2</sub> assimilation in photosynthesis and water loss via transpiration. These traits are important to boost plant production and water use efficiency. However, getting accurate and representative gas exchange data from large field trials is tricky and labour intensive. We have recently developed a novel gas exchange device for breeding work. Instruments now produced by <u>PlantInvent Ltd</u> are capable of analysing hundreds of plants per day and enable high throughput collection of gas exchange data. Data collected during 2020 field season indicates significant variation of gas exchange traits among 20 BARISTA varieties.





In BARISTA, we use our expertise in plant gas exchange measurements to find links between in situ gas exchange traits and realized yield values in the field. These data allow to clarify the breeding potential of gas exchange traits to increase crop yield in the future climatic conditions.



# ABA mutants for drought tolerance

Several barley mutants in ABA-related genes exhibited interesting phenotypes when exposed to drought at the seedling stage. BARISTA has tested their sensitivity to drought at the pre-flowering stage to prove their usefulness in barley breeding.

The most exciting phenotype concerned the *hvera1.b* mutant carrying a mutation in the *HvERA1* gene. After severe drought stress lasting ten days hvera1.b fully recovered its transpiration rate and stomatal conductance within two days of re-watering, while the WT (cv. 'Sebastian') recovered only two third of the original performance showing a permanent damage after the severe stress.

WUE (Water Use Efficiency) was much higher in the mutant than in the WT, although the number of seed/spike and the seed weight did not differ from WT after drought stress.

*hvera1.b* demonstrated lower stomatal conductance than its WT already under optimal conditions.

Although the mechanism of ERA1 action in barley under stress is still under investigation, the results make ERA1 an interesting candidate for future research and potential application. We are introgressing the mutation into elite cultivars to test the effect of hvera1.b in different genetic background.





### Quantitative disease resistance

At a time scientists are attempting to secure yield from attacks of pathogens and pests. In BARISTA we tested 160 spring barley single (SSL) and quadruple-stack lines (QSL) containing between one and three selected quantitative resistance candidate genes, conferring field resistance against important barley pathogens like powdery mildew and leaf rust in Germany, Italy, Spain and Finland. The study will help to select and use pathogen resistance lines in future barley breeding programs. Simultaneously, we generated another set of lines by crossing one of the QSL with the elite barley cultivar Explorer using speed breeding. So far, we selected 81 SSL and QSL lines for seed multiplication and testing in multiple field trials across Europe.



#### The partners of BARISTA

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FOR SUSTAINABLE BARLEY

# BARISTA people: Johanna Maria Würtz

From Spain to Scotland on foot. The story of one student's determination to study flowering in barley



Last year, an undergraduate from University of Halle, accepted an Erasmus placement at the James Hutton Institute in Dundee, to work on the BARISTA project with Luke Ramsay. However, this was no ordinary student, let me introduce you to Johanna Maria Würtz and her Shetland pony, Hechizo. Their adventure started in Segovia, where Johanna and Hechizo set out on foot (and hoof!) to hike the 1,150-mile, across northern Spain to France's Atlantic coast, crossing the channel, arriving in East Sussex and making their way North to Dundee, completing the journey just before the UK went into a second lockdown. Despite limited work hours during lockdown, Johanna managed to set up a large, replicated, randomised glasshouse experiment to study flowering time in the backcross and SSD populations developed as part of BARISTA.

Around 588 lines from three crosses, including parents from Syria, Mexico and Iraq and the progeny, were scored for awn emergence and DNA extracted for KASP analysis using flowering related genes. Considerable variation was observed in awn emergence ranging from 33 to 110 days after sowing and interestingly the KASP markers developed for 4 major genes controlling flowering could not fully explain the variation of this complex interaction. These populations are now being multiplied by partners in Spain and Italy and we will continue to explore the research that Johanna has contributed to.

Johanna has now returned to Germany to continue her studies, and she says of her research experiences 'I'd love to come back for my PhD after two years of master's studies and further training in biological vegetable breeding, as I really embraced this beautiful piece of the world and its people, and there is so much still to do and get to know that wasn't possible because of COVID. We're going home with a heart full of amazing memories of incredible people and unique experiences!" Makes what we do all worthwhile and good to know there is an enthusiastic and excited next generation of plant scientists.

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