

## Modifying canopy architecture and photosynthesis to maximize barley biomass and yield for different end-uses

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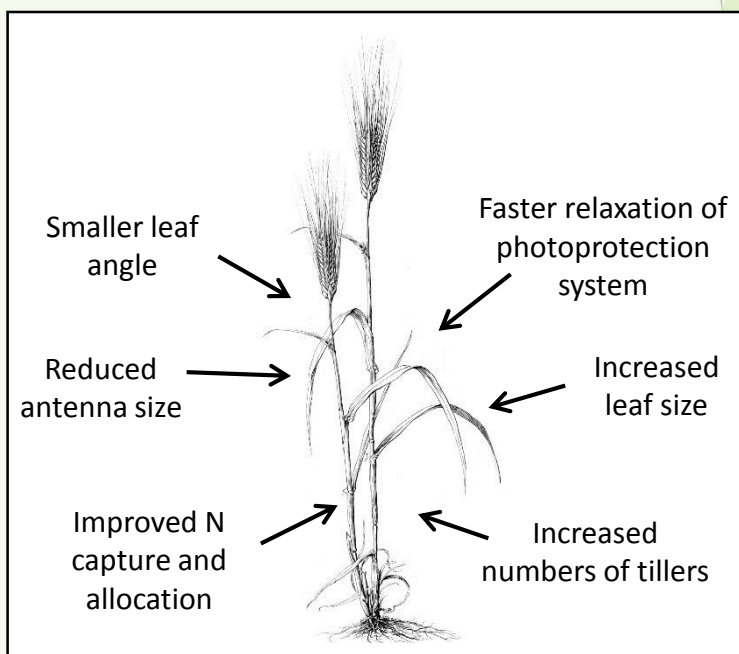
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### Welcome to the BarPLUS project!

BarPLUS is a three years project undertaken under the framework of FACCE SURPLUS ERA NET program. It is aimed at the identification of genes, alleles and barley lines needed to increase barley plant biomass, without penalty on grain yield.

BarPLUS focuses on the improvement of the number of stems, leaf size and angle, photosynthesis antenna size

and the photoprotective mechanisms, nitrogen nutrition and leaf nitrogen distribution.



## Welcome to the BarPLUS project cont...

BarPLUS takes advantage of genetic, physiological and molecular biology tools combined with in silico modeling to produce knowledge on genes and alleles and provide lines to breed a new barley ideotype.

**Allele mining** – search for allelic variants in candidate genes related to biomass production using natural genetic variation resources from the WHEALBI barley accession panel (<http://www.whealbi.eu/>).

**Forward screening** of the *HorTillus* population in search for mutants in traits related to biomass production.

**Exome sequencing** of mutants to map the loci and identify candidate genes responsible for specific phenotypes.

### Mapping-by-sequencing

isolation of selected genes for broad leaf character.

Reverse genetics – TILLING of candidate genes related to biomass production.

**Field evaluation of mutants and elite barley cultivars** – biomass production and yield estimation, physiological and morphological parameters evaluation.

**Modeling** – design and in silico evaluation of a barley ideotype characterized by high biomass production and yield.

**LCA** – life-cycle assessment of the ideotype in agro-climatic and management scenarios predicted for the year 2030.

## BarPLUS Team

The BarPLUS consortium is a multidisciplinary group of scientists providing knowledge and skills in plant physiology, plant genetics and genomics, molecular biology, bioinformatics and modeling.

**Five institutions from different countries are involved in the BarPLUS project.** The coordinator, professor Paolo Pesaresi represents University of Milano, as leader of the PhotoLab group at Department of Biosciences,



## BarPLUS Team cont...

which specializes in the study of the regulatory networks that control photosynthesis using genetics approaches combined with functional genomics, molecular biology, biochemistry and biophysics.

Partner research groups are:

- A multidisciplinary team, led by Dr. Laura Rossini from Department of Agricultural and Environmental Sciences (DiSAA) from University of Milano, Italy – provides expertise in the use of genomic tools, mutant resources and natural genetic diversity for the genetic dissection of morphological traits in barley, as well as modeling and LCA analysis,
- A group led by Dr. Alessandro Tondelli from Genomics Research Centre of Fiorenzuola d'Arda from Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria – CREA, Italy - who specializes in the molecular biology, bioinformatics, genetic and genomics of barley and wheat with the emphasis on GWAS studies,
- A research team led by Dr. Roxana Savin from Crop Physiology Lab of the University of Lleida, Spain – which provide the expertise in the applications of crop physiological knowledge to breeding and agronomy,
- A group led by Prof. Michael Lenhard from the Institute for Biochemistry and Biology, University of Potsdam, Germany - with extensive experience of the phenotypic and genetic characterization of leaf-size mutants,
- A group led by Dr. Agnieszka Janiak from the Department of Genetics, University of Silesia in Katowice, Poland - experienced in genomics, NGS techniques in cereals and in barley genetics, with special emphasis on the use of mutagenesis for induction and evaluation of genetic diversity in cereals, provider of "HorTILLUS" TILLING population, a resource of induced genetic diversity in barley.





## Screening *HorTILLUS* population for biomass-related traits

During several laborious days BarPLUS Team have screened *HorTILLUS* – a population of chemically mutagenized barley plants derived from 'Sebastian' variety, which serves as a resource for induced genetic variation in barley

In the spring and early summer of 2016, members of the BarPLUS consortium have gathered together in Poland to evaluate the barley mutant population developed at the Department of Genetics, University of Silesia in Katowice, for the traits related to biomass

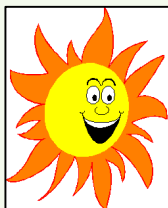
production. At that time, around 9 500 plants were screened for leaf size, number of tillers, leaf angle and photosynthesis efficiency. In total 37 lines with interesting traits have been found and will be the subject of further analysis.



leaf angle 1



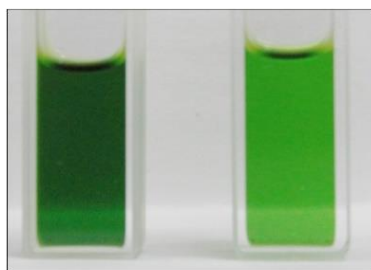
Sebastian



## Happy under the sun!

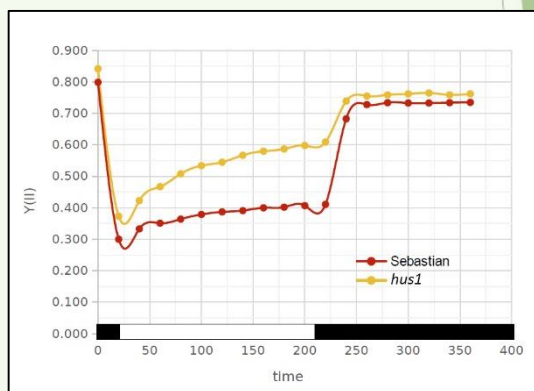
The screening of the *HorTILLUS* population resulted in the identification of an interesting mutant with more efficient photosynthesis rate compared to Sebastian parent variety

The mutant was named *Happy Under the Sun 1 (hus1)*, and is characterized by paler leaves, related to the lower content of total chlorophyll and different chlorophyll a to b ratio in comparison to the parent variety.



	Sebastian	<i>hus1</i>
Chl µg/mg	1,45	1,16
Chl a/b	2,86	3,50

The mutant produces wider leaves than Sebastian variety and has a very peculiar thylakoid protein composition typical of a mutant adapted to environmental stress conditions.



The mutant uses higher amount of energy for the photochemistry in photosystem II and has diminished photoprotection comparing to its parent variety. It also shows differences in the composition of thylakoid proteins and their degradation and turnover rate.

The mutant will be subjected to exome capture sequencing and the efforts to discover the underlying genetic mechanism of the phenotype are now underway.



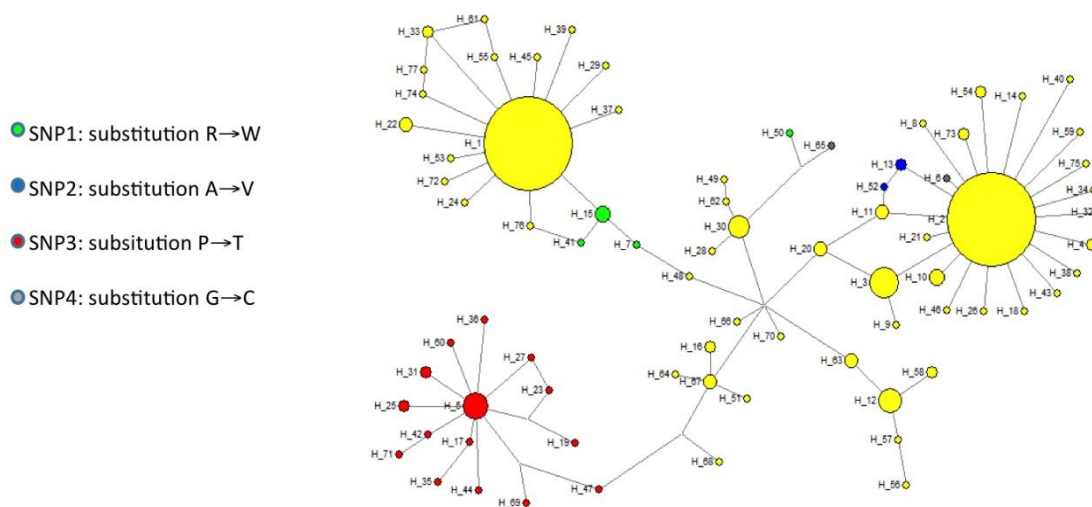


## The importance of natural variation and data mining

An important part of the BarPLUS project is to use the wealth of barley germplasm resources to evaluate the significance of natural allelic variation of selected candidate genes in the production of biomass.

A total of 70 candidate genes were selected based on previous knowledge of their involvement in the regulation of traits related to biomass production. Their sequences are now being used for the identification of natural sequence variation by using WHEALBI exome capture data for 403 barley accessions kindly provided to BarPLUS by the WHEALBI consortium.

This resource along with careful curation of gene models and use of tools for predicting the impact of aminoacid sequence variants provide a unique opportunity to study natural genetic diversity in barley and identify new alleles of potential interest. These will be characterized at the phenotypic level to evaluate their effect on biomass-related traits.



Gene haplotype networks such as the one depicted here can help to understand the origin of genetic variants of interest

## BarPLUS consortium meetings and exchanges

BarPLUS partners exchange ideas, update on research progress and plan new activities through regular meetings and frequent contacts via internet conferences.

The kick-off meeting took place at the Genomics Research Centre of Fiorenzuola d'Arda (CREA, Italy) and it was a great opportunity to know each other and set up the working plan for material evaluation and further visits in partner institutions. The collaboration and mutual work exchange initiated in Fiorenzuola d'Arda have borne the first fruits during the second meeting at the University of Potsdam (Germany), where the first project's results were discussed and plans the next year were set up.

Members of BarPLUS consortium will meet again in the spring 2018 in Spain at the University in Lleida.



University of Lleida, Spain

## BarPLUS consortium:



<http://www.unimi.it/>



<http://www.crea.gov.it/>



<http://www.udl.cat/ca/en/>



<http://www.uni-potsdam.de>



<http://www.us.edu.pl/>



## Partner project:



<http://www.whealbi.eu/>