

BARLEY CAP Coordinated Agricultural Project CSREES

Barley CAP Update

Joel Ransom
Extension Agronomist – Cereal Crops
North Dakota State University Extension

BARLEY CAP

What is BarleyCAP?

Coordinated Agricultural Project for Barley
This USDA/CSREES-funded project involves government, public and private laboratories, links laboratory and field research with education and outreach in an effort to use modern tools of genomics to facilitate classical plant breeding efforts to develop superior barley varieties.

Lead PI/Institution:
Gary Maebbauer, University of Minnesota

UNIVERSITY OF CALIFORNIA: Dale Brinkman, Tracy Blythe, Robert C. Anderson, Robert C. Anderson, Robert C. Anderson
 COLORADO: Robert C. Anderson, Robert C. Anderson
 IDAHO: Robert C. Anderson, Robert C. Anderson
 MINNAPOLIS: Gary Maebbauer, Gary Maebbauer
 MONTANA: Gary Maebbauer, Gary Maebbauer
 NORTH DAKOTA: Gary Maebbauer, Gary Maebbauer
 SOUTH DAKOTA: Gary Maebbauer, Gary Maebbauer
 UTAH: Gary Maebbauer, Gary Maebbauer
 WISCONSIN: Gary Maebbauer, Gary Maebbauer

DNA

- Deoxyribonucleic acid – a long polymer that consists of 4 different building blocks (called nucleotides) that contains the genetic instructions used in the development and functioning of all known living organisms.

Barley Breeding

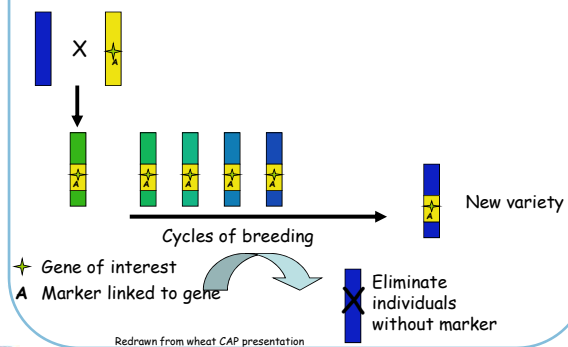
- Barley breeding is the art and science of improving the characteristics of the barley plant for the benefit humankind (adapted from Poelhman and Sleper, Breeding Field Crops, 4th edition, 1995).
- Traditionally required crossing plants with observable (color, disease resistance, etc.) or measureable characteristics (height, yield, protein content, etc.) and selecting from offspring for types meeting the criteria of the breeder
- Requires very large numbers of plants (progeny) and a bit of luck to make progress for certain traits

Marker Assisted Selection

- Marker assisted selection (MAS) is an indirect selection process where a trait of interest is selected not based on the outward appearance of the trait itself but on a genetic marker (keyword) near the trait (gene) on the DNA.
- If we think of DNA as a road, and sign posts as markers on the road, MAS allows the selection of desirable segments of the road based on known signposts without having to actually drive the segment to determine if it is desirable.
 - This is extremely valuable if the trait is hard to observe under normal field conditions (i.e. scab, UG99 stem rust, etc.)
 - And when crossing a trait into an otherwise very desirable variety.



Marker Assisted Selection



Advantages MAS

- Non-destructive:
 - Useful in early generations.
 - Ability select for recessive or masked traits.
- Circumvent costly screening methods.
- Fast (once you have reliable markers).
 - Marker development is costly and benefits from a “team” approach.



Barley CAP activities

- Identify markers that can effectively be used by barley breeders
- Develop a shared genotype and phenotype database
- Develop new methods of identifying markers
- Centralized genotyping equipment




High Density Genetic Maps

We will develop a detailed genetic "road map" of the barley genome using SNPs, or Single Nucleotide Polymorphisms. SNPs are single "letter" changes in the genetic code of the DNA.

DWB-D	GGATACTTGGAGTGATAAA
DWB-R	GGATACTTGGAGTGATAAA
GP	GGATACTTGGAGTGATAAA


Polymorphism



Current genetic maps have hundreds of markers, but many are difficult to use for MAS. The new barley SNP map will add 3,000 new markers that will be useful for MAS and will cover the entire genome.


Centralized Marker and Trait Database

Barley CAP will gather information, e.g., on yield, malt and food quality, disease resistance, SNP markers, from each breeding program, and put that information in a central database – essentially consolidating many breeding programs into one. This information will be used to map locations of genes that control these important traits. All genotype and phenotype data from the Barley CAP will be web accessible in 'The Hordeum Toolbox' database.




Trait Mapping Software

Traditional Mapping Approach



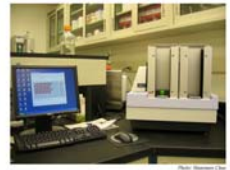
Barley CAP Approach



Barley CAP will develop new genetic mapping software, called QTL Miner, to identify SNP markers linked to genes controlling important traits using large trait and genotype datasets. Traditional gene mapping has utilized experimental populations that generally consist of the progenies from two parents. Barley CAP will use the actual breeding lines from breeding programs to conduct trait mapping.

High-Throughput Genotyping

USDA created four Regional Genotyping Centers to service small grain breeding programs. These centralized facilities vastly increase the efficiency of generating marker data and eliminate the need for individual researchers to equip their own labs to carry out genotyping.



How will this help the barley breeders (and ultimately you)?

- Cooperative, multistate project allows for:
 - Access to technology that otherwise would be too expensive
 - Sharing of knowledge and data on single platform.
- Ability to improve the efficiency in the breeding program as selection intensities can be increased.
- Faster gain from selection, especially for difficult traits like malting quality and disease resistances.



Will this replace the need for traditional breeding?

- These are tools that can improve efficiency, but will not replace the need for crosses and yield plots
- Potentially could reduce the number of plots used for selecting for certain traits
- Increases the success of selecting plants with traits that are not expressed in all environments

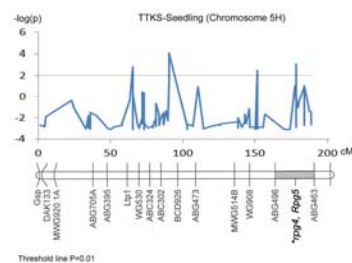


What are recent achievements?

- 1,820 lines from 10 US barley breeding programs have been genotyped
 - Allowing identification of potential markers for:
 - Malting quality
 - Fusarium head blight resistance
 - Winter hardiness in winter types
- Increased use of MAS by participating breeders
 - Less than 1/2 the breeders use MAS extensively currently
- CAP provides a format to address constraints to more widespread use of MAS
 - Cost of supplies, equipment and personnel
 - Lack of reliable markers
- Identification of location of stem rust resistant genes



Location of important genes for resistance to stem rust was identified in 2008



Conclusions

- The barley CAP is an important project fostering integration among breeding programs and expanding resources of molecular based techniques to assist in the development of new varieties of barley
- Good progress to date has been achieved in improving markers and in assisting breeders to increase their use of marker assisted selection in their breeding programs

