

**P0813****ClimBar: An Integrated Approach to Evaluate and Utilize Genetic Diversity**

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European agriculture anticipates an unprecedented combination of stress factors, production threats and quality needs due to climate change. Various regions of Europe will be affected differently. Barley & wheat domestication, and landrace formation in Europe, were under very different climates than those emerging now. Alleles needed for sustainable, resilient, quality yields in a changed climate are likely not combined in current haplotypes of elite barley cultivars. These alleles are likely found in diverse landraces and wild relatives in the Mediterranean basin and Fertile Crescent -- areas that prefigure expected climate change. New precision, high-throughput phenotyping tools are essential to find trait-allele associations needed for future-climate breeding. Combining genetics, genomics, modelling, molecular biology, morphology, and physiology, ClimBar takes an interdisciplinary approach to develop a strategy for breeding an increased resilience to climate change in barley. ClimBar, a new project under the framework of FACCE ERA-NET Plus Joint Programming Initiative on Climate Smart Agriculture, will identify genome regions, genes, and alleles conferring the traits needed to breed resilient barley varieties adapted to the climatic conditions predicted for 2070 in different European environments. Adapted, resilient germplasm created using ClimBar data, tools and models will provide food-chain security, economic stability and environmental sustainability.

Website: [http://plen.ku.dk/english/research/plant\\_soil/breeding/quality/climbar/](http://plen.ku.dk/english/research/plant_soil/breeding/quality/climbar/)

## Handouts

[ClimBar\\_poster\\_10\\_2015.pdf](#) (775.6 kB)

Back to: [Genome Mapping, Tagging & Characterization: Wheat, Barley, Oat, and related](#)

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**Meeting Information**

**When:**

January 08 - 13, 2016

**Where:**

San Diego, CA