Single CCT domain proteins play an essential role in chloroplast development and cause albostrians-type leaf variegation in barley

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Albostrians is a long known leaf-variegation mutant in barley that shows a non-perfect penetrance of the variegation phenotype. We isolated the underlying gene by map-based cloning and mutant analysis. A single CCT domain protein was identified as the causal gene and depending of the position of the mutation the phenotype became more severe and turned into full albino, indicating that the original mutant protein must have retained some residual functionality. We performed a phylogenetic analysis and observed that the gene is present in all angiosperms and is always retained as a paralogous pair of genes per diploid genome. We performed mutational analysis of the paralog of albostrians and could show that the two genes are not redundant in their function but both genes have a fundamental role in early chloroplast development or maturation. Studies of the respective genes in Arabidopsis suggest only partly conserved functions in Arabidopsis and barley raising the question about the level of conservation of basic regulatory processes in chloroplast development and maturation between dicot and monocot species.

Barley diversity now and 6000 years ago: archaeogenetics and genebank genomics

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The cereal grass barley was domesticated about 10,000 years before the present in the Fertile Crescent and became a founder crop of Neolithic agriculture. After domestication, during a process of widespread range extension, barley adapted to a broad spectrum of agricultural environments. Today, barley remains an important crop that is used around the world as animal fodder and raw material for the malting industry. In this presentation, I report on the genetic relationship of 6000-year old barley grains found in a cave in the Judean Desert to extant populations. DNA were extracted from archeological remains and used for high-throughput sequencing. Comparison to whole-exome sequence data from a diversity panel of present-day barley genebanks accessions showed the close affinity of ancient samples to extant landraces from the Southern Levant and Egypt. Our findings suggest that barley landraces grown in present-day Israel have not experienced major lineage turnover over the past six millennia, although there is evidence for gene flow between cultivated and sympatric wild populations. We demonstrate the usefulness of ancient genomes from archaeobotanical remains together with sequence data from genebank collections for domestication research.

Wheat pre-breeding: germplasm into practice

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In 2007, the National Institute of Agricultural Botany (NIAB) embarked on a programme of wheat pre-breeding to deliver systematically developed and validated resources for wheat improvement. This translational programme aimed to bridge the gap between fundamental discoveries in model plant species and commercial breeding. The material generated encompasses sets of defined near-isogenic lines, advanced lines from CIMMYT synthetics, novel synthetics plus over 10,000 winter and spring derivatives. We have also created two MAGIC populations: a 1,000-line population sampling eight elite varieties and a 600-line population sampling variation from sixteen varieties released between 1930 and 2010. We have further characterised two large pan-European association mapping panels, encompassing over 1,000 winter wheat varieties.

This presentation will describe the breadth of wheat pre-breeding activities at NIAB with emphasis on the recent downstream uses of pre-breeding resources for the dissection of yield and yield components, the prediction of flowering time and the optimisation of nitrogen use.