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FA

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Tritigen: Triticeae genomics for the advancement of essential European crops

tritigen.ari.gov.cy/

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Participating countries: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GR, HR, HU, IE, IL, IS, IT, LT, LV, NL, NO, PL, PT, RS, SE, SK, TR, UK + GE, RU, UA

Objectives:

- Develop the tool box needed to identify and exploit qualitative and QTL alleles for improving wheat, barley and rye.
- Resistance against fungal diseases and abiotic stresses; quality, yield stability and sustainability under low input
- Database of existing and planned Triticeae genomics research, platforms and applications in Europe
- Development of new tools and platforms for “omic” and bioinformatic analyses, portal for those recommended
- Dissemination of new and efficient methods for linkage mapping and molecular breeding
- Collaborative development and dissemination of comparative genomics methods
- Coordinated development and collaborative application of high-resolution mapping populations in the Triticeae; database of existing and planned populations.
- Coordinated transfer of know-how and tools to manage, maintain, and exploit natural genetic diversity
- Coordination of high-throughput phenotyping facilities for association genetics
- Development of a framework for Triticeae physical mapping.

Working Group 1. Tools for assessing, harvesting and applying genetic diversity (DivGen)

Karl Schmid (Chair) and Hikmet Budak (Vice-Chair)

Development and deployment of more rapid and robust, less expensive, and denser molecular markers in order to assess germplasm diversity and haplotype, phylogeographic patterns of diversity, marker-assisted selection, association genetics and genome evolution.

Working Group 2. Accessing the physical genome for sustainability and quality (PhysGen)

Pierre Sourdille (Chair) and Nils Stein (Vice-Chair)

Development of contig-based physical maps for barley and hexaploid wheat genomes that will serve as the basic resources for high-throughput gene isolation and large-scale sequencing. The overall synteny and colinearity of the Triticeae genomes and the sequenced genomes of rice and *Brachypodium* will be exploited.

Working Group 2a. Bioinformatics

Thomas Wicker(Chair) and David Marshall (Vice-Chair)

Genomic analyses will generate huge amounts of data of different kinds that will need to be integrated with phenotype and pedigree information. This represents a major challenge within TritiGen. The TritiGen Action will seek to bring them together in new collaborations so that data can be mined using common platforms or interfaces.

Working Group 3. Implementation of genomics approaches for understanding cereal traits (TraitGen)

Nils Rostoks (Chair) and Hilde-Gunn Opsahl-Sorteberg (Vice-Chair)

Technologies to identify differentially expressed genes and to analyze gene expression levels on a genomic scale and to analyze the proteome will be used to better understand traits in the Triticeae that control the sustainability, yield, quality, and value of the crop.

Working Group 4. Functional genomics for testing and validation of candidate genes (FuncGen)

Søren Rasmussen (Chair) and Patrizia Galeffi (Vice-Chair)

In order to assess gene function, RNAi and VIG strategies, transient and stable transformation, TILLING populations for reverse genetics, and SNP association mapping will be used. Advances in Triticeae transformation by partners in TritiGen is also making possible insertional mutagenesis strategies applying T-DNA and transposons.

Recent Achievements:

- 1536 SNP markers applied in association mapping analyses for key barley traits
- New information on effects of domestication on agronomically important candidate genes
- Development of a complete physical map for chromosome 3B of wheat
- Large scale sequencing of Triticeae BACs
- Exploitation of synteny for development of COS markers and fine mapping of genes
- Application of transcriptional profiling to identify genes responding to drought and disease in wheat and barley

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