

## Poster & Session Search



**Date:** Sunday, January 13  
8:00 am - 10:10 am

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### QTL Cloning #1573

**Location:** Town and Country

**Moderators/Organizers:** Roberto Tuberosa *DipSA - University of Bologna*, Roberto Tuberosa *DipSA - University of Bologna*

**8:00 AM - 8:20 AM**

**Presenters:** Benjamin Kilian *IPK Gatersleben*

#### W653 - Exploring Environmental Adaptation In Cultivated Barley Using a Novel Divergent Selection Strategy

As early farming spread from the Fertile Crescent in the Near East around 10,000 years before the present, domesticated crops encountered considerable ecological and environmental change. Spring-sown crops that flowered without the need for an extended period of cold to promote flowering and day length-insensitive crops able to exploit the longer, cooler days of higher latitudes emerged and became established. To investigate the genetic consequences of adaptation to these new environments, we identified signatures of divergent selection in the highly differentiated modern-day spring and winter barleys. In one genetically divergent region, we identify a natural variant of the barley homolog of Antirrhinum CENTRORADIALIS2 (HvCEN) as a contributor to successful environmental adaptation. The distribution of HvCEN alleles in a large collection of wild and landrace accessions indicates that this involved selection and enrichment of preexisting genetic variants rather than the acquisition of mutations after domestication.

**8:20 AM - 8:40 AM**

**Presenters:** Christian Bachem *Wageningen-UR*, Bjorn Kloosterman *Keygene NV*, Bjorn Kloosterman *Wageningen-UR*, José Antonio Abelenda *Centro Nacional de Biotecnología-CSIC*, Salomé Prat *Centro Nacional de Biotecnología-CSIC*, María-del-Mar Carretero-Gomez *Wageningen-UR*, Richard Visser *Wageningen UR, Plant Breeding*

#### W654 - Cloning and Analysis Of The Gene Responsible For The Plant Maturity QTL In Potato: Molecular Pathways Of Potato Domestication

Potato (*Solanum tuberosum* L.) originates from the Andes and most wild genotypes are short-day dependent for tuber-formation. In diploid research material as well as in tetraploid cultivars the presence of a major-effect QTL for Plant Maturity and Earliness of tuber formation has been mapped on Chromosome 5 close to the R1 resistance gene cluster. Using map based cloning together with deep bi-allelic sequence data of chromosome 5, we have now identified a gene coding for a central regulator underlying this major-effect QTL. We show that this gene belongs to the family of DOF transcription factors and regulates tuberisation and plant life-cycle length, by acting as a mediator between the circadian clock and the mobile tuberisation signal. We also show that naturally occurring allelic variants of this protein, evade post-translational light regulation. We propose that this adaptation has allowed the cultivation of potato outside the centre of origin, under long-day conditions of spring and summer that prevail in northern temperate latitudes.

**8:40 AM - 9:00 AM**

**Presenters:** Xuehui Huang *National Center for Gene Research, SIBS, CAS*, Bin Han *National Center for Gene Research, SIBS, CAS*

#### W655 - Sequencing-Based GWAS For Cloning QTLs In Wild and Cultivated Rice

Cultivated rice evolved from its wild progenitor under natural and human selection. Identifying the genetic basis of the diverse varieties will provide important insights for breeding elite varieties for sustainable agriculture. We sequenced 950 world-wide rice varieties including *Oryza sativa indica* and *japonica* subspecies, and constructed a high-density haplotype map of rice genome by using a data imputation method. We performed genome-wide association studies (GWAS) for cloning QTLs underlie

multiple agronomic traits. The peak signals at six loci tied closely to the previously identified genes. To characterize various gene alleles and complex genetic variation, we developed an analytical framework for haplotype-based *de novo* assembly of the low-coverage sequencing data in rice. Candidate genes were identified for some associated loci through detailed annotation, expression profiling and identification of putative causal mutations. Moreover, we sequenced and analyzed the genomes of 446 geographically diverse accessions of the wild rice species *Oryza rufipogon*, the immediate ancestral progenitor of cultivated rice. Compared with cultivated rice, its wild progenitor *O. rufipogon* has a higher genetic diversity, a weaker population differentiation and a more rapid LD decay rate, suggesting that the wild rice collection would be an ideal system for GWAS. We phenotyped each accession of the *O. rufipogon* population for several traits and perform GWAS in the wild population. The details will be presented.

#### **9:00 AM - 9:20 AM**

**Presenters:** Xiaoguang Yu *Fondazione Edmund Mach, San Michele all'Adige (TN), Italy*, Francesco Emanuelli *Fondazione Edmund Mach, San Michele all'Adige (TN), Italy*, Silvia Lorenzi *Fondazione Edmund Mach, San Michele all'Adige (TN), Italy*, Paula Moreno-Sanz *Fondazione Edmund Mach, San Michele all'Adige (TN), Italy*, Laura Costantini *Fondazione Edmund Mach, San Michele all'Adige (TN), Italy*, Sergio Moser *Fondazione Edmund Mach, San Michele all'Adige (TN), Italy*, Juri Battilana *Fondazione Edmund Mach, San Michele all'Adige (TN), Italy*, Roberto Larcher *Fondazione Edmund Mach, San Michele all'Adige (TN), Italy*, M. Stella Grandi *Fondazione Edmund Mach*

#### **W656 - Identification Of Causal Genes Of mQTLs Associated To Grape and Wine Flavor**

Secondary metabolites produced in grapevine berries play an essential role in high-quality wines and also contribute to the quality of table grapes. Some of the most prevalent wine odor constituents are monoterpenoids which biosynthesis via the plastidial methyl-erythritol-phosphate (MEP) pathway has been demonstrated in grapevine.

Based on a double pseudo-testcross mapping strategy, we detected a major QTL on LG 5 for linalool, nerol and geraniol content in grapevine berries at ripening time, and also an additional QTL for linalool on LG 10. Further testing indicated that gain-of-function mutations in the structural gene of the MEP pathway *1-deoxy-D-xylulose-5-phosphate synthase (VvDXS1)* - colocalized with the mQTL on chromosome 5 - are the major determinants for terpenoid accumulation in Muscat grape varieties and have direct effects on the enzymatic or regulatory properties of the DXS protein. Similarly, association of genetic variants with the content of several volatile aromatic compounds (VOC) is being tested for candidate genes in the mQTL interval on chromosome 10.

#### **9:20 AM - 9:40 AM**

**Presenters:** Yusaku Uga *National Institute of Agrobiological Sciences*

#### **W657 - Molecular Cloning Of Dro1, a Rice Quantitative Trait Locus That Controls Deep Rooting**

Lowland rice (*Oryza sativa* L.), which is generally grown under flooded conditions, is susceptible to drought stress owing to its shallow root distribution and limited capacity to extract water from deep soil layers. Therefore, introducing deep rooting characteristics into lowland rice cultivars might be one way to improve their drought avoidance. However, the gene(s) responsible for deep rooting has not been identified in plants and it is still unclear whether it would affect drought avoidance. In this study, we cloned *Deeper rooting 1 (Dro1)*, a rice quantitative trait locus controlling deep rooting, using mapping populations derived from a cross between IR64, a lowland rice with shallow roots, and Kinandang Patong, an upland rice with deep roots. To elucidate the role of *Dro1* at the whole-plant level in a natural environment, we developed a near-isogenic line for *Dro1* (Dro1-NIL) in the IR64 genetic background. The maximum root depth of IR64 and Dro1-NIL in upland conditions was ca. 20 and 45 cm, respectively. To clarify whether *Dro1* improves drought avoidance, both lines were exposed to drought stress under upland conditions. The yield of Dro1-NIL was significantly higher than that of IR64, demonstrating that *Dro1* contributes to drought avoidance in rice and that it can improve the productivity of rice under soil drought stress.

#### **9:40 AM - 10:00 AM**

**Presenters:** Tanja Gerjets *INRA GDEC*, Sonia Vautrin *INRA-CNRGV*, Pierre Barret *INRA GDEC*, Walid Alfares *University of Aleppo*, Pierre Sourdille *INRA GDEC*, Frederic Choulet *INRA GDEC*, François Balfourier *INRA GDEC*, Helene Berges *INRA Toulouse*, Catherine Feuillet *INRA GDEC*

#### **W658 - Map-Based Cloning Of SKr, a Major QTL Involved In Crossability Of Wheat With Rye**

Although wheat can be crossed with a wide range of related species, most adapted bread wheat varieties are non-crossable because of the failure of pollen to fertilize the ovary, thereby reducing the possibilities to reintroduce genetic diversity in the elite wheat gene pool through intra- and interspecific crosses. Only ancient wheat and landraces are crossable, in particular those originating from the Asian gene pool. Inhibition to crossability between wheat (*Triticum aestivum* L.) and related species such as rye (*Secale cereale* L.) is genetically controlled and dominant. A number of QTL have been identified to date, including Kr1 on chromosome 5BL and

SKr, a strong QTL mapped at the distal end of chromosome 5BS. Fine mapping of SKr was initiated using a HIF population of 223 individuals derived from a cross between the French variety Courtot (non crossable with rye) and the variety Chinese Spring (crossable). Using shotgun sequences from Chinese Spring BAC clones identified by chromosome walking as well as the homologous relationships with rice and barley, 9 markers and 5 candidate genes were identified in a genetic interval of 0.6 cM spanning SKr. SSR markers cosegregating with SKr were developed to support primary triticale breeding programs. Finally, more than 200 lines from various gene pools (European, Asian) have been phenotyped and genotyped to perform association studies with the candidate genes and for analyzing the spatio-temporal origin of crossability. An update of the project will be presented.