P3.28

Discovery and detection of ISBP allelic variation in bread and durum wheat

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The routine use of molecular markers in wheat breeding programmes has long been hampered by the difficulties in achieving cheap, polymorphic and locus-specific markers. Recently, insertion site-based polymorphism (ISBP) markers have been evidenced as very specific and polymorphic tools for genomics and genetic studies in hexaploid wheat, capable of homogeneously saturating the wheat genome.
While their suitability for high-throughput detection methods has been recently demonstrated, the possibility of the high-resolution-melting (HRM) analysis for their detection has not been previously explored. In this work, we set up a medium-throughput and cost effective methodology with potential for wheat germplasm analysis and marker-assisted selection that can be carried out in-house by the breeders. The developed markers derive from the wheat 4A chromosome sequence survey developed within the framework of the International Wheat Genome Sequencing Consortium (IWGSC).

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Poster session – Friday 5th July 2013

P3.29

QTL discovery in barley landraces through genome-wide association mapping

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A core collection of 159 Spanish barley landraces has been extensively phenotyped over the years, constituting an excellent resource for new QTL and gene discovery. Accessions from this collection have shown some advantageous traits such as high grain yield under low productivity conditions, surpassing modern cultivars, and outstanding resistances to scald and powdery mildew.
Appropriate accessions have been introduced in biparental crosses and several projects to find out the genetic control of target traits are underway. To further explore the genetic diversity of this collection, an association mapping approach is being followed, taking advantage of the existence of SNP platforms that provide enough marker coverage for the level of linkage disequilibrium detected in the collection.
Some duplicates were found and removed from the analysis. We have performed association mapping of several sets of phenotypic data (agronomic, physiological, morphological, disease resistance) with an iSelect panel of close to 8,000 SNPs, using a mixed model analysis with a kinship matrix calculated using 500 SNPs evenly distributed over the genome, and a false discovery rate of 0.20. A few high-confidence QTLs were found for several traits, some in accordance with previously known genes or QTLs detected in biparental populations.

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P3.30

Waking up too early: Combating pre-harvest sprouting and pre-maturity amylase in wheat

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The occurrence of pre-harvest sprouting (PHS) and pre-maturity amylase (PMA) in wheat grains constitutes a major challenge to wheat production resulting in yield and economic losses. PHS is the precocious germination of grains before harvest with an accompanying burst in α-amylase production. PMA however is the late production of α-amylase in grains without any visible sign of germination. Both traits increase amylase activity within grains making such grains unsuitable for bread-making purposes. Tolerance to PHS and PMA is multi-genic and controlled by quantitative trait loci (QTLs). In this study, we selected six stable QTL that affect PHS and PMA for characterization. Our results show that most of the QTLs affect the dynamics of dormancy loss in wheat grains as measured by the germination index test. However, the timing of these QTL effects was different. While some of the QTLs showed effects at early stages of grain maturation (20–40% grain moisture content), others only showed effects at late stages of grain maturation (10% grain moisture content) and after-ripening. Furthermore, it was observed that temperature influences the expression of the QTL effects. For instance, some of the QTL effects were found to be greater when grains were germinated at 22°C than at 17°C. In summary, we have validated and demonstrated the potential of six QTL for PHS and PMA resistance. We will use this understanding of the effects to help fine map these QTLs and to deploy them in rational combinations to help develop PHS and PMA tolerant varieties.

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Initial study on activity of enzymes, participating in nitrogen and energy metabolism in *Brachypodium distachyon*

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Glutamate plays central role in nitrogen metabolism. The principal carrier of glutamate catabolism is NAD-dependent glutamate dehydrogenase. For cereals the activity of enzymes of nitrogen and energy metabolism are important indicators. The main task of the experiment was the preliminary study on those in leaves of 14-days old seedlings of *Brachypodium distachyon*.
Cell-free extracts were subjected to gel-chromatography on column with Sephadex G 50. Malate, NAD, glutamate served as substrates for the MDH-GOAT assay. Malate, NAD served as substrates for the MDH assay. 2-oxoglutarate, NADH, ammonium sulphate served as substrates for GDH assay. The optical measurement was carried out by spectrophotometer Ultrospec-110 pro. Determination of total protein content was carried out by microbiurete Bailey method using Benedict's reagent under the wave length of 330 nm. Activity (μM coenzyme per ml) of nitrogen metabolism and energy metabolism enzymes, GDH, MDH-GOAT and MDH, correspondingly, was determined at 340 nm.
The results of study have shown that the activity of MDH-GOAT in leaves of seedlings was equal to 36.29 μM/ml, while GDH – 4.03 μM/ml. MDH activity – comprised 209.68 μM/ml. It is generally known, that MDH-GOAT is responsible for the nitrogen metabolism in plants and plays important role in detoxification of the products of protein degradation, taking place during the processes of abiotic and biotic stress, i.e. salinity, drought, etc. Thus, plants with high MGH-GOAT activity and low GDH activity are regarded as more resistant to adverse environmental factors, what will be shown by further studies.

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