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Proteomics evidence of quality stresses caused by changing environment

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Several reviews have already been proposed showing that plant proteomics is a useful approach to understand the effects of environmental factors on gene expression. Heat stress during the accumulation of grain components is known to have a strong influence on wheat grain physiology, leading to reduced grain size and increased protein concentration and modification of the rheological properties. To illustrate the usefulness of the proteomics approach, analysis of the endosperm responses to heat stress was carried out in three experiments with three different bread wheat cultivars. Experiment 1, where day /night temperature throughout grain formation was 34°C/10°C for stressed (S) and 18°C/10°C for control (C), showed that the kinetics of accumulation of both total proteins and albumins globulins (AG) were significantly different between S and C. At physiological maturity, 60 proteins were up-regulated and 20 were down-regulated in S compared with C samples. In experiment 2, after the 4 days of heat shock on cv Récital (exposed to 4-hour periods at mid-day at 38°C for four consecutive days), 109 AG spots had changed: including 29 new spots, 37 up- and 43 down- regulated spots. At physiological maturity (i.e: 25 days after the end of the heat shock treatment) 21 AG still had significantly different % spot volume compared with control grains. In the experiment 3, crops were subjected to two day/night thermal regimes from 4-5 daa to grain maturity: 23°C/11°C (C) and 28°C/15°C (T). Individual storage proteins did not display identical kinetics in C and T. Two omega-gliadins were 200% over-expressed, whereas one gamma-gliadin and one LMW-GS were 50% under-expressed at three consecutive sampling stages in 28°C/15°C compared with 23°C/11°C. All together the three experiments indicate that regulation of the amount of glutenins and gliadins was not related to specific HSPs or PDIs. Many other enzymes associated to proteins accumulation and starch synthesis were identified. Some possible influences of heat stress responsive proteins on the accumulation of grain components, or on dough properties and quality characteristics will be presented.

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Characterization of polyphenol oxidase and phytoene synthase genes and development of their functional markers in common wheat

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Characterization of polyphenol oxidase (PPO) and phytoene synthase (Psy) genes and development of their functional markers are of importance for marker-assisted selection in wheat breeding. In the present study, complete genomic DNA sequences of two PPO genes, one each located on chromosomes 2A and 2D, as well as one Psy gene on chromosome 7A, and their allelic variants were characterized by means of in silico cloning and experimental validation. Both of the PPO genes on chromosomes 2A and 2D contain an ORF of 1731 bp, encoding a PPO precursor peptide of 577 amino acids with a predicted molecular mass of ~64 kD. An STS marker *PPO18* was developed based on the 191-bp difference between two allelic variants detected in the first intron of PPO gene on chromosome 2A, amplifying a 685-bp and 876-bp fragments in the cultivars with high and low PPO activity. Two complementary dominant STS markers, *PPO16* and *PPO29*, were developed based on the PPO gene haplotypes located on chromosome 2D, generating a 713-bp fragment in cultivars with lower PPO

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activity and a 490-bp fragment in those with higher PPO activity, respectively. The cloned *Psy* gene comprises six exons and five introns, 4175 bp in total, and an ORF of 1284 bp. A co-dominant marker, *YP7A*, was developed based on polymorphisms of two haplotypes of the gene, yielding 194-bp and 231-bp fragments in the cultivars with high and low yellow pigment content, respectively.

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International collaboration for unifying *Glu-3* nomenclature system in common wheats

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Low molecular weight glutenin subunit (LMW-GS) composition in common wheats is one of the critical determinants for gluten properties. However, the nomenclature of *Glu-3* encoding LMW-GSs was not consistent among laboratories, due to the complexity of LMW-GSs and different separation methods used by researchers. It is very important to unify the nomenclature system for sharing information about the effects of individual LMW-GS on gluten properties. Therefore, we decided and shared 25 cultivars as standards representing each *Glu-A3*, *Glu-B3* and *Glu-D3* alleles and additional local 88 cultivars from Argentina, China, France, Japan and Mexico. Using SDS-PAGE and 2D analyses, we found differences of the nomenclature particularly for *Glu-A3* and *Glu-B3* among laboratories. We also found new *Glu-3* alleles among local cultivars. The possibility to establish standard methods to identify *Glu-3* alleles will be discussed.

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Genetic improvement of Chinese noodle quality by combination of conventional testing and molecular markers

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The integration of molecular markers with conventional breeding program is crucial for improving breeding efficiency and for the successful application of marker-assisted selection (MAS) in practical breeding program. Noodle is a major wheat product consumed in China and improvement of noodle quality has become an important breeding objective. A standardized laboratory testing procedure and a new scoring system were developed for noodle quality evaluation. Major traits affecting noodle quality were identified, i.e., gluten strength, starch viscosity, grain hardness, protein content, and flour color associated traits. Molecular markers such as *Glu-A3d* and *Glu-B3d* (gluten quality), *Wx-7A* (starch viscosity), *Pinb-D1b* (grain hardness) have been validated as important markers for noodle quality improvement. The full-length genomic DNA sequence of two phytoene synthase genes (*Psy-A1* and *Psy-B1*) controlling yellow pigment, and three polyphenol oxidase genes (*Ppo-A1*, *Ppo-B1*, and *Ppo-D1*) responsible for discolor during storage, were characterized by in silico cloning and experimental validation. Four co-dominant STS markers including *YP7A*, *YP7B*, *PPO18* and *PPO29* were developed and they were closely associated with yellow pigment and PPO activity, respectively. 1B.1R translocation was identified to have significant effect on yellow pigment by QTL mapping.

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Jinmai 20 and Yumai 34 are leading cultivars characterized with high yield potential, outstanding noodle quality, and broad adaptation.

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Dormancy in white-grained wheat: Mechanisms and genetic control

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Grain dormancy is a major component of resistance to PHS resistance in red- and white-grained wheat. A QTL in chromosome 4A both types on has been associated with a component of this dormancy that is reflected in sensitivity of the embryo to ABA. Genetic studies involving reciprocal F₁s and doubled haploids suggest that 2 or more, genes are involved in dormancy in white-grained wheat and that at least one is expressed in the seed coat. By analogy, it is tempting to suggest that the seed coat effect in white-grained wheats may be similar to that in red wheat and be controlled by a gene(s) on one of the group 3 chromosomes. A doubled haploid population involving parents that both contain the 4A QTL but vary in dormancy phenotype was analysed and a new QTL located on chromosome 3B close to the likely position of *R-B1a*. This QTL appeared to be linked to increased expression of genes controlling key enzymes in the flavonoid pathway and a significantly greater accumulation of soluble flavonoids. Interaction between a factor produced by the dormant seed coat and the ABA-sensitive embryo during early imbibition would appear to explain a significant part of dormancy in white-grained wheat and be consistent with the evolution of white wheat.

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An integrated approach to predicting end-product quality of wheat

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One of the most important tasks of cereal science is to relate end-product quality to genes involved in determining certain attributes of quality. It requires a good understanding of the complex nature of quality that can lead to the proper measurements of these attributes. Most of our knowledge about the genetics of quality derives from two different experimental approaches : i) direct measurements of quality traits on samples with systematically altered chemical composition; ii) relating quality and chemical composition/genetics of large sample populations using statistical methods. An overview on the recent achievements of these two approaches will be given introducing a novel prediction procedure relating the individual and interactive contribution of HMW and LMW glutenin alleles to specific dough parameters and end-product quality attributes. The results shown are based on a statistical investigation of more than 3000 samples covering most of the glutenin alleles and allelic combinations appearing the Australian bread wheat cultivars.