

Sheedy JG, Raupp WJ, Thompson AL, and Smiley RW. 2008. Resistance to root lesion nematodes of addition lines derived from Chinese Spring x *Aegilops speltoides*, 2007. Plant Dis Management Rep (online), Report 2:XXXX, DOI: 10.1094/PDMR02 (submitted).

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Research interests.

1. Biochemistry and genetic control of factors that cause deterioration of wheat quality prior to harvest (preharvest sprouting and tolerance to preharvest sprouting, grain dormancy, late maturity α -amylase, and black point).
2. Biochemical and genetic control of color and color stability in Asian noodles (grain and flour constituents involved in color of wheat flour and color and color stability in Asian noodles - xanthophylls, flavonoids, polyphenol oxidase, peroxidase, lipoxygenase, and nutritive aspects of cereal xanthophylls - lutein and lutein esters).
3. Durum germ plasm with tolerance to hostile soils and root diseases and better adaptation to southern Australia.

Dormancy in white-grained wheat: mechanisms and genetic control.

Daryl Mares, Judith Rathjen, and Kolumbina Mrva, and Judy Cheong (SARDI, GPO Box 397, Adelaide SA 5001, Australia).

Grain dormancy is a major component of resistance to PHS resistance in red- and white-grained wheat. A QTL on chromosome 4A of both types has been associated with a component of this dormancy that is reflected in sensitivity of the embryo to ABA. Genetic studies involving reciprocal F_1 s and doubled haploids suggest that two 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 analyzed, and a new QTL was 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.

Pathway for water movement into dormant and nondormant wheat grain.

Judith R. Rathjen and Daryl J. Mares, and Ekaterina V. Strounina (Centre for Magnetic Resonance, University of Queensland, Brisbane, Qld 4072, Australia).

The movement of water into harvest-ripe grains of dormant and nondormant genotypes of wheat was investigated using magnetic resonance micro-imaging (MRMI). Neither the rate of increase in water content nor the pattern of water distribution within the grain was significantly different in closely related dormant and nondormant genotypes during the first 18 h. Water entered the grain through the micropyle. By 2 h, water was clearly evident in the micropyle channel, embryo, and scutellum. After 12 h, embryo structures such as the coleoptile and radicle were clearly visible and water had accumulated between the inner and outer layers of the seed coat as well as in the crease. Varying the point of access

to water, distal versus proximal end of the grain, did not affect the pattern of water distribution significantly. Germination was, however, delayed significantly in grains imbibed from the distal compared to proximal end, and this effect was more pronounced in the dormant genotype. This observation suggested that dormant genotypes may contain an inhibitor in the seed coat that is transferred to the embryo by water during imbibition.

Late maturity α -amylase: semidwarfing genes impose a cool temperature shock requirement.

Kolumbina Mrva and Daryl Mares, and Judy Cheong (SARDI, GPO Box 397, Adelaide SA 5001, Australia).

Late maturity α -amylase (LMA) in wheat involves the premature synthesis of high pI α -amylase isozymes during the middle to later stages of grain development. Expression of LMA in wheat is dependent on QTL on chromosomes 7B and 3B, however, the level of expression is affected by a range of factors that include genotype (GA insensitivity genes, T1B·1R translocation), environment (temperature, light), and agronomy. GA insensitive/semidwarfing genes, *Rht1* and *Rht2*, reduce expression of LMA and appear to introduce a requirement for a cool temperature shock as a trigger for α -amylase synthesis. For the majority of LMA-prone genotypes, exposure to a significant temperature differential (i.e., a cool temperature shock), rather than cool temperature alone appears to be important for consistent and maximum expression of LMA. The aims of this study were to investigate LMA expression in synthetic wheats with and without a semidwarf (*Rht1*) phenotype, to define the window of sensitivity to cool temperature shock, to determine the minimum duration of cool temperature for initiation of α -amylase synthesis and finally to examine the quantitative relationship between the duration of the cool temperature shock and α -amylase activity.

Publications.

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