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Genetic modification of wheat for dry environments – a trait based approach to crop improvement

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Empirical breeding continues to deliver improved wheat varieties for water-limited environments. A disadvantage of this approach is that the expression of important traits for dry environments may remain sub-optimal. Combining conventional and molecular breeding methods with a trait-based approach focussed on physiological understanding has the potential to hasten yield progress, and also uncover and develop new genetic variation for important traits.

Drought tolerance can be defined in a host of ways, but the definition of most importance to farmers and agronomists is greater production per unit of water used (or rainfall), or ‘more crop per drop’. A smorgasbord of traits and genes has been proposed to improve drought tolerance and possibly yield in water-limited environments. However, most have been unsuccessful. To improve yield a trait must increase one or more of the following without limiting the others: (i) crop water use, (ii) water use efficiency, and/or (iii) harvest index. The relative importance of each component will depend on the region where crop improvement is being targeted and the underlying limitations. Each component will vary according to the timing and expression of key plant characteristics, and each will have a genetic basis. A summary of the key traits for water-limited environments, the extent of genetic variation and their known genetic control will be presented, together with selection progress made for these traits.

A range of selection methodologies will be discussed including advances in phenotypic selection, the use of surrogate traits, the use of marker assisted selection for key traits and for dissecting the physiological basis of some important traits. Furthermore, examples will be given where new genetic variation for use in breeding has been identified or developed. Finally, methods for validating putatively important traits using conventional breeding or transgenic methods will be discussed.

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Comparison of global gene expression between wild emmer wheat genotypes contrasting in drought resistance

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Plants adapt to drought at the molecular, cellular and whole plant levels by a range of physiological and biochemical mechanisms, controlled by a network of genes which could be activated or repressed in response to drought stress. Wild emmer wheat (*Triticum dicoccoides*), the progenitor of cultivated wheat, is a promising source for improvement of drought resistance. The aim of this study was to identify candidate genes for drought resistance derived from wild emmer wheat. We describe here a comparison of global gene expression between drought resistant and drought susceptible genotypes of wild emmer wheat, under normal irrigation vs. drought stress conditions, using Affymetrix GeneChip® technology. ANOVA analysis revealed 1,091 differentially expressed transcripts ($p < 0.0001$) in at least one of the four genotype/treatment combinations. Further analysis showed that a

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group of 60 genotype-specific transcripts were highly expressed under drought stress in the resistant genotype. Gene annotation showed that 70% of these transcripts are functional proteins, 9% are regulatory proteins and 21% were not identified. The identified functional proteins are involved in important biological pathways, such as: membrane structure; metal ion, hormone and water transport; carbohydrate and protein metabolism; and senescence processes. Furthermore, some of these proteins are known to be involved in drought tolerance in other plant species. Therefore, these transcripts are considered as potential candidates genes for drought resistance. We show here that the wild emmer wheat gene pool is a promising source for improvement of drought resistance in cultivated wheat.

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Effects of post-anthesis heat stress and nitrogen levels on grain yield and grain growth of wheat (*T. durum* and *T. aestivum*) genotypes

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In order to study the effects of post-anthesis heat stress and nitrogen levels on grain yield and yield component of wheat genotypes, two separate field experiments were conducted in delayed and optimum sowing dates under Ahvaz conditions (2006-2007). Plants in delayed sowing experienced heat stress from post-anthesis growth stage. Each split-plot experiment had a randomized complete block design with three replications. The application rates of N at three levels (50, 100, and 150 KgNha⁻¹) were in main-plots. Sub-plots were consisted of six bread and durum wheat genotypes. The results indicated that the grain yield reduction in 50 and 100 KgNha⁻¹ compared with 150 KgNha⁻¹ treatment was 41% and 21% under optimum and 44% and 26% under heat stress conditions, respectively. In all genotypes, grain yield and 1000-grain weight (TGW) reduction under post-anthesis heat stress conditions was 42% and 33%, respectively. The highest and the lowest grain yield reduction due to heat stress were observed in Star (39%) and Vee/Nac (27%) cultivars. The Grain yield reduction in low nitrogen levels treatments and post-anthesis heat stress were due to significant reduction in number of grains.m⁻² and TGW, respectively. In low nitrogen levels treatments grain number per area was reduced due to reduction in number of fertile florets/spikelets, spikes.m⁻², and spikelets per spike. Grain growth period averages were 23 and 16 days under optimum and post-anthesis heat stress conditions, respectively. Heat stress after anthesis reduced the grain growth rate (12%) and grain growth period (30%) compared with optimum conditions. Further research are recommended for full understanding of the effects of heat stress and N deficiency on yield and yield components of recommended wheat genotypes under agroclimatic conditions of southern Iran.

Key words: wheat, post- anthesis heat stress, nitrogen levels, grain yield and grain growth

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Wheat production in a changing environment - low temperature adaptation

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To ensure survival and maintain a competitive advantage, a plant must be programmed to recognize and respond to the environmental cues that signal seasonal changes. Wheat, which is one of the most widely adapted food crops in the world, has evolved a broad range of complex systems that are expressed in anticipation of and during exposure to temperatures that approach freezing. Exploitation of these highly responsive mechanisms has allowed early farmers and plant breeders to produce

cultivars that are adapted to a wide range of environments. However, the highly integrated quantitative systems of structural, regulatory, and developmental genes that make wheat such a malleable species has also made the separation of cause-and-effect adjustments to changing temperatures a difficult challenge. Phenotypic studies have shown that developmental genes regulate the duration of low temperature (LT) tolerance gene expression and rate component regulates the degree that the LT induced genes are up-regulated. In this system, the point of transition from the vegetative to the reproductive growth stage is pivotal in determining the duration of LT tolerance gene expression. Integration of the mechanisms determining phenological development and LT response efficiently accommodates both short term and seasonal adjustments to LT stress, but it adds to the complexity of the responses. The rapidly expanding discipline of plant genomics has provided us with the tools and opportunity for detailed exploration of LT tolerance at the molecular level and a virtual flood of information has arisen from investigations using model plant systems and innovative technology. This increased understanding will strengthen our ability to maintain and improve wheat production in a changing environment, but its application must be tempered by the knowledge that LT adaptation is determined by pathway dependent teams of environmentally induced genes working in concert rather than the action of single genes operating in isolation.

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Can ABA signaling be used to develop drought tolerant wheat?

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Wheat yield and quality can be compromised by drought stress and preharvest sprouting (PHS) on the mother plant. PHS is one barrier to the adoption of hard white wheat varieties as a new market class in the U.S. It is believed that problems with PHS are due to lack of grain dormancy partly resulting from lack of ABA sensitivity (McKibbin et al, 2002). The long term goal is to wheat mutants with increased sensitivity to ABA to increase grain dormancy and drought tolerance. ABA is needed to set up seed dormancy and embryo desiccation tolerance during embryo maturation, and stimulate storage of nutrients. ABA also inhibits germination of mature seeds and stimulates stomatal closure in response to drought stress. A screen for wheat mutants with altered response to ABA in seed germination has been used as a first step to isolate wheat plants with increased ABA sensitivity. Mutants have been characterized for changes in ABA dose-response. In addition, ABA hypersensitive grain germination appears to correspond to reduced vegetative transpiration under drought stress and decreased carbon isotope discrimination.

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Stay-green wheat for Australia's changing, dry environment

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Stay-green phenotype has been successfully used to select for yield and yield stability of sorghum in the Australian northern cereal belt and shows promise for selection in wheat. CIMMYT line SeriM82 exhibits a stay-green phenotype by maintaining green leaf area longer during the grain filling period than the current northern cultivar Hartog. Yield of SeriM82 ranged from 6 to 28% greater than Hartog in 6 environments with differing moisture availability. SeriM82 exhibited stay-green phenotype in all environments where yield was significantly greater than Hartog. However, where the availability of

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deep soil moisture was limited, SeriM82 failed to exhibit significantly greater yield or to express the stay-green phenotype. Thus, deep soil moisture was important for expression of the high-yielding, stay-green phenotype. SeriM82 and Hartog also differ in root architectural traits. In large soil-filled chambers, SeriM82 had a narrower root system and extracted more soil moisture per soil volume, particularly deep in the profile, late in the growing season when marginal WUE is high. In small gel-filled chambers, SeriM82 exhibited a more vertical seedling seminal root angle indicating that seminal root angle is closely related to the vertical root distribution of mature plants. Gel-filled chambers provided a rapid and effective method of screening for seminal root angle suitable for genetic mapping studies. We postulate that SeriM82 is able to extract a small amount of extra soil moisture from deep in the profile late in the season. The stay-green phenotype of SeriM82 involving a narrower root system would be expected to confer a yield advantage in areas where moisture is available in deep non-constrained soils. However wider angled, shallower root systems might prove advantageous where deep soil moisture is unavailable and where plants rely on smaller, in season rainfall. In addition to seminal root angle, a number of shoot- and root- related traits are likely to be involved in the expression of high-yielding, stay-green phenotype in SeriM82.