**Triticum monococcum**: A Source of Novel Genes for Improving Several Traits in Hexaploid Wheat

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**ABSTRACT**

The diploid ‘A’ genome progenitor gene pool of wheat, comprising three closely related species *T. monococcum* ssp *monococcum* (*T. monococcum*), *T. monococcum* ssp *aegilopoides* (*T. boeoticum*) and *T. urartu*, harbours useful genes for many economically important traits, including resistance to diseases and micronutrient content. Their genomes share considerable homology with the A genomes of cultivated tetraploid and hexaploid wheat enabling the transfer of desirable alleles from the ‘non-progenitor’ A genome chromosomes into their ‘cultivated’ homologues without any significant linkage drag. A spring type *T. monococcum* (acc. pau14087) has maintained a high level of resistance to stripe rust, leaf rust, cereal cyst nematode, Karnal bunt and powdery mildew. Using a RIL population generated from a cross of *T. boeoticum* acc. Pau5088 with *T. monococcum* acc. pau4087, a linkage map with 179 loci was generated. This population showed segregation for stripe rust, leaf rust, cereal cyst nematode, Karnal bunt, powdery mildew, evolutionary traits like two grains vs one grain per spikelet, and grain iron and zinc content. Using QTL analysis, genes for stripe rust resistance were mapped in *T. monococcum* and *T. boeoticum* have been transferred to hexaploid wheat cultivars PBW343 and WL711 without any apparent linkage drag. Leaf rust resistance genes transferred from *T. monococcum* are being mapped in hexaploid wheat background.

**STRIPE RUST RESISTANCE**

Forty genes for stripe rust resistance have been catalogued so far but none has been identified from diploid ‘A’ genome species. *T. monococcum* (acc. pau14087) and *T. boeoticum* (acc. pau5088), being maintained at PAU Ludhiana, are susceptible to prevalent stripe rust races at the seedling stage but show resistant reaction at adult plant stage. Genetic analysis of the RIL population revealed the presence of two genes for stripe rust resistance, with one gene contributed by each of the parental lines. QTL analysis of the RIL population led to identification of two QTLs, one each in *T. monococcum* and *T. boeoticum* respectively. The QTL from *T. monococcum* mapped on chromosome 2A in a 3.6 cM interval between *Xwmc407* and *Xwmc170* with R^2^ value of 14%, whereas the QTL from *T. boeoticum* mapped on 5A in 8.9 cM interval between *Xbarc151* and *Xcvd12* with R^2^ value of 24%. These were designated as *QYrtm.pau-2A* and *QYrtb.pau-5A*, respectively. *T. monococcum* acc. pau14087 and three resistant RILs were crossed to hexaploid wheat cvs WL711 and PBW343, using *T. durum* as a bridging species with the objective of transferring these genes into hexaploid wheat. The B genome of *T. durum* suppressed resistance in the F1 plants, but with subsequent backcrossing one resistance gene could be transferred from one of the RILs to the hexaploid wheat background. Inheritance studies at the hexaploid level showed that the gene transferred from the RIL is a major gene (Table 1).
identified. The QTL on 1A, designated as Qcre.pau-1A, appeared to be a major gene with 34% contribution to the overall phenotypic variance whereas the QTL on 2A designated as Qcre.pau-2A contributed 12% to total phenotypic variation. Qcre.pau-1A is novel, being the only CCN resistance gene mapped in any ‘A’ genome species and none of the other known genes have been mapped on chromosome 1A. The QTL Qcre.pau-2A, might be allelic to Cre5, a CCN resistance gene transferred from Ae. ventricosa and mapped on 2AS in the same chromosomal region. Qcre.pau-1A was transferred to cultivated wheat using T. durum cv. PBW114 as the bridging species. Selected CCN resistant F₈ homozygous introgression lines with 2n=28 and 2n=42 showed the introgression of the molecular markers identified to be linked with CCN resistance locus Qcre.pau-1A indicating that this gene alone reduced cyst multiplication to a threshold level. These introgression lines can be used for marker-assisted transfer of Qcre.pau-1A to elite wheat cultivars.

**CEREAL CYST NEMATODE RESISTANCE**

Cereal cyst nematode (CCN), *Heterodera avenae* Woll., is a root nematode of cereals found in more than 31 wheat growing countries of the world (Nicol et al 2003). The effects can be reduced to some extent by crop rotation and chemical and biological control measures, but host plant resistance is the most economically and environmentally sustainable method for managing CCN. So far, only a few sources of resistance viz. Cre1, Cre8 and a QTL QCre.srd-1B have been identified in cultivated hexaploid wheat germplasm. In India, several thousand accessions of bread and durum wheat have been screened against CCN but none of the lines of Indian origin showed any resistance except line AUS15854, from exotic collections, which has a dominant resistance gene and has been used for developing CCN resistant varieties (Sharma et al 2004). Sources of resistance for *H. avenae* have been identified primarily in wild relatives of wheat. *T. monococcum* accession 14087 is resistant whereas *T. boeoticum* acc. 5088 is susceptible to *Heterodera avenae* (cereal cyst nematode, CCN) population of Punjab. The RIL population showed continuous variation (Figure 1). With composite interval mapping, using the genotypic data of the RIL population (Singh et al 2007), two QTLs, one each on chromosome 1AS and 2AS, conferring resistance to CCN in *T. monococcum* were identified. The QTL on 1A, designated as Qcre.pau-1A, has on average 30-35 spikelets per ear compared to 20-22 spikelets per ear in commercial hexaploid wheat cultivars. One of the RILs with higher seedling stage resistance genes have been transferred to cultivated wheat using *T. monococcum* has, in general, one grain per spikelet. The *T. monococcum* - *T. boeoticum* introgression lines can be used for marker-assisted transfer of Qcre.pau-1A to elite wheat cultivars.

**LEAF RUST RESISTANCE**

At seedling stage, the RIL population showed susceptible reactions against race 104-2, resistant reactions against the race 77-5 but segregated against the race 77-2. However, at adult plant stage, the population showed complete resistance against mixture of the above races, thereby indicating that, in addition to seedling resistance genes, the parents have some common gene that is operative at adult plant stage. The genes showing segregation at seedling stage have not been mapped in the diploid species so far. However, both adult plant and seedling stage resistance genes have been transferred into a hexaploid wheat background and are being mapped. Details can be found in another paper (Kaur et al – in these proceedings).

<table>
<thead>
<tr>
<th>Progeny ID</th>
<th>No. of progenies</th>
<th>Total</th>
<th>( \chi^2 ) (1:2:1)</th>
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<tr>
<td>452</td>
<td>96</td>
<td>118</td>
<td>2.34</td>
</tr>
<tr>
<td>480</td>
<td>84</td>
<td>59</td>
<td>4.81</td>
</tr>
</tbody>
</table>

HR = homozygous resistant, HS = homozygous susceptible and Seg. = segregating

**VARIABILITY FOR EVOLUTIONARY AND PRODUCTIVITY RELATED TRAITS**

*T. monococcum* has, in general, one grain per spikelet whereas *T. boeoticum* has two grains per spikelet. The RIL population showed variation for grains per spikelet as well. The two accessions also showed variation in grain size with *T. monococcum*, having bolder seeds compared to *T. boeoticum*. Data for the traits was recorded for three consecutive years 2005-2007. The QTL analysis (CIM) identified two QTLs, one each on chromosomes 1A and 4A, that govern the grain number per spikelet. The QTL on 1A maps in the marker interval *Xcfd65-Xwmc470* and for the pooled data. The grain weight QTL on 3A, having bolder seeds *T. monococcum* showed complete resistance against mixture of the above races, thereby indicating that, in addition to seedling resistance genes, the parents have some common gene that is operative at adult plant stage. The genes showing segregation at seedling stage have not been mapped in the diploid species so far. However, both adult plant and seedling stage resistance genes have been transferred into a hexaploid wheat background and are being mapped. Details can be found in another paper (Kaur et al – in these proceedings).

**PRODUCTIVITY RELATED TRAITS**

The QTL on 1A, designated as Qcre.pau-1A, has on average 30-35 spikelets per ear compared to 20-22 spikelets per ear in commercial hexaploid wheat cultivars. One of the RILs with higher spikelets per ear was also crossed to hexaploid wheat...
using *T. durum* as a bridging species primarily for the purpose of transferring rust resistance into hexaploid wheat. One BC1F1 population derived from a cross N59/RIL130/ 2*PBW343 (N59 is a *T. durum* cultivar whereas PBW 343 is a *T. aestivum* cultivar) showed segregation for ear size (spikelets per spike). Yield data of about 90 apparently good-looking leaf and stripe rust resistant plants was recorded and compared with the recurrent parent. More than 70% of plants showed higher yields than that of the recurrent parent (Fig. 2) PBW 343. Higher yield in these plants was due to increase in number of spikelets per spike (data not shown). Theses lines are being analysed for introgression from the *T. monococcum* or *T. boeoticum.*

![Fig. 2. Yield per plant of BC1F1 plants of the cross N59/RIL130/ 2*PBW343. Arrow indicates yield per plant of the recurrent parent PBW 343.](image)

**HIGH GRAIN IRON AND ZINC CONTENT**

Iron and Zinc are the two micronutrients that are deficient in the diet of people of the third world countries. Iron deficiency ranks among the most widespread nutrient deficiencies, estimated to affect over two billion people worldwide. About 800,000 child deaths worldwide per year are attributable to Zn deficiency in underdeveloped countries. Efforts are under way to increase the Fe and Zn content of major food crops through biofortification. Evaluation of primary and secondary gene pool of wheat showed that *T. boeoticum, T. monococcum, T. dicoccoides, Aegilops tauschii* and S genome species have a wider range of grain micronutrient density (Chhuneja et al. 2006, Ortiz-Monasterio, I, and Graham R D (2000) Breeding for trace minerals in wheat. Food Nutr. Bull. 21, 392–396.

**REFERENCES**


Chhuneja P., Dhaliwal H S., Bains NS. and Singh K. (2006) *Aegilops kotschyi* and *Aegilops tauschii* as sources for higher levels of grain Iron and Zinc. Plant Breeding 125, 529—531


