In summary, our data on the array and amino acid sequences of D defensins provide new evidence for the closer relationship between the polyploid wheat *T. kiharae* and *T. urartu* than with *T. monococcum* subsp. *aegilopoides*. Of particular interest are that the amino acid sequences of D defensins are highly conserved and persisted for about 10 thousand years that followed from the origin of polyploid forms. This observation provides strong evidence in favor of vital functions of this AMP family in plants.

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ITEMS FROM THE REPUBLIC OF SOUTH AFRICA

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Triticale breeding.

Widespread stem rust and leaf rust infections occurred during 2007. All our established commercial cultivars proved to be highly susceptible and are being phased out. However, the recently released cultivar US2007 remained completely resistant. Another advanced line (to be named AgBeacon) that also has complete resistance and excellent yield potential is being multiplied for release in 2009 and has the pedigree: Massa/Nimir 3/3/Yogui 1/Tarasca 87 3// Hare 212/4/Ibis/8/Ibis/7/Hare 212/3/Champlain/Aronde 68//VPM/Moisson/4/Juanillo 100/5/ANDAS'S'/6/Durum wheat/Balbo//BOK'S'/3/ANDAS'S'//TJ/BGL'S'.

Wheat recurrent mass selection.

New material developed in each phase of the program included approximately 60,000 new, potentially different F_1 genotypes. For the second year, an F_7 nursery consisting of 204 pure lines was distributed to local breeders (PANNAR, SGI, Monsanto, Cengen, and Afgri-Seed). The same material was evaluated in Uganda for resistance to the UG99 stem rust virulence. A genotyping system (microsatellite and AFLP loci) to distinguish F_6 inbred lines from one another and from released commercial cultivars was tested and found to discriminate among the majority of lines.

Genetic studies.

Chromosomal mapping of rust-resistance genes derived from wild *Triticum* species were continued, including the last two of a number of leaf and stripe rust-resistance genes transferred in the wide-crosses program: (i) linked leaf and stripe rust-resistance genes (*LrS20*/*YrS20*) from *Ae. neglecta* were mapped to chromosome 6A using microsatellites and monosomic and telosomic analyses and (ii), monosomic analyses to determine the location of a leaf rust resistance gene (*Lrmac*) derived from *Ae. biuncialis* are being completed.

Attempts to reduce the amount of foreign chromatin associated with genes that were transferred earlier, were continued. (i) Following allosyndetic pairing induction, resistant testcross F_1 involving the *Lr59* (*Ae. peregrina*), *Lr56*/*Yr38* (*Ae. sharonensis*) and *LrS20*/*YrS20* (*Ae. neglecta*) translocations are being screened with appropriate microsatellite markers to physically map each translocation and to identify the most useful recombinants. (ii) Crosses to shorten the *Lr54*/*Yr37* translocation (*Ae. kotschyi*) thus far yielded ten recombinants. The shortest of these, S14-74, appears to have retained both resistances but has lost an associated dwarfing (*Rht*) gene. An attempt is being made to find a suitable STS marker for S14-74. (iii) Four putative recombinants of a translocation (carrying resistance genes *LrS13*/*SrS13* as well as linked gametocidal genes) derived from *Ae. speltoides* were physically mapped. Recombinant 04M127-3A is the most useful and is, therefore, being tested for presence of gametocidal genes and to determine if it can be shortened further.

A strategy to transfer genes for salt tolerance from *Th. distichum* chromosomes $2J_1^d$, $3J_1^d$, $4J_1^d$, and $5J_1^d$ to wheat and triticale was continued. (i) Putative triticale translocations involving $3J_1^dS$ and $3J_1^dL$ were tested for their ability to complement addition chromosome $2J_1^d$ in salt-tolerance tests. The $3J_1^dS$ translocation may carry the salt tolerance gene(s) associated with chromosome $3J_1^d$. Testcross progeny are being screened in an attempt to also find translocations involving $2J_1^d$. (ii) Triticale addition lines of chromosomes $2J_1^d$, $3J_1^d$, $4J_1^d$, and $5J_1^d$ also are being used to identify further AFLP and SSR marker loci for these chromosomes.

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