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Registration of W4909 and W4910 Bread Wheat Germplasm Lines with High Salinity Tolerance

Two spring habit bread wheat (*Triticum aestivum* L.) germplasm lines W4909 and W4910 (Reg. no. GP-730 and GP-731, PI 631164 and PI 631165) with high salinity tolerance were developed at USDA-ARS Forage and Range Research Laboratory, Utah State University, Logan, UT. They were jointly released by USDA-ARS and Utah Agricultural Experiment Station on 10 April 2002.

The germplasm lines W4909 and W4910 were derived from hybrids between a disomic addition line AJDAj5 ($2n = 44$; $21''$ **AABBDD** + $1''$ $\mathbf{E^b}$) having a pair of $\mathbf{E^b}$-genome chromosomes from *Thinopyrum junceum* (L.) A. Löve ($2n = 42$; $\mathbf{E^bE^bE^bE^bE^eE^e}$) and the wheat line Ph^I carrying *Ph*^{I}, the inhibitor gene dominant to the *Ph* allele. The disomic addition line, developed by Charpentier (1992), is a derivative of backcrosses of 'Chinese Spring' (CI*tr* 14108) to the Chinese Spring × *Th. junceum* partial amphidiploid ($2n = 56$; **AABBDDEE**). It was found to possess higher salt tolerance than Chinese Spring in a greenhouse test at USDA-ARS Forage and Range Research Laboratory in 1995. The wheat line Ph^I, originated from a hybrid of Chinese Spring and *Aegilops speltoides* Tausch. (Chen et al., 1994), and was used in the cross to suppress the *Ph* gene for promoting homoeologous pairing between the *Th. junceum* chromosome and wheat chromosomes in the F_1 hybrids.

The F_2 plants of original hybrids were screened for salt tolerance with Chinese Spring as the control, because both parental lines are in a Chinese Spring background that has a moderate salt tolerance. F_3 families of the survived F_2 plants were screened again in 1997. Three F_3 families had survival rates greater than 90%, indicating that they were not progeny of monosomic addition lines. The plants in one family were sterile, whereas the other two families (W2407 and W2457) produced seeds. All F_4 plants of the two families (W3574 and W3586) were euploids with $2n = 42$ (Li et al., 1997). Fluorescent genomic in situ hybridization (F-GISH) and molecular studies on these two lines indicated that they had a very small interstitial translocation of *Th. junceum* chromatin in a metacentric wheat chromosome whose homoeologous relationship has not been determined (Wang et al., 2003). Three F_5 families derived from the cross were tested at the USDA-ARS U.S. Salinity Laboratory, Riverside, CA, in 2000. Grown in a greenhouse under regular irrigation with salt solution up to the EC = 22 dS/m, two lines (W4909 and W4910) were more salt tolerant than AJDAj5 and Ph^I (the two parental lines), both of which were more salt tolerant than Chinese Spring, the common genetic background (Wang et al., 2003). This conclusion was substantiated by 2-yr observations at CIMMYT's field plots in La Paz, Baja California Sur, Mexico. Irrigated with diluted sea water at EC = 12 dS/m, the salt-tolerance in lines W4909 and W4910 was better than that in Chinese Spring and close to that in 'Kharchia 65' (from India), the most salt-tolerant landrace of wheat in the world (A. Mujeeb-Kazi, personal communication). Analyses of shoot ion contents indicate that W4909, W4910, and Ph^I have the true tolerance to high internal Na^+ concentrations, in contrast to the sodium exclusion mechanism in Chinese Spring and Yecora Rojo (CI*tr* 17414) that kept the Na^+ concentrations lower (C. M. Grieve, personal communication).

W4909 and W4910 are morphologically similar to Chinese Spring, except that they are later in maturity. W4910 is more similar to AJDAj5 in plant height and heading date, whereas W4909 is closer to the Ph^I line, which is taller and earlier than AJDAj5. W4909 and W4910 are also different from each other by a few molecular markers originated from the two parental lines (Wang et al., 2003), suggesting that they have different genomic organizations arising from different recombination events. These germplasm lines should be of interest to breeders who may pyramid QTLs for salt tolerance from W4909 or W4910 with those from other sources such as Kharchia 65 and Yecora Rojo. Seed (F_6) of W4909 and W4910 will be available at 10 seeds per written request by bone fide wheat researchers. The seed request should be addressed to the corresponding author. Appropriate recognition of the source should be noted if these germplasm lines contribute to the development of molecular tools, new breeding lines, or cultivars.

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References

Charpentier, A. 1992. Production of disomic addition lines and partial amphiploids of *Thinopyrum junceum* on wheat. C.R. Acad. Sci. Paris 315(III):551–557.

Chen, P.D., H. Tsujimoto, and B.S. Gill. 1994. Transfer of *Ph*^{I} gene promoting homoeologous pairing from *Triticum speltoides* into common wheat and their utilization in alien genetic introgression. Theor. Appl. Genet. 88:97–101.

Li, X.M., C. Jaussi, R.R.-C. Wang, and S. Naimov. 1997. Salt-tolerant Triticeae germplasm from plant introductions and wide hybridization. p. 77. *In* Agronomy Abstracts. ASA, Madison, WI.

Wang, R.R.-C., X.-M. Li, Z.-M. Hu, J.-Y. Zhang, S.R. Larson, X.-Y. Zhang, C.M. Grieve, and M.C. Shannon. 2003. Development of salinity-tolerant wheat recombinant lines from a wheat disomic addition line carrying a *Thinopyrum junceum* chromosome. International J. Plant Sci. 164(1):25–33.

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Registration of TTU-LRC Castor Germplasm with Reduced Levels of Ricin and RCA_{120}

An open-pollinated germplasm population of castor (*Ricinus communis* L.) TTU-LRC (Reg. no. GP-3, PI 631156) was developed at Texas Tech University and released in 2002. The eight F_6 parental lines of TTU-LRC were selected for reduced levels of two toxins found in castor seeds, ricin and *R. communis* agglutinin (RCA_{120}), as well as dwarf-internode