ITEMS FROM JAPAN

IBARAKI UNIVERSITY
College of Agriculture, 3-21-1 Chuo, Ami, Inashiki, Ibaraki 300-0393, Japan.

Nobuyoshi Watanabe.

Cytological and microsatellite mapping of mutant genes for spherical grain and compact spikes in durum wheat.

Two mutants for sphaerococcoid seed (MA 16219) and compact spike (MA 17648) were isolated from the M_3 progeny of the durum wheat cultivar,Altaiskaya Niva mutagenized with chemical mutagens. The chromosomal locations of the genes involved were determined by the use of a complete set of D-genome disomic substitutions in durum cultivar Langdon. The gene for sphaerococcoid grain, s^{16219}, was allelic to *S2*, located in the centromeric region of chromosome 3B in hexaploid wheat. The gene for compact spike, C^{17648}, was located on chromosome 5AL distal to the *Q* locus. Using microsatellite markers, C^{17648} and the awn inhibitor gene *B1* were located in the F_2 of 'LD222 / MA17648'. The gene order was *Xbarc319* – C^{17648} – *Xgwm179* – *Xgwm126* – *Xgwm291* – *B1*.

Exploration of genetic diversity among Xinjiang Triticum and Triticum polonicum by AFLP markers.

Seventy-two Xinjiang *Triticum* and *T. turgidum* subsp. *polonicum* accessions were subjected to AFLP analyses to discuss the origin of *T. petropavlovskyi*. A total of 91 putative loci were produced by four primer combinations; 56 loci were polymorphic, which is equivalent to 61.53% of the total number of putative loci. Genetic diversity among 11 *T. petropavlovskyi* accessions was narrow due to the lowest number (32) of polymorphic loci among the wheat species. Forty-four polymorphic loci were found in *T. aestivum* subsp. *aestivum* and *T. aestivum* subps. *compactum*, whereas the highest polymorphism was observed in *T. turgidum* subsp. *polonicum*. On the basis of the UPGMA clustering and PCO grouping and genetic similarity estimates from the AFLPs, we noted that *T. petropavlovskyi* was more closely related to the Chinese accessions of *T. turgidum* subsp. *polonicum* than to accessions from other countries. Two accessions of *T. aestivum* subsp. *aestivum* were grouped with *T. petropavlovskyi* in the UPGMA clustering; both were similar to *T. petropavlovskyi* in respect of spike structure, i.e., presence of awn, glume awn, and leaf pubescence. Six loci, which were commonly absent in Chinese *T. turgidum* subsp. *polonicum*, also were absent in nearly all of the *T. petropavlovskyi* accessions. The findings of this study reduced the probability of an independent allopolyploidization event in the origin of *T. petropavlovskyi* and indicated a greater degree of gene flow between *T. aestivum* subsp. *aestivum* and *T. turgidum* subsp. *polonicum* leading to *T. petropavlovskyi*. Most likely, the *P* gene of *T. petropavlovskyi* hexaploid wheat was introduced from *T. turgidum* subsp. *polonicum* to *T. aestivum* subsp. *aestivum* via a spontaneous introgression or breeding effort.

Comparative genetic diversity of T. aestivum subsp. aestivum–T. turgidum subsp. polonicum introgression lines with long glume and T. petropavlovskyi by AFLP-based assessment

Genetic diversity of a set of introgression lines of *T. aestivum* subsp. *aestivum* L./*T. turgidum* subsp. *polonicum* with long glume and *T. petropavlovskyi* were analyzed by AFLP. Small-scale, bulk-breeding method was used throughout until the F_6 generation to develop the introgression lines. Thirty-eight hexaploid F_7 plants with long glume phenotype and their parents were subjected to AFLP analysis by four primer combinations. A total of 47 polymorphic loci were detected between the parents and 15 were introgressed across the 38 lines. We hypothesized that approximately 50% of A or B genomes associated polymorphic loci were introgressed. The variation of introgression lines was limited within the diversity between their parents, *T. aestivum* subps. *aestivum* cv. Novosibirskaya 67 (N67) and *T. turgidum* subsp. *polonicum* cv. IC12196. N67 was closer to 38 introgression lines than that of IC12196. The UPGMA cluster and principal coordinate analysis (PCO) grouping showed 0.84 to 0.98 similarity values between N67 and the introgression lines. Eleven *T. petropavlovskyi* accessions were distinguished from introgression lines with UPGMA clusters and PCO groupings, and *T. petropavlovskyi* was located between the introgressions lines and IC12196. Several introgression lines

Table 1. Near-isogenic lines of durum wheat cultivar LD222.

Code	Character	Allele	Donor
Chromosome 1A			
ANW 1A	Black glume	*Bg*	*T. turgidum* subsp. *durum* var. *reichenbachii*
ANW 1B	Black glume, hairy glume	*Bg, Hg*	*T. turgidum* subsp. *carthlicum #521*
ANW 2A	Hairy Glume	*Hg*	*T. turgidum* subsp. *durum* var. *melanopus*
Chromosome 3A			
ANW 9A	Red grain	*R-A1b*	DS LDN (DIC 3A)
ANW 10A	Brittle rachis	*Br2*	DS LDN (DIC 3A)
ANW 11B	Sphaerococcoid	*S3*	MS 1453, a mutant of Saratovskaya 29 (2n=42)
Chromosome 5A			
ANW 16C	Reduced height	*Rht 12*	Mv 17 (Karcagi 522 5A, 2n=42)
ANW 22A	Compact spike	C^{17648}	MA17648, a mutant of Altaiskaya Niva
Chromosome 7A			
ANW 5A	Long glume	*P1*	*T. turgidum* subsp. *polonicum* var. *vestitum*
ANW 5C	Long glume	*P1*	*T. petropavlovskyi* Maystrenko's line (2n=42)
ANW 5D	Long glume	*P1*	*T. turgidum* subsp. *polonicum* var. *abyssinicum*
ANW 5E	Long glume	*P1*	*T. petropavlovskyi* k44126
ANW 5F	Long glume	*P1*	*T. aestivum* subsp. *aestivum* PI 191834
ANW 5G	Long glume	*P1*	*T. aestivum* subsp. *aestivum* AUS 20561 (2n=42)
ANW 7A	Chlorina	*cn-A1d*	CDd6, a mutant of Langdon
Chromosome 2B			
ANW 3A	Nonglaucousness	*WI1*	*T. turgidum* subsp. *durum* var. *pyramidale*
ANW 3B	Nonglaucousness	*w1*	AUS 2499
ANW 12A	Ligulelessness	*lg1*	A variant of Marvroullos
Chromosome 3B			
ANW 9B	Red grain	*R-B1b*	DS LDN–TDIC (3B)
ANW 10B	Brittle rachis	*Br3*	DS LDN–TDIC (3B)
ANW 11C	Sphaerococcoid	*S2*	MSK 2454, a mutant of Skala (2n=42)
ANW 11D	Sphaerococcoid	S^{16219}	M-16219, a mutant of Altaiskaya Niva
Chromosome 4B			
ANW 4A	Reduced height	*Rht-B1b*	*T. turgidum* subsp. *durum* cv. Cando
ANW 4B	Reduced height	*Rht-B1c*	Maringa NIL (2n=42)
ANW 4C	Reduced height	*Rht-B1d*	*T. aestivum* subsp. *aestivum* cv. Saitama 27 (2n=42)
ANW 4D	Reduced height	*Rht-B1e*	*T. aestivum* subsp. *aestivum* cv. Krasnodari 1 (2n=42)
ANW 4E	Reduced height	*Rht-B1f*	*T. aethiopicum* W6824D
ANW 4F	Reduced height	*Rht-B1h*	*T. turgidum* subsp. *polonicum* IC 12196
ANW 4G	Reduced height	*Rht-B1f*	*T. aethiopicum* W6807C
ANW 14A	Hairy peduncle	*Hp*	Hp-S615, an S615 NIL (2n=42)
ANW 20A	Blue grain	*Ba2*	UC66049
Chromosome 7B			
ANW 5B	Long glume	*P2*	*T. ispahanicum*
ANW 7B	Chlorina	*cn-B1b*	CDd2, a mutant of Langdon
ANW 6A	Purple culm	*Pc*	DS CS–Hope (7B)
ANW 13A	Chocolate black chaff	*cc*	Vic CBC mutant
Location unknown			
ANW 8A	Yellow leaf	digenic	Yellow mutant (15:1)
ANW 11A	Sphaerococcoid	digenic	Sphaerococcoid mutant
ANW 16D	Reduced height	*Rht 14*	Castelporziano
ANW 16F	Reduced height	*Rht 16*	Edmore M1
ANW 16G	Reduced height	*Rht 18*	Icaro
ANW 16H	Reduced height	*Rht 19*	Vic SD1 line b

resembled with *T. petropavlovskyi* for awning and glume length. The genetic variation among 38 introgression lines was much wider than that of *T. petropavlovskyi*. We concluded that *T. petropavlovskyi* was established by intensive selection of hybrid between *T. aestivum* subsp. *aestivum*/*T. turgidum* subsp. *polonicum*.

Quantitative trait loci for soil-penetration ability of roots in durum wheat.

Increasing the ability of root penetration (RP) into hard soil is important to improve drought resistance in durum wheat. Traits related to RP ability were evaluated in 110 RILs derived from the cross 'Jennah Khetifa /Cham1' using paraffin-Vaseline (PV) discs. QTL analyses were made for the number of roots penetrating the PV disc (PVRN), total number of seminal and crown roots (TRN), RP index (PVRN/TRN), and root dry weight (DW). Jennah Khetifa had higher PVRN, RP index, and root DW values than those of Cham1, and the RILs showed significant differences for these traits. Two closely-linked markers, *Xgwm617a* and *Xgwm427b*, on the long arm of chromosome 6A were associated with PVRN and RP index. For root DW, a QTL was linked to marker *Xgwm11* on chromosome 1B. Alleles of Jennah Khetifa were associated with increased PVRN, RP index, and root DW. No QTL was detected for TRN in this mapping population. The absence of co-located QTL suggested that RP ability was controlled separately from TRN and root DW. Although the population size and number of replications were small, this study helps in understanding the complexity of root growth and the potential of marker-assisted selection for selecting genotypes with high RP ability in durum wheat populations.

Development of near-isogenic lines in durum wheat.

The NILs for sphaerococcoid seed and compact spike were established as ANW 22A and ANW 11D. Multiple alleles at the *Rht-B1* locus were introduced into the genetic background of cultivar LD222. *Triticum turgidum* subsp. *polonicum* IC 12196 may be considered as new source of *Rht* gene. The NILs for GA-sensitive *Rht* genes (*Rht14*, *Rht16*, *Rht18,* and *Rht19*) were developed, although their chromosomal locations have not been determined. The effort to develop NILs was extended to introduce taxonomy-related traits such as spelt, squarehead, and glume awns. Table 1 (p. 80) summarizes presently developed near-isogenic lines of durum wheat cultivar LD222. Several NILs are available upon request. The information is also available at the website: http://seimei.agr.ibaraki.ac.jp/ibaraki_public_html/catalogue.htm.

Publications.

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