ITEMS FROM BRAZIL

BRAZILIAN AGRICULTURAL RESEARCH CORPORATION — EMBRAPA
Rodovia BR 285, km 294, Caixa Postal 451, Passo Fundo, RS, Brazil.

Wheat in Brazil – the 2009 crop year.

Eduardo Caierão and Flávio Martins Santana.

Brazilian wheat production was about 5 x 10^6 tons (Conab 2009) in the 2009 crop year, which is enough to supply 50% of the domestic demand (Table 1). The deficit in production makes Brazil the largest wheat importer. The south region, comprised of the states of Rio Grande do Sul, Santa Catarina, and Paraná, accounts for 90% of the national production. Nonetheless, due to the characteristics of the cultivation system utilized, average grain yield is not the highest in the country.

Table 1. Cultivated area, total production and grain yield of wheat in Brazil in 2009 (Source: CONAB, 2010).

Region	Area (ha x 1,000)	Production (t x 1,000)	Grain yield (kg/ha)
North	—	—	—
Northeast	—	—	—
Central-west	67.5	171.8	2,546.0
Southeast	84.1	225.0	2,675.0
South	2,276,4	4,629.4	2,034.0
Brazil	2,428.0	5,026.0	2,070.0

The wheat area planted in 2009 was similar to that in 2008. However, the total production and average grain yield/hectare achieved in 2009 were about 16.7% and 16.8% smaller than those of 2008, respectively. In the state of Rio Grande do Sul (south region), high rainfall conditions observed in October and November (harvest months) affected the grain quality for milling industries. In the state of Paraná, the high incidence of wheat blast and Fusarium head blight in the north of the state reduced dramatically the average grain yield in some fields.

In 2010, there is no evidence that the Brazilian wheat area will increase or remain the same.

Reference.

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ITEMS FROM THE PEOPLES REPUBLIC OF CHINA

UNIVERSITY OF ELECTRONIC SCEINCE AND TECHNOLOGY OF CHINA
School of Life Science and Technology, Chendgu 610054, Sichuan, PR China.

The genomic evolution of the Thinopyrum and Dasypyrum: Evidence from α-gliadin sequences.

G.R. Li, C. Liu, T. Zhang, J. Zhou, and Z. Yang.

The genus *Thinopyrum* represents a vast reservoir of useful agronomic traits for wheat and forage improvement. Wide hybridization and chromosomal engineering enabled the incorporation of alien genetic material from *Thinopyrum* into common wheat in the last four decades (Chen et al. 2005; Li and Wang 2009). Chen et al. (1998) analyzed *Thinopyrum*

species in detail with genomic *in situ* hybridization using an S^t-genomic DNA probe, which can detect detail in the physical organization of the DNA sequences of *Thinopyrum* chromosomes. The basic genomes of the *Thinopyrum* species are J, J^s, and S^t, where J is closely related to *Th. bessarabicum* and J^s is a modified version of the J genome with the signal of the S^t genome (Wang et al. 1994). Kishii et al. (2005), using the *Daypyrum* genomic DNA to hybridize with *Th. intermedium*, considered that the genomic formula of *Th. intermedium* can be tentatively redesignated as $S^tS^tJ^sJ^s$(V-J-R)^s(V-J-R)^s. Recently, Liu et al. (2009) distinguished the J^s genome from *Th. intermedium* using FISH of the Sabrina-like LTR sequences. The hybridization pattern of the J^s genome was similar to that of the V genome of *Dasypyrum*, implying that the constitution of J^s genome in *Th. intermedium* may have the V genome. In this study, we investigated a number of α-gliadin sequences, which represent a evolutionariyy fast gene family of seed-storage proteins, in order to provide evidence to the relationship between *Thinopyrum*, in particular *Th. intermedium* with *Dasypyrum* species.

Materials and Methods. The *Dasypyrum villosum*, *Th. intermedium*, *Lophopyrum elongatum*, *Th. bessarabicum*, and *Pseduoroengeria spicata* lines were kindly provided by Dr. Harold Bockelman, National Plant Germplasm System, USDA–ARS, Aberdeen, Idaho, USA. Diploid *D. breviaristatum* was obtained from Dr. Shoji Ohta, Department of Bioscience, Fukui Prefectural University, Matsuoka, Yoshida, Fukui, Japan. The PCR amplification, cloning, and sequence analysis of α-gliadin genes were according to Li et al. (2009).

Results and Discussion. A Total of 137 unique clones were sequenced from the six species (Table 1). The nucleotide comparison of these entire sequences showed a high degree of homology with other α-gliadin sequences in wheat. On the basis of the deduced amino acid sequence of the α- gliadin genes, 58 sequences included complete ORFs, whereas 79 sequences were pseudogenes, because they contained a typical in-frame premature stop codon. Among the species, different frequencies of pseudogenes were observed, including 19 of 21 *Th. bessarabicum* α-gliadin sequences and 6 of 16 *D. villosum* α-gliadin sequences. The general structure of the α-gliadin protein consists of a short N-terminal signal peptide (S) followed by a repetitive domain (R) and a longer nonrepetitive domain (NR1 and NR2), separated by two polyglutamine repeats (Q1 and Q2). In the first glutamine repeat (Q1), the *L. elongatum* α-gliadin sequences contained 6–24 (average 18) glutamine residues. In the second glutamine repeat (Q2) region, *D. villosum* had 12–24 (average 18.6)

Table 1. The α-gliadin sequences from six species. Q1 and Q2 are polyglutamine repeats.

Species	Genomic formula	Putative full-ORF	Pseudogenes	Length of ORF	Length of Q1	Length of Q2	Glia-α
D. breviaristatum	V^b	13	14	810–954	8 (3–14)	6 (2–11)	3
D. villosum	V	10	6	846–897	14 (8–10)	18 (12–24)	10
L. elongatum	E	15	10	855–884	18 (6–24)	8 (7–9)	11
Ps. spicata	S^t	10	18	812–1,073	6 (3–8)	13 (6–28)	5
Th. intermedium	JJ^sS^t	8	12	831–861	5 (3–8)	5 (3–10)	6
Th. bessarabicum	J	2	19	855–872	8 (7–9)	5 (3–7)	2

The reported T cell stimulatory epitopes Glia-α (QGSFQPSQQ), Glia-α-2 (PQPQLYPQ), Glia-α-9 (PFPQPQLPY), and Glia-α-20 (FRPQQPYPQ) have their own conserved position in the wheat α-gliadin protein (van Herpen et al. 2006). All the α-gliadin sequences from six species lacked Glia-α-2, Glia-α-9, and Glia-α-20, which were all found in the first repetitive (R) domain. The Glia-α in the second nonrepetitive (NR2) domain was found in all species with different frequency. Only 3 of 13 full-ORF of *D. breviaristatum* sequences contained epitope Glia-α, whereas all 10 *D. villosum* ORFs possessed epitope Glia-α (Table 1).

Sequence comparisons were performed among the α-gliadin genes to understand the relatedness and the divergent time by construction of phylogenetic trees. In addition to the α-gliadin nucleotide sequence, two γ-gliadin sequences from wheat were used as an outgroup. The phylogenetic tree indicated that the sequences from *D. breviaristatum* were clearly separated from other groups, indicating the earlt divergence of the *D. breviaristatum* α-gliadins (Fig. 1, p. 43). Genes from *L. elongatum* and *Ps. spicata* were clustered into two different groups, suggesting that the α-gliadin genes in the two species exhibit higher diversity than those in *D. villosum* and *Th. intermedium*. The sequences from *D. villosum*, *L. elongatum*, *Th. bessarabicum*, and *Ps. spicata* were clustered in one subgroup. These results suggested that the J, S^t, E, and V genomes are closely related to the *Th. intermedum* genome. Because only a part of the *L. elongatum* and *Ps. spicata* α-gliadin sequences were closely clustered to *Th. intermedium*, *Th. intermedium* may have lost diversity after polyploidization.

Based on the calculation of the evolutionary rates of the α-gliadin sequences, *D. breviaristatum* possibly evolved 15–20 MYA, the separation of genomes J, S^t, E, and V occurred at 8–13 MYA, and the *Th. intermedum* genome generated 7–8 MYA.

We speculate that the *Dasypyrum* species are relatively close to *Thinopyrum* and its putative ancestry species *L. elongatum*, *Th. bessarabicum*, and *Ps. spicata*. *Dasypyrum villosum*, not *D. breviaristatum*, most likely joint the *Th. intermedium* evolution. The relationship between *Dasypyrum* and *Thinopyrum* also is supported by the phylogenetic studies from several chloroplast and nuclear single-copy genes. We also expect to develop the molecular markers to help trace the transfer of both *Dasypyrum* and *Thinopyrum* chromatin to wheat (Liu et al. 2009).

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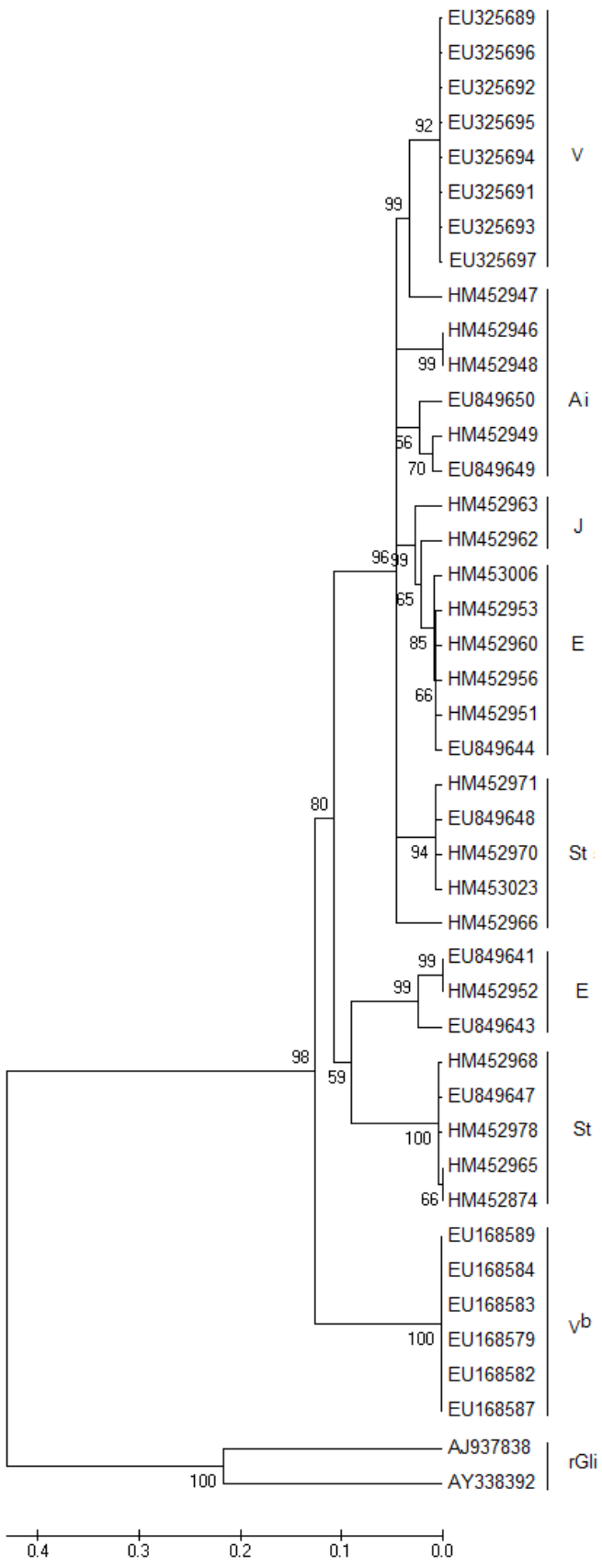

Fig. 1. A phylogenetic tree was developed with NJ and MP analyses using the MEGA4 with 1,000 iterations.

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ITEMS FROM CROATIA

BC INSTITUTE FOR BREEDING AND PRODUCTION OF FIELD CROPS
Rugvica, Dugoselska 7, 10370 Dugo Selo, Croatia.
Department of Cereal and Forage Crops, Botinec, Zagreb, Croatia.
www.bc-institut.hr

Slobodan Tomasović, Rade Mlinar, Ivica Ikić, Branko Palaveršić, Katarina Jukić, and Tomislav Ivanušić.

A study of the technological traits of high-quality, Bc wheat cultivars in different environments.

The technological traits of the Bc winter cultivars Mihelca and Zdenka, which are widely grown in Croatia, Slovenia, and Bosnia and Herzegovina, as well as the newly registered cultivars Bc Mira and Bc Renata, were analyzed. Samples were taken partly from small-scale trials at locations in Botinec, Lovas, Rugvica, and Osijek (Table 1) and partly from wheat production fields throughout Croatia (Table 2, p. 45). Over a three-year period, each sample was tested for dough rheological traits using a farinograph and an extensograph. Preliminary results showed a high and stable quality for cultivars Mihelca, Zdenka, Bc Mira, and Bc Renata and during the following years it was confirmed in wide produc-

Table 1. Test results of bread-making quality for BC Institute wheat cultivars from small-scale trials at locations in Botinec, Lovas, Rugvica, and Osijek, Croatia.

Location	Farinogram							Extensogram			
	Water absorance (%)	Dough develop time (min)	Stability (min)	Resist-ance (min)	Degree of softening (FJ)	Quality number	Quality group	Energy (cm^2)	Extensi-bility (mm)	Resist ance (EJ)	R/E
Zdenka (2006–07)											
Botinec	66.5	8.5	6.5	15.0	0	100.0	A1	135.3	190	313	1.65
Rugvica	65.8	2.0	1.7	3.7	24	77.7	A2	141.8	176	388	2.20
Lovas	65.9	7.0	2.7	9.7	16	88.0	A1	120.4	202	270	1.34
Osijek	65.1	2.1	1.9	4.0	65	61.5	B1	133.7	178	370	2.08
Zdenka (2007–08)											
Botinec	66.2	2.3	1.3	3.6	65	62.0	B1	130.9	178	360	2.02
Mihelca (2006–07)											
Botinec	57.9	6.8	8.2	15.0	0	100.0	A1	130.1	178	350	1.97
Rugvica	58.6	10.3	3.0	13.3	3	92.1	A1	125,.7	185	308	1.66
Lovas	57.4	7.2	7.5	14.7	3	94.5	A1	106.5	190	260	1.37
Osijek	56.0	1.8	0.6	2.4	65	56.2	B1	136.3	180	350	1.94
Mihelca (2007–08)											
Botinec	57.2	1.6	0.7	2.3	70	57.7	B1	100.5	172	290	1.69