Table 5. Participation of public and private institutions in the wheat seed market (%) in the Brazilian state of Paraná from 2000 to 2008.

Breeder	Profile	2000	2001	2002	2003	2004	2005	2006	2007	2008
Coodetec	Public/Private	14	14	26	28	31	46	41	34	35
Embrapa	Public	23	27	24	16	22	23	33	44	48
Iapar	Public	38	37	30	30	27	18	10	8	8
OR Seeds	Private	21	14	17	23	18	13	15	13	6
Other	—	4	8	3	3	2	0	1	1	2
Totals	Public	61	64	54	46	49	41	43	52	56
	Public/Private	14	14	26	28	31	46	41	34	35
	Private	21	14	17	23	18	13	15	13	5
	Others	4	8	3	3	2	0	1	1	2

In Rio Grande do Sul, Embrapa was the market leader in 2003, 2004, and 2005, but its participation has decreased drastically, down to 14% of the market share in 2008. From 2005 to 2008, Fundacep increased its participation, growing from 18% to 48%. The participation of public companies was once larger, especially in 2002, 2003, and 2004. In 2007, an equilibrium between the participation of public and private companies was achieved (Table 4, p. 44).

In Paraná, the current participation of Embrapa in the wheat seed market is highly significant, having reached its highest rate in nearly 10 years (55%). On the other hand, the participation of Iapar (a traditional breeder in the state) has abruptly dropped since 2000, reaching only 7% in 2008. Coodetec, which led the market in 2004, 2005, and 2006, also has shown a reduction in its participation in the last 2 years. The participation of OR Seeds in the Paraná market is rather modest and achieved its highest rate (23%) in 2003 (Table 5).

ITEMS FROM THE PEOPLES REPUBLIC OF CHINA

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Characterization of low-molecular-weight glutenin subunit Glu-B3 genes and the development of STS markers in common wheat.

To characterize the LMW-GS genes at the *Glu-B3* locus, gene-specific PCR primers were designed to amplify eight near-isogenic lines and Cheyenne with different *Glu-B3* alleles (*a*, *b*, *c*, *d*, *e*, *f*, *g*, *h*, and *i*) defined by protein electrophoretic mobility. The complete coding regions of four *Glu-B3* genes with the complete coding sequence were obtained and designated as *GluB3-1*, *GluB3-2*, *GluB3-3*, and *GluB3-4*. Ten allele-specific PCR markers designed from SNPs present in the sequenced variants discriminated the *Glu-B3* proteins of electrophoretic mobility alleles *a*, *b*, *c*, *d*, *e*, *f*, *g*, *h*, and *i*. These markers were validated on 161 wheat cultivars and advanced lines with different *Glu-B3* alleles, thus confirming that the markers can be used in marker-assisted breeding for wheat grain processing quality.

Characterization of novel LMW-GS genes at the Glu-D3 locus on chromosome 1D in Aegilops tauschii.

The objectives of this study were to clarify the relationship between LMW-GS *Glu-D3* gene of *Ae. tauschii* registered in GenBank and the six *Glu-D3* genes, including 12 allelic variants of common wheat characterized in our previous studies, and identify novel *Glu-D3* genes and haplotypes from *Ae. tauschii* using gene-specific PCR amplification. By searching

the NCBI database, 13 LMW-GS genes/pseudogenes of *Ae. tauschii* were retrieved and classified into five gene families based on their nucleotide similarity with the six *Glu-D3* genes of common wheat. Of these, four *Ae. tauschii* genes *AY585350*, *AY585354*, *AY585355*, and *AY585356* matched to *GluD3-4*, *GluD3-5*, *GluD3-1*, and *GluD3-2* of common wheat, respectively, and one pseudogene *AY585351* matched to *GluD3-6*; none matched to *GluD3-3*. In order to identify the *Glu-D3* genes from *Ae. tauschii* corresponding to *GluD3-3* and *GluD3-6* of common wheat, gene-specific primers were developed to amplify 8-18 *Ae. tauschii* entries. As a result, two novel *Glu-D3* genes, designated *GluDt3-3* and *GluDt3-6*, were identified. *GluDt3-3* showed seven allelic variants or haplotypes at the DNA level in eight *Ae. tauschii* entries, designated as *GluDt3-31*, *GluDt3-32*, *GluDt3-33*, *GluDt3-34*, *GluDt3-35*, *GluDt3-36*, and *GluDt3-37*. Two to eight SNPs were found among the seven haplotypes and 1–4 amino acid substitutions among the deduced peptides. Multiple-sequence alignments showed that the DNA similarity was 99.6–99.9% among the seven *GluDt3-3* haplotypes, and 99.4–99.7% between these haplotypes and those of common wheat *GluD3-3* gene. *GluDt3-6* presented seven haplotypes in 18 *Ae. tauschii* entries, designated as *GluDt3-61*, *GluDt3-62*, *GluDt3-63*, *GluDt3-64*, *GluDt3-65*, *GluDt3-66*, and *GluDt3-67*. *GluDt3-61*, from *Ae. tauschii* entry Ae38, was the only one haplotype with complete coding sequence, and the other six were all pseudogenes. Compared with *GluD3-6* gene of common wheat, *GluDt3-61* exhibited a 3-bp insertion, a 42-bp deletion, and 11 base substitutions, leading to a glutamine insertion in position 52, a 14 amino acid deletion in position 84–97, and 10 amino acid mutations in its deduced peptide. *GluDt3-62* and *GluDt3-63* showed a 6-bp insertion, a 24-bp deletion, and a 15–21 base substitution in the coding region, of which a nonsense mutation from C to T at position 622 resulted in pseudogenes. *GluDt3-64* had five base substitutions, including a nonsense mutation at the position 742. *GluDt3-65*, *GluDt3-66*, and *GluDt3-67* all had a base deletion at position 247, as well as 7–8 base substitutions, which resulted in frameshift mutations in the three haplotypes. These results indicated that *Ae. tauschii* also contains six *Glu-D3* genes, and their allelic variants are even richer than those in common wheat.

Allelic variation at the Glu-D3 locus in Chinese bread wheat and effects on dough properties, pan bread, and noodle qualities.

Glutenin subunit alleles at the *Glu-D3* locus and their effects on dough properties, pan bread, and dry white Chinese noodle (DWCN) qualities were investigated using 106 winter and facultative wheat cultivars and advanced lines. Allele *Glu-D3c* (42.5%) was the most frequent glutenin subunit, followed by *Glu-D3b* (25.5%) and *Glu-D3a* (23.6%). *Glu-D3d* and *Glu-D3f* occurred in only three and six cultivars, respectively. The effect of *Glu-D3* was significant for DWCN quality, accounting for up to 16% of the variation, but there were no significant differences between individual *Glu-D3* alleles on dough properties and qualities of DWCN and pan bread. Interaction effects '*Glu-A1* × *Glu-D3*' and '*Glu-B1* × *Glu-D3*' were significant for DWCN quality and loaf volume. More work is needed to understand the effects of *Glu-D3* variation on the determination of dough properties and end-use quality.

Characterization of a phytoene synthase 1 gene (Psy1) located on common wheat chromosome 7A and development of a functional marker.

Phytoene synthase (Psy), a critical enzyme in the carotenoid biosynthetic pathway, demonstrated high association with the yellow pigment (YP) content in wheat grain. Characterization of Psy genes and the development of functional markers for them are of importance for marker-assisted selection in wheat breeding. We characterized the full-length genomic DNA sequence of a Psy gene (*Psy-A1*) located on chromosome 7A by *in silico* cloning and experimental validation. The cloned *Psy-A1* comprises six exons and five introns, 4,175 bp in total, and an ORF of 1,284 bp, encoding a Psy precursor peptide of 428 amino acids with a calculated molecular weight of ~47.7 kD. A co-dominant marker, YP7A, was developed based on polymorphisms of two haplotypes of *Psy-A1*, yielding 194-bp and 231-bp fragments in cultivars with high and low YP content, respectively. The marker YP7A was mapped on chromosome 7AL using a RIL population from cross 'PH82-2/Neixing 188', and a set of Chinese Spring nullisomic-tetrasomic lines and ditelosomic line 7AS. *Psy-A1*, co-segregating with the STS marker YP7A, was linked to SSR marker *Xwmc809* on chromosome 7AL with a genetic distance of 5.8 cM, and explained 20–28% of the phenotypic variance for YP content across three environments. A total of 217 Chinese wheat cultivars and advanced lines were used to validate the association between the polymorphic band pattern and grain YP content. The results showed that the functional marker YP7A was closely related to grain YP content and, therefore, could be used in wheat-breeding programs targeting of YP content for various wheat-based products.

Cloning and phylogenetic analysis of polyphenol oxidase genes in common wheat and related species.

Cloning and phylogenetic analysis of polyphenol oxidase (PPO) genes in common wheat and its relatives would greatly advance the understanding of molecular mechanisms of grain PPO activity. Six wheat relative species, including *T. urartu*, *T. monococcum* subsps. *monococcum* and *aegilopoides*, *T. turgidum* subsps. *dicoccoides* and *durum,* and *Ae. tauschii*, were sampled to isolate new alleles at *Ppo-A1* and *Ppo-D1* loci corresponding to common wheat PPO genes,. Seven new alleles were identified from these species, which were designated as *Ppo-A1c* (from *T. urartu*), *Ppo-A1d* (*T. monococcum* subsp. *aegilopoides*), Ppo-A1e (*T. monococcum* subsp. *monococcum* and *T. turgidum* subsp. *durum*), *Ppo-A1f* (*T. turgidum* subsp. *dicoccoides*), *Ppo-A1g* (*T. turgidum* subsp. *durum*), and *Ppo-D1c* and *Ppo-D1d* (*Ae. tauschii*). Five out of the seven alleles detected in the wheat relatives contained an open reading frame (ORF) of 1,731 bp encoding a polypeptide of 577 residues, which is the same as those of *Ppo-A1* and *Ppo-D1* genes in common wheat, whereas the full-length ORF of the allele *Ppo-A1g* from *T. turgidum* subsp. *durum* was not obtained, and a 73-bp deletion occurred in the third exon of *Ppo-D1d*, an allele from *Ae. tauschii*, resulting in a shorter polypeptide of 466 amino acids. The 191-bp insertion in the first intron reported previously in common wheat was also found in *T. turgidum* subsp. *dicoccoides* lines, implying that more than one tetraploid wheat lines may be involved in the origination of common wheat. Phylogenetic trees were constructed using the genomic DNA sequences of the seven alleles, together with four from common wheat and four partial PPO gene sequences deposited in GenBank. The genome tribe A was divided into two clusters, one of which contained *Ppo-A1d* and *Ppo-A1e*, and the other included the remaining five alleles at the *Ppo-A1* locus. The alleles from different clusters showed high sequence divergences, indicated by dozens of SNPs and five to six InDels. The genome tribe D comprised the alleles *Ppo-D1a*, *Ppo-D1c*, *Ppo-D1d*, and *Ppo-D1b*, and the former three were clustered together, showing significant sequence divergence from *Ppo-D1b*.

Association between percent SDS-unextractable polymeric protein (%UPP) and end-use quality in Chinese bread wheat cultivars.

The effect of genotype and environment on the size distribution of polymeric proteins was studied in two trials, Trial I with 33 spring cultivars and Trial II with 21 winter cultivars sown in four environments in the northwestern China spring wheat region and northern winter wheat region, respectively. The association between quantity and size distribution of polymeric protein and dough properties (both trials), and northern-style Chinese steamed-bread (CSB) (Trial I) and pan bread (Trial II) qualities also were investigated. In Trial I, all protein attributes, i.e., flour protein content, SDS-extractable polymeric protein in the flour (EPP), SDS-unextractable polymeric protein in the flour (UPP), and percent UPP in total polymeric protein (%UPP), were largely determined by environment, whereas variation in dough strength resulted from variation in UPP and %UPP across environments. In Trial II, EPP was largely determined by environment, and UPP and %UPP were largely determined by genotype. These differences might result from different levels of protein content and dough strength in the two trials. EPP was positively correlated with dough extensibility and was generally negatively correlated with dough stability and maximum resistance in both trials. However, %UPP was significantly positively correlated with dough stability and maximum resistance and end-use quality in both trials. In Trial I, the correlation coefficients between %UPP and maximum resistance and CSB score were 0.90 and 0.71, respectively, whereas in Trial II, the correlation coefficients between %UPP and maximum resistance and pan bread score were 0.96 and 0.87, respectively. Therefore, selection for high %UPP together with high-quality-glutenin subunits should lead to improved dough strength and end-use quality in Chinese wheats.

Molecular characterization of Pina and Pinb allelic variations in Xinjiang landraces and commercial wheat cultivars.

Our objective was to characterize allelic variations at the *Pina* and *Pinb* loci in Xinjiang wheat germ plasm for further understanding the mechanisms involved in endosperm texture formation and the status of grain texture in Chinese bread wheat. A total of 291 wheat cultivars, including 56 landraces, and 95 introduced and 140 locally improved cultivars, grown in Xinjiang, were used for SKCS measurement and molecular characterization. Among the harvested grain samples, 185 (63.6%), 40 (13.7%), and 66 (22.7%) were classified as hard, mixed, and soft, respectively. Eight different genotypes for the *Pina* and *Pinb* loci were identified, including seven previously reported genotypes, i.e., *Pina-D1a*/*Pinb-D1a*, *Pina-D1a*/*Pinb-D1b*, *Pina-D1b*/*Pinb-D1a*, *Pina-D1a*/*Pinb-D1p*, *Pina-D1a*/*Pinb-D1q*, *Pina-D1a*/*Pinb-D1aa*,

Pina-D1a/*Pinb-D1ab*, and a novel *Pinb* allele, *Pinb-D1ac*. This new allele, detected in the local landrace Kashibaipi and Red Star (from Russia) had a double mutation at the 257th (G to A substitution) and 382nd (C to T substitution) nucleotide positions of the coding region. *Pina-D1b*, *Pinb-D1b*, and *Pinb-D1p* were the most common alleles in Xinjiang wheat germ plasm, with frequencies of 14.3%, 38.1%, and 28.6% in hard textured landraces, 25.5%, 56.9%, and 11.8% in hard introduced cultivars, and 24.8%, 47.8%, and 26.5% in hard locally improved cultivars, respectively. The restriction enzymes *Apa*I, *Sap*I, *Bst*XI, and *Sfa*NI were used to identify *Pinb-D1ab* or *Pinb-D1ac*, *Pinb-D1b*, *Pinb-D1e*, and *Pinb-Dg,* respectively, by digesting PCR products of the *Pinb* gene. The unique grain hardness distribution in Xinjiang bread wheat and the CAPs markers for identification of the *Pinb* alleles provided useful information for breeding wheat cultivars with optimum grain textures.

HarvestPlus wheat.

A study of the effects of processing method including pan bread, steamed bread, and Chinese dry white noodles on mineral element including Fe, Zn, and P concentrations has been completed. High and significant processing and genotype effects on all the traits were found, with processing method contributing the largest for concentration of K, whereas the other traits were influenced mainly by genotype. Genotype, environment, and their interactions all had highly significant effects on all mineral element concentrations and kernel characteristic traits including 1,000-kernel weight and protein content.

Distribution of the photoperiod insensitive Ppd-D1a allele in Chinese wheat cultivars.

Photoperiod response is of great importance for optimal adaptation of bread wheat cultivars to specific environments, and variation is commonly associated with allelic differences at the *Ppd-D1* locus on chromosome 2D. A total of 926 Chinese wheat landraces and improved cultivars collected from nine wheat-growing zones were tested for their genotypes at the *Ppd-D1* locus using allele-specific markers. The average frequency of the photoperiod-insensitive *Ppd-D1a* allele was 66.0%, with frequencies of 38.6% and 90.6% in landraces and improved cultivars, respectively. However, the *Ppd-D1a* allele was present in all improved cultivars released after 1970, except for spring wheats in high latitude northwestern China and winter wheats in Gansu and Xinjiang. The presence of the *Ppd-D1a* allele in landraces and improved cultivars increased gradually from north to south, illustrating the relationship between photoperiod response and environment. *Ppd-D1a* in Chinese wheats is derived from three sources, the Japanese landrace Akagomughi and the Chinese landraces Mazhamai and Youzimai. The current information is important for understanding the broad adaptation of improved Chinese wheat cultivars.

Resistance to rusts and powdery mildew.

Stem rust. In total, 134 differential cultivars were sown in 29 locations, and stem rust only was observed in Guizhou and Keshan. Twe;ve differential cultivars from North America were used to characterize races of 52 Chinese stem rust samples,and the frequencies of major races CFM, CFR, MFM, and MFC were 50.0%, 15.4%, 15.4%, and 11.5%, respectively. Three dominant, Chinese races, 21C3CTH, 21C3CFH, and 34MKG, were used to characterize the resistance of 367 Chinese advanced lines and 131 CIMMYT lines (first stem rust nursery) giving 92 and 310 resistant genotypes, respectively.

Six Australian races were used to identified the stem rust resistance genes in 70 Chinese wheat cultivars, and *Sr5*, *Sr7b*, *Sr8a*, *Sr8b*, *Sr9g*, *Sr10*, *Sr18*, *Sr21*, *Sr23*, *Sr24*, *Sr31*, and *Sr38* were present in 43 genotypes; 11 genotypes conferred resistance to *Sr31*. Molecular markers for *Sr24*, *Sr31*, and *Sr38* were used to confirm the results from gene postulations and indicated that the data from molecular marker shares 90% agreement with gene postulation.

More than 300 Chinese cultivars were sent to Kenya for screening to Ug99. Four cultivars from the Sichuan Province were identified to be MR in Kenya in 2007, and a 5-ha seed increase/pilot plot per cultivar for three cultivars will be sown in October 2008. A total of 380 Chinese cultivars, including the those with an MR response identified in the 2007 season in Kenya, were sent to Kenya for field testing. The first Stem Rust Resistance Nursery and 60 Stem Rust Resistance Materials for China and Turkey were increased and distributed to 16 Chinese institutes. Forty key

agronomic parents from five representative institutes were sent to Cornell University. A stem rust workshop was held in June, with 35 participants from 25 institutes. Five Chinese scientists attended the Ug99 Rust Workshop in Australia.

Molecular mapping of leaf rust resistance gene LrZH84 in Chinese wheat line Zhou 8425B.

With the objectives of identifying and mapping new genes for resistance to leaf rust, F_1 and F_2 plants and F_3 lines from a cross between resistant line Zhou 8425B and susceptible line Chinese Spring were inoculated with Chinese *P. triticina* races THTT and MBHP in the greenhouse. A total of 793 pairs of SSR primers were used to test the parents and resistant and susceptible bulks. Seven polymorphic, chromosome-1B markers were used for genotyping the F_2 and F_3 populations. Zhou 8425B carried a single dominant resistance gene, temporarily designated *LrZH84*, linked to SSR markers *Xgwm582-1B* and *Xbarc8-1B* with genetic distances of 3.9 cM and 5.2 cM, respectively. The *Xbarc8* allele co-segregated with *Lr26* in the F_3 population. The *Xgwm582* allele associated with *LrZH84* was identified as a wheat gene and shown to be present in the Predgornaia 2 parent of Zhou 8425B. The seedling reaction pattern of *LrZH84* was different from those of lines with *Lr26*, *Lr33*, *Lr44*, and *Lr46*, all of which are located in chromosome 1B. We concluded that *LrZH84* is likely to be a new leaf rust-resistance gene.

A novel homeobox-like gene associated with reaction to stripe rust and powdery mildew in common wheat.

Stripe rust and powdery mildew, caused by *P. striiformis* f. sp. *tritici* and *B. graminis* f. sp. *tritici*, respectively, are severe diseases in wheat worldwide. In our study, differential amplification of a 201-bp cDNA fragment was obtained in a cDNA-AFLP analysis between near-isogenic lines Yr10NIL and Avocet S, inoculated with *P. striiformis* f. sp. *tritici* race CYR29. A full-length cDNA (1,357 bp) of a homeobox-like gene, TaHLRG (GenBank accession EU385606), was obtained in common wheat based on the sequence of GenBank accession AW448633 with high similarity to the above fragment. The genomic DNA sequence (2,396 bp) of TaHLRG contains three exons and two introns. TaHLRG appeared to be a novel homeobox-like gene, encoding a protein with a predicted 66-amino-acid homeobox domain and was involved in race-specific responses to stripe rust in real-time quantitative PCR analyses with Yr9NIL, Yr10NIL, and Avocet S. TaHLRG also was associated with adult-plant resistance to stripe rust and powdery mildew based on the field trials of doubled haploid lines derived from the cross 'Bainong 64/Jingshuang 16' and two $F_{2:3}$ populations from the crosses 'Lumai 21/Jingshuang 16' and 'Strampelli/Huixianhong'. A functional marker, THR1, was developed based on the sequence of TaHLRG and located on chromosome 6A using a set of Chinese Spring nulli-tetrasomic lines.

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