Table 3. Estimated losses in winter wheat due to rust in 2013 (T = trace, less than 1% loss statewide; — no state estimates available; and * = preliminary 2013 Kansas wheat disease loss estimate).

State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
				%	1,000 bu	%	1,000 bu	%	1,000 bu
NJ	29	54.0	1,566	—	—	—	—	—	—
NM	70	44.0	3,080	—	—	—	—	—	—
NY	115	68.0	7,820	0.0	0	T	T	0.0	0
NC	920	57.0	52,440	0.0	0	2.0	1,070	T	T
ND	205	44.9	8,815	T	T	T	T	0.0	0
OH	665	70.0	46,550	T	T	T	T	T	T
OK	3,400	31.0	105,400	0.0	0	0.0	0	T	T
OR	780	62.1	48,360	0.0	0	0.0	0	2.0	987
PA	160	68.0	10,880	—	—	—	—	—	—
SC	255	54.0	13,770	0.0	0	1.0	139	T	T
SD	670	42.2	26,130	T	T	T	T	T	T
TN	540	71.0	38,340	0.0	0	T	T	2.0	T
TX	2,250	29.0	65,250	—	—	—	—	—	—
UT	110	44.5	4,840	—	—	—	—	—	—
VA	275	62.0	17,050	—	—	—	—	—	—
WA	1,660	66.9	114,540	0.0	0	T	T	1.0	1,157
WV	7	52.0	364	—	—	—	—	—	—
WI	265	58.0	15,370	T	T	2.0	314	2.0	314
WY	120	24.0	2,880	—	—	—	—	—	—
U.S. % loss				T		0.3		0.7	
U.S. total	32,402	47.4	1,534,253		T		3,924		10,378

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SOUTH DAKOTA

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Fine mapping and metabolic and physiological characterization of the glume glaucousness inhibitor locus Iw3 derived from wild wheat.

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Cuticular wax constitutes the outermost layer of plant skin and its composition greatly impacts plant appearance and plant-environment interaction. Epicuticular wax in the upper part of adult wheat plants can form the glaucousness, which associates with drought tolerance. We characterized the glume-specific, glaucousness inhibitor *Iw3* by fine mapping and physiological and molecular approaches. *Iw3* inhibits glaucousness formation by altering wax composition. Compared to the wild type, *Iw3* eliminates β-diketone, reduces primary alcohols by 47%, but increases aldehyde 400-fold and alkanes fivefold, which leads to a 30% reduction of total glume wax load. Loss of glaucousness increased cuticle permeability, suggesting an important role in drought sensitivity. Genetically, the glaucousness-inhibiting effect of *Iw3* is partially dominant in a dosage-dependent manner. We localized the *Iw3* locus within a 0.13-cM interval delimited by marker loci *Xpsp3000* and *XWL3096*. Of the 53 wax genes assayed, we detected transcription changes in nine genes by *Iw3*, down-

Table 4. Estimated losses in spring and durum wheat due to rust in 2013 (T = trace, — = no state estimate available, N/A = data not available, * U.S. total does not includestates for which loss or production data is not available).

SPRING WHEAT

				Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	%	1,000 bu	%	1,000 bu	%	1,000 bu
CA	N/A	N/A	N/A	0.0	0	0.0	0	T	T
CO	9	82.0	738	0.0	0	0.0	0	0.0	0
ID	510	77.0	39,270	0.0	0	0.0	0	5.0	2,067
MN	1,160	57.0	66,120	0.0	0	T	T	0.0	0
MT	2,850	37.0	105,450	0.0	0	0.0	0	3.0	3,261
ND	5,060	46.0	232,760	0.0	0	T	T	0.0	0
NV	3	75.0	225	—	—	—	—	—	—
NY	N/A	N/A	N/A	0.0	0	T	T	0.0	0
OR	88	63.0	5,544	0.0	0	T	T	2.0	1,046
SD	1,165	44.0	51,260	T	T	T	T	T	T
UT	14	48.0	672	—	—	—	—	—	—
WA	495	60.0	29,700	T	T	T	T	T	T
U.S. % loss				T		T		1.2	
U.S. total *	11,354	46.8	531,739		T		T		6,374

DURUM WHEAT

				Losses due to:					
				Stem rust		Leaf rust		Stripe rust	
State	1,000 acres harvested	Yields in bushels per acre	Production in 1,000 of bushels	%	1,000 bu	%	1,000 bu	%	1,000 bu
AZ	79	102.0	8,058	—	—	—	—	—	—
CA	67	100.0	6,700	0.0	0	0.0	0	T	T
ID	11	62.0	682	0.0	0	0.0	0	0.0	0
MT	490	34.0	16,660	0.0	0	0.0	0	0.0	0
ND	770	38.0	29,260	0.0	0	T	T	0.0	0
OR	N/A	N/A	N/A	0.0	0	0.0	0	0.0	0
SD	4	42.0	168	0.0	0	0.0	0	0.0	0
U.S. % loss				0.0		T		T	
U.S. total *	1,421	43.3	61,528		0		T		T

regulation of Cer4-1 and up-regulation of other five Cer4 and three KCS2 homologs. All these results provided initial insight into the *Iw3*-mediated regulation of wax metabolism and paved the way for an in-depth characterization of the *Iw3* locus and the glaucousness-related β-diketone pathway.

W3 is a new wax locus that is essential for biosynthesis of β-diketone, development of glaucousness, and reduction of cuticle permeability in common wheat.

Zhengzhi Zhang, Wenjie Wei, Huilan Zhu, Ghana S. Challa, and Wanlong Li; Caili Bi (Department of Biology, Hebei Normal University, Shijiazhuang, Hebei 050024, PR China); and Harold N. Trick (Department of Plant Pathology, Kansas State University, Manhattan, KS 66506, USA).

The cuticle plays important roles in plant development, growth, and defense against biotic and abiotic attacks. Different from the model plants, cuticles of adult wheat and barley plants are rich in hentriacontane-14,16-dione and its hydroxy isoforms (also known as β-diketone), but their biosynthetic pathway largely remains unknown. We identified a novel wax mutant in the wheat cultivar Bobwhite. The mutation is not allelic to the known wax gene loci *W1* and *W2*, and is designated as *W3*. Genetic analysis localized *W3* on chromosome arm 2BS. The *w3* mutation reduced by 99.0% β-diketones, which account for 63.3% of the total wax load, but increased the hydroxy-β-diketones to β-diketone ratio

11-fold, suggesting differential roles of *W3* in β-diketone biosynthesis and its hydroxylation. Loss of β-diketones caused failure to form glaucousness and a significant increase in cuticle permeability in terms of water loss and chlorophyll efflux in the *w3* mutant. Transcription of 23 cuticle genes from five functional categories was altered in the *w3* mutant; 19 down-regulated and four up-regulated, suggesting a possibility that *W3* encodes a transcription regulator coordinating expression of cuticle genes. Biosynthesis of β-diketones in wheat and their implications in glaucousness formation and drought and heat tolerance were discussed.

Fine mapping of shattering locus Br2 revealed local chromosomal structure differentiation between the two lineages of Aegilops tauschii.

Zhengzhi Zhang, Huilan Zhu, and Wanlong Li, and Bikram S. Gill (Wheat Genetics Resource Center, Department of Plant Pathology, Kansas State University, Manhattan, KS 66506, USA).

Chromosome inversions often accompany population differentiation and capture local adaptation during speciation. *Aegilops tauschii*, the D-genome donor species of hexaploid wheat, consist of two genetically isolated lineages, L1 and L2, but little is known about the genetic mechanisms underlying the population split in this diploid species. During fine-mapping of shattering gene *Br2* using a large F_2 population derived from a cross between *Ae. tauschii* accessions TA1604 (an L1 accession) and AL8/78 (an L2 accession), we found contrasting patterns of crossover distribution in the *Br2* interval and neighboring regions despite the high, local gene synteny with *Brachypodium distachyon* and rice. *Br2* is localized in an 0.08-cM interval, and 13 marker loci formed a block, where single-crossover was completely suppressed, but a double crossover was enriched with a recombination rate of ~11 cM/Mb. In a neighboring region, no double crossover was recovered, but the single-crossover rate reached 24 cM/Mb, much higher than the genome-wide average. This result suggests a tentative inversion polymorphism between the parental lines in the *Br2* region. Genotyping using the markers from the *Br2* region divided a collection of 55 randomly sampled *Ae. tauschii* accessions into two major groups, and they are largely isolated in genetics. The two groups correspond to the lineages L1 and L2 based on their geographic distribution patterns. This data provides first line of evidence that inversion may underlie the evolution of *Ae. tauschii* lineages.

The chloroplast view of the evolution of polyploid wheat.

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Polyploid wheats comprise four species: *Triticum turgidum* (AABB genomes) and *T. aestivum* (AABBDD) in the emmer lineage, and *T. timopheevii* (AAGG) and *T. zhukovskyi* ($AAGGA^mA^m$) in the timopheevi lineage. Genetic relationships between chloroplast genomes were studied to trace the evolutionary history of the species. Twenty-five chloroplast genomes were sequenced, and 1,127 plant accessions were genotyped, representing 13 *Triticum* and *Aegilops* species. *Aegilops speltoides* (SS genome) diverged prior to the divergence of *T. urartu* (AA), *Ae. tauschii* (DD), and *Aegilops* species of the Sitopsis section. *Aegilops speltoides* forms a monophyletic clade with the polyploid emmer and timopheevi wheats, which originated within the last 0.7 and 0.4 million years, respectively. The geographical distribution of chloroplast haplotypes of the wild tetraploid wheats, as well as of, illustrates the possible geographic origin of the emmer lineage in the southern Levant and the timopheevi lineage in northern Iraq. *Aegilops speltoides* is the closest relative of the diploid donor of the chloroplast (cytoplasm), as well as the B and G genomes to the timopheevi and emmer lineages. Chloroplast haplotypes were often shared by species or subspecies within major lineages and between the lineages, indicating their contribution in introgression to the evolution and domestication of polyploid wheats.