International Plant Resistance to Insects Newsletter

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EDITORS' PAGE
2003 Newsletter

Welcome from the Department of Entomology at Kansas State University to volume 27 of the International Plant Resistance to Insects Newsletter (IPRI Newsletter). We hope the present format of the newsletter is helping plant resistance researchers continue to move into the world of 21st century digital communications; however, submissions have become very low, and so we are wondering if there is a need to continue the Newsletter. This issue will be discussed at the 2004 IPRI workshop.

For those of you reading the newsletter for the first time, we welcome your comments and contributions. If you wish to contribute items to future newsletters, they should be Word files of two pages or less of text in length (tables are not printed) and submitted as e-mail file attachments to jreese@oznet.ksu.edu.

Other types of plant resistance to insects information continue to be accessible also. The KSU Plant Resistance to Pests listserv, established by Donna Schenck-Hamlin of the KSU Hale Library and now administered by John Reese (JREESE@OZNET.KSU.EDU), is intended for continuous information exchange among individuals globally interested in plant resistance to pests about professional meetings, conferences and research grants, as well as new research developments concerning plant resistance to arthropods and plant pathogens. To subscribe to the bulletin board, send an e-mail message to: <listserv@ksuvm.ksu.edu>, with the subject line blank, and the message "SUB PRP firstname lastname."
Use the e-mail address <PRP@KSUVM.KSU.EDU>to send a message to the entire bulletin board group. Kansas State University plant resistance to insects information is available on the Worldwide Web at http://www.oznet.ksu.edu/dp_entm/welcome.htm. Items available include the Painter Reprint Collection, archive editions of IPRIN, and links to related websites including the Crop Science Society of America, CGIAR (Consultative Group for International Agricultural Research), and the Technology ISB Monthly News Report. Information is also available on how to subscribe to Plant Breeding News.

Thank for your interest in the IPRIN 2003. Please send your suggestions for improvement to John Reese at jreese@oznet.ksu.edu, or Department of Entomology, Waters Hall, Kansas State University, Manhattan, KS 66506-4004. Your continued support, through contributions and/or financial assistance is much appreciated. Financial contributions may be sent to Sherry Figge, Department of Entomology, Waters Hall, Kansas State University, Manhattan, KS 66506-4004, Attention IPRIN.

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Dissertation Abstracts

KANSAS

A high-density genetic map of the *Aegilops tauschii* Genome includes genes, retrotransposons and microsatellites, and provides unique insight into cereal chromosome structure and function.

Elena Boyko, Department of Entomology, Kansas State University, Manhattan, KS; Ruslan Kalendar, Alan H. Schulman Institute of Biotechnology, Plant Genomics Laboratory Finland; University of Helsinki, Victor Korzun, Institute of Plant Genetics, Gatersleben, Federal Republic of Germany; Abraham Korol, Instutue of Evolution, Univeristy of Haifa, Haifa, Israel and Gill Bikram, Department of Plant Pathology, Kansas State University, Manhattan, KS USA

Aegilops tauschii (Coss.) Schmal. (2n=2x=14, DD) (syn. *Ae. squarrosa* L.; *Triticum tauschii*) is well known as the D-genome donor of bread wheat (*T. aestivum*, 2n=6x=42, AABBDD). Because of the highly syntenic nature of the genomes within the Triticeae, a high-density map of the Ae. tauschii Coss. genome will be useful for breeding and genetics within this tribe of grasses which includes bread wheat, barley, and rye. We have placed 248 new loci onto a high density genetic map of *Ae. tauschii* for a total 727 loci making it one of the most extensive maps produced to date for the Triticeae species. Seventy four of the mapped loci are defense-related genes.

The retrotransposon marker system recently developed for cultivated barley (*Hordeum vulgare L.*) was successfully applied to *Ae. tauschii* with the placement of 80 retrotransposon loci onto the map. A total of 50 microsatellite and ISSR loci also were added.

The resistance and defenseresponse genes are organized into separate clusters. A significant correlation between the physical density of markers (number of markers mapped to the chromosome segment/ physical size of the same segment in micrometers) and recombination rate (genetic size of a chromosome segment/physical size of the same segment in micrometers) was demonstrated. Discrete regions of negative or positive interference (an excess or lack of double crossovers in adjacent intervals relative to the expected rates on the assumption of no interference, respectively) was observed in most of the chromosomes. Eighty percent of the markers located in the pericentromeric regions showed negative interference. Islands with negative and/or no interference were present in interstitial and distal regions in both short and long chromosome arms. Most of the positive interference was restricted to the long arms of *Ae. tauschii* chromosomes.

A DNA Marker in Bread Wheat Linked to a Gene Expressing Resistance to the Greenbug. E. V. Boyko, S. R. Starkey, C. M. Smith, Department of Entomology, Kansas State University; and B. S. Gill, Department of Plant Pathology, Kansas State University.

The greenbug, *Schizaphis graminum*, (Rondani) and the Russian wheat aphid, *Diuraphis noxia* (Mordvilko) are the major aphid pests of wheat worldwide, especially in the southwestern and western United States. Cultivars of bread wheat (*Triticum aestivum* L. em Thell, 2n=6x=42, AABBDD) containing *Gb* (*Schizaphis graminum*) and *Dn* (*Diuraphis noxia*) resistance genes have begun to be produced and cultivated. However, the existence of biotypes of both aphids may result in the eventual development of additional biotypes that overcome presently used greenbug and Russian wheat aphid resistance genes. Therefore, it is important to develop a basic understanding of the chromosome location of known aphid resistance genes and new genes as they are identified. In the present study, molecular marker-assisted selection was used to identify resistance in a segregating population of plant genotypes from a cross between two *Triticum aestivum* wheats; PI220127 (*D. noxia* resistant) and "Sando's 4040" (*S. graminum* resistant). Restriction fragment length polymorphism (RFLP) probes covering all seven wheat homeologous groups of chromosomes were evaluated for linkage between probe loci and putative aphid resistance genes. Grouping molecular markers at a LOD threshold of 3.0 yielded a linkage group of 23 EST,RFLP, and SSR loci, including wheat SSR 332 (wheat chromosome 7A), and ESTs for a putative zinc finger protein, (*XZnfp*) and a pathogenesis-related protein (*Prlb*). *Gby* was linked to two flanking RFLP loci on the short arm of wheat chromosome 7A – *Xcdo91-7A.1*, distally at 11.3cM, and *Xbcd385*, proximally at 7.5cM. A cytogenetic map created using makers common to our 7A genetic map and group 7 physical maps further suggests that *Gby* is located in the subtelomeric region of the short arm of wheat 7A. The distal regions of group 7 chromosomes are characterized as having a high recombination rate and a high marker density. Thus, *Gby* is a very good candidate for map-based cloning. This is a first report of chromosome location of and molecular markers linked to new genes expressing resistance to greenbug in wheat.

Publications:

Boyko, E.V., Gill, K.S., Mickelson-Young, L., Nasuda, S., Raupp, W. J., Ziegler, J. N., Singh, S., Hassawi, D. S., Fritz, A. K., Namuth, D., Lapitan, N.L.V. and Gill, B. S. 1999. A high-density genetic linkage map of *Aegilops tauschii*, the D-genome progenitor of bread wheat. *Theor. Appl. Genet.* 99:16-26.

Boyko, E.V., Kalendar, R., Korzun, V., Korol, A., Schulman, A. and Gill, B.S. 2002. A high-density cytogenetic map of the *Aegilops tauschii* genome incorporating retrotransposons and defense-related genes: insights into cereal chromosome structure and function. *Plant Mol. Biol. (Special Issue)* 48:767-790.

Plant, Animal & Microbe Genomes X. Final Abstracts Guide. January 12-16, 2002, San Diego, CA, P384.

Identification of *Aegilops* Germplasm with Multiple Aphid Resistance. C. M. Smith and S. Starkey, Department of Entomology, Kansas State University; H. Havlickova and V. Holubec, Research Institute of Crop Protection, Ruzyne, Prague, Czech Republic; and B. S. Gill, Wheat Genetic Resource Center, Kansas State University, Manhattan, KS.

The greenbug, *Schizaphis graminum*, (Rondani), the Russian wheat aphid, *Diuraphis noxia* (Mordvilko), and the bird cherry oat aphid, *Rhopalosiphum padi* (L.), cause several million dollars worth of wheat production losses annually in Europe and the United States. In this study, *Triticum* and *Aegilops* accessions from the Czech Research Institute of Crop Protection and the Kansas State University Wheat Genetic Resources Center were evaluated for resistance to these aphids. Accessions with aphid cross-resistance were examined for expression of the antibiosis, antixenosis, and tolerance categories of resistance.

Aegilops neglecta accession 8052 exhibited antibiotic effects toward all three aphids in the form of reduced intrinsic rate of increase (r_m). The r_m of greenbug (biotype I) on *Ae. neglecta* 8052 was significantly lower than that of greenbugs on plants of the susceptible U. S. variety Thunderbird. The r_m of Russian wheat aphids was significantly lower on foliage of both *Ae. neglecta* 8052 and *T. araraticum* accession 168 than on Thunderbird. r_m values for bird cherry oat aphids fed both *Ae. neglecta* 8052 and *T. araraticum* 168 were also significantly lower than those for bird cherry oat aphids fed the susceptible Czech variety Zdar. Neither *Ae. neglecta* 8052 or *T. araraticum* 168 exhibited tolerance to either greenbug biotype I or Russian wheat aphid. Preliminary data suggest that *T. araraticum* 168 may also possess tolerance to bird cherry oat aphid. New genes from *Ae. neglecta* and *T. araraticum* expressing aphid antibiosis can be used to develop multiple aphid resistant wheats in the U. S. and Central Europe.

Publications:

Flinn, M. F., C. M. Smith, J. C. Reese and B. S. Gill. 2001. Categories of resistance to greenbug (Homoptera: Aphididae) biotype I in *Aegilops tauschii* germplasm. *J. Econ. Entomol.* 94: 558-563.

Srinivas, P., S. D. Danielson, C. M. Smith and J. D. Foster. 2001. Induced resistance to bean leaf beetle (Coleoptera: Chrysomelidae) in soybean. J. Entomol. Sci. 36:438-444.

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C.A. Baker, J.D. Burd, N.C. Elliot, S.D. Kindler, D.W. Mornhinweg, D.R. Porter, K.A. Shufran.

Russian wheat aphid, *Diuraphis noxia* (Mordvilko)

Wheat

Efforts are ongoing to develop Russian wheat aphid (RWA)-resistant wheat germplasm. Advanced wheat lines derived from 13 different RWA resistance sources were planted for seed increase, evaluation, and purification in preparation for germplasm release and possible varietal release; these include 48 hard white winter lines, 35 hard red winter lines, 40 hard red spring lines, 55 soft white spring lines, and 54 hard white spring lines. Topcrossed seed was screened for resistance to RWA, and resistant plants were transplanted to the greenhouse for increase and progeny testing. Homozygous RWA-resistant lines will be selected for germplasm release. Field evaluations of winter RWA-resistant wheat lines were made in Goodwell, Oklahoma.

Durum wheats maintained by USDA–ARS GRIN have been evaluated for resistance to RWA. Resistant plants were identified, rescued, and grown for seed increase. Approximately 87 winter durum lines and 13 spring durum lines were grown for evaluation. Purified selections will be reintroduced to the GRIN collection, and crosses will be made with agronomically acceptable durum wheats.

Genetic diversity studies are ongoing for all resistant lines to determine if these lines carry different genes for resistance to RWA.

Barley

Efforts continue to develop adapted RWA-resistant germplasm lines for all barley producing areas of the U.S.

Spring Barley

Ten adapted spring barley germplasm lines, developed in conjunction with Phil Bregitzer, were evaluated in advanced yield nurseries at 4 locations in Idaho, 2 locations in

Colorado and 2 locations in Nebraska. Cooperators for these field trials were: Phil Bregitzer, Idaho; Bob Hammon, Colorado; and David Baltensperger, Nebraska. These lines have potential for cultivar release. 187 adapted, advanced generation RWA-resistant germplasm lines were evaluated in the field in 4 locations in Idaho. These lines involved 14 susceptible backgrounds and 23 resistant sources. Seventy lines were selected for further yield testing in 2002. Multiple germplasm releases are planned from these lines after the 2002 season. A preliminary yield trial was conducted in a dryland barley production area of Colorado with the cooperation of Frank Peairs. This trial involved 114 RWA-resistant lines developed in an Otis background with 3 sources of resistance. Eighteen lines were selected for further testing at several locations in Colorado in 2002. A smaller preliminary yield trial was conducted with 30 of these lines in Idaho by Phil Bregitzer. One thousand adapted, advanced generation germplasm lines were evaluated in observation rows in Idaho with Phil Bregitzer.

Winter Barley

Thirty-three adapted RWA-resistant germplasm lines were evaluated in a preliminary yield trial in Idaho with the cooperation of Charles Erickson involving 3 susceptible backgrounds and 9 resistant sources. Five hundred and sixty headrows and 600 observation rows were also evaluated. From these, 37 lines were selected for further testing in replicated yield trials in 2002. One thousand advance generation germplasm lines were tested for adaptation to Western Colorado with the cooperation of Bob Hammon. These lines involved 2 susceptible backgrounds and 7 resistant sources. Seventy-five lines were selected for a replicated yield trial in 2002.

Genetics

Development of genetic populations to study inheritance of RWA resistance and genetic diversity in all 109 RWA-resistant barley lines previously identified at Stillwater continued.

Greenbug, *Schizaphis graminum* (Rondani)

A regional field study to characterize the occurrence of the greenbug holocycle and assess its overwintering ability was conducted during the past three wheat-growing seasons at research locations ranging from South Dakota to Texas. Sexual morph production began in mid October and peaked in November while oviposition began each year in November. Greenbugs were capable of producing oviparae and viable eggs throughout the primary hard red winter wheat production area of the Great Plains, and thus for any given year, failure of greenbug sexual reproduction was due to local climatic conditions and host availability. Collaborative studies with West Texas A&M University have been initiated to optimize the process of artificially generating the greenbug holocycle and improving egg-hatch success.

Rice root aphid, *Rhopalosiphum rufiabdominalis (Sasaki)*

An obscure aphid was found infesting wheat in Oklahoma in the fall of l999 and identified as the rice root aphid. Rather high numbers of this aphid has been found infesting wheat since the initial observation in 1999 beginning in October and continuing through the middle of January. During October and the first half of November of 200l this aphid was the most abundant aphid found infesting wheat in Garfield County, Oklahoma. During the same time the aphid was found to be infesting almost every field sampled in the western half of Oklahoma and was found infesting experimental plots of several varieties of cereal ryes and wheat located at Hays, Kansas. Based on greenhouse conducted aphid confinement test, all small grains were suitable hosts for the rice root aphid based on reproductive rates and aphid survival. Rice and sorghum were poor hosts, while corn was a non-host. Forage grasses were, for most part, found to be inferior hosts for the rice root aphid when compared to small grains. The results of greenhouse conducted experiments indicated the rice root aphid can cause a significant reduction in the forage yield of both wheat and barley. Since considerable acreage of wheat planted in Oklahoma is grazed by cattle, the aphid's ability to reduce forage yield of wheat may be of significant economic importance. In addition to the direct feeding damage, it can also transmit barley yellow dwarf disease, which can be devastating to a wheat crop.

Bird cherry oat aphid, *Rhopalosiphum padi* , L.

Efforts continue to develop a seedling screening technique for BCO. A small-scale replicated study was conducted in the greenhouse on 10 barley lines previously identified in the literature as either susceptible or resistant to BCO or resistant to BYDMV. Seedlings were infested with BCO at the one leaf stage and measurements on shoots and roots recorded in an attempt to identify a trait showing visual damage symptoms from BCO feeding. The same measurements were made on an identical planting grown in the greenhouse at the same time but kept aphid free by repeated insecticide applications. Analysis is ongoing.

Personnel

Matt Greenstone left USDA-ARS-PSWCRL to be science editor for Bioscience and has since become Research Leader with the ARS in Beltsville.

Old faces new positions:
D.W. Mornhinweg – Research Geneticist
K.A. Shufran – Research Entomologist

Publications.

Burd, J. D. 2002. Physiological modification of the host feeding site by cereal aphids (Homoptera: Aphididae). J. Econ. Entomol. 95: 463-468.

Anstead, J. A., J. D. Burd, and K. A. Shufran. 2002. Mitochondrial DNA sequence divergence among Schizaphis graminum isolates from non-cultivated hosts: Haplotypes and host associations. Bul. Entomol. Res. 92: 17-24.

Kindler, S.D., N.C. Elliott, K.L. Giles, T.A. Royer, R. Fuentes-Granados, and F. Tao. 2002. Effect of greenbugs on winter wheat yield. J. Econ. Entomol. 95:89-95.

Kindler, S.D., T.L. Harvey, G.E. Wilde, R.A. Shufran, H.L. Brooks and P.E. Sloderbeck, and R.A. Shufran. 2001. Occurrence of greenbug biotype K in the field. J. Agric. Urban Entomol. 18:23-34.

Mornhinweg, D.W., D.R. Porter, and J.A.Webster. Inheritance of RWA-resistant spring barley germplasm line Stars-9577B. Crop Science (In Press).

Royer, T.A., K.L. Giles, S.D. Kindler, and N.C. Elliott. 2001. Developmental response of three geographic isolates of *Lysiphlebus testaceipes* (Cresson) (Hymenoptera: Aphididae) to temperature. Environ. Entomol. 30:637-641

Wilde, G.E., R.A. Shufran, S.D. Kindler, H.L. Brooks, and P.E. Sloderbeck. 2001. Distribution and abundance of insecticide resistant greenbugs (Homoptera: Aphididae) and validation of a bioassay to assess resistance. J. Econ. Entomol. 94:547-551.

JAPAN

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Summary of current plant resistance research

Nephotettix cincticeps Uhler (green rice leafhopper, GRH) is one of the most serious insect pests of rice in temperate Asia. GRH is a vector for the transmission of rice stripe and rice dwarf viruses. Utilization of resistance gene to GRH is effective for protecting rice plants against virus diseases. Three genes for antibiosis type of resistance to GRH were identified by RFLP mapping using near-isogenic lines (NILs) derived from two kinds of crosses between susceptible Japonica and resistant Indica varieties. In the first cross combination between Asominori and IR24, IR24 and F_1 were highly resistant with above 80 % nymph mortality, but Asominori was susceptible with 0 % nymph mortality. The self-pollinated progeny of the NIL heterozygous for the resistant gene showed 3 resistant and 1 susceptible segregation. A single dominant gene for resistance, which corresponds to *Grh1*, was mapped on chromosome 5. In the second cross combination between Kinmaze and DV85, DV85 and F_1 were highly resistant, but Kinmaze was susceptible. Using NILs, two dominant genes for resistance, those would correspond to *Grh4* and *Grh2*, were mapped on chromosomes 3 and 11, respectively. The NIL only for *Grh2* showed moderate resistance. *Grh2* was necessary for *Grh4* to express strong resistance to GRH.

DISSERTATION ABSTRACTS

Ph.D. Dissertation. Xuming Liu, Department of Entomology, Kansas State University.

Molecular Mapping of Wheat Genes Expressing Resistance to the Russian Wheat Aphid, *Diuraphis Noxia* (Mordvilko) (Homoptera: Aphididae). December, 2001. Major Advisor, C. M. Smith.

The Russian wheat aphid (RWA), *Diuraphis noxia* (Mordvilko), is a serious, worldwide, economic pest of wheat (*Triticum aestivum* L. em. Thell). The results of our experiments identified microsatellite markers linked to several known genes as well as new genes expressing RWA resistance in wheat. Wheat microsatellite marker *Xgwm111* located on chromosome 7DS (short arm) is tightly linked to *Dn* (*Diuraphis noxia*) genes *Dn1, Dn2*, and *Dn5*, as well as *Dnx* in wheat at approximately 3.0 cM. The markers *Xgwm44* and *Xgwm111* are linked to *Dn6* near the centromere on chromosome 7DS at 14.6 cM and 3.0 cM, respectively. This is the first report of the chromosome location of *Dn6*, which is either allelic or tightly linked to *Dn1, Dn2*, *Dn5*, and *Dnx*. The chromosome arm locations of markers *Xgwm44* and *Xgwm111* (and the linked genes) were confirmed to be chromosome 7DS by di-telosomic and nulli-tetrasomic analyses. *Xgwm106* and *Xgwm337* flanked *Dn4* on chromosome 1DS at 7.4 cM and 12.9 cM, respectively.

Xgwm635 (near the distal end of 7DS) clearly marked the location of a previously suggested resistance gene in PI 294994, which we have designated as *Dn8. Xgwm642*, in a defense gene-rich region of chromosome 1DL, marked another new gene (*Dn9*) from PI 294994. A third new gene (*Dny*) from the Chinese wheat Lin-Yuan207, was localized on chromosome 1DL between *Xgdm111* and *Xgwm337*.

A new type of molecular marker-based inheritance**,** semi-codominant inheritance, was demonstrated in a wheat segregating population. The mechanism proposed for this inheritance is the competitive PCR amplification of the primer-matched DNA template of one parent over the primer-mismatched DNA template of another parent due to sequence mutation in the primer binding sites. Genetic maps of the above *Dn* genes and linked markers were constructed for wheat chromosomes 1D and 7D. These markers will be useful in marker-assisted breeding for RWA-resistant wheat.

Publications:

Liu, X.M., Smith, C.M., Gill, B.S. and Tolmay, V. 2001. Microsatellite markers linked to six Russian wheat aphid resistance genes in wheat. *Theor. Appl. Genet.* 102:504-510.

Liu, X. M., C.M. Smith, and B. S. Gill. 2002. Identification of microsatellite markers linked to Russian wheat aphid resistance genes *Dn4* and *Dn6*. *Theor. Appl. Genet. 104:1042-1048.*

Ph.D. Dissertation. Renu Malik, Department of Entomology, Kansas State University.

Molecular Genetic Characterization of Wheat Curl Mite, *Aceria tosichella* Keifer (Acari: Eriophyidae), and Wheat Genes Conferring Wheat Curl Mite Resistance. December, 2001. Major Advisor, C. M. Smith.

The wheat curl mite (WCM), *Aceria tosichella* Keifer, a serious pest of wheat in North America, is the only vector known to transmit wheat streak mosaic virus (WSMV), which consistently reduces wheat yields. Genetic resistance to WCM has shown direct and indirect suppression of WCM and WSMV, respectively, in the field. Here we report the mapping of a new gene, designated as *Cmc4*, in common wheat derived from *Ae. tauschii* that provides resistance to the six known WCM strains. Monosomic analyses showed that *Cmc4* is located on chromosome 6D and is inherited as a single dominant gene. Molecular mapping placed *Cmc4* on the distal end of chromosome 6D towards the telomere. The locus containing *Cmc4* is flanked by markers- GDM141 (4.1cM) and KSUG8 (6.4cM). Only a small segment of chromosome 6D containing *Cmc4* was transferred from *Ae. tauschii* to the common wheat germplasm KS96WGRC40. This is the first report of the genetic mapping of a gene providing resistance to WCM. Thus, the flanking markers identified may be used in wheat breeding programs for the selection of lines resistant to WCM.

The development of virulence in WCM to mite-resistant wheat varieties demands an understanding of the evolutionary dynamics of different WCM strains existing in different geographic locations. Methods are required for accurate and fast identification of different WCM strains for successful and effective deployment of wheat cultivars resistant to WCM. A nuclear ribosomal DNA marker was identified that differentiates a highly virulent Nebraska (NE) strain of WCM from all other North American WCM strains that transmit wheat streak mosaic virus. The marker amplified a 495-bp fragment containing the partial 3′ end of 18S rDNA, the complete intergenic spacer –1 (ITS-1) and the partial 5′ end of the 5.8S region. When digested with the *HhaI* restriction enzyme, the amplified fragment showed a differential banding pattern between DNA of the Nebraska (NE), Kansas (KS), Montana (MT), and Alberta, Canada (AB) strains of WCM. Sequence analysis of DNA bands of different WCM strains indicated that the NE strain was 1.97 % more variable in the ITS-1 region than all the other strains of WCM. Maximum parsimony method produced a phylogenetic tree representing two clades of WCM strains. One group comprised the KS, MT, and AB strains and the second group comprised the NE strain. *Aceria cajani* and *Aceria pongamiae* were included as outgroups. The NE strain comprises a distinct gene pool from all the other strains.

Aegilops tauschii, the wild diploid D-genome progenitor of wheat (*Triticum aestivum* L.) is an important source of resistance to several arthropod pests and pathogens. One hundred and eight *Ae. tauschii* accessions from different geographic regions were evaluated for resistance to KS, NE, and MT strains of WCM. WCM resistance was detected from all the geographic locations where *Ae. tauschii* occurs. The highest percentage of resistant accessions originated from Turkey, followed by Afghanistan and the Caspian Sea region of Iran. Sixty-seven percent of the accessions were resistant to at least one strain of WCM and at least 19% of the total were resistant to all the three strains of WCM. Resistance to the NE and KS strains occurred more frequently in the accessions tested than did resistance to the MT strain of WCM. Thus, *Ae. tauschii* is a very useful source for WCM resistance genes for common wheat.