ANNUAL WHEAT NEWSLETTER

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Kansas State University, Manhattan.

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III. CULTIVARS AND GERMPLASM

IN DEDICATION TO
DR. SHIVCHARAN SINGH MAAN

Dr. S.S. Maan, a world renowned wheat geneticist, born 11 January, 1926, in Karnal, Punjab, India passed away on 1 November, 2016, at home in Davis, California, while in the care of his wife Ranjit Kaur and daughter Ajit Kaur.

After receiving his B.S. degree in Botany from Punjab University in 1948. He studied at Kansas State University, Manhattan, obtaining an M.S. degree in 1958 and a Ph.D. in 1961. While working as a postdoctoral fellow at the University of Nebraska, Lincoln (1961–63), he made a seminal discovery of a genetic system for producing hybrid wheat. He would then devote his life to hybrid wheat research as a faculty member at North Dakota State University, Fargo, from 1964 until his retirement in 2000.

Dr. Maan was a deep thinker and his discoveries and vision for hybrid wheat were ahead of their time, only now attracting huge interest from industry and academia. Currently, hundreds of millions of dollars are being spent working with materials that Dr. Maan developed to realize the dream of hybrid wheat. The genetic stocks and breeding lines that Dr. Maan and his collaborator Karl Lucken developed underpin hybrid wheat programs around the world, helping to increase wheat yield so that we may be able to feed 9.5 billion people by 2050. Dr. Maan trained many graduate students and postdoctoral fellows, collaborated with many scientists around the world, and published over 100 research papers. For his outstanding research achievements, Dr. Maan was honored as Fellow of the Crop and Agronomy Societies of America and received the Crop Science Research award in 1980. He was awarded the first Distinguished Professorship at North Dakota State University among many other awards and recognitions.

He is survived by his wife of 61 years, Ranjit Kaur Maan, his son Paul Singh Maan, and his daughter Dr. Ajit Kaur Maan, and his grandchildren Sohni Shivan Maan-Davie and Simrin Ruchi Maan-Davie.

Genetic mapping of germination and termite tolerance under drought stress in durum wheat.

An attempt was made to map loci regarding germination and termite tolerance under drought stress under field conditions in a set of 114 recombinant inbred durum wheat lines (RILs) at the NIAB, Pakistan, in 2016–17. The population was developed by making a cross between a drought tolerant cultivar Omrabi5 (O5) with a heat and salt tolerant cultivar Belikh2 (B2) at ICARDA, Syria. The genetic map, constructed at IPK-Gatersleben using 265 markers, was available for genetic mapping. Seeds of 104 RILs were successfully regenerated in the 2015–16 season at the NIAB fields, Pakistan. The regenerated population was grown on 1 November, 2016, in 2-m rows with 9 inches distance between at 5 g seed/line. One set was tested under control conditions and two were tested under drought stress. Irrigation was applied 14 days after sowing to the control, whereas the stress treatments were kept free of any irrigation. Germination data were recorded 3 weeks after planting. Termite infection in drought replicates happened naturally, because drought favors termite attack. Data for termite resistance were recorded on 12 January, 2017, using a visual scale of 0–4, where 0 = no damaged/infected plants, 0.5 = 12.5% plants damaged/infected, 1 = 25% plants damaged/infected, 1.5 = 37.5% plants damaged/infected, 2 = 50% plants damaged/infected, 2.5 = 62.5% plants damaged/infected, 3 = 75% plants damaged/infected, 3.5 = 87.5% plants damaged/infected, and 4 = 100% plants damaged/infected.

Mean germination under control (Gr) ranged between 50% and 100%, with a mean value of 81.86±9.6%. Germination under drought (GrD) reduced the mean to 72.16±9.6% and ranged between 47.5% and 92.5%. Relative germination in drought (RGrD) ranged from 66.7% to 100%, where the mean value was 88.38±8.1%. The mean value of termite tolerance (TT) was 1.37±0.6 and ranged from 0.5 to 3. Genetic mapping, using QTL cartographer v2.5, revealed a total of seven (five major (with $R^2 > 0.1$) and two minor (with $R^2 < 0.09$)) QTL. There were three QTL (one minor and two major QTL) for Gr; two were detected on chromosome 5A (onw associated with marker *Xbarc342* at 73.7 cM with LOD score of 2.51 and $R^2 = 0.086$ contributed by O5 and the other associated with marker *Xgwm1171b* at 171.8 cM with LOD score of 3.6 and $R^2 = 0.18$ contributed by B2) and one on 6B (associated with marker *Xbarc178* at 147.1 cM with LOD score of 3.03 and $R^2 = 0.12$ contributed by B2). For GrD, one minor QTL was observed on chromosome 6B (associated with marker *Xbarc247* at 149.9 cM with LOD score of 2.56 and $R^2 = 0.09$ contributed by B2). Two major QTL were discovered for RGrD on chromosomes 2A (associated with marker *Xgwm1256* at 179.9 cM with LOD score of 2.73 and $R^2 = 0.11$ contributed by O5) and 4B (associated with marker *Xgwm736b* at 140.2 cM with LOD score of 3.2 and $R^2 = 0.11$ contributed by O5). In the end, there was one major QTL for TT that was observed on chromosome 5B (associated with marker *Xgwm1043* at 140.2 cM with LOD score of 3.7 and $R^2 = 0.15$ contributed by B2). This study will be extended to genetic mapping of yield and yield related traits under field conditions in future.

Induction of tolerance to Fusarium head blight.

Fusarium graminerarum (*Fg*) infests a wide range of hosts, including wheat, corn, and barley, producing yield losses, deterioration of the quality, and grain contamination with mycotoxins, which constitute a risk to human and animal health. Few sources of Fusarium head blight (FHB) resistance have been reported, and several resulted in a lack of tolerance when these lines were tested with local populations of *Fg*.

For 8 years, several wheat recombinant and dihaploid populations were tested against a wide range of *Fg* strains in Argentina. We identified lines with SAR and ISR types of tolerance activated by the spray with plant hormones. In the last year, we assessed if the pretreatment with gibberellic acid (GA) and jasmonic acid (J) elicited inducible defences against *Fg*. Two experimental lines (M and P) and a commercial cultivar (ACA 315) were used. The trials were performed in two localities, La Plata and Tres Arroyos, Argentian, with a complete factorial design in blocks with three replicates for every treatment.

At anthesis, spikes of every wheat line or cultivar were sprayed with water (control plants (C)), GA (10^{-4} M), or J (10^{-4} M). After 48 h, half of the pretreated spikes were inoculated with *Fg*. Such a technique helps to highlight the mechanism of resistance to spread of the pathogen (Type-II mechanism). The following treatments were recorded: control-*Fg*, gibberellic-*Fg*, jasmonic-*Fg*. At harvest, spikes were maintained at room temperature until these were manually hacked. Total grain number (GT), the damaged grain (GD), and the 1,000-kernel weight (TKW) were recorded. An ANOVA included the assessment of genotype, treatment, locality, and the interactions. The mean analysis showed the gibberellic-*Fg* treatment significantly increased the total number of grains in both experimental lines compared with the controls and the plants treated with jasmonic acid. Experimental line M produced a higher number of GT compared to that of the commercial cultivar ACA 315; when both were treated with J these wheats presented similar GTs. The number of GD was reduced under the J treatment in line M, compared to the rest of inoculated treatments (C-*Fg* and G-*Fg*). ACA 315 showed a low number of GD when infested compared with their controls. The TKW was significantly lower in ACA315 J and J-*Fg* treatments. Locality influenced the TKW, with the highest values obtained in Tres Arroyos, in the experimental line P, when plants were treated with G and inoculated (G-*Fg*). This value was significantly higher compared with the rest of the treatments at both localities. Treatment with hormones could induce Type-II FHB tolerance in wheat lines carrying this mechanism of resistance.

Isoenzyme profiles of grain esterases in hexaploid wheat.

Esterases represent a large group of enzymes that catalyze cleavage of multiple-ester bonds. In general, esterases are divided into four types: cholinesterases (most frequently, these are identified using ordinary electrophoretic analysis), acetylesterases, arylesterases, and carboxyl esterases. Plant carboxyl esterases catalyze conversion of the esters into bioactive acids and alcohols, thereby playing a key role in many biological processes. Lack of epistatic interactions and a co-dominant nature of inheritance of the esterase isozymes makes them meaningful for quick and accessible investigation of the processes of biochemical adaptation to environmental changes. Such a marker, which is convenient for solution of practical problems of selection, can be used as a tool that can speed up and simplify the selection of significant material. Our aim was to estimate the isoenzyme profile of esterases isolated from mature seed and, to ascertain using such a biochemical marker, the polymorphism among samples of promising breeding material of hexaploid wheat. Ripe seed from following wheat cultivars were used as samples: Zlata, Lyubava, Agatha, Lisa (spring wheat), and Mera (winter wheat) (originated from the Moscow Agricultural Research Institute «Nemchinovka», Moscow District, Russian Federation); lines AFI91 and AFI177 (spring wheat) (originated from the Agrophysical Research Institute–AFI, St. Petersburg, Russian Federation); and RILs 7, 10, 29, 32, 44, 47, 57, 83, 88, 89, and 115 of the ITMI mapping population (spring wheat). The seeds were ground in a porcelain mortar and the flour sieved. Enzymes were extracted from the flour and subjected to vertical native electrophoresis using 4% concentrating and 8% separating polyacrylamide gels. Molecular weight markers were Page Ruler Prestained Protein Ladder (Thermo Scientific, Lithuania). After electrophoresis, gels were treated with a reagent for a nonspecific esterase and scanned. The individual electrophoretic profile of each sample was estimated. Heterozygosity and its dispersion were calculated.

The esterase complex in the wheat seed studied was represented by 10 isoforms. Between nine and ten isoforms of various electrophoretic mobility were identified in cultivars Zlata, Lyubava, Agatha, Lisa, and Mera, seven were found in line AFI91, eight in AFI177, and from seven to ten in the ITMI RILs. All samples were characterized by the presence of esterases isoforms *Est-8*, *Est-9*, and *Est-10*. Heterogeneity was found only in the qualitative and quantitative composition of esterases with a greater molecular weight, *Est-1*, *Est-2*, *Est-3*, *Est-4*, *Est-5*, *Est-6*, and *Est-7*. Each cultivar among the 18 had a genotype different from that in the other samples. The average heterozygosity (H) of samples within ten loci encoding esterase isoforms was 0.924; the dispersion of heterozygosity for all the samples studied was $\mathrm{Var}(H) = 0.0004$. As a result of the analyses, the most promising breeding parental forms are cultivars Zlata and Mera and lines AFI91, AFI177, ITMI7, ITMI44, ITMI83, and ITMI115. Because of the existence of ten isoforms in hexaploid wheat, the esterases might represent a convenient biochemical marker suitable for examination of samples of the hexaploid wheat at physiological, biochemical, and genetic levels.

Studies on drought stress in spring wheat using genome-wide association mapping.

As a result of climate change, drought severity is expected to increase in the future, which will limit the global production of different crops. Bread wheat is one of the most important crops worldwide facing drought that will result in yield loses. Today, tolerance against abiotic stress is an important goal in wheat breeding. Identification of wheat genotypes that tolerate drought conditions and detect QTL for drought stress were the aims of a study using 111 spring wheat genebank accessions from 27 countries and genotyped with the 15k chip. Drought stress was applied by chemical desiccation using potassium iodide (KI, 0.5% w/v). KI was applied 14 days after anthesis to simulate drought in two subsequent years. The accessions were evaluated for a number of morphological and agronomical traits, such as plant height, spike length, grain number, and 1,000-kernel weight. Genome-wide association mapping studies were performed to reveal significant marker-trait associations under drought and control conditions. The analysis showed that chemical desiccation had a strong impact on yield parameters and significant differences between the genotypes. Genome-wide association mapping analysis revealed major marker-trait associations on different chromosomes.

VIII. VOLUME 64 MANUSCRIPT GUIDELINES.

The required format for Volume 64 of the *Annual Wheat Newsletter* will be similar to previous editions edited from Kansas State University.

CONTRIBUTIONS MAY INCLUDE:

—Current activities on your projects.
—New cultivars and germ plasm released.
—Special reports of particular interest, new ideas, etc., normally not acceptable for scientific journals.
—A list of recent publications.
—News: new positions, advancements, retirements, necrology.
—Wheat stocks; lines for distribution, special equipment, computer software, breeding procedures, techniques, etc.

FORMATTING & SUBMITTING MANUSCRIPTS:

Follow the format in volume 44–63 of the *Newsletter* in coördinating and preparing your contribution, particularly for state, station, contributor names, and headings. Use Microsoft Word™ or send an RTF file that can be converted. Please include a separate jpg, gif, or equivalent file of any graphic in the contribution. Submit by E-mail to jraupp@k-state.edu.

DISTRIBUTION:

The only method of distribution of Volume 64 will be electronic PDF either by email or through download from the Kansas State University Research Exchange (K-REx) (https://krex.k-state.edu/dspace/browse?value=Raupp%2C+W.+J.&type=author).

The *Annual Wheat Newsletter* also will continue to be available (Vol. 37–64) through the Internet on GrainGenes, the USDA–ARS Wheat Database at http://wheat.pw.usda.gov/ggpages/awn/.