

2021 Hard Winter Wheat Rust Symposium

April 6th & 8th, 2021

U.S. Time Zones				Tuesday, April 6th
Pacific	Mountain	Central	Eastern	
				Stripe Rust
7:00am	8:00am	9:00am	10:00am	Plenary Session Welcome: Bob Bowden, USDA-ARS Chair: Katherine Frels, University of Nebraska
7:10am	8:10am	9:10am	10:10am	Erick DeWolf, Kansas State University Documenting Changes in Virulence and Tolerance to Heat Stress in Great Plains Populations of <i>Puccinia striiformis</i> f.sp. <i>tritici</i> 20 min talk / 10 min Q & A
7:40am	8:40am	9:40am	10:40am	Xianming Chen, USDA-ARS Races of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> and stripe rust resistance relevant to the hard red winter wheat region 20 min talk / 10 min Q & A
8:10am	9:10am	10:10am	11:10am	10 min Break
8:20am	9:20am	10:20am	11:20am	Kim Garland-Campbell, USDA-ARS Stripe Rust Gene Introgression & Stewardship 20 min talk / 10 min Q & A
8:50am	9:50am	10:50am	11:50am	5 min Break
8:55am	9:55am	10:55am	11:55am	FLASH TALKS Chair: Jeff Boehm, Jr., USDA-ARS 5 min per speaker
				Shuyu Liu Adult plant resistance in a popular cultivar TAM 111
9:00am	10:00am	11:00am	12:00am	Elena Gulyaeva Studies of <i>Puccinia striiformis</i> f. sp. <i>tritici</i> in Russia
9:05am	10:05am	11:05am	12:05pm	Wardah Mustahsan Mapping Wheat Stripe Rust Resistance in Overlay x Overland Population
9:10am	10:10am	11:10am	12:10pm	Buket Sahin Phenotypic Evaluation of Stripe Rust, Leaf Rust and Stem Rust Resistance in A-genome Diploid Relatives of Wheat
9:15am	10:15am	11:15am	12:15pm	FLASH TALK Q & A Session / 15 min
9:30am	10:30am	11:30am	12:30pm	LUNCH BREAK

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U.S. Time Zones				Tuesday, April 6th
Pacific	Mountain	Central	Eastern	
				Leaf Rust
11:00am	12:00pm	1:00pm	2:00pm	Plenary Session Chair: Mary Guttieri, USDA-ARS
11:05am	12:05pm	1:05pm	2:05pm	Jim Kolmer, USDA-ARS Leaf Rust Virulence Overview and Resistant Cultivars with APR 20 min talk / 10 min Q & A
11:35am	12:35pm	1:35pm	2:35pm	John Fellers, USDA-ARS Molecular Biology of <i>Puccinia triticina</i> 20 min talk / 10 min Q & A
12:05pm	1:05pm	2:05pm	3:05pm	10 min Break
12:15pm	1:15pm	2:15pm	3:15pm	Amir Ibrahim, Texas A&M AgriLife Research Overview of Texas Germplasm and Castroville Rust Nursery 20 min talk / 10 min Q & A
12:45pm	1:45pm	2:45pm	3:45pm	5 min Break
12:50pm	1:50pm	2:50pm	3:50pm	FLASH TALKS Chair: Jeff Boehm, Jr., USDA-ARS 5 min per speaker
				Marshall Clinesmith Genomic Regions Associated with Resistance to Leaf Rust in Hard Winter Wheat
12:55pm	1:55pm	2:55pm	3:55pm	Joe Hahn QTL Analysis of Wheat Leaf Rust in the Lakin/Roelfs F2007 Backcross Population
1:00pm	2:00pm	3:00pm	4:00pm	Zoia Sikharulidze Exploring the main characteristics of wheat genotypes selected from international nurseries in Georgia
1:05pm	2:05pm	3:05pm	4:05pm	FLASH TALK Q & A Session / 15 min
1:20pm	2:20pm	3:20pm	4:20pm	ADJOURN

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U.S. Time Zones				Thursday, April 8th
Pacific	Mountain	Central	Eastern	
				Stem Rust
7:00am	8:00am	9:00am	10:00am	Plenary Session Chair: Allan Fritz, KSU
7:05am	8:05am	9:05am	10:05am	Yue Jin, USDA-ARS Diversity and novelty of virulence detected in global stem rust 20 min talk / 10 min Q & A
7:35am	8:35am	9:35am	10:35am	Dave Marshall, USDA-ARS Identifying Germplasm with Resistance to African Stem Rust Races 20 min talk / 10 min Q & A
8:05am	9:05am	10:05am	11:05am	10 min Break
8:15am	9:15am	10:15am	11:15am	Les Szabo, USDA-ARS Adventures in phylogenetics and diagnostics of the wheat stem rust fungus in the U.S. and abroad 20 min talk / 10 min Q & A
8:45am	9:45am	10:45am	11:45am	Matt Rouse, USDA-ARS Characterization and introgression of wheat resistance to stem rust 20 min talk / 10 min Q & A
9:15am	10:15am	11:15am	12:15pm	10 min Break
9:25am	10:25am	11:25am	12:25pm	FLASH TALKS Chair: Jeff Boehm, Jr., USDA-ARS
				Dylan Mangel Wheat Bacterial Leaf Blight Susceptibility is Tightly Linked to Sr2 (10 minutes)
9:35am	10:35am	11:35am	12:35pm	Max Fraser Identification of a new adult plant resistance locus in Khorasan wheat conferring adult plant resistance to the Ug99 stem rust race group
9:40am	10:40am	11:40am	12:40pm	FLASH TALK Q & A Session / 15 min
9:55am	10:55am	11:55pm	12:55pm	LUNCH BREAK

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U.S. Time Zones				Thursday, April 8th
Pacific	Mountain	Central	Eastern	
				Stewardship of <i>R</i>-genes
11:00am	12:00pm	1:00pm	2:00pm	Plenary Session Chair: Amir Ibrahim, Texas A&M AgriLife Research
11:05am	12:05pm	1:05pm	2:05pm	Allan Fritz, Kansas State University Stewardship of Rust <i>R</i>-genes and Breeding with a Universal Donor 20 min talk / 10 min Q & A
11:35am	12:35pm	1:35pm	2:35pm	Mary Guttieri, USDA-ARS Rust Resistant Germplasm Update and Gene Stewardship 20 min talk / 10 min Q & A
12:05pm	1:05pm	2:05pm	3:05pm	10 min Break
12:15pm	1:15pm	2:15pm	3:15pm	Rust Panel Open Discussion: Coordinated Breeding Stewardship of Rust <i>R</i> genes 30 minutes
12:45pm	1:45pm	2:45pm	3:45pm	RUST SYMPOSIUM END

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ABSTRACTS FOR PLENARY SPEAKERS

Documenting Changes in Virulence and Tolerance to Heat Stress in Great Plains Populations of *Puccinia striiformis* f.sp. *tritici*

Erick DeWolf¹, Heather Gardner¹, and Robert Bowden²

¹Kansas State University, Department of Plant Pathology, Manhattan, KS 66506

²USDA-ARS, Hard Winter Wheat Genetics Research Unit, Manhattan, KS 66506

In 2001, stripe rust emerged as a yield-limiting constraint to wheat production in Kansas. Field observations indicate that the virulence of the *Puccinia striiformis* f.sp. *tritici* (*Pst*) population has changed since 2001 with critical shifts occurring in 2010, 2012, and 2017. These observations also suggest that current *Pst* populations remain active at temperatures previously considered unfavorable for disease development. The objective of this study is to document changes in virulence and evaluate heat stress tolerance with pathogen isolates collected between 2010-2020. In these studies, wheat varieties were selected to represent widely used sources of genetic resistance over the past decade. These varieties were inoculated with pathogen isolates collected between 2010-2020 with a focus on isolates representing putative virulence changes in the *Pst* population. Heat tolerance was evaluated by exposing plants with incubating lesions of stripe rust to 2-7 days of heat stress (simulated diurnal temperature cycles with Max T=35C and Min T between 18, 20, 22 or 24C). Results support field observations of key virulence shifts in 2010 (*Yr17*), and 2012 (*QYr.tamu-2B*). There was also evidence that the virulence to both the *Yr17* and *QYr.tamu-2B* resistance emerged around 2017 and was common by 2020. Heat stress experiments indicate that *Pst* isolates from 2020 were able to tolerate diurnal cycles of heat stress as long as there was a cool period (<24C) for the fungus to recover.

Races of *Puccinia striiformis* f. sp. *tritici* and stripe rust resistance relevant to the hard red winter wheat region

Xianming Chen, USDA-ARS Wheat Health, Genetics, and Quality Research Unit and Department of Plant Pathology, Washington State University, Pullman, WA

Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, is an important disease of wheat in the hard winter wheat production region in the U.S. Great Plains. Samples of wheat stripe rust collected by collaborators in the region, together with those from other regions, were tested on a set of 18 *Yr* single-gene differentials for identifying races. Races identified in the recent years will be presented in comparison with other regions. Frequencies of virulence to the 18 *Yr* genes over the years will be presented. Molecular characterization of the pathogen population revealed high diversity and rapid structural changes in the country. Genetic relationships of the population in the hard wheat region with other regions will be discussed. Every year, entries of the hard wheat regional nursery are tested in multiple locations in Washington States under natural infection and in the greenhouse with predominant races in both seedling-low temperature (4-20°C) and adult-plant-high temperature (10-30°C) conditions to identify wheat lines with race-specific all-stage resistance and non-race specific high-temperature adult-plant (HTAP) resistance to stripe rust. The data of the recent years will be presented and discussed. A winter wheat panel of 857 entries including cultivars and breeding lines from the hard wheat region were studied with specific molecular markers and through genome-wide association study for identifying genes or QTL for resistance to stripe rust. As *Yr17* is a major gene presented in cultivars and breeding lines in this region and other regions and the pathogen populations are highly virulent to this gene, the results of our recent study for identifying a HTAP resistance gene linked to *Yr17* will be discussed. Genes for effective all-stage resistance or HTAP resistance will be proposed for diversifying stripe rust resistance in breeding programs.

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Leaf Rust of Wheat in the Great Plains and Prospects for Durable Resistance

James Kolmer, USDA-ARS Cereal Disease Laboratory, St. Paul, MN

Leaf rust, caused by *Puccinia triticina*, is a common disease of wheat in the Great Plains region. In 2019 and 2020 yield losses of 2-8% due to leaf rust occurred in Texas, Oklahoma, and Kansas. In 2019 and 2020 races MNPSD and MPPSD, which are virulent to the leading cultivar SY Monument, increased in frequency in the southern Great Plains. Races MNPSD and MPPSD are virulent to genes *Lr24*, *Lr26*, *Lr37* and *Lr39* which are present in many hard red winter wheat cultivars. In 2020 races with virulence to durum wheat were collected from rust detection plots in the Rio Grande Valley. The durum races are also virulent to common wheat cultivars that have *Lr39*, and may potentially spread to northern durum growing regions. Cultivars with race-specific seedling resistance have constantly selected virulent races of *P. triticina* for over 70 years. Hard red winter wheat cultivars with combinations of the adult plant resistance genes *Lr34*, *Lr46*, *Lr77*, and soft red winter cultivars with *Lr74* have had durable leaf rust resistance over years. Hard red winter wheat cultivars with combinations of adult plant resistance genes can be selected by utilizing tightly linked markers in addition to evaluation and selection in rust nursery plots. In the spring wheat region of Minnesota and North Dakota, races with virulence to *Lr21* were the most common in 2020 having been selected by cultivars with this gene. Hard red spring wheat cultivars with combinations of *Lr13*, *Lr16*, *Lr23*, and *Lr34* have had moderate to high levels of durable resistance. Tightly linked markers should facilitate selection for these resistance genes.

The Multi-State Rust Evaluation Nursery and Texas Wheat Germplasm

Amir M.H. Ibrahim, Texas A&M University, College Station TX 77843, Email address: Aibrahim@tamu.edu

South Texas is at the forefront of *Puccinia*, where inoculums of wheat leaf rust, caused by *Puccinia triticina* Eriks., stem rust, caused by *Puccinia graminis* f. sp. *tritici*, and stripe rust, caused by *P. striiformis* Westend. f. sp. *tritici* Eriks, overwinter. Our program evaluates hard red winter (HRW) and soft red winter (SRW) wheat regional nurseries at the Multi-state Rust Evaluation Nursery at Castroville, TX. Eighty released SRW cultivars from 15 U.S. programs went through regional testing at this nursery from 2011 to 2020. The nursery is also a hub for deriving resistance by several programs. Breeding material screened ranges from 18,000 to 25,000 entries per year. First sightings of new leaf and stripe rust race changes usually occur in South Texas. This nursery is indispensable for evaluating segregating populations and advanced breeding lines and documenting and forewarning about race changes in popular cultivars in early to mid-April when the crop is in its early stages in other wheat-growing areas in the Great Plains. The U.S. Great Plains breeding programs continue to make steady progress in wheat rust resistance. Screening nurseries and molecular markers allowed these programs to increase resistance levels and lower the production cost for U.S. wheat producers. I will discuss the current status of this nursery and approaches to sustain it and expand screening efforts. I will also provide an overview of the Texas germplasm.

Diversity and novelty of virulence detected in global stem rust populations

Yue Jin, Matthew Rouse and Les Szabo, USDA-ARS Cereal Disease Lab, St. Paul, MN

Pablo Olivera, University of Minnesota

Douglas Luster, USDA-ARS Foreign Disease-Weed Science Research Unit

In the last two decades, wheat stem rust outbreaks and epidemics at various scales have occurred in Africa, Central Asia and Europe, indicating that the disease has re-emerged as a serious threat to wheat production. Working with international partners, we have characterized stem rust pathogen isolates that have contributed to these epidemics/outbreaks. We have closely monitored the evolution and spread of the Ug99 race group and detected variants that rendered some of the most important stem rust resistance genes, such as *Sr24*, *Sr36* and *SrTmp*, or

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combination thereof, ineffective. The occurrence of these variants has substantially increased the potential vulnerability of US wheat to Ug99. Novel virulences or virulence combinations attacking genes thought to be universally resistant or highly effective against the Ug99 race group have been detected in stem rust populations that are likely sexual in origin in Europe, Caucasus, and Central Asia. Continued efforts are needed to monitor these populations, and to identify others that are playing a large role in generating novel virulences in order to effectively guide gene deployment strategies, such as selecting sources of resistance in breeding and selecting suitable candidates for constructing resistance gene pyramids or cassettes.

Identifying Germplasm with Resistance to African Stem Rust Races

David Marshall, USDA-ARS, Raleigh, NC

Following the detection and confirmation of Ug-99 stem rust in Uganda in 1999, the global wheat rust community joined together with a common purpose to manage stem rust. One of the objectives was to have a common location where all the world's wheats could be evaluated for resistance. As a result, each year since 2005, the USDA-ARS has conducted a screening nursery for stem rust in Njoro, Kenya. This nursery is in cooperation with CIMMYT (International Maize and Wheat Improvement Center) and KALRO (Kenya Agricultural and Livestock Research Organization). Between 2005-2010, improvements were made in the infrastructure of the Njoro site to enable improved irrigation and plant growth. Between that time and in subsequent years, protocols were improved in order to reliably grow U.S. winter wheat germplasm in Njoro. To date, we have screened about 60,000 winter wheats from both public and private breeding programs in the U.S. We have identified those resistances based more on adult-plant (non-race specific) factors, as well as the effectiveness of race-specific genes. This screening has enabled us to evaluate and sort-out those combined resistances under field conditions to multiple stem rust races each year. Breeders can use this, along with genotypic information, to select lines having stem rust resistance prior to these races arriving in the U.S.

Adventures in phylogenetics and diagnostics of the wheat stem rust fungus in the U.S. and abroad

Les J. Szabo, Yue Jin, USDA-ARS Cereal Disease Laboratory, St. Paul, MN

Pablo Olivera, University of Minnesota, Department of Plant Pathology, St. Paul, MN

Over the last decade the development of genomic resources has facilitated the genotypic characterization of *Puccinia graminis* f. sp. *tritici*. Phylogenetic analysis of representative isolates from asexual populations in Africa, Central Asia, and Europe has identified 12 genetic groups which belong to four clades. Members of the Ug99 race group belong to clade I. This group is evolving, making the relationships between genotypes and phenotypes complex and dynamic. Isolates derived from collections from the Ethiopian epidemic (2013/2014) and the outbreak in Europe (2013) belong to clade IV. This clade is a complex group, containing seven genetic groups and several examples of convergent evolution. Analysis of isolates derived from sexual populations in the Caucasus region and Central Asia are genetically diverse. The U.S. asexual *P. graminis* f. sp. *tritici* population belongs to clade VI, composed of nine genetic groups that cluster into three subgroups. Rapid diagnostic assays, based on SNPs, have been developed that are being used as part of an international surveillance program. These assays allow for in-depth surveys using non-living samples.

Stewardship of Rust R-genes and breeding with a universal donor

Allan Fritz, Dept. of Agronomy, Kansas State University, Manhattan, KS

The Kansas State University wheat breeding program has strategically focused on using race non-specific resistance for leaf and stripe rust. The nearly twenty-year effort has resulted in a high percentage of lines in the breeding program having resistance based on race non-specific genes. The resistance levels are adequate for

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leaf rust but are not generally sufficient to manage heavy stripe rust infections. The goal of the breeding program is to supplement the race non-specific resistance with all-stage resistance that is more likely to be race-specific. The breeding challenge is to maintain or increase the frequency of race non-specific alleles in the breeding program while simultaneously deploying all-stage resistance genes. Our approach is to use a “universal donor” for rust resistance. ‘Bob Dole’ is currently being used as the recurrent parent to build a line that has *Yr5*, *Yr15*, *Yr36*, *Lr42* and *Lr52/Yr47*. BC1s will be created using lines advanced to from the Preliminary Yield Trial to the Advance Yield Trial phase of the breeding program (~60 lines per year) as the recurrent parent and the universal donor as the donor parent. Lines advanced to the elite stage of the program will continue to be backcrossed while lines dropped from consideration will be discarded. Markers can be used for background selection to seed the backcrossing program. This approach should result in a maximum of a one-year delay of release relative to our conventional approach.

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ABSTRACTS FOR FLASH TALKS

Adult plant resistance in a popular cultivar TAM 111

Shuyu Liu, Bhoja R. Basnet, Yan Yang, Jackie C. Rudd, Amir M. H. Ibrahim, Xianming Chen, Esten R. Mason, Robert L. Bowden, Ravi P. Singh, Qignwu Xue, Dirk B. Hays, Paul St Amand, Guihua Bai

Stripe rust epidemics occur when susceptible cultivars meet rust-prone weather conditions and virulent rust pathogen races. After the *Yr17* resistance gene became less effective, several lines including TAM 111 provided resistance to the *Yr17* virulent-race. After TAM 111 resistance was broken down in 2012, the combinations of both *Yr17* and *QYr.tamu.2B* could provide some protections until 2017. A set of 124 recombinant inbred lines from the cross of TAM 112/TAM 111 were phenotyped for rust resistance in eight field experiments and one greenhouse from 2010 to 2012 to understand TAM 111 resistance. Both infection type (IT) and disease severity (DS) were collected from field natural or artificial inoculations and from greenhouse with race PST-100 inoculation. We mapped field and GH resistance to stripe rust in TAM 111 on chromosomes 1A, 2A, 2B, 6B and 7D with the major QTL *QYr.tamu.2B* at 154.3 Mbp. This major QTL could reduce IT by 1.9 (0-9 scale) and DS by 22.4% with the largest R^2 up to 76.1% for IT and 57.1% for DS. We developed KASP markers for this QTL, which have been used to screen lines in regional nurseries (SRPN and RGON) in the USDA Central Small Grains Genotyping Laboratory. However, the markers only work in some genetic backgrounds.

STUDIES OF PUCCINIA STRIIFORMIS F. SP. TRITICI IN RUSSIA

Elena Gulyaeva, Ekaterina Shaydayuk, Darya Iyakovleva
All Russian Institute of Plant Protection, St. Petersburg-Pushkin, Russia

The causative agent's virulence of wheat yellow rust (*Puccinia striiformis*) in large scale of Russia firstly was studied. Leaves with urediopustules were collected in 2019-2020 on soft and durum wheat, triticale and wild grasses in the North Caucasus (Dagestan, Krasnodar), Central Black Earth region (Tambov), and Volga regions (Saratov, Kirovsk) regions, North-West (Saint Petersburg), East (Krasnoyarsk) and West Siberia (Novosibirsk). 82 single pustule isolates were pathotyped using Avocet lines with genes *Yr1*, *Yr5*, *Yr6*, *Yr7*, *Yr8*, *Yr9*, *Yr10*, *Yr15*, *Yr17*, *Yr18*, *Yr24*, *Yr26*, *Yr27*, *YrAR*, *YrSp* as well as set of wheat differential lines (Chinese 166, Lee, Heines Kolben, Vilmorin 23, Moro, Strubes Dickkopf, Suwon 92/Omar), Hybrid 46, Reichersberg 42, Heines Peko, Nord Desprez, Compair, Carstens V, Spaldings Prolific, Heines VII). Genomic DNA was extracted from each isolate for detection of the two invasive strains PstS1 and PstS2. All Russian isolates were avirulent to genes *Yr5*, *Yr10*, *Yr15*, *Yr24* и *Yr26* and Moro variety and virulent to *Yr2*, *Yr6* and Suwon 92/Omar. Virulence to *Yr17* was revealed in one collection from Saratov (Volga region). Variability in virulence was observed on the other *Yr*-lines. Using molecular markers, the four isolates of invasive strains PstS2 were detected in the North-Western region.

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Mapping Wheat Stripe Rust Resistance in Overlay x Overland Population

Wardah K. Mustahsan, Mary J. Guttieri, Robert L. Bowden, Kimberley Garland-Campbell, Guorong Zhang

Stripe rust, also known as yellow rust, (causal organism *Puccinia striiformis f. sp. tritici*) is a major disease hindering wheat production and global food security. Recent race changes have reduced the effectiveness of host plant resistance genes and increased the importance of polygenic resistance. The goal of this study is to understand the genetic mechanisms of disease resistance that can aid in producing durable wheat varieties for producers. In this study, stripe rust resistance was evaluated in a Overlay x Overland RIL population. Overlay carries the *Ae. ventricosa* 2NS segment that contains *Yr17*. Both cultivars had functionally effective field stripe rust resistance until pathogen race changes in 2010-12. We hypothesize, our population will find more useful genomic regions with the Jagger genome than the Chinese Spring genome for discovering novel stripe rust resistance genes. Disease ratings of infection type (IT) and severity (SEV) were evaluated in four field trials 2018-2020: Rossville, KS, Hays, KS, Pullman, and Century Ferry, WA. Environment affected both types of disease ratings. A genetic linkage map for Chinese Spring was constructed using 1,071 SNPs and Jagger was constructed using 1,115 SNPs (GBS). A KASP marker for the 2NS segment was properly positioned on linkage group 2A. QTLs were identified on chromosomes 2A, 2B, and 2D associated with IT and SEV using BLUPs. Informative SNP sequences will be converted to KASP assays to support breeding efforts for stripe rust resistance in hard winter wheat germplasm.

Phenotypic Evaluation of Stripe Rust, Leaf Rust and Stem Rust Resistance in A-genome Diploid Relatives of Wheat

Buket Sahin, Dept. of Plant Pathology, Kansas State University, Manhattan, KS

Global food security relies on increasing production of two main grain crops – rice and wheat. Among these, wheat has greater significance in terms of tonnage. The various rust diseases that attack this crop – leaf rust (*Puccinia triticina*), stripe rust (*Puccinia striiformis* Westend. f. sp. *tritici*) and stem rust (*Puccinia graminis* Pers. f. sp. *tritici*) are important limitations for increasing wheat production in the world. In order to stay ahead of constantly evolving rust pathogens, it is necessary to increase genetic diversity by identifying genetic resistance from sources besides common wheat. Wild relatives of wheat are tractable sources of wheat rust resistance genes. The mini core collection of diploid A-genome species covering about 90 percent of the genetic variation of these species, including 59 accessions of *Triticum monococcum* subsp. *aegilopoides*, 24 accessions of *T. monococcum* subsp. *monococcum*, and 26 accessions of *T. urartu*, spanning their whole area of geographic distribution has been established by using genotype-by-sequencing (GBS). These accessions are being evaluated for their seedling resistance to leaf rust, stripe rust, and stem rust under greenhouse conditions and also being screened for adult plant resistance under both greenhouse and field conditions. This information will be crucial for directed gene transfer from these accessions into advanced wheat breeding lines.

Genomic Regions Associated with Resistance to Leaf Rust in Hard Winter Wheat

Marshall Clinesmith, Allan Fritz, Bob Bowden, Mary Guttieri, Nora Bello, Eduard Akhunov, Cristiano Lemes

Leaf rust caused by *Puccinia triticina* is an important foliar disease in wheat with significant impacts on grain yield. Primary control of leaf rust is through fungicide applications and the deployment of resistant cultivars. The objective of this study was to identify genomic regions associated with adult plant resistance (APR) to leaf rust in the hard winter wheat cultivars Everest and Cedar using a doubled haploid (DH) population. The DH population and parents were phenotyped for leaf rust infection type and severity at the adult plant stage in greenhouse experiments using artificial inoculation with the leaf rust race TFBJQ determined to be virulent on both parents at the seedling stage, and at Castroville, TX under natural inoculum. Cedar was associated with resistance alleles for three genomic regions on chromosomes 2AS, 5AL and 7DS. *QLr.ksu-7DS* from Cedar was identified in all

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datasets conferring the largest effect for both traits and was confirmed to be the APR race non-specific gene *Lr34*. Everest was associated with resistance alleles for six genomic regions on chromosomes 1BL, 2AL, 2BS, 3BL, 4DL, and 7BL. *Q_{Lr.ksu-2AL}* was relatively stable providing the largest effect of any QTL from Everest. These findings suggest the durable APR resistance to leaf rust observed in Everest could be the result of multiple minor effect genes.

QTL Analysis of Wheat Leaf Rust in the Lakin/Roelfs F2007 Backcross Population

Joseph Hahn, Dept. of Plant Pathology, Kansas State University, Manhattan, KS

Leaf rust, caused by the fungus *Puccinia triticina*, is a major disease of wheat in North America. Breeding efforts to achieve resistance have historically been plagued by a cycle in which a resistance gene is discovered, deployed, and rapidly defeated, thus wasting valuable sources of native resistance. Slow-rusting genes, however, can potentially contribute to race-nonspecific resistance to the pathogen for many years. In this study, the adapted Kansas moderately susceptible winter wheat cultivar, 'Lakin', was backcrossed to the Mexican spring wheat, 'Roelfs F2007', which is known to possess adult plant resistance (APR) to leaf rust. The 297 BC1F6-derived progeny of this cross were screened for resistance in five location-years at field nurseries in Kansas and Texas, as well as in two greenhouse studies. Genotyping-by-Sequencing (GBS) generated 2,549 high-quality genome-wide markers used for the construction of a linkage map covering all 21 chromosomes. Quantitative trait locus (QTL) analysis identified reproducible QTLs on chromosome arms 3BS, 5DS, 7BS, and 7BL. Three QTLs contributed by Roelfs F2007 appeared to correspond to locations of known APR genes *Lr74* (3BS), *Lr78* (5DS), and *Lr68* (7BL). The APR QTL on 7BS contributed by Lakin appeared to be novel. Together, the four QTLs accounted for 45.13% and 46.05% of the variation in least squares means for disease severity and infection type, respectively. These results confirm that Roelfs F2007 contains multiple APR loci which may be used in breeding for resistance to infections by *P. triticina*.

Exploring the main characteristics of wheat genotypes selected from international nurseries in Georgia

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Wheat (*Triticum aestivum* L.) is the essential food for Georgians. It is a very important crop for the East Georgia drylands, where it has no practicable alternative in crop rotations. Therefore, strengthening the grain production in the country through growing improved varieties, is one of the internal priorities for the Georgian agricultural sector. Although the climate in Georgia is very favorable for wheat production, wheat yields are very low, averaging 2.5-5 ton/ha. The main reason for the current situation is that the farmers continue to plant old or poorly adapted imported cultivars. The researches conducting in the frame of project #FR-18-978 will identify improved wheat genotypes, which will be superior to the current commercial cultivars of Georgia in terms of adaptation, yield, resistance to diseases and grain quality. In total nine genotypes of wheat from International Nurseries (IN) of ICARDA and CIMMYT including local variety Lomtagora 126 were tested at four locations of Georgia (Dedoplistskharo, Mtskheta, Borjomi, Akhalkalaki) in 2019-2020. Each yield trial was planted on 10 m² plots in four replications using a randomized block design. In accordance with the results of yield trials, the highest yield showed the genotypes: F885K1.1/SXL/3/OMBUL/A1AMO//MV11/4/BONITO-36 (IN-20IWWIT-IR-22) - and HBK0935W-24/K...105W2.1 (IN - 17IWWIT-IR-9807) with an average yield 8kg/10m² and 1000 kernel weight – 45-53g. The average yield of the rest genotypes was between 3.3 – 6.2kg/10m². The grain quality and the bread-making quality of the majority varieties excluding genotypes:SG-RU24/BILINMIYEN96.55(IN-20IWWIT-IR-13) and

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KUV/LJILN//ORACLE/ PEHLIVAN(IN- 20IWWIT-IR-17) were good. The promising genotypes were characterized with adult plant resistance to rusts. The research will be continued in 2021 also.

Wheat Bacterial Leaf Blight Susceptibility is Tightly Linked to Sr2

Dylan Mangel, Elizabeth Elmore, Katherine Reinhart, Jessica Rupp, and Bob Bowden

Bacterial leaf blight (BLB) of wheat has been attributed to the pathogen *Pseudomonas syringae* pv. *syringae* (Pss). Disease development occurs in conditions of high humidity and cool temperatures during the boot stage. The symptoms of BLB are large gray-green lesions or blotches on the upper leaves that quickly become necrotic and bleached to gray or white. However, the symptoms are sporadic under field conditions, which has led to equally sporadic research on the disease. Recently, a correlation was identified between the BLB phenotype and the *Sr2*-linked phenotypes pseudo-black chaff and stem melanism. This suggested that the resistance gene *Sr2* may play a role in BLB pathogenesis. Three recombinant inbred line populations, containing three unique *Sr2* parents ('Kingbird', 'Thunder CL', and 'KS84HW196'), were genotyped and rated for the disease phenotype. All three populations segregated for severity of BLB. Preliminary QTL analysis with the cv. 'Kingbird'-derived population have identified three QTLs related to the BLB phenotype. QTLs associated with increased disease severity were centered on *Sr2* (3BS) and *Lr34* (7DS). There was also a QTL on chromosome 5D, which was associated with a decrease in disease severity. This evidence confirms the tight linkage of *Sr2* and the BLB phenotype. Isolation studies to date have not shown a clear and constant association of Pss with the BLB phenotype. Ongoing research intends to determine if Pss is required for symptom development.

Identification of a new adult plant resistance locus in Khorasan wheat conferring adult plant resistance to the Ug99 stem rust race group

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The *Puccinia graminis* f. sp. *tritici* (Pgt) Ug99 lineage of races presents a major challenge to global wheat production as it is virulent to most resistance genes presently deployed. Our ability to satisfy current and future caloric and nutritional demands hinges on the discovery of new sources of resistance to this pathogen. Therefore, it is imperative that efforts be made to improve the durability and diversity of Ug99 resistance by identifying, characterizing, and deploying novel resistance genes. While the primary gene pool of resistance genes in bread wheat (*Triticum aestivum*) is narrow, the secondary gene pool of wild relatives has proven to be a rich source of genetic diversity. The Khorasan wheat (*Triticum turgidum* ssp. *turanicum*) accession 'Citr 11390' ('Sun Ray'), is resistant to the Ug99 race group at adult growth stages. A population of 121 backcross inbred lines (BILs), developed from 'Sun Ray' and the recurrent parent 'MN07098-6', an advanced breeding line susceptible to Ug99, was used to map the source of resistance carried by 'Sun Ray'. The population was evaluated for stem rust resistance in field nurseries in Njoro, Kenya and Debre Zeit, Ethiopia in 2019 and 2020. A QTL conferring adult plant resistance to Ug99 races was identified on the distal portion of chromosome 2AL, roughly 20Mb from *Sr21*. However, the susceptibility of both parents to TTKSK, as well as the lack of *T. monococcum* in either pedigree, indicates that this is a new locus. Further validation is ongoing, as well as marker development.