XIX INTERNATIONAL WORKSHOP ON SMUTS AND BUNTS

BOOK OF ABSTRACTS

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Editors

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THE MINISTRY HAS BEEN INSTRUMENTAL
IN IMPROVING WHEAT BY SUPPORTING
INTERNATIONAL WINTER WHEAT
IMPROVEMENT PROGRAM

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OPENING SESSION

WHEAT IMPROVEMENT RESULTS, CHALLENGES AND PERSPECTIVES

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Wheat is a key food staple that provides around 20 percent of protein and calories consumed worldwide. Demand for wheat is projected to continue to grow over the coming decades particularly in the developing world to feed an increasing population, and with wheat being a preferred food, continuing to account for a substantial share of human energy needs in 2050. Based on recent trends, an increasing number of poor consumers in low- and middle-income countries will want to eat wheat-based food at an affordable price as populations and economies grow, women and men seek employment in cities, and dietary habits change.

Projections regarding wheat demand growth to 2050 abound and vary widely around an average of approximately +50% relative to 2010. Wheat productivity levels are at a critical juncture. The unfolding scenario implies a wheat demand growth of 1.4% p.a. to 2030 at constant prices. World wheat area has not increased over the last 20 years and there are limited prospects for it to increase. Achieving the yield growth target of 1.4% p.a. would protect (net) wheat consumers (urban and rural) from increasing staple food prices whereas wheat producers, including smallholders, would benefit from increased productivity and the associated producer surplus.

Just over half of global wheat production comes from 75 developing countries, characterized by smallholdings and more than 90% of globally irrigated wheat is grown in developing countries. Over the period 1993 to 2013 world wheat yield grew at 1.0 % p.a. (relative to 2010 average yield), considerably below the 1.4 % p.a. target above. In addition, the future brings new yield constraints only now beginning to be seen in yield statistics, in particular limitations on irrigation water and climate change. The water constraint arises because of over-pumping of ground water in many regions of the world. The climate change threat is most clear in terms of projected warming (rates vary between 0.1 and 0.4 0C per decade, with wheat yield reduced by around -5% to -8%/ 0C). Uncertainty surrounds projected rainfall change, but many models suggest Mediterranean climates may face increased drought. The conclusion from these demand and supply considerations is that developing countries and indeed the world must lift wheat yield growth rate by about 40% over the current rate, whilst increasing stresses will be exerting increasing downward pressure. Furthermore, stakeholders expect this to be achieved sustainably, with greater input use efficiency and minimal off site environmental impact, while preserving or improving the productive capacity of the land under wheat.

The 2008 food-price crisis has highlighted the extreme vulnerability of global Wheat Agri-Food Systems. Effects of local production problems, like droughts, flooding or disease outbreaks, are amplified by global markets, causing price spikes and food insecurity for disadvantaged consumers. Maynard (2015) estimated that in a multiple climate and crop production shock, prices for wheat would increase 4-fold (Maynard, 2015). Building on such broader analyses, research under WHEAT is looking at different ‘what if’ scenarios, such as worse climate change, increased heat stress or repeated multi-year poor harvests in bread baskets. On top of this already challenging setting, biotic stresses continue to evolve in virulence – with the earlier outbreak of Ug99 stem rust causing major upheaval. Now, for the first time, Bangladesh and India reported wheat blast (Magnaporthe grisea) in early 2016, which has thus moved outside Latin America. The bulk of global wheat consumption is met by national and regional production, with about 20% or 160 M tons traded on world markets; predicted to grow by 2050, as imbalances become more frequent and acute (Abis, 2015). Improving access to markets through more effective value chains will become even more important, as global and regional trade will grow to compensate for greater production and productivity variability.

The presentation will discuss the major intervention points whet breeders have to achieve the needed genetic gains of 0.7% p.a. in areas of raising yield potential, enhancing heat and drought tolerance, biotic stresses, industrial processing and nutrition.

WHEAT PRODUCTION, DISTRIBUTION AND VARIATION OF DISEASES, BUNTS AND SMUTS IN TURKEY

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Wheat is a leading field crop throughout the world and Turkey. Turkey has very suitable ecology for wheat production and is part of the center of origin for wheat. Therefore, Turkey has advantages for the development of productive and high-quality varieties of wheat, which is a strategic national product. Wheat production in Turkey, which had been about 2.5 million tons in the 1930s, reached 10 million tons in 1967 and 20.6 million tons in 2009. This increase in production was primarily due to the increase in planting areas from the 1930s till the 1960s. The grain yield per unit area was 920 kg/ha in 1930 and reached 1250 kg/ha in 1967. Since then, genetic gains and appropriate agronomic techniques have made important contributions to increased productivity. The increase in planting areas between 1967 and 2010 was only 1.0%, and the increase in yield was 104.8%. This increase per unit area was realized due to the important contributions made by both the genetic value of the varieties used and improved agronomic techniques like irrigation and fertilization. The main diseases for winter wheat areas of Turkey are yellow rust, leaf rust and soil borne pathogens (nematodes and root rots). For spring wheat coastal areas leaf rust and *Septoria* are dominant diseases. Seed transmitted diseases like common bunt only occur in areas with less industrialized production where certified seeds are not used. However, their damage to grain quality is devastating and development of resistant varieties represents a viable option.

MAPPING RESISTANCE GENES FOR COMMON BUNT IN WHEAT

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Organic wheat production is increasing in Denmark, Europe and in wheat producing areas, in general. The seed borne disease common bunt is a particular challenge for organic seed production because systemic pesticides that is used to control common bunt in conventional agriculture is not permitted in organic farming. Therefore, selecting and breeding for resistance to common bunt in wheat has high priority for organic breeding but have been neglected in conventional breeding. As result little is known about the underlying genetic mechanisms, and the number and chromosomal locations of the resistance factors for common bunt resistance in wheat.A double haploid (DH) population segregating for common bunt resistance was used to identify the chromosomal location of common bunt resistance gene Bt9. DH lines were phenotyped in three environments, and genotyped with DArTseq and SSR markers. Bt9 was mapped to the distal end of chromosome 6D. Since wheat common bunt resistance gene Bt10 is also located on chromosome 6D the possibility of their co-location was investigated. Comparison of marker sequences linked to Bt9 and Bt10 on physical maps of chromosome 6D confirmed that Bt9 and Bt10 are two distinct resistance factors located at the distal (6DL) and proximal (6DS) end of chromosome

6D, respectively. Flanking markers for Bt9 can now be developed and used in marker assisted selection. A search for new resistance genes was also carried out by a genome-wide association study of 248 wheat accessions phenotyped in 2 growth seasons for the reaction to common bunt and two QTL could be identified. The possibilities for maintaining a sustainable wheat production will be discussed.

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DISEASES DISTRIBUTION AND LOSSES SESSION

MULTILOCAL RESISTANCE ASSESSMENT AGAINST COMMON BUNT OF WHEAT GENOTYPES

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The use of plant resistances against common bunt is the most efficient, durable and environmentally sound strategy against common bunt in wheat and other *Triticeae*. Resistant varieties do not cause additional cost for the farmer and can be made available in all concerned wheat producing areas of the world. Common bunt resistance is based on Flors' gene for gene principle with an effector of the pathogen and a resistance gene in the host plants, able to detect the effector and to unleash the appropriate resistance mechanisms.To efficiently use this type of resistance, it is important to characterize the effectors in the pathogen population as well as to monitor the presence and the efficacy of the resistance genes. While many of this information is available at local and regional level, only little is known at an interregional or even continental dimension. In order to obtain a better overview on the efficacy of resistances and the presence and distribution of pathogen races, 12 researchers from 10 countries (spanning Europe, the USA and Iraq) have initiated the European *Tilletia* ringtest (ETR). The ringtest consists of the common testing of a set of 65 wheat accessions including differentials to characterize the pathogens stains but also NN modern varieties and landraces with specific resistance features. The ringtest takes place in 2015 and 2016. First results display the diversity of pathogen strains and allowing to recommend the deployment of the most appropriate resistance genes in the different cropping areas. After the first year, the accessions that resulted susceptible in all areas have been discarded.

FAO ACTIVITIES ON PLANT PRODUCTION AND PROTECTION IN CENTRAL ASIA

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Wheat is the main staple crop in all countries in Central Asia. The consumption rate of wheat is therefore the highest in the world, at over 200 kg/year/ capita. Based on official statistics, wheat production in general is increasing, but production per capita is slightly declining and yield is remaining very low. In addition to this, the serious infestation of quarantine and transboundary pests and diseases severely damage crop yield. Every year the farmers observe damage caused by locusts, rusts, nematodes, gypsy moth, American white fly, and other dangerous pests and diseases. To control pests and diseases the farmers apply pesticides but the registration and quality control system of pesticides and pesticide application equipment is not in place. That imposes serious risks to the environment and to human health.

Central Asia counts as one of the centers of origin and diversity of several crop species. However the efficiency of conservation and utilization of plant genetic resources for food and agriculture is very low. An informal seed system dominates over a formal system, and use of high-quality seed of superior varieties requires further development of seed quality control and certification.

With the purpose of responding to the challenges on crop production in the sub-region, the new FAO paradigm "Save and Grow" is translated into following four areas:

1. The first area is intensification and diversification of cropping systems that foresees the provision of technical assistance to the

countries in developing their policies and strategies on sustainable crop production intensification and diversification of cropping systems, organic farming, preparedness for drought and climate change mitigation, promotion of conservation agriculture, and sustainable pasture and grassland management.

2. The second area for cooperation is the strengthening capacity of the National Plant Protection Organizations. In this regard FAO cooperates with the countries and provides support to the omproving policies on plant protection, implementation of international conventions and standards (e.g., ISPM) and harmonization of regional phytosanitary legislation. FAO continues support for developing capacities to control transboundary pests and diseases (locusts, wheat rusts) and carrying out the monitoring, surveillance and control of wheat rust (e.g. SMS monitoring). The key activities in both areas will be the training of young plant breeders and pathologists in cooperation with CIMMYT and ICARDA and the development of training programs and curriculums.

3.The third area is focused on strengthening national frameworks for pesticide management, covering improvement of the national systems for pesticide registration, testing, quality control, management, inventory and disposal of obsolete pesticides, adoption and promotion of efficient pest control, enhancing the membership of countries in the international organizations, and implementation of international conventions like IPPC and Rotterdam Conventions and the International Code of Conduct on Pesticide Management. Promotion of integrated pest management (IPM) by developing Farmer Field Schools is a comparative advantage of FAO that was implemented in different countries around the world.

4. The fourth direction is providing assistance in better management of plant genetic resources (PGR) and seed systems, focusing on improving conservation, efficient utilization of plant genetic resources, and seed sector development, especially formulation and implementation of seed policies and harmonization of the national seed legislation with the internationally accepted norms and standards.

Strong cooperation and partnerships have been established between public and civil society organizations in successful implementation of the projects and the program in the sub-region. The cornerstone of FAO's technical assistance in plant production and protection is safeguarding and intensifying crop production. In this sense, for a strong and healthy harvest, FAO is helping farmers incorporate innovative techniques into traditional farming practices.

GENETIC VARIATION IN *TILLETIA TRITICI* AND *T. LAEVIS* ISOLATES THE CAUSAL AGENTS OF COMMON BUNT DISEASE IN IRAQ

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Common bunt disease incited by *Tilletia caries,* is one of the most destructive disease of wheat in Iraq, that can cause severe yield losses when the susceptible cultivars are grown without chemical dressing. The study has been conducted to determine the possible genetic variations in the pathogen population and to identify the physiological races of the pathogen. Collections of common bunt were prepared from bunt-infected spikes from the main wheat growing areas during 2012/13 seasons. Eighteen isolates from these collections were selected based on high germination percent of the teliospores and used for artificial inoculation of international differential set genotypes at faculty of agricultural sciences field in Sulaimania. Results revealed that there is a wide genetic diversity among *T. caries* isolates representing different locations. 18 races of *Tilletia caries* and *T. foetida* pathogens were identified according to the international nomenclature system. Ten of these races match the international races T1, (T1, L1, L2), T2, T4, T9, T11, T13, T17, T18 and T20, while the rest eight races could be new races and not be recoded previously in the world. It has been found that the resistance genes *Bt2*, *Bt6*, *Bt14* and *Bt15* were ineffective against most of the pathogen races while *Bt4* and *Bt8* were ineffective against four races, *Bt1* was found to be ineffective against 5 races, and genes *Bt3* and *Bt5* were ineffective against three races only. Al the identified races

were unable to overcome resistance of the known resistant genes *Bt11* and *Bt12*, while only two races were found to be able to overcome the resistant gene *Bt7*, *Bt9*, *Bt10* and *Bt13*. Confirmation of the identification of these races on the molecular bases is further needed.

Table 1. Differential varieties reaction against 18 isolates of Tilletia spp representing different agro ecological zones of Iraq

Iso No	Location	Resistant gene															
		Bt0	**Bt1**	**Bt2**	**Bt3**	**Bt4**	**Bt5**	**Bt6**	**Bt7**	**Bt8**	**Bt9**	**Bt10**	**Bt11**	**Bt12**	**Bt13**	**Bt14**	**Bt15**
T1	Baghdag, Twaitha	**S**	**S**	**R**	**R**	**S**	**R**	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**S**
T2	Diala, Bladroze	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**S**	**R**
T3	Wasit, Sheix Saad	**S**	**S**	**R**	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**S**	**R**	**R**	**R**	**S**	**R**
T4	Mesan, Ali Gharbi	**S**	**R**	**R**	**R**	**R**	**S**	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**S**	**R**
T5	Dewania, Mhnawia	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**
T6	Salahdhin, Bejee	**S**	**R**	**R**	**R**	**R**	**R**	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**S**
T7	Mosul, Hamdania	**S**	**R**	**S**	**R**	**R**	**R**	**R**	**R**	**S**	**R**	**R**	**R**	**R**	**R**	**S**	**R**
T8	Mosul, Rabiaa	**S**	**S**	**S**	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**S**
T9	Mosul, Sherqat	**S**	**R**	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**S**	**S**
T10	Garmian, Kalar	**S**	**S**	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**S**
T11	Sulaimani, Halabja	**S**	**R**	**S**	**R**	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**S**
T12	Sulaimani, Bakrajo	**S**	**R**	**S**	**R**	**S**	**R**	**R**	**R**	**S**	**S**	**R**	**R**	**R**	**S**	**R**	**R**
T13	Sulaimania Penjwen	**S**	**R**	**S**	**R**	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**S**	**R**	**R**
T14	Erbil, Rania	**S**	**R**	**R**	**R**	**R**	**R**	**S**	**R**	**R**	**R**	**S**	**R**	**R**	**R**	**R**	**S**
T15	Erbil, Kwesanjaq	**S**	**R**	**R**	**R**	**R**	**S**	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**
T16	Duhok, Zakho	**S**	**S**	**R**	**R**	**R**	**R**	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**
T17	Duhok, Malta	**S**	**R**	**R**	**R**	**R**	**S**	**R**	**R**	**S**	**S**	**R**	**R**	**R**	**R**	**S**	**R**
T18	Duhok, Feshkhabor	**S**	**R**	**R**	**S**	**R**	**R**	**R**	**R**	**S**	**R**	**R**	**R**	**R**	**R**	**R**	**R**

KARNAL BUNT OF WHEAT (*TRITICUM* SPP.) IN INDIA AND OTHER SOUTH ASIAN COUNTRIES

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Karnal bunt (KB) of wheat (*Tilletia indica* (Mitra) = (*Neovossia indica* (Mitra) Mundkur) was first reported from Karnal, undivided Punjab (India) in 1931. Since then it has been reported in other countries of South Asia (Afghanistan, Pakistan and Nepal) and from other countries of the world including Iran, Iraq, South Africa, Mexico and USA. The disease results in grains filled with masses of fungal spores and can be damaging even at low incidence as color and palatability of wheat products are adversely affected. Hence, it has serious consequence on wheat trade especially for those countries planning to export wheat. In India, KB has been mostly severe in the north western plains zone (NWPZ) which provides wheat to the national buffer stock. But it was also reported from north-eastern and central India. The affected states are - Punjab, Haryana, Rajasthan, Uttar Pradesh, parts of Madhya Pradesh, Bihar, West Bengal, lower altitudes of Himachal Pradesh and Jammu region of Jammu and Kashmir. The disease has not been recorded in Maharashtra, Gujarat, Orissa, Assam, Meghalaya, Karnataka, Andhra Pradesh, Tamil Nadu and Kerala. The incidence of KB in India has increased in NWPZ during last four years. In last cycle 2014-15, a large grain samples (12295) revealed KB in 42.67

% samples with maximum infection range upto 5.15 % in samples from NWPZ. Weather analysis of last ten years indicated that February rain aggravated KB. Though KB is in existence in India for the last 70 years, the losses in total wheat production even in worst years (such as 1969-70) were not more than 0.5 %. However, it impairs seed viability and flour quality due to production of trimethylamine. Like India, KB has long been present in Afghanistan and Pakistan, with occasional outbreaks. It has become serious in last few years with the changed rainfall pattern and, thus, several popular wheat varieties being susceptible to KB. In Pakistan KB is more prevalent in Khyber Pakhtunkhwa province in the north with decreasing severity towards central and South parts of the country. In case of Afghanistan, KB is present in the eastern region bordering Pakistan, which is an important seed-producing area within Afghanistan. In Nepal, KB was reported in 1986-87 in the Doti district. Since then has shown sign of increase in that area. Due to increased incidence of KB in recent years, it is being given special attention in India, Pakistan and Afghanistan. KB isolates from different Indian states have been characterized through host-pathogen interaction and molecular markers. Monosporidial lines of *T. indica* have been developed and compatible monosporidial pairs identified. The *Ustilago hordei* whole genome (21.15 Mb) was mined for SSR motifs using WebSat. A total of 8226 SSR motifs were identified consisting mono (22%), di (14%), tri (43%), tetra (3%), penta (6%) and hexa (12%) repeats. Primers for 36 randomly selected SSR motifs are being used for variability in *Tilletia indica*. Use of resistant varieties is the most economical and sustainable approach to manage this disease. Immunity to KB in *Triticum aestivum* is lacking. Most of the widely cultivated varieties (HD 2009, WL 711, UP 262) of early 70s were highly susceptible to KB as they were not selected for resistance. In later years, KB screening was intensified and tolerant bread wheat cultivars (WL 1562, PBW 154, HD 2281, PBW 502, PBW 34, DWL 5023, PBW 215, PDW 233) were released. A number of bread wheat resistant lines were identified, namely HD 29, HD 2300, HD 2499, HD 4571. Likewise, six KB free lines (KBRL 10, KBRL 13, KBRL 15, KBRL 18, KBRL 22, KBRL 24) were developed at Ludhiana. Resistance to KB was also identified in *S. cereale*, *Triticale* and accessions of *Aegilops* spp. Experiments indicated low incidence of KB under zero tillage as compared to conventional tillage. The climate change trend (warmer temperature and more rainfall during grain filling) has shown that most varieties in heavily infected locaitons of South Asia are prone to KB. Hence a more systematic and concerted efforts are required at the regional level to combat the threat of KB in the region and its spread beyond the region.

CURRENT AND FUTURE PROSPECTS OF KARNAL BUNT IN PAKISTAN

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Wheat, a staple food of inhabitants of the Indian subcontinent is increasingly affected by both biotic and abiotic stresses under changing climates. Karnal bunt (KB) is one of the fungal diseases caused by Tilletia indica; that seriously affects the quality of the grains. The fungus emits fishy odour of tri-methylamine which makes the flour quality unacceptable for human consumption. Recent environmental fluctuations support the increased prevalence/occurrence of the pathogen. Yield losses resulting from KB are generally low, however the current climatic trends reflects the alarming situations of significant increase in the incidence level of KB in all cultivated varieties of bread wheat studied. Twenty wheat varieties were screened at Barani Agricultural Research Station, Kohat against KB infection for three years (2012-15) consecutively. Total rainfall as well as heavy showers in post heading stage during first and last year was higher than second year of the experiment, resulting in higher KB infection during the first and third year. Significant increase in KB infection were observed with the increase in rainfall in almost all the genotypes tested. No commercial variety were found to be immune to KB infection; however certain level of resistance against the disease exists in the wheat germplasm tested. Among commercial cultivars INQ-91, FSD-85, Shafaq-06, Uqab-2000, AS-2002, BK-2002, Lasani and Sehar-06 remained moderately susceptible (MS) and susceptible (S) while PS-13, Shahkar-13, Lalma,

NARC-11, FS-08 and Kohat-2000 exhibited reasonable good resistant (R) response against the disease. To avoid the spread and control KB, awareness of farming community to plant fresh seed of cultivars with moderate level of resistance, avoid seed production in hotspot areas, following cultural practices like crop rotation, reduced irrigation/fertilizer, deep plowing after harvest and seed treatment with hot water and solar energy could possibly help in reducing and combating KB infection in the country.

PATHOGEN VARIATION AND DIAGNOSIS SESSION

DETECTION OF TILLETIA CONTROVERSA USING IMMUNOFLUORESCENT MONOCLONAL ANTIBODIES

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Tilletia controversa is an internationally quarantined pathogenic fungus that causes dwarf bunt of wheat and is similar to *Tilletia caries* in both teliospore morphology and genetic structure. This study developed a rapid and sensitive immunofluorescence method for differentiating the teliospores of *T. controversa* from *T. caries*. The method utilizes monoclonal antibody D-1 against teliospores of *T. controversa* as well as a PE-Cy3-conjugated goat anti-mouse antibody (overlapping light excitation of 495 and 555 nm).

The orange cycle fluorescent signal was stronger against *T. controversa* teliospores in the outer spore wall and net ridge, whereas only the green signal was observed for the protoplasm of *T. caries* teliospores. The detection limit of this method was 2.0 µg/ml of the D-1 monoclonal antibody. This study describes the production and diagnostic application of a novel mouse monoclonal antibody specific to *T. controversa* teliospores. This method could be used for the on-site identification of *T. controversa* teliospores in the near future and will help in selecting fungicides to control dwarf bunt of wheat as further technical developments are achieved.

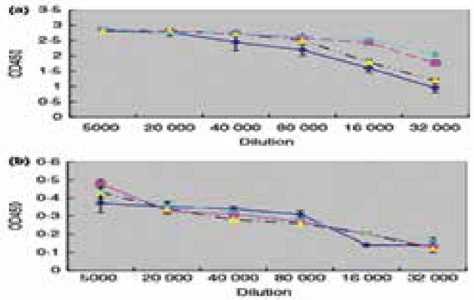

Figure 1. The binding of *anti-Tilletia controversa* mAbs in diluted hybridoma media to salt-soluble components (a) and washed *T. controversa* spores (b). All of the results represent the mean and standard deviations from three replications.D-1, D-3, D-4, D-5 were represented by the following symbols separately: -◆-, -■-, --- and -•-.

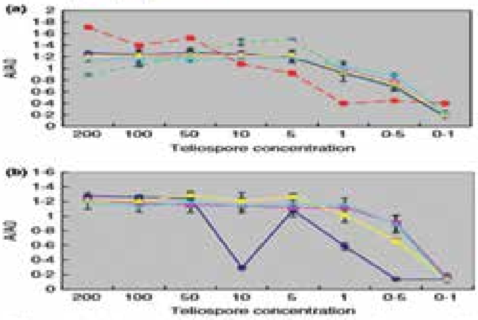

Figure 2. (a) Interday calibration curves from the competitive assays using D-1, D-3, D-4 and D-5 at a 1:45000 dilution and D-2 and D-6 at a 1:1000 dilution. (b) Interday calibration curves from the subtractive inhibition assays; no subtractive inhibition was performed from D-2 or D-6. The concentration of *T. controversa* telisopores was 0.5mg/ml, and the volumes of the antibody and teliospores were both 50 μ l. The data presented are the mean and standard deviations from three replications, the subtractive inhibition assay had a detection limit of 0.1 mg/ml, whereas the competitive assay had a detection limit of 0.5mg/ml. D-1, D-3, D-4, D-5, D-2 and D-6 were represented by the following symbols separately: -◆-, -■-, -▲-, -×-, -•- and -■- .

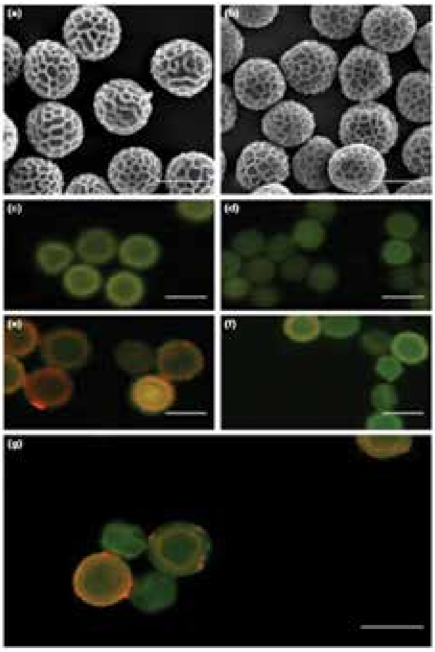

Figure 3. Morphology of *Tilletia controversa* (a) and *Tilletia caries* (b) teliospores using scanning electron microscopy (SEM) with 17000X magnification. The reaction of monoclonal antibody D-1(2.0 µg/ml) in the immunofluorescence assay against teliospores of *T. controversa*(c), *T.caries* (d) or a mixture of teliospores from *T. cotroversa* and *T. caries* (e). The detection of a mixture of teliopsores from *T. controversa* and *T. caries* with monoclonal antibody D-1 applied at 4.0 μ g/ml)(e) or 2.0 μ g/ml (f, g). Absorbance at 495 nm is shown in c and d, and absorbance at 495 and 555 nm is shown in e, f, and g, respectively, the magnification was 25.2x in c, d, e and f, 50.0x in g. Note the orange teliospores in e, f, and g, which indicate *T. controversa*, and the green teliospores in e,f, and g, which indicate *T. caries*. Scale bars= 20 μ m.

DEVELOPMENT OF A LOOP-MEDIATED ISOTHERMAL AMPLIFICATION (LAMP) ASSAY FOR *TILLETIA INDICA*

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Introduction

T. indica causes the disease Karnal bunt in wheat and is subjected to very strict quarantine regulations especially in Australia. The current international diagnostic protocol to distinguish this pathogen from its closest relative, *T. walker,* uses PCR technology (conventional and real-time) based on a small sequence region that differs by only one nucleotide between them. The objective of this work was to develop a more sensitive molecular diagnostic assay that is easy to perform and cost-effective without the need for expensive instrumentation.

Methods

Mycelium was harvested from the germination of teliospores of an isolate of *T. indica* (PS2). DNA was extracted from the ground mycelium and a shotgun library of sequences of about 650 bp was prepared using the TruSeq DNA Sample Preparation kit. The library of random DNA fragments was sequenced on the MiSeq Sequencer at the Ramaciotti Centre for Genomics, University of NSW.

BLAST analysis of the assembled contigs has retrieved a contig of 61,110 bp which aligned with the reference mitochondrial genome of *T. indica* (DQ993184) and *T. walkeri* (EF53675). The alignment enabled the selection of target regions for the design of four primers for the LAMP detection of *T. indica*. LAMP reactions were performed using the *Bst* DNA Polymerase.

Results and Discussions

Alignment of the mitochondrial genomes of *T. indica* and *T. walkeri* found small [single nucleotide polymorphisms (SNPs)] and big [large deletions or insertions (indels)] genetic changes in the mitochondrial genomes of *T. indica* isolates. Comparative analysis of the *T. indica* and *T. walkeri* mitochondrial genomes also found numerous SNPs and big indels. The gene order is found to be conserved between *T. indica* and *T. walkeri.* Four primers, two inner primers (FIP and BIP) and two outer primers (F3 and B3) were designed from a target region specific to *T. indica* isolates. This assay has been found to be specific to *T. indica* from BLAST analysis and the screening of other *Tilletia* species including *T. walkeri*, *T. tritici*, *T. ehrhartae.* A positive reaction is visualized by the formation of a white precipitate that makes the solution turbid (Fig. 1). The amount of turbidity correlates with the amount of DNA. The fluorescent DNA dye, Sybr green, can be added to distinguish a negative and a positive reaction (Fig. 2). The products were also analyzed on a gel and visualized by a fluorescent stain, GelRED (Fig. 3).

Conclusion

A LAMP assay has been developed for *T. indica*. This method is highly sensitive and specific and can be performed on a simple heating block, making it a very cost-effective tool. A positive result can be easily visualized by the turbidity of the reaction (Fig. 1). Thus a LAMP assay can be performed in a resource-limited laboratory.

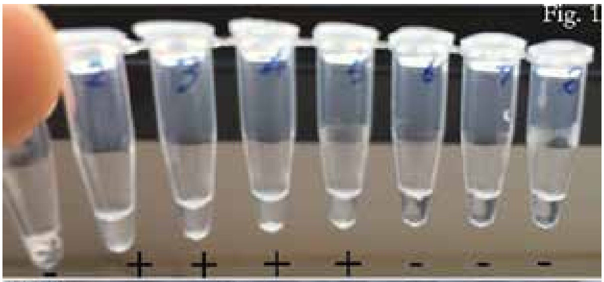
Fig. 1

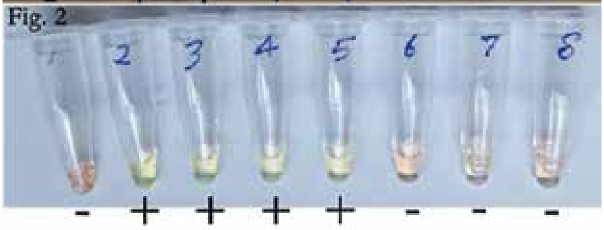
Fig. 2

Fig. 3

SCREENING WHEAT VARIETIES FOR RESISTANCE WITH PURIFIED VIRULENCE RACES OF COMMON BUNT (*TILLETIA CARIES*)

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Introduction

Trials screening wheat for resistance to common bunt sometimes suffers from inconsistent results because spores used often are divers, and contains a variable mixture of virulent and avirulent races to certain resistance genes. An attempt has in this study been made to screen varieties using spores purified with specific virulence.

Methods

From 2012 and onwards, resistant varieties were infected with spores collected from the same varieties if infected spikes were found. In this way, a collection of 98 virulence races were build up specific to the 98 wheat varieties, including differential varieties with known resistance genes. In 2013-14 and in 2014-15, spores from 7 selected varieties were used to infect the other varieties. The varieties were sown in 0.5 rows without replication with 5g seed per row.

Results

Some of the varieties that had low infection in previous trials, and therefore earlier were recorded as almost fully resistant, could indeed be infected if they were re-inoculated with the spores from the few infected plants of the variety. For example, varieties with the resistance gene *Bt10* had no or low infection when infected with the diverse spore collection, and it was concluded that Danish spores were avirulent to *Bt10*. However, when varieties with *Bt10* were inoculated with spores from varieties with *Bt10*, they turned out to be highly susceptible. The spore collection is therefore a mixture of virulent and avirulent spores against *Bt10*. The same is the case for *Bt2*, *Bt7*, *Bt13* and *BtZ*. When varieties were inoculated with spores that had been purified on other varieties, they were normally either more resistant or more susceptible compared with inoculation with the spores mixture. It is likely that varieties that react in a similar way to different origins of spores may have the same resistance genes. However, this is not always the case. Some (or maybe most) varieties carry more than on gene affecting the susceptibility, and certainly most virulence races of the pathogen are virulent to more than one resistance gene. For example, all spores virulent to *Bt10* are in this study also virulent to *BtZ*, and I have been unable to distinguish between these two genes. Some varieties have so far been resistant in all studies, and even if a few plants were infected, spores from these plants have been unable to create a high infection level. Some of these varieties may have a resistance gene to which no virulence have been found, and some varieties may have a combination of pyramided genes. I have been unable to develop virulence races specific to the resistance genes *Bt3*, *Bt4*, *Bt5*, *Bt6*, *Bt8*, *Bt9*, *Bt11*, *Bt12*. It is possible that the varieties NGB9014, NGB-9015, Tambor, Kuban, Begra, Maribos, Fold, Monopol, Tarso, Torrild, Cardos, Kranich, Türkis, Gluten, Folke have *Bt7*, since they react in a similar way to the 7 different sources of spores used in 2014-15. It is possible that the varieties Format, Curier, Complet, Solstice, Bussard, Paroli, Dream, Butaro, Ochre, PG3540 and Hereward have *Bt2*. The varieties Korrund, Aron, Karat, Tulsa, Xenos, Tataros, Erbachshofer Braun and Indigo have in some trials shown resistance, but in 2014-15, they have been susceptible to most or all virulence races. Spores harvested on the variety Tommi in Sweden in 2014 were able to give a high infection in the Tommi, Globus and Segor, and a medium infection was achieved with spores from Austria, even though these varieties have so far been resistant or shown low susceptibility to spores from Denmark. The spores from Sweden were unable to infect differential lines resistant to all the Danish spores. The variety Quebon could be infected by spores collected in Czech Republic, but was resistant to all other spores tested on other varieties. This indicates that Tommi, Globus and Segor may carry the same resistance gene, which is different to the gene in Quebon, and different to the known *Bt*-genes.

RESISTANCE GENETICS AND BREEDING SESSION

INTERNATIONAL WINTER WHEAT IMPROVEMENT PROGRAM: REDUCTION OF DISEASE LOSSES THROUGH BREEDING

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The IWWIP (www.iwwip.org), based in Turkey, develops germplasm for Central and West Asia (CWA). IWWIP is a cooperative program between the Ministry of Food, Agriculture and Livestock of Turkey, CIMMYT, and ICARDA, and has operated since 1986. Its breeding activities are implemented through a multilocational network in Turkey in close cooperation with the key wheat breeding programs in the region. The main emphasis of IWWIP breeding is broad adaptation, disease resistance, and grain quality. Annually, IWWIP germplasm is sent to cooperators throughout the CWA region and globally for evaluation and selection. More than 65 varieties originating from IWWIP germplasm have been released in the CWA region and occupy more than 2.5 mln ha. IWWIP operates a multi-locational network of breeding sites in Turkey integrated with national research system institutes and stations.

The crosses are made in Izmir, resulting F1s are also grown in Izmir. F2 populations are subjected to leaf rust pressure in Trakya region of Edirne and resistant plants are selected and bulked. The F3 is subjected to stripe rust pressure in Diyarbakir and individual spikes are selected. The F4 headrows are grown in Eskisehir and selection of the best progenies is made. From F5 preliminary yield trials onwards the material is tested across key locations for most important diseases: Haymana near Ankara and Izmir for stripe rust, Adapazari and Edirne for leaf rust, Kastamonu for stem rust, Eskisehir and Yozgat for soil-born pathogens (nematodes and root rots). The key location for common bunt screening is in Eskisehir with around 1000 entries evaluated annually. In the course of the last 3-5 years IWWIP was able to identify a number of common bunt entries of diverse origin. They re-evaluated again for common bunt as well as for rusts and the best selections were multiplied. The set of common bunt resistant germplasm comprising 70 entries was distributed in 2015 globally to more than 300 cooperators. Though the genetic control of resistance in this set is not defined, based on pedigree we suspect that there is sufficient genetic variation. Most of this germplasm is high-yielding background and possess resistance to rusts.

QTL MAPPING OF DWARF BUNT RESISTANCE IN WINTER WHEAT

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A number of genes conferring resistance to the diseases of common bunt [*Tilletia caries* (D.C.) Tul. (syn. *Tilletia tritici*) and *Tilletia foetida* (Wallr.) Liro (syn. *Tilletia laevis*)] and dwarf bunt [*Tilletia contraversa* Kühn (syn. *Tilletia controversa*)] have been used by breeding programs for nearly one hundred years. However markers that are useful in diverse populations have been particularly difficult to develop.

While readily controlled by seed treatments, common bunt is a reemerging disease of wheat in organic production in the world. While host resistance genes are effective against both diseases, reliable phenotypic screening of dwarf bunt resistance can be challenging as the infection of dwarf bunt requires specific environmental conditions of prolonged snow cover. Year to year climatic variation results in non-uniform infection in the best of screening nurseries.

A recombinant inbred line (RIL) population derived from the bunt resistant parent, IDO444 and the susceptible parent, Rio Blanco, was evaluated for phenotypic reaction to dwarf bunt inoculation in five trials of two locations over three years. The population was genotyped with the Diversity Arrays Technology (DArT) and the Illumina Infinium 9K iSelect platform. Two QTLs on 1A and 2B were consistently detected in the populations over years and locations, which explained 6-11% and 6-12% of the phenotypic variation, respectively. A single DArT marker on the short arm of chromosome 7D (corresponding to *wPt-2565*) explained up to 60% of the variation for resistance to dwarf bunt in this population. Three PCR-based STS markers were designed based on the sequence of *wPt*-2565 and validated in the RIL population. The STS markers were further assessed in dwarf bunt differential lines and elite breeding lines.

REACTION OF WINTER WHEAT AND SPELT WHEAT GENOTYPES TO COMMON BUNT AND DWARF BUNT

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The contribution presents data on common bunt resistance from the years 2013 – 2015 and data on dwarf bunt resistance obtained since the year 2008 at the Crop Research Institute in Prague-Ruzyně.

Common bunt inoculation was done by shaking seed with teliospores in Erlenmayer flasks for 1 - 2 min. Inoculation and sowing (1 m long rows, 4 replications) was carried out in early October. For dwarf bunt tests rows 1 m long with 8 replications were sown in late October. Teliospores were evenly spread on the soil surface after sowing. In absence of a snow cover the plots covered with straw or white nonwoven fabric. The resistant checks Globus and Bill and the susceptible check Batis were included in the tests.

Out of the recently registered winter wheat cultivars in the Czech Republic only cv. Genius proved common bunt resistance in the both years of testing. Cv. Sailor proved high resistance to common bunt only in one year, while in the other years it was more or less susceptible. Cvs Saturnus and Potenzial showed the lowest bunt incidence in the trials with dwarf bunt.

In addition to winter wheat cultivars, 80 spelt wheat genotypes were evaluated for common bunt in 2015. Two spelt wheat genotypes were free of infection, 49 genotypes showed bunt incidence below 10%.

The tested sources of resistance obtained by courtesy of Dr. B.J.Goates proved high resistance to dwarf bunt. As they were recorded resistant to common bunt as well, they offer a suitable genetic material for resistance breeding both to the common and dwarf bunt.

Acknowledgements: Supported by Ministry of Agriculture of the Czech Republic project No. QJ1210189. The research leading to the results presented on spelt wheat has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement n° 613609.

DETERMINATION OF REACTIONS OF SOME TURKISH BREAD WHEAT CULTIVARS TO COMMON BUNT IN ANKARA

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Common bunt (*Tilletia foetida* (Wallr.) Liro, *Tilletia caries* (D.C.) Tul.) is an important fungal disease of wheat in many wheat producing countries. Common bunt is also an important problem of the seed industry. Chemical control with seed treatment is practical, cheap and effective. On the other hand chemical control have important some disadvantages such as environmental concerns, phytotoxicity for wheat, cost increasing nature and limitations for organic wheat production. Therefore, resistance breeding is necessary to give more emphasis to for the control of common bunt. The aim of the study is to identify reactions of some Turkish bread wheat cultivars to the bunt. Experiment was carried out at the research facilities of Central Research Institute for Field Crops CRIFC at İkizce location in Ankara. In total 130 Turkish wheat cultivars were treated with bunt spores before planting. Materials were sown in a 1 m rows with 2 replications by hand in October, 2014. The infected spike was counted in total spike and calculated percentage of the disease in July, 2015. As a result, 10 (8%) genotypes were determined resistant (disease percentage ≤10 %), while 96 (74%) genotype were determined as susceptible (disease percentage between 41-100 %) infected heads. Resistant cultivars were cv. Atay-85, cv. Çetinel 2000, cv. Karahan 99, cv. Ekiz, cv. Kıraç 66, cv. Zencirci-2002, cv. Yayla 305, cv. Porsuk 2800, cv. Sönmez 2001 and cv. Süzen 97. The utilization of these genotypes in the breeding programs and production is recommended.

Acknowledgement: This study was financed and supported by General Directorate of Agricultural Research and Policy of the Ministry of Food, Agriculture and Livestock of Turkey (Project no: TAGEM/TBAD/12/A12/P01/01-004)

IDENTIFICATION AND DISTRIBUTION OF NEW HIGH YIELDING GENOTYPES WITH RESISTANCE TO KARNAL BUNT OF WHEAT

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Karnal bunt or partial bunt, first identified in Karnal-India in 1931, is a quarantine disease of wheat, durum, and triticale, caused by the fungus *Tilletia indica*. Spores can be carried in soil, surfaces of plant parts including seed, farm equipment and humans. Karnal bunt has the potential to reduce grain yield, quality and marketability significantly and is reported to occur in India, Pakistan, Nepal, Iran, Iraq, Mexico, USA, South Africa, Brazil, and Afghanistan. Karnal bunt cannot be easily detected in growing plants and grains must be removed from the head and examined for bunt infection wherein the bunted kernels are fragile, dark in color, and smell fishy. The kernels usually remain unbroken although part of the germ may be eroded. Crack in the surface reveal a black powdery spore mass within the endosperm at the embryo end of the kernel or along the kernel grove. Hence screening for Karnal bunt is long and tedious process.

International Maize and Wheat Improvement Center (CIMMYT) in collaboration with Instituto Nacional de Investigaciones Forestales y Agropecuarios (INIFAP) have reinitiated the identification of resistant wheat genotypes and their worldwide distribution through Karnal Bunt Screening Nursery (KBSN). Identification of Karnal bunt resistant germplasm was done in an artificially inoculated Karnal bunt nursery at the INIFAP-CIRNO, Campo Experimental Norman E. Borlaug, Cd. Obregón. Based on multi-environment testing of the elite germplasm from CIMMYT's breeding programs the constituents of KBSN were selected. Although the frequency of resistant lines in improved wheat germplasm is low, we could identify low frequency of highly resistant and somewhat higher frequency of moderately resistant germplasm. Wheat line Munal#1 and some synthetic wheat derived lines are among the highly resistant group. The 17th KBSN was assembled based on Karnal bunt screening in 2012-13 and 2013-14 and distributed in 2015. It comprised 97 resistant and moderately resistant germplasm and was distributed in 30 locations. Targeted breeding with proper testing are needed to incorporate Karnal bunt resistance in popular varieties.

IDENTIFICATION AND CHARACTERIZATION OF NEW SOURCES OF COMMON BUNT RESISTANCE IN SPRING WHEAT

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Common bunt, caused by two species of fungi genus *Tilletia* [*T. tritici* (syn. *T. caries*) and *T. laevis* (syn. *T. foetida*)], can significantly reduce grain quality and yield of wheat. It can be controlled with either host resistance or fungicide seed treatments. The use of host resistance is considered the most effective way to control common bunt in wheat. Common bunt is considered a priority one disease of wheat in western Canada, hence, breeding for common bunt resistance is also a priority along with other diseases. In order to identify novel sources of resistance, four doubled haploid (DH) populations were developed utilizing four uncharacterized resistant germplasm lines and three registered susceptible cultivars (AC Reed, Sadash and Andrew) of spring wheat. These populations along with parents and checks were screened for common bunt severity under controlled conditions during 2012 (AC Reed/N9195), 2013 (Andrew/P2626, Sadash/P2634), 2014 and 2015 (Sadash/P2624) and field conditions during 2013 (Andrew/P2626, Sadash/P2634). Analysis of disease severity data showed the presence of major [single (in N9195), two (in P2624), three (in P2634)] and minor (in P2626) additive gene(s). The analysis also indicated segregation of two sets of two minor additive genes (along with major genes) in cross Sadash/P2624. DH population AC Reed/N9195, which carried a major gene, was utilized for genotyping using 90K SNP Infinium iSelect assay and a high density genetic linkage map was constructed (map density: 1.25). This linkage map along with

phenotypic data was utilized for QTL analysis which identified one major QTL for common bunt on wheat chromosome 1A. DH population Sadash/P2624 is again being grown in the greenhouse to generate adequate disease severity data to be utilized in QTL mapping experiments. The identification of these new sources of resistance will facilitate marker-assisted breeding for common bunt resistance.

MAPPING BUNT RESISTANCE IN WINTER WHEAT

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During the last two decades, bunt diseases have re-emerged in organic winter wheat throughout Europe. Currently, no bunt resistant and adapted varieties are available for organic farming in Austria. Whereas the predominantly seed-borne disease common bunt (*Tilletia tritici, Tilletia laevis*) can be managed by careful seed hygiene, control of the soil-borne dwarf bunt (*Tilletia controversa*) is more challenging, as soils once contaminated with the long lived teliospores cannot be used for organic winter wheat production for up to 10 years. Host resistance therefore constitutes the most important tool for bunt control in organic farming. Breeding for bunt resistance is time and cost intensive and molecular marker technology could greatly facilitate the development of resistant winter wheat varieties. Knowledge regarding the genetic basis of bunt resistance – the main prerequisite for the development of useful molecular markers – is limited, and reflected by the fact that only a subset of bunt resistance genes can be allocated to specific wheat chromosomes. Furthermore, little is known about the interaction between dwarf and common bunt resistance.

Here, we report the identification of novel common and dwarf bunt resistance loci in winter wheat, which will be useful to develop molecular markers for application in bunt resistance breeding: Three mapping populations of 100 to 120 recombinant inbred lines (RIL) were developed from crosses between bunt resistant material – namely the North American cultivars ‘Blizzard’, ‘Bonneville’ and the Turkish landrace and bunt differential line ‘PI119333’ – and ‘Rainer’, a susceptible Austrian winter wheat cultivar. These RIL populations along with parents and checks were tested for common and dwarf bunt resistance in field trials with artificial inoculation at multiple sites in Austria and the USA in 2014 and 2015. All three populations were genotyped with genome wide SNP markers. Resistant parental lines conferred durable protection against a broad spectrum of bunt races across locations and years. The segregation patterns of individual RIL populations suggested the presence of major QTL in each of these populations. Accordingly, major bunt resistance QTL were identified by the combined statistical analysis of phenotypic and genotypic data, conferring bunt resistance in collaboration with minor effect QTL. Epistatic interactions between identified QTL were found to play a significant role in the disease reaction. Interestingly, different resistance loci were responsible for common bunt and dwarf bunt resistance.

Acknowledgments: The project „COBRA Austria“ is funded within the framework of the ERA-Net project Core Organic 2 by the Austrian Federal Ministry of Agriculture, Forestry, Environment and Water Management (project number 100898).

NOVEL SOURCES OF RESISTANCE TO COMMON BUNT AND OTHER DISEASES

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Common bunt used to be one of the main wheat production constraints in Turkey and neighboring countries. After sources of resistance are identified and introgressed into modern wheat cultivars it became a less important problem. However, new sources of resistance for different diseases are needed to identify and incorporate the resistance into wheat germplasm. One of the novel sources would be wild relatives of wheat. The aim of this study is to evaluate the amphidiploid wheat to common bunt, nematode and some other diseases. The material have been developed based on two diverse Durum wheat germplasm; one group is based on Langdon, spring durum wheat, and the other group is based on several winter durum wheat genotypes from Ukraine and Romania. Several T. tauschii entries used in developing the synthetics had been collected mainly from Central Asia and Caucasian countries.

Material has been tested under field conditions for common bunt; the seeds have been inoculated with common bunt spores artificially collected in previous crop cycle and planted. After the flowering the infected spikes were counted and per cent resistance/susceptibility is determined. For rusts, they were tested under artificially inoculated field conditions and natural epidemic conditions in multiple locations and in greenhouse for seedling tests. For nematode resistance/susceptibility, they were tested in greenhouse under artificially inoculated conditions.

The results showed that Synthetic wheat has resistant genotypes for all diseases studied. While 66 % of Winter Synthetics are highly resistant to Common bunt, the resistance percentage was 59 % in Spring synthetics. For rust diseases resistance percentages were lower in both types than common bunt resistance. It was around 3 % For yellow rust in both types under artificially inoculated conditions. 74 % of winter synthetics were resistant-medium resistant to leaf rust under natural epidemic conditions; Spring types were not tested for Lr resistance. While 12 winter synthetic germplasm were selected for nematode resistance, 9 spring synthetic genotypes were selected for nematode resistance. 15 winter synthetic genotypes and 12 spring synthetic genotypes were identified as Crown rot resistance and they were selected for further evaluation and to be used in breeding programs. The results showed that synthetic wheat can be novel sources of number of diseases to be used in breeding programs.

ON-FARM BUNT-RESISTANCE BREEDING IN WHEAT AT "FORSCHUNG UND ZÜCHTUNG DOTTENFELDERHOF" – EFFORTS, RESULTS AND CHALLENGES

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Common bunt causes serious problems in organic cultivation and seed multiplication of wheat. However, resistance to common bunt is not required for the registration of new varieties in Germany and therefor was neglected in private and public breeding programs over decades. Beyond that, agronomic measures to prevent infections and seed treatments approved in organic agriculture are limited. Soil-borne infections often increase the problem.

In the early 1980s, 'Forschung & Züchtung Dottenfelderhof' began working on the development of strategies to control common bunt in organic farming. Alongside the evaluation of prophylactic agronomic measures, a resistance breeding program was started, first for winter wheat and later on for spring wheat.

As a pre-breeding measure, a wide range of varieties, gene bank accessions and breeding lines are evaluated for resistance against common bunt every year using the local common bunt emergence as an inoculum. Candidates showing no or low infection rates (<8%) are tested for 3 consecutive years. Lines with approved resistance are used as parents in about 100 crosses done every year in both winter and spring wheat. Adapted material, genetic resources and (exotic) landraces are intercrossed in mainly double-crosses or back-crosses. F2-progenies are sown as a bulk under low infection-pressure (2’000 spores per kernel) to eliminate highly susceptible offspring and to visually select non-infected single plants with desirable agronomic traits. In F3 to F5, resistant pure lines are developed following an ear-to-row pedigree scheme applying artificial inoculation with 20’000 spores per kernel. In F6-F9, candidate lines are sown ear-to-row without inoculation which serves further selection of the pure lines and production of clean seeds for trials and multiplication. Simultaneously, a bulk of each selected line is checked in parallel trials from F6 on to avoid loss of resistance. Beginning in F7, the most promising candidates are evaluated for resistance properties in trials of cooperating institutions.

Up to now, more than 850 winter wheat cultivars/lines have been tested at Dottenfelderhof. Less than 20 were without infection. Among the roughly 200 currently registered varieties available in Germany, Austria and Switzerland less than 5 were without infection and only nine indicated a very low level of infection. The examination of over 30 currently approved spring wheat varieties revealed three resistant varieties and eight with a very low susceptibility. Most of them showed low agronomic suitability for organic production. Following the above described scheme, Forschung und Züchtung Dottenfelderhof has developed a broad range of diverse breeding material adapted to the needs of organic farming. So far, four officially approved varieties of winter wheat with resistance to common bunt were released. Three candidates of spring wheat with resistance to common bunt are in the process of registration. Testing in multiple location trials (International *Tilletia* Ringtest) found one of the FZD-varieties to be stable in resistance over all locations. Most of the other lines react with varying infection rates depending on locations.

Results of resistance evaluation of a broad range of wheat material at Dottenfelderhof reveal that the overall resistance level in currently available varieties adapted to the needs of organic farming is still low. By the means of intercrossing adapted material and different sources of resistances followed by selection under artificial infection in a pedigree-scheme under the conditions of organic farming, suitable and resistant varieties can be developed. However, resistances are race-specific. Therefore, breeding lines and registered varieties with resistance to common bunt need to be characterized with respect to their pedigree and resistances should be checked at multiple locations before recommendation for cultivation.

IDENTIFICATION OF GENETIC RESISTANCE SOURCES IN ADVANCE BREAD AND DURUM WHEAT GENOTYPES TO COMMON BUNT CAUSED BY *TILLETIA LAEVIS* KUHN IN IRAN

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Common bunt with causing agent (*Tilletia laevis* Kuhn) is one of the destructive diseases of wheat in dryland areas. In order to evaluate resistance of 230 rainfed bread and durum wheat genotypes to common bunt, this experiment was carried out in Maragheh and Kordestan in 2014 and 2015 cropping seasons. Eight grams of each genotype were artificially inoculated with spores of related local isolates in ratio of 0.005. Seeds were planted in 2 rows, with one-meter length. At harvesting time, the numbers of infected spikes were assessed for each genotype and their reaction was grouped base on the Mamluk and Van Slageren methods.

The results of this study showed, differences among isolates in their virulence at different locations, and resistance differences between wheat genotypes to the diseases were observed. Based on the results in Maragheh, 72 genotypes without infection, 88 genotypes resistant, 45 genotypes moderately resistant, 19 genotypes moderately susceptible, 3 genotypes susceptible, and 3 genotypes were very susceptible. And in Kordestan, 26 genotypes without infection, 46 genotypes resistant, 50 genotypes moderately resistant, 27 genotypes moderately susceptible, 14 genotypes susceptible, and 67 genotypes were very susceptible.

Compilation of results in Maragheh and Kordestan regions shows that, 18 genotypes were immune and 14 genotypes were resistant in both

locations. Usage of these genotypes recommended for release or in breeding programs. Also results showed that, relative percentage of resistant genotypes in durum wheat is more than bread wheat. So we recommended durum wheat for planting in infected areas.

EVALUATION OF SYNTHETIC WHEAT FOR RESISTANCE TO COMMON BUNT

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With the aim to increasing global wheat production up to 2030 the potential wheat yield must be increased up to 30-40%. Each year the crop productivity must be increased up to 1.6-1.8 %, including 1 % due to genetic and breeding methods. It could be more realistic in case of utilization of wild relatives of wheat. Important direction for improving of genetic potential of wheat is connected with resistance to biotic and abiotic stresses.

In Almaty oblast condition have been conducted researches of F1 generation in crosses of nursery of hexaploid synthetic wheat and local cultivars of winter wheat - Ajarly, Farabi, Naz, Steklovidnaya and Zhetisu on experimental base of Kazakh scientific research institute for plant growing and farming in 2014-2015 agricultural year.

The of diseased plants on local cultivars were between 8,3-25%. High resistance to common bunt was demonstrated by 5 lines, disease occurrence were absent on LANGDON/KU-20-8//AJARLY, LANGDON/KU-2075//AJARLY, LANGDON/KU-2092//FARABI, LANGDON/KU-2144//STEKLOVIDNAYA, LANGDON/KU-2100//NAZ. One line LANGDON/KU-2075//FARABI showed practical resistance to common bunt (with number of diseased plants 4,3%). Low susceptibility to common bunt was demonstrated by 3 lines (number of diseased plants 10,5-20%), and one line showed moderate susceptibility (28,5%) to disease.

REACTION OF TAJIK WHEAT VARIETIES AND BREEDING LINES TO COMMON BUNT UNDER DIFFERENT CONDITIONS

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Common bunt remains the important seed-borne disease worldwide. The disease caused by two related fungi: *Tilletia tritici* (Bjerk.) Wint. and *T. laevis* Kühn, in Tajikistan common bunt predominantly caused by *T. laevis*. The pathogen mostly controlled through seed treatment with fungicides since 1950's due to rapid development of chemical industry and production of wide range of pesticides. Therefore, in most wheat breeding programs the selection of bunt resistant varieties was given lower priority. However, still the poor farmers cannot afford application of pesticides for disease control. Thus, breeding of resistant varieties to common bunt will significantly contribute to improving grain yield and increasing farmers' income.

A study of Tajik wheat varieties and breeding lines originated from the international nurseries of CGIAR Centres was carried out. The aim was to assess their reaction to common bunt and identify resistant sources for further utilisation in breeding programs.

Screening of 19 advanced lines and 3 commercial varieties (control varieties) to common bunt reaction was conducted in natural and artificial conditions. Study in Tajikistan was carried out under natural conditions in two different agro-climatic zones. Seeds were inoculated with local common bunt spores in Turkey and screening conducted in the field. In Sweden the seeds were treated with spores originated from Tajikistan and planted in the greenhouse and resistant to common bunt local variety Stava served as a check. The reaction of genotypes was recorded as follows: Resistant (R) - less than 5% plants infected; Moderate-resistant (MR) - 5 to 10% plants infected; Susceptible (S) – more than 10% plants infected.

In Tajikistan under the natural conditions the plants were less infected by common bunt during two years of field experiments. However, the presence of pathogen was identified through conducting seed health tests in majority of seed samples. Only two wheat lines - PRINIA/STAR (originated from 6WWEERYT nursery) and SHARK/F4105W2.1 (originated from 5WWEERYT nursery) - moderately reacted to the pathogen under the artificial inoculation in Turkey. The remaining genotypes were susceptible to the disease. Advanced line SHARK/F4105W2.1 was the only genotype with MR reaction in the greenhouse test conducted in Sweden. All other breeding lines and check varieties were susceptible, among them 16 were highly susceptible to common bunt.

The study shows that major commercial wheat varieties widely grown in Tajikistan and most of advanced breeding lines are not resistant to common bunt. Besides one MR line not any resistant variety was identified. Therefore, developing wheat varieties resistant to seed-borne diseases, especially to common bunt, has to be high priority and in breeding strategies.

SCREENING TURKISH AND IWWIP GERMPLASM (INTERNATIONAL WINTER WHEAT IMPROVEMENT PROGRAM) FOR COMMON BUNT (*TILLETIA FOETIDA* (WALLR.) *LIRO, ILLETIA CARIES* (D.C.) TUL.) RESISTANCE UNDER ESKISEHIR FIELD CONDITIONS

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The main control method of the common bunt of the wheat in our country is chemical applications. Chemical applications are cheap, practical and have precise result. But they also have a negative effect on the environment, human health and also economic issues. Therefore, it seems that the main and the best way to control bunt are breeding the resistant cultivars. In the light of this, it is important to study breeding resistant cultivars and work on their improvements. This study was conducted in 2011-2015 years at Transitional Zone Agricultural Research Institute's disease surveillance trial nursery. The aim of the study was to determine reactions of some registered bread and durum wheat cultivars against bunt disease. In this study, 1890 winter wheat advanced lines some of which are improved by IWWIP and introduced were used, as well as 165 bread and 56 durum registered wheat varieties.

Before planting in the field all seeds were contaminated with 0.5% bunt spore suspension that collected from institute experimental field previous year. Varieties and lines were planted on 1 row x 1 Mt. and 30 cm the distance between rows was and 40 cm between blocks was arranged before cultivation. Disease observations were done at exact period of full wheat maturity. In each row infected spikes and healthy spikes were counted and % of disease incidence estimated. Spike infected 0-5% bunt was considered as resistant (R), 5-10% bunt moderate resistant (MR), 11%+ susceptible (S). The inoculums were collected from Eskisehir region. Its virulence to *Bt2*, *Bt3*, *Bt4*, *Bt6*, *Bt7*, *Bt12* genes was determined on set of differential varieties carrying individual Bt genes. Genotypes with *Bt1*, *Bt5*, *Bt8*, *Bt9*, *Bt10*, *Bt11* and *Bt13* genes were resistant to the inoculums.

As a result, 557 (29%) of the genotypes were found resistant and 164 (9%) moderately resistant. The resistant and moderately resistance entries were again inoculated and re-checked one more season. This systematic screening procedure resulted in identification of 70 genotypes from IWWIP, Iran, Romania and Russia with proven resistance to common bunt. With relation to bread wheat varieties, Kıraç66, Porsuk2800, Süzen 97, Çetinel, Müfitbey, Nacibey, Karahan99, Zencirci02, Dağdaş94, Ekiz and Claudio as well as 18 durum wheat varieties were found resistant against the common bunt's Eskişehir race. The results indicate that there are good numbers of common bunt resistance resources among the germplasm. The utilization of these sources in the breeding program and production is recommended.

POSTER PRESENTATIONS

RESISTANCE IN AUSTRALIAN DURUM AND BREAD WHEAT VARIETIES TO KARNAL BUNT (*TILLETIA INDICA*)

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Karnal bunt, a disease of wheat caused by the fungus *Tilletia indica*, is not present in Australia, but any potential incursion would cause severe damage to the Australian wheat industry through quality losses as well as huge losses in export markets. This study was undertaken to determine the vulnerability of Australian durum and bread wheat germplasm to infection by *T. indica*. One hundred and sixty-two bread (*Triticum aestivum*) and six durum (*Triticum durum*) varieties were tested using the phenotyping facilities of CIMMYT (International Maize and Wheat Improvement Center), Mexico. Inoculations on two separate dates showed a high degree of consistency in genotypic rankings for resistance (rank correlation = 0.91). Of the 168 wheat varieties tested, 55 showed high levels of resistance (with % infected grains ≤ 5%), and 12 of those had zero percent infection, which was as good a resistance as the resistant check, Munal#1. This indicates existence of a high level of resistance to Karnal bunt in the current Australian wheat germplasm. All varieties are being re-screened, and if confirmed, the level of inherent resistance will influence the likelihood of establishment of *T. indica* in the event of an incursion into Australia, and the subsequent economic losses.

GRAIN YIELD COMPARISON OF ELITE AUSTRALIAN WHEAT VARIETIES AND WHEAT GERMPLASM WITH KARNAL BUNT RESISTANCE

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Karnal bunt, a disease of wheat caused by the fungus *Tilletia indica*, has the potential to seriously damage the Australian wheat industry because of its use as a quarantine barrier to international trade. International research collaboration with CIMMYT (International Maize and Wheat Improvement Center, Mexico) has developed new wheat germplasm carrying Karnal bunt resistance genes, and these will be made available to Australian breeders for variety development. Because Karnal bunt is not present in Australia, breeders may be reluctant to adopt and use improved germplasm in their programs for fear of upsetting the established phenology and yield profiles. In a large field trial carried out at Wagga wagga, Australia, we found no significant difference in grain yield between new wheat lines carrying Karnal bunt resistance, and currently adapted, commercial varieties, indicating no evidence of yield penalty. On the contrary, three of the new lines yielded over 7 t ha-1, a yield performance that compared favorably with the highest yielding of the commercial varieties. The result support the view that incorporation of Karnal bunt resistance genes into elite Australian wheat varieties

would provide the best and most sustainable protection against any potential incursion, as it would have no obvious deleterious phenotypic effect.

HIGH-DENSITY GENOTYPING WITH SNPS IDENTIFIES A NEW GENOMIC REGION FOR KARNAL BUNT (*TILLETIA INDICA*) RESISTANCE IN WHEAT

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Identification of quantitative trait loci (QTL) associated with resistance to Karnal bunt in wheat is greatly desired because phenotyping is labor intensive, expensive, and the disease is highly influenced by environmental factors. Previous research with bi-parental populations has identified QTLs using microsatellite markers, but it can be argued that the mapping populations used only captured a portion of the genetic diversity available in wheat. In the present study, we used high-density genotyping with single-nucleotide polymorphic (SNP) markers to further search for allelic variants that might be linked to Karnal bunt resistance in wheat. A 9K wheat SNP array was assayed across 118 wheat varieties, followed by genome-wide association analysis with simultaneous corrections for population structure and genetic relatedness. At a P-value ≤ 0.001 [$-\log10(P) \geq 3.0$], the analysis identified a genomic region on chromosome 3AL, comprising a haplotype block of 8 significant SNP loci, mapped within an interval of 4.3 cM. Longer sequences containing the SNPs were extracted and a BLAST search showed significant (Evalue = 0.0) hits with a rice gene on chromosome 1 that encodes the ABC transporter, ATP-binding protein, putative,

expressed. If validated, these SNPs would provide alternative markers and germplasm conferring Karnal bunt resistance and increase the options of achieving greater resistance by combining the positive alleles into elite wheat cultivars in breeding programs.

DETERMINATION OF SPRING WHEAT LINES AND VARIETIES'S REACTION TO COMMON BUNT (*TILLETIA CARIES* (DC.) TUL. – *TILLETIA FOETIDA* (WALL.) *LIRO)* AT MENEMEN CLIMATIC CONDITIONS

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Common bunt is an important disease observed at wheat producing areas. As well as common bunt has direct effects on yield infected plants become more sensitive to other diseases compare to healthy plants. Although seed treatment with chemical can control the disease, the best and economical control is to develop resistant varieties.

This study was conducted to determine the reaction of some varieties and lines to common bunt at bread wheat crossing block and bread wheat observation nursery. At this study, 316 entries from bread wheat crossing block and 133 entries from bread wheat observation nursery were evaluated. Before sowing, seeds were contaminated with the rate of 0.5 % common bunt spores collected in previous year. Materials were sown at rows with 1m x 1m dimensions. Disease rate were determined by counting diseased and healthy plants within the same row. Scoring rates were; 0-5 % resistant, 6-10 % moderate resistant, 11-15 % moderate sensitive and 16+ % sensitive.

We identified 57 genotypes being resistant, 137 - moderately resistant, 122 - moderately susceptible and 133 susceptible.

THE INCIDENCE OF SMUT AND BUNT DISEASES IN WHEAT AND BARLEY FIELDS IN AEGEAN COASTAL CITIES OF TURKEY

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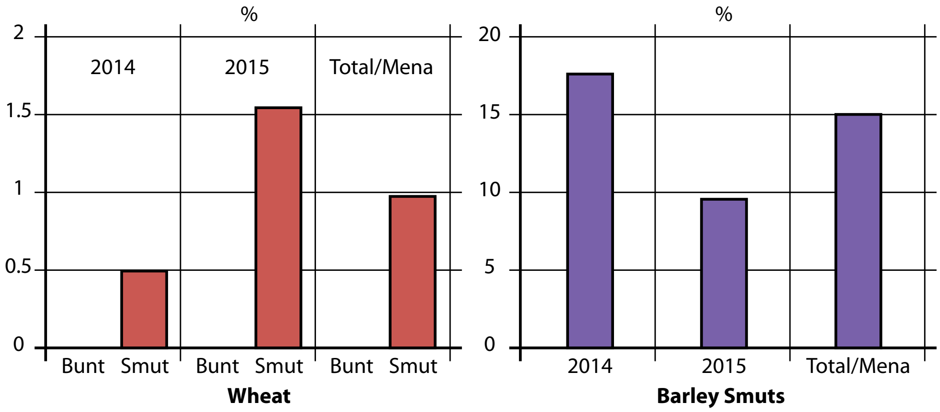
Smut and bunt diseases of cereal cause damage by reducing yield and quality of harvested grain. A 2-year survey in the Aegean coastal cities of Turkey in 2014 and 2015 was conducted to detect incidence of the smut and bunt diseases of wheat and barley. Survey studies were carried out between milky and dough stages (Zadoks 61-79) of wheat and barley in seven cities including Aydın, Balıkesir, Canakkale, Denizli, Izmir, Manisa and Mugla in April, May and June. In 2014, 189-wheat and 69-barley field were observed while, in 2015, 127-wheat and 33-barley field were examined in terms of presence of smut and bunt diseases. Any bunt diseases (*Tilletia* spp.) were not found in the examined fields in both years. However, wheat smut disease (*Ustilago tritici*) was detected at the rates of 0,53% and 1,57% in 2014 and 2015, respectively. In addition, average incidence of bayley smut diseases (*Ustilago hordei* + *U.nigra* + *U.nuda)* in inspected areas were 17,91% and 9,09% in 2014 and 2015, respectively. Smut incidence in the barley fields examined was 15%, while it was 0,95% in the wheat fields (Diagram 1).

As a result, no any bunt disease was observed and smut diseases were seen at a low level in inspected wheat fields. These findings were attributed to sowing certificated seed and applying registered fungicides against these diseases. Smut infections in the barley fields were higher than the wheat. It seems that the smut diseases in the barley fields are

primary problem leading to significant economic losses (15%) currently. It is concluded that in general, barley growers sow their own seed harvested in previous year mostly without any chemical seed treatment. These diseases are well-managed with regular application of registered fungicide seed dressing for susceptible varieties. Resistant varieties should be used to avoid of these diseases. In addition, necessary cultural measures (e. g. balanced fertilization, irrigation,) should be taken.

Diagram 1. Smut and bunt diseases incidence (%) of Aegean coastal cities of Turkey for wheat and barley in 2014 and 2015



BUNT REACTIONS IN A BUNT RESISTANCE NURSERY IN 2015

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Common bunt (*Tilletia foetida* (Wallr.) Liro, *Tilletia caries* (D.C.) Tul.) is the principal yield and quality limiting factors for wheat production in the wheat growing areas. The aim of the study was to determine of the resistance of Bunt Resistance Nursery (BRN) developed by Central Research Institute for Field Crops to the current bunt population.

In this study, 50 genotypes were inoculated artificially with current local *Bt* (virulent on *Bt0, Bt2, Bt3, Bt4, Bt6* and *Bt7*) populations before planting. Materials were sown in a 1 m rows with 2 replications by hand. Infected spike were counted and calculated percentage in total spike. The disease percentage of susceptible check cv.Yakar reached 90-100%. Infected spike rate that under 25% were considered to be resistant.

All genotypes were found resistant to current bunt populations. These resistant germplasm is a potential sources to common bunt.

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SOME LANDRACES BREAD WHEAT BUNT RESISTANCE GENOTYPES REACTIONS TO BUNT

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Landraces are important sources for disease resistance. Common bunt (*Tilletia* spp.) was not important disease for modern cultivation system due to seed treatment with fungicide. However improvement resistant genotypes are needed for organic farming applications and rural area. Landraces were collected from central and south east Anatolia and tested to bunt. The aim of the study was to determine reactions of selected resistant genotypes to bunt obtained from Ankara locations. Evaluations were carried out at the research facilities of Central Research Institute for Field Crops CRIFC at İkizce location in Ankara in the 2014–2015 growing season.

The seeds of the genotypes were inoculated artificially with bunt spore population (virulent on *Bt0, Bt2, Bt3, Bt4, Bt6* and *Bt7*) before planting. Materials were sown in a 1 m. rows with 2 replications by hand. The percentage of infected spikes was used for the comparison of resistance of the entries end of the season.

All materials (21) were resistance to bunt. The results indicate that these genotypes are very valuable resistance source to common bunt.

Acknowledgement: This study was financed and supported by General Directorate of Agricultural Research and Policy of the Ministry of Food, Agriculture and Livestock of Turkey

OCCURRENCE OF DWARF BUNT IN WINTER BREAD WHEAT IN KAYSERI PROVINCES IN TURKEY

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Dwarf bunt caused by *Tilletia contraversa* is an important disease of winter wheat. It has a limited geographic area due to specific winter climate requirements. Dwarf bunt teliospores are soilborne, long-lived, and can retain viability in soil at least 10 years. *T. contraversa* spores germinates only at low temperatures under snow cover on unfrozen ground thus dwarf bunt occurs in areas having prolonged snow cover. The disease has very special conditions to occur in highland areas.

In this study, surveys were conducted in Kayseri provinces in 2013. Infected spikes were collected from 5 different fields in Kayseri (Pınarbaşı district) province in Central Anatolia in Turkey. Field locations, where disease had appeared, were very mountainous, highland and arid area. There were suitable conditions for disease occurrence. Infected plants were severely stunted and with numerous tillers. Heads were more spherical and rigorous than the healthy ones. All of the infected spikes were observed under the microscope and teliospores were detected as dwarf bunt. Dwarf bunt teliospores are bigger and rough than common bunt spores.

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SCREENING OF ADVANCED BREAD WHEAT LINES AGAINST COMMON BUNT DISEASE

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Wheat (*Triticum aestivum* L.) is an important crop of Turkey. Fungal diseases cause to low yield and quality in Turkey. Common bunt (*Tilletia foetida* (Wallr.) Liro, *Tilletia caries* (D.C.) Tul.) is one of the spike diseases of wheat. One of the control methods of the disease is developed and used of resistant genotypes. Wheat germplasm improved by Central Research Institute for Fields Crops (CRIFC) Wheat Breeding Unit were screened against common bunt disease in the field experimental area of the CRICF Department of Plant Pest and Diseases Resistance. The screening was carried out in the 2014-2015 growing season of. In this study, 56 genotypes from the advanced bread lines materials were tested.

Each of the material was sown in a single row of 1 meter length with row to row spacing 30-33 cm. and 2 replications. The seeds of the total genotypes were inoculated artificially with local *Bt* (virulent on *Bt0, Bt2, Bt3*, *Bt4*, *Bt6* and *Bt7*) population before planting. A cultivar Yakar 99 was included as a highly susceptible check. The susceptible check was 90-100% disease severity in August 2015. Below 25% were considered to be resistant. As a result, 17 genotypes (30% in total) were determined resistant (infected spike rate ≤1-25 %), while 39 genotypes (70% in total) were determined as susceptible (%41-100) infected heads.

Acknowledgement: This study was financed by TÜBİTAK 1003 programme (113O115) and supported by General Directorate of Agriculture Research and Policy, Republic of Turkey Ministry of Food, Agriculture and Livestock.

BUNT REACTIONS OF BREAD WHEAT GENOTYPES IN CROSSING BLOCK NURSERIES FROM BAHRI DAGDAŞ INTERNATIONAL A.R.I.

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Common bunt (*Tilletia foetida* (Wallr.) Liro, *Tilletia caries* (D.C.) Tul.) as the biotic stress and drought as the abiotic stress are the principal yield-limiting factors for wheat production on the Central Anatolian Plateau of Turkey. Combined disease resistance and drought tolerance in the breeding program is an important issue for Central Anatolia. In this study, 90 genotypes in the Crossing Block Bread Wheat nurseries were tested to bunt. Wheat germplasm improved by Bahri Dağdaş International Agricultural Research Institute Wheat Breeding Unit were screened by the CRICF Department of Plant Pest and Diseases Resistance against common bunt disease in the field experimental area in the 2014-2015 growing season of.

Each material was sown in a single row of 1 meter length with row to row spacing 30-33 cm. and 2 replications. The seeds of the total genotypes were inoculated artificially with local *Bt* population (virulent on resistance genes *Bt0, Bt2, Bt3, Bt4, Bt6* and *Bt7*) before planting. Infected spikes were counted in July. The susceptible check cv.Yakar 99 reached up to 90-100% disease severity. Infected spike percentages less than 25% in total was considered to be resistant.

As a result, 6 genotypes (7% in total) were determined resistant (infected spike rate ≤ 10 %), while 84 (93%) genotypes were determined as susceptible (between 11 to 100 %). The resistant lines can be used as genetic resources among the germplasm.

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DETERMINATION OF THE REACTIONS OF GENOTYPES IN BREAD WHEAT YIELD TRIAL TO COMMON BUNT

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Wheat is one of the most important daily calories sources for human. Common bunt (*Tilletia foetida* (Wallr.) Liro, *Tilletia caries* (D.C.) Tul.) is among the most important fungal stress factors limiting wheat production in wheat growing area. The disease causes significant yield losses of grain. One of the most important control methods of the disease is development and usage of resistant genotypes. Determination of the reactions of resistant varieties against different races of bunt fungus is important. In this study, the OBVD (Common Wheat Yield Trial) set which includes cultivars and advanced lines developed by Agricultural Research Institutes governed by the General Directorate of Agricultural Research and Policy was tested against bunt in 2014-2015 growing season. Evaluations were carried out at the research facilities of Central Research Institute for Field Crops CRIFC at İkizce location in Ankara.

There were 31 bread wheat genotypes and 9 durum wheat genotypes in the studied set. Each genotype was planted to 1 meter and 2 replications by hand. The wheat cultivar Yakar 99 was used as the susceptible control. The % of infected spike was used for the comparison of resistance of the test materials.

Twenty genotypes including 11 bread (33%) and 9 durum (100%) wheat were found as resistant (infected spike rate ≤1-25 %) to bunt. The results indicate that there are resistant genotypes to common bunt in the germplasm and these genotypes can use in the breeding programs and production.

Acknowledgement: This study was financed and supported by General Directorate of Agricultural Research and Policy of the Ministry of Food, Agriculture and Livestock of Turkey (Project no: (TAGEM/TBAD/14/A12/P01/002)

DETERMINATION OF REACTIONS OF GENOTYPES IN SPECIAL BREAD WHEAT- CROSSING BLOCK NURSERY TO COMMON BUNT

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Common bunt of wheat, caused by *Tilletia* spp., is an important disease in certain wheat growing areas of the world. Seed treatment is effective; the use of resistant genotypes is an important in rural areas and organic production. Crossing Block - Special Bread Wheat (CB-SB) contained 149 some advanced lines and cultivars for use as parents in the crossing program.

The aim of the research was to determine the reaction of 149 genotypes in Special Bread Wheat - Crossing Block nursery developed by Central Research Institute for Fields Crops (CRIFC) Wheat Breeding Unit to bunt.

Genotypes were sown in a single row of 1 meter length with row to row spacing 30-33 cm. and 2 replications. The experiment was conducted as the seeds of the total genotypes were inoculated artificially with local *Bt* (virulent on *Bt0, Bt2, Bt3, Bt4, Bt6* and *Bt7*) population before planting. The susceptible check (cv. Yakar 99) was 90-100% disease severity in July, 2015.

As a result, 43 (29%) genotypes were determined resistant (infected spike rate ≤25 %), when 106 (71%) genotypes were determined as susceptible (infected spike rate between 41 to 100). The results indicate that there are resistant materials to bunt in the germplasm and these genotypes can be used in the breeding programs.

Acknowledgement: This study was financed by TÜBİTAK 1003 program (113O115) and supported by General Directorate of Agriculture Research and Policy, Republic of Turkey Ministry of Food, Agriculture and Livestock.

DETERMINATION OF REACTION OF ADVANCED WHEAT LINES TO COMMON BUNT

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Common bunt (*Tilletia foetida* (Wallr.) Liro, *Tilletia caries* (D.C.) Tul.) is important disease is considered issue during breeding process. The aim of the research was to determine reactions of 40 advanced wheat lines developed by Wheat Breeding Unit of Central Research Institute for Fields Crops to bunt.

Each of the material was sown in a single row of 1 meter length with row to row spacing 30-33 cm. and 2 replications. The seeds of the total genotypes were inoculated artificially with local *Bt* (virulent on *Bt0, Bt2, Bt3, Bt4, Bt6* and *Bt7*) population before planting. The susceptible check (cv. Yakar 99) reached 90-100% disease severity in July 2015.

As a result, 2 (5%) genotypes were determined as resistant (infected spike rate ≤25 %), while 38 (95%) genotypes were determined as susceptible (infected spike rate between 41 to 100 %). These advanced lines can be released directly as commercial cultivars.

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RESISTANCE OF SYNTHETIC WHEAT TO COMMON BUNT AND CHARACTERISTICS FOR BREEDING

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Synthetic forms of winter wheat, including germplasm of Ae.triaristata, Ae.cylindrica, Tr.militinae, Tr.timopheevi, Tr.kiharae were evaluated for resistance to bunt in Eskisehir conditions (Candidates for 22nd FAWWON). Resistant genotypes were identified: Bezostaya-1/Ae.cylindrica; Bezostaya-1//2*Tr.militinae (entries 1721-6 and 1721-4) and Erythrospermum-350/Tr.kiharae. The respective grain yield was 5.7 t/ha, 4.6 t/ha, 2.3 and 7.5 t/ha. Genotype Bezostaya-1/Ae.cylindrica combines the resistance to bunt and resistance to yellow rust. Erythrospermum-350/Tr.kiharae combines resistance to bunt with stable grain productivity (Turkey and Kazakhstan). Spring bread wheat advanced yield trial of Kazakh Research Institute of Farming were evaluated for resistance to bunt. On average more than 60% of resistant forms were identified.

SCREENING OF KAZAKHSTAN WINTER BREAD WHEAT GERMPLASM FOR RESISTANCE TO COMMON BUNT

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Common bunt (CB) caused by *Tilletia caries* (DC) Tul. (syn. *Tilletia tritici*) and *Tilletia foetida* (Wallr.) Liro (syn. *Tilletia laevis*) can cause considerable losses to yield and quality in wheat. The most feasible approach for managing the bunt diseases of wheat is to use resistant cultivars. Such cultivars directly benefit farmers by assuring production [Blair J., Goates; Harold E. Bockelman, 2012]. In Kazakhstan the study of the material world and national breeding for resistance to CB local population were initiated in 50 years. Evaluation was carried out by conventional methods in plant pathology [V. Krivchenko, 1972]. In 50-70 years the degree of damage by CB of Kazakhstan commercial varieties - Albidium 43, Kazakhstanskay 126, Saratovskay 29, Cesium 111 reached 50-80%. [Z. Dzhiembaev, Ishpaykina E., 1955; Bukenova R. 1974]. Formula virulence of seven spore populations of CB from Almaty region (Kazakhstan origin) shows 3 resistance genes - *Bt3* (Ridit); *Bt9* (Sel. M -65-3157); *Bt10* (Sel. M -66) [V. Krivchenko 1984].

In 1991-2000 collection of more than 600 accessions (varieties and biotypes, promising material of national winter wheat breeding) was screened for resistance to CB. The assessment showed variable types of reactions. Dominated (60.3%) mixed reaction type - I (10-41% losses), 11.9% were resistant material - R (up to 10% losses), 27.8% of the material were affected by more than 41,0% (S type). In 2010-2012 resistance to CB of international nursery CAC (CIMMYT) was analyzed, which includes material of Central Asia countries. In most cases predominant types were I and S - reaction susceptibility. From Kazakhstan winter wheat breeding relatively high resistance was shown by commercial varieties - Naz, Steklovidnay 24, Krasnovodopadskay 25 (16.1; 19,7; 31,1% respectively) [Kulmuratov N.,Sarbaev A., Yessimbekova M., Kokhmetova A., Dutbaev E., 2013]. Formula virulence of the local pathogen population in the conditions of a foothill zone of Trans-Ili Alatau, including 3 of the most effective gene - Bt8, Bt9, Bt10, the presence of which in the breeding material is important for practical breeding for resistance to Tilletia caries. In 2013 we identified 18 promising crosses, that were resistant or immune with dominance of resistance to CB provided by genes Bt9, Bt10. These materials that were resistant to all bunt races should be valuable for broadening the genetic diversity of CB resistance in national breeding programs. Although seed treatments are available for control CB, growing resistant cultivars is the most economic and environmentally friendly option in bunt control, especially important in organic agriculture systems because of decrease in the use of chemical seed treatments [Ciuca M; Saulescu N. 2008].

Nazgul Zhumakadyrova (Kyrgyzstan, State center for varieties testing and genetic resources) Resistance of released varieties of winter and spring wheat to smut in Kyrgyzstan conditions.

EVALUATION OF DISEASE TOLERANCE OF SYNTHETIC HEXAPLOID WHEAT GENOTYPES IN DIFFERENT REGIONS OF AZERBAIJAN

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Wheat diseases are the principal yield limiting factors in wheat production. Synthetic - hexaploid wheat (SHW) (*Triticum turgidum* x *Ae. tauschii*) lines carry potentially novel alleles for biotic and abiotic stress resistance. A collection of SHWs created at CIMMYT (Mexico) has not been evaluated in Azerbaijan condition as a source of breeding. The main objective of the current study was to evaluate the synthetic wheat collection for resistance to diseases and select the best sources to use in breeding. To identify new sources of resistance, 117 accessions (80 SYNT-Elite, 37 SYNT-Japan) of SHW were screened for stripe (yellow) rust, stem rust and powdery mildew under different soil and climatic field conditions (irrigated, rain-fed and salinity) of Azerbaijan, during 2015.

Eighty synthetic elite (SE) lines showed different responses to stripe rust depending on climate conditions. Under irrigated condition 96.1% of SE lines were resistant/moderately resistant and 3.9% moderately susceptible to stripe rust. In contrast under rain-fed condition only 14.1% of lines were scored as resistant/moderately resistant, while 39.4% were moderately susceptible and 46.5% susceptible to stripe rust. About 91.0% of SE lines showed resistance/moderate resistance and 9.0% moderate susceptibility under salinity condition. Most of the SYNT-Japan lines were susceptible to stripe (yellow) rust in all conditions. Stem rust was not severe enough to detect differences among all accessions. Most of the lines showed moderate susceptibility to powdery mildew only under irrigated condition. Karnal bunt and smut diseases were not observed among studied accessions. Based on agronomic traits and disease resistance, 50 lines from 117 accessions were selected for further evaluation in different soil and climatic conditions (irrigated, rain-fed and salinity) of Azerbaijan in 2016. Selected valuable genotypes can be used as a source material for breeding and genetic research.

EFFICACY OF PROTECTANTS AGAINST HEAD SMUT IN THE SOUTH OF RUSSIA

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One of the most common diseases is head smut. In the south of Russia species *Tilletia caries* Tul. is usually found in winter wheat. The pathogen spreads with seed material. The danger of the pathogen is not only in reducing the crop yield, but also the toxic properties of head smut spores containing alkaloid trimethylamine, which negatively affect the human and livestock health. The anti-head smut system, along with agronomic techniques includes pre-sowing treatment using chemicals. The aim of our research was to study the effect of seed protectants on the development of the pathogen by artificial infection with spores and the identification of the most effective preparations.

Research Methods.

Seeds of winter wheat cultivar Batko were used in the experiments (2014-2015). They were infected with head smut pathogen teliospores and then treated with fungicides. Infectious load was 2 g spores per 1 kg of grain. Seeds were sown on an area of 1m^2 plots, four-time repetition. Counting head smut was conducted at the end of the milk-wax ripeness. The prevalence of the disease was determined according to the standard formula, reflecting the ratio of the number of affected ears to their total number, expressed as a percentage.

Results

Seven protectants with different active substances were used in the studies. It was found that preparations Maxim extreme, KS (18.7 g/l fludioxonil + 6.25 g/l cyproconazole) 1.5 liters/t, Inshur Performa, KS (80 g/l of triticonazole + 40 g/L of pyraclostrobin) 0.6 liters/t, Kinto Duo, KS (20 g/l of triticonazole + 60 g/l prochloraz) 2.5 l/t Stsenik combi KS (250 g/l 37.5 g clothianidin +/l fluoxastrobin + 37.5 g/l prothioconazole + 8 g/l tebuconazole) 1.6 liters/t, Celeste TOP, KS (262.5 g/l thiamethoxam + 25 g/l difenoconazole + 25 g/l fludioxonil) in the norm of 1.2 liters/t completely suppressed the development of smut pathogen prevalence at the controls (untreated infected) - 37.0%. Preparations Maxim, KS (25 g/l fludioxonil) and Lamador, CA (250 g/L prothioconazole + 150 g/liter tebuconazole) were less efficient and reduced the incidence of disease at 99.5% and 95.1% respectively. Protectants, completely inhibiting the development of the pathogen on a high artificial infectious background, are recommended to agricultural producers for the application in wheat seed protection against *Tilletia caries*.

SCREENING SPRING COMMON WHEAT CULTIVARS AND LINES OF CIMMYT SELECTION TO THE MOST HARMFUL DISEASE AGENTS IN RUSSIA

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Genetic uniformity of wheat cultivars in all parts of Russia and uncontrolled use of the race-specific resistance genes affected distribution and losses of fungi on wheat. Intensive dynamics of biotrophs has been caused also by their high plasticity and high migratory ability. The increase of wheat grain losses is possible due to the worsening phytopathologic conditions connected with the advent of new aggressive races of fungi. The strategic direction of struggle to harmful diseases dominating over modern agriculture in the world is creation of wheat resistant to fungi. The success of selection for diseases' resistance entirely depends on germplasm of wheat. The initial material should have genetic varietion of created cultivars, long protection to diseases, constraining reproduction of pathogen and possessing group resistance to pathogenic organisms. In this connection the best cultivars and lines of spring common wheat selected shuttle nurseries of CIMMYT were evaluated for resistance to Puccinia triticina Eriks., Puccinia graminis Pers., Septoria tritici Rob. et Desm., Stagonospora nodorum Berk., Ustilago tritici Jens., Blumeria graminis (DC). Speer f. sp. tritici Marchal in the Non-chernozem zone of the Russian Federation. In 2013-2015 wheat samples were tested on an artificial infectious background of P. triticina, S. tritici and Stagonospora nodorum, and natural infectious background of P. graminis, U. tritici, B. graminis. The most of tested samples were very resistant to leaf rust and characterized low dynamics of Septoria. Stem rust was noted at the end of vegetation when grain in an ear was already generated. The dynamics of powdery mildew was observed only on leaves of the bottom circles and crop was damaged insignificant. U. tritici has been identified only on 5 samples of common wheat. Resistant wheat cultivars to diseases have been identified: lines Ug 99 Res HL possessed resistance to leaf and stem rusts, several of them were characterized by low dynamics of Septoria. Those abilities were observed for wheat cultivars Fiton 82, Fiton, ShSel-9-77-31, Ecada 204, Eritrospermum 102-13, Gordeiforme 748, etc. Wheat samples ShSel-9-34-15, Ecada 186, Fiton 58, Lutescens 124-13, Leucurum 1469-21, № 20 RAZSIB 134 (ShSel), etc. have possessed resistance to leaf rust and powdery mildew.

PERFORMANCE OF SOME EGYPTAIN WHEAT VARITIES TO LOOSE SMUT OF WHEAT.

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Improvement of wheat (*Triticum aestivum* L.) is a major goal of plant breeders and pathology to ensure food security and self-sufficiency. Wheat attacked by many destructive diseases such as rusts, powdery mildew and smuts. Wheat loose smut ranked the second serious disease in Egypt. The main objective of this study is to evaluate some Egyptian wheat varieties to loose smut under field conditions. Artificial inoculation was done during heading stage for wheat varieties *i.e.* Giza 168, Gemmaiza 9, Gemmaiza 11, Gemmaiza 12, Sahka 94 and Sids 12. Disease incidence (%) was estimated for each variety and the effect of loose smut on the number of tillers was studied. Results obtained revealed that, Giza 168 showed the least disease incidence% (12.53%), whereas Sids 12 showed the highest disease incidence% (40.12%). The rest of the varieties showed intermediate disease incidence%. On the other hand loose smut affect the number of tiller/plant, whereas Giza 168 was the least affected one.

RESISTANT PROMISING VARIETIES OF WINTER AND SPRING BREAD WHEAT TO BUNT UNDER THE KYRGYZSTAN'S CONDITIONS

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Introduction

Cereals (wheat, barley, corn) - the strategic agricultural crops of the Kyrgyz Republic, as they are the main sources of the most important food products for the population of the country, as well as concentrated and of roughage for agricultural animals. They occupy more than half of planting area (54%) from the total area of cultivated crops in the republic [Dzhunusova, 2006]. Last year wheat yields has fallen sharply, this is connected, firstly, with the violation of agrotechnical methods in the cultivation of crop varieties, and most importantly - the absence of resistant varieties of grain crops to particularly dangerous harmful pathogen. As is known, the most harmful diseases of winter and spring wheat are infectious diseases. In moderate expression of wheat diseases the yield losses make 10-20%, and in the epidemic years can reach 30-50% or more.

Materials and methods

Entomological and phytopathological field studies were conducted at the demonstration plots in Sokuluk district, Chui region by the State

Center for varieties testing and plant genetic resources. In our studies attention was given to studying stability of the released and promising varieties of winter and spring bread wheat to infectious diseases on a background of artificial infection of plants. Severity was recorded, and dynamics of the development of disease was determined by generally accepted methods in plant pathology. Artificialy infected seeds with spores of local bunt was used. The observations and assessments focused on immunological parameters varieties reaction to pathogens. The harmfulness bunt in Kyrgyzstan was influenced by genetic characteristics of varieties and climatic conditions in autumn and spring growing season.

Results and research

During the period of 2012-2014 evaluation for resistance to bunt on infectious background in entomological and phytopathological demonstration plot (Sokuluk district, Chui region.) was conducted on varieties of winter and spring bread wheat of domestic and foreign selection. The results have shown that some released and promising winter and spring bread wheat varieties were moderately infected by bunt except variety Moskovskaya 39. In 2012-2014 years winter wheat Moskovskaya 39 under artificially infected bunt showed highly resistant reaction from 0 to 3%. Varieties Intensivnaya, Don 105 shown high susceptibility to disease up to 83.5%, as well as the variety Afina and promising variety Zhanym showed moderate susceptibility with infection up to 21.4 to 54.5%.Variety Donskoy was infected by 53.4% in 2013, but in the rest of 2012-2014 is was moderately susceptible from 21.8 to 30.5%. In 2014 year variety Berezit in our experiments shown reaction up to 20%, but in 2012-2013 years the infection was higher.

Conclusions

The results demonstrated that the only highly resistant to bunt variety was Moskovskaya 39 among all the released and promising varieties of winter and spring wheat. At the same time, resistant in different years and were varieties Berezit and Donskoy. The most effective in protection of winter and spring bread wheat from bunt should be considered introduction into production of immune varieties. Varieties of wheat possessing high and moderate resistant to bunt pathogen can be employed as the parental form for creating new varieties of wheat.

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WHEAT KARNAL BUNT (TILLETIA INDICA) IN PAKISTAN AND ITS IMPLICATIONS FOR EXPORT

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A fungal disease of wheat and triticale known as Karnal bunt (KB) may reduce the yield as well as quality of the grains. Planting infected seed is the primary means of disseminating the pathogen (Tilletia indica) over long distances, therefore many countries declared the disease as quarantine pest. Two sets of over 700 wheat advanced lines and varieties were assembled and examined for KB at the Crop Disease Research Institute (CDRI) Islamabad using washing test. The first set of entries contributed by various national programs when tested showed 42% samples infected with KB. Planting of infected seeds and lack of management practices for KB resulted in high percentage (76%) of infection in samples from 2014-15 wheat harvest. The late rain in previous years could also be the contributor to the increased incidents of KB. Though the tested samples received from research institutes, there is likelihood of even more infection in the farmer's field as well. Pakistan produced surplus wheat in the last couple of years and planning to export which would require concerted efforts both at management and breeding level to control KB spread and introduce varieties with certain level of resistance.

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XIX INTERNATIONAL WORKSHOP ON SMUTS AND BUNTS

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