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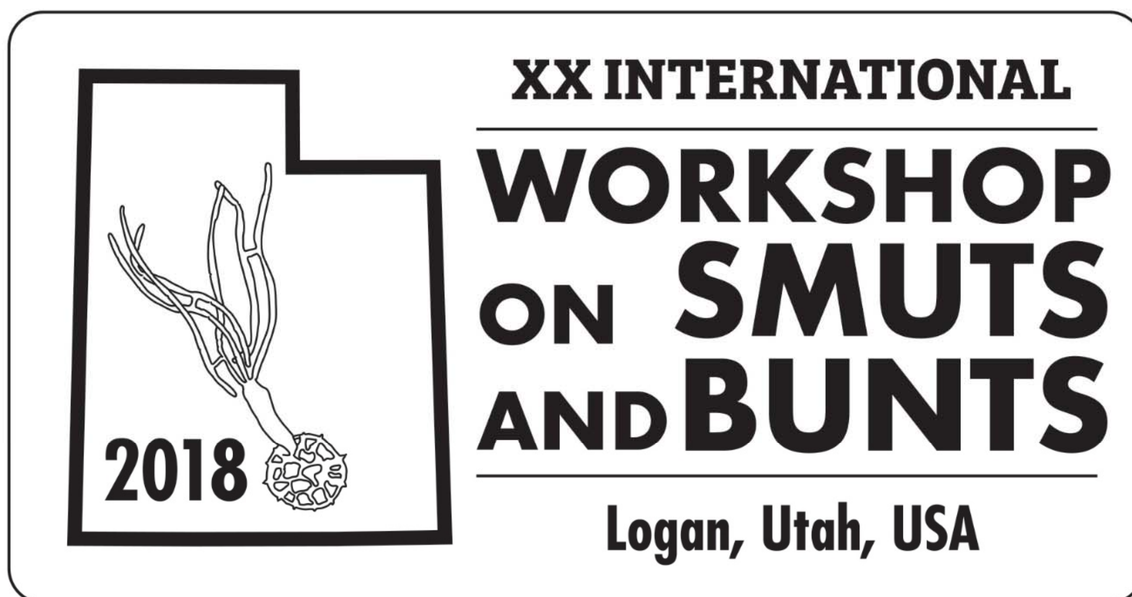

29 May 2018, Tuesday

Arrival of participants to Logan

Hampton Inn by Hilton
1665 North Main Street
Logan, Utah 84341 USA
Phone +1-435-713-4567

18:30 – 20:30	Welcome Reception: The Italian Place: 48 Federal Ave, Logan, UT 84321

30 May 2018, Wednesday

09:00-09:30	Welcome to the conference by Dr. Paul Johnson, Department Head, Plants, Soils and Climate, Utah State University.
09:25-10:00	Introduction and logistics, Utah Bunt nursery details – David Hole
10:00-10:30	Break.

Scientific session:
Pathogens: Diversity, Pathogenicity, Methodology
Session chair: Hermann Bürstmayr

10:30-11:00	**iTRAQ-based Proteomic Analysis of Wheat Bunt Fungi *Tilletia controversa*, *T. caries* and *T. foetida*** Li Gao
11:00-11:30	**Classification of wheat bunt diseases (*Tilletia* spp.) and the importance of reliable reference material for the development of new detection methods** Monika K. Grundler

11:30-12:00	**Tracing *Tilletia caries* in wheat during the endophytic phase** Fabio Mascher

Lunch – 12:00 – 13:30
Session chair: Juliet Marshall

13:30-14:00	**Three new species of flag smut of grasses from the United States** Kyryll G. Savchenko
14:00-14:30	**Determination of the genome composition of *Sporisorium reilianum* f. sp. *reilianum* (Kühn) Langdon and Fullerton, the sorghum head smut pathogen** Chunlai Zhang
14:30-15:00	**Historical records of *Urocystis* in North America from the U.S. National Fungus Collections** Lisa A. Castlebury
15:00-15:30	Break

Sightseeing in Logan or hiking in Logan canyon to wind caves 16:00-

Dinner on your own

31 May 2018, Thursday

Scientific session:
Disease Control
Session chair: Anders Borgen

09:00-09:30 **Genome-Wide Association Mapping for Dwarf Bunt Resistance in the National Small Grains Collection**

Tyler Gordon

09:30-10:00 **Virulence pattern of Czech bunt samples and sources of resistance**

Veronika Dumalasová

10:00-10:30 **Evaluation of Nordic heritage varieties and NILs for resistance to common bunt (*Tilletia caries* syn. *T.tritici*)**

Anders Borgen

10:30-11:00 Break
Session chair: Veronika Dumalasova

11:00-11:30 **Strategic use of virulence pattern to develop genetic markers for resistance to common bunt (*Tilletia caries*) in wheat**

Anders Borgen

11:30-12:00 **New tools available to control the common bunt of wheat: development of an early detection test on plantlet by qPCR.**

G. Orgeur.

12:00-12:30 **Mapping QTLs conferring additive resistance to Karnal bunt in bread wheat in two recombinant inbred lines populations**

P.K. Singh

12:30 – 14:00 – Lunch
Session chair: Fabio Mascher

14:00-14:30	**Prospects and challenges for breeding bunt resistant wheat using molecular marker assisted selection** Rui Wang
14:30-15:00	**Comparative mapping of bunt resistance genes in winter wheat** Hermann Bürstmayr
15:00-15:30	**Organic methods of controlling common bunt at the farm level.** Lars Wiik

15:30-16:00 Break
Session chair: David Hole

16:00-17:00	Business Meeting - Discussion

Banquet – 19:00 – 21:00
Smithfield Golf Course Reception

01 June 2018, Friday

09:00-09:30	Travel to Logan Bunt nursery
10:30-12:00	Travel to Pocatello, ID
12:00-13:00	Lunch on own at Portneuf Valley Brewing
13:30-16:00	USDA small grains collection Aberdeen, ID **(Passport or Gov't ID required)**
16:00	Travel back to Logan or SLC airport hotels.

Strategic use of virulence pattern to develop genetic markers for resistance to common bunt (*Tilletia caries*) in wheat

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When assesssing races of common bunt for virulens pattern within a region, it is important to take into account that collected spores may represent a diverse population of different virulence races. When screening spores on a differential set of wheat lines with known resistance genes, a low infection rate on a resistant wheat variety does not necessarily demonstrate that virulence is absent in the spore collection, but could be a sign that virulence is present, but only present in a low frequency among the spores. If just a few spores within a spore sample are indeed virulent, they may infect some plants and from there multiply the virulence quite rapidly next years. Previous studies have shown that virulence against most resistance genes were present in Denmark after purifying races of common bunt (*Tilletia caries*) on resistant varieties. So far, only wheat differential varieties with *Bt4, Bt6, Bt9, Bt11* and *Bt12* cannot be infected with bunt races purified from Danish collections [1, and later own unpublished data]. Virulence against *Bt4, Bt6* and *Bt9* has been found in other European studies [2], and *Bt11* may not be only one gene but a combination of at least two genes [3]. Therefore, *Bt12* seems to be the only gene for which virulence have not been found in European population of common bunt. This leads to the conclusion that if resistance breeding shall safely control common bunt in wheat, we need not only one effective gene, but a combination of pyramided genes. Since it is very difficult to test if a resistant line has only one gene or more genes, the most effective tool to achieve this at present are genetic markers.

Using Genome Wide Association Studies (GWAS) to find QTLs and markers for the major resistance genes in wheat have so far led to only few commercial useful markers. Till now, only markers for *Bt9* [6] and *Bt10* are used in practice, but a marker for *Bt12* [4] and Blizzard [7] have also been found. One of the problems in developing markers for bunt resistance have been that spores used in GWAS trials have been divers or unknown in virulence, and that phenotypic results not distinguishes between different resistance genes. Therefore, the most successful studies have used segregating populations of single crosses where the resistance gene is known on before hand [5].

In the LIVESEED project, we have the ambition to develop genetic markers on several different resistance genes at the same time. We will do so by testing segregating populations of several different crosses between varieties with 7 different resistance genes, and infect them with 7-11 different virulence races of common bunt able to distinguish between the resistance genes. A total of 300 varieties will be pheno- and genotyped. Using this experimental design, we attempt during

2018 and '19 to develop markers for *Bt1, Bt2, Bt5, Bt7, Bt13, BtZ* and Quebon-resistance, and hopefully also a couple of minor QTLs.

Acknowledgement: The research is part of the LIVESEED project supported by EU Horizon2020 program.

References

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