

**Proceedings of the  
2020 National Fusarium  
Head Blight Forum**



**VIRTUAL**  
**December 7-11, 2020**

---

Proceedings compiled and edited by: S. Canty, A. Hoffstetter and R. Dill-Macky

Credit for photo on cover: Siemer Milling Company Whitewater Mill at West Harrison, IN  
Photo courtesy of Carl Schwinke, Siemer Milling Co.

©Copyright 2020 by individual authors.

All rights reserved. No part of this publication may be reproduced  
without prior permission from the applicable author(s).

Copies of this publication can be viewed at <https://scabusa.org>.

## **Guideline for Referencing an Abstract or Paper in the Forum Proceedings**

When referencing abstracts or papers included in these proceedings, we recommend using the following format:

Last Name and Initial(s) of Author, [followed by last names and initials of other authors, if any].  
Year of Publication. "Title of paper" (Page Numbers). In: [Editor(s)] (Eds.), *Title of Proceedings*;  
Place of Publication: Publisher.

### ***Sample Reference:***

Arshani Alukumbura, Dilantha Fernando, Sabrina Sarrocco, Alessandro Bigi, Giovanni Vannacci and Matthew Bakker. 2020. "Analysis of Effectiveness of *Trichoderma gamsii* T6085 as a Biocontrol Agent to Control the Growth of *Fusarium graminearum* and Development of Fusarium Head Blight Disease in Wheat" ( p. 25). In: Canty, S., A. Hoffstetter, and R. Dill-Macky (Eds.), *Proceedings of the 20120 National Fusarium Head Blight Forum* . East Lansing, MI: U.S. Wheat & Barley Scab Initiative.

---

---

## FORUM ORGANIZING COMMITTEE

Chair: Carl Bradley, University of Kentucky, Princeton, KY

Members: Rick Boyles, Clemson University, Florence, SC  
Jason Cook, Montana State University, Bozeman, MT  
Jason Fiedler, USDA-ARS, Fargo, ND  
Pat Hayes, Oregon State University, Corvallis, OR  
Guixia Hao, USDA-ARS, Peoria, IL  
Amir Ibrahim, Texas A&M University, College Station, TX  
Dave Kendra, BASF, Research Triangle Park, NC  
John McLaughlin, Rutgers University, New Brunswick, NJ  
Jaijai Rao, North Dakota State University, Fargo, ND  
Damon Smith, University of Wisconsin, Madison, WI  
Jessica Rutkoski, University of Illinois, Urbana, IL  
Darcy Telenko, Purdue University, West Lafayette, IN  
Xiang S. Yin, Rahr Corporation, Shakopee, MN

USWBSI Co-Chairs: Ruth Dill-Macky, University of Minnesota, St. Paul, MN  
Doyle Lentz, Private Grower, Rolla, ND

### ORGANIZED BY THE:



U.S. Wheat & Barley  
Scab Initiative

---

---



---

# Table of Contents

---



---

## BARLEY COORDIANATED PROJECT

<b>Fusarium Head Blight Biomass in Spring Barley Comparing 2018 to 2019 in U.S. Nurseries</b>	
Sidrat Abdullah, Eninka Mndowla, Suzette Arcibal Baldwin, Ellen Kress, Ruth Dill-Macky, Mark Earl Sorrells, Patrick Gross, Robert Brueggeman, Carl Griffey, Joshua Fitzgerald, Juliet Marshall, Kathy Klos and Thomas Baldwin .....	Poster #41 .....3
<b>Development of TR18262 Two-row Feed Barley with Desirable Agronomics and Disease Resistance Including Lower DON Accumulation</b>	
Ana Badea, William Legge, James Tucker, Xiben Wang, Adam Foster, Dan MacEachern, Raja Khanal and Barbara Blackwell .....	Poster #1 .....4
<b>Determining Fusarium Head Blight Resistance of Spring Barley in Idaho</b>	
Suzette Arcibal Baldwin, Belayneh A. Yimer, Thomas T. Baldwin, Yanhong Dong and Juliet M. Marshall .....	Poster #2 .....5
<b>2020 Hindsight on the North American Barley Evaluation Nursery (NABSEN)</b>	
Thomas Baldwin, Patrick Gross, Richard Horsley, Kevin Smith, Ruth Dill-Macky, James Tucker, Ana Badea, Marie Timmerman, Austin Case and Robert Brueggeman .....	Invited Talk .....6
<b>Exploring Variation for FHB Resistance in Naked Barley</b>	
John Hawkins and Kevin P. Smith .....	Poster #3 .....8
<b>Quantitative Trait Loci Associated With Resistance to Fusarium Head Blight and DON Accumulation in Barley Populations Derived from Moderately Resistant Six- and Two-Rowed Parents</b>	
Rae Page, Tamas Szinyei, Matthew Martin, Ahmad H. Sallam, Oadi Matny, Joseph Wodarek, Yanhong Dong, Patrick Hayes and Brian Steffenson.....	Poster #4 .....9
<b>Biofilm Formation in <i>Fusarium graminearum</i></b>	
Rebecca Shay and Frances Trail.....	Poster #5 .....11
<b>Five years in: Outlook for Breeding for FHB Resistance in Barley in New York</b>	
Daniel Sweeney, James Tanaka, David Benscher and Mark Sorrells .....	Poster #6 .....12

---



---

## DURUM COORDIANATED PROJECT

<b>Impact on Durum Wheat of Small Introgressions from Wild <i>Thinopyrum</i> Species Conferring Effective Resistance to <i>Fusarium</i> Diseases: Breeding Performance and Metabolic Responses</b>	
Ljiljana Kuzmanović, Giuseppina Fanelli, Silvio Tundo, Giulia Mandalà, Gloria Giovenali, Alessandra Capoccioni, Sara Rinalducci and Carla Ceoloni .....	Invited Talk ..... 15

---

IMPACT ON DURUM WHEAT OF SMALL  
INTROGRESSIONS FROM WILD *THINOPYRUM*  
SPECIES CONFERRING EFFECTIVE RESISTANCE  
TO *FUSARIUM* DISEASES: BREEDING  
PERFORMANCE AND METABOLIC RESPONSES  
Ljiljana Kuzmanović<sup>1</sup>, Giuseppina Fanelli<sup>2</sup>, Silvio Tundo<sup>1,3</sup>,  
Giulia Mandalà<sup>1,4</sup>, Gloria Giovenali<sup>1</sup>, Alessandra Capoccioni<sup>1</sup>,  
Sara Rinalducci<sup>2</sup> and Carla Ceoloni<sup>1\*</sup>

---

<sup>1</sup>University of Tuscia, Department of Agriculture and Forest Sciences (DAFNE), Viterbo, Italy;

<sup>2</sup>University of Tuscia, Department of Ecological and Biological Sciences (DEB), Viterbo, Italy;

<sup>3</sup>Present address: University of Padova, Department of Land, Environment, Agriculture and Forestry (TeSAF), Legnaro, Italy; and <sup>4</sup>Present address: University of Verona, Department of Biotechnology, Verona, Italy

\*Corresponding Author: PH: 39 (0) 761-357202; Email: ceoloni@unitus.it

---

## ABSTRACT

Durum wheat (*Triticum durum*,  $2n = 4x = 28$ , DW) covers only 8% of the global wheat surface, yet it represents a strategic commodity for countries spanning many and diversified world areas, primarily the Mediterranean Basin. Recent climate changes have not only contributed to modify the DW conventional distribution areas, but also exposed the crop to unfamiliar pathogens. This is the case for fungal pathogens of the *Fusarium* genus, responsible for some of the most threatening diseases of wheat and other cereals, namely Fusarium head blight (FHB), or scab, and Fusarium crown rot (FCR). For DW, which results more vulnerable to both FHB and FCR than 6x bread wheat (BW), this condition is particularly worrying. In fact, being typically devoted to human consumption, the DW crop greatly suffers, besides yield and quality reduction, the safety problems associated with health-dangerous *Fusarium* mycotoxins, such as deoxynivalenol (DON). Since effective resistant sources are not available in breeding pools, a profitable and sustainable approach to arm the species with appropriate defense means consists of the exploitation of genetic variability present in related gene pools, such as those of the *Thinopyrum* genus. Of specific interest is the distal end of 7L arm of several congeneric species, enriched with genes/QTL for resistance to relevant wheat diseases. Among them, the *Lr19+Sr25* genes (leaf and stem rust resistance, respectively), located on the 7e<sub>1</sub>L arm of 10x *Th. ponticum*, and also major QTL contributing resistance to both FHB and FCR, namely *Fhb7*, identified on the 7e<sub>2</sub>L arm of a different *Th. ponticum* accession, as well as its likely ortholog present on 7EL of the 2x *Th. elongatum* (1, 2, 3, 4, and refs. therein). The extraordinary efficacy against FHB of both *Fhb7* QTL (indicated hereafter as *Fhb7e<sub>2</sub>* and *Fhb7E* for the sake of distinction), was initially established in laboratory BW lines, such as Thatcher 7DS·7e<sub>2</sub>L centric translocation line, and Chinese Spring (CS) 7E(7D) substitution line. Besides contributing to cytogenetic mapping of *Fhb7* QTL (e.g. 2), we have successfully exploited chromosome engineering strategies to incorporate firstly *Fhb7e<sub>2</sub>* (1) and more recently *Fhb7E* (3) into DW. In both transfer schemes, previously produced DW recombinant genotypes, with 7e<sub>1</sub>L segments (including *Lr19*, *Sr25* and *Yp* genes) spanning 23% (named R5) and 28% (R112) of their 7AL arms, were used as recipient lines. As donor of *Fhb7e<sub>2</sub>*, the 7DS·7e<sub>2</sub>L BW-*Th. ponticum* translocation line was used, whereas previously obtained BW 7DS·7DL-7e<sub>1</sub>L/7EL recombinant types (named R69-9 and R74-10), carrying a terminal 7EL portion, including *Fhb7E*, embedded into a 7e<sub>1</sub>L *Th. ponticum* segment present on wheat 7DL



## Durum Coordinated Project

(2), were employed. In both cases, transfer of the *Fhb7* QTL was achieved by homologous pairing and recombination between the 7e<sub>1</sub>L portions shared by donor and recipient recombinant chromosomes in 5x F<sub>1</sub>s. Stable DW recombinants with either *Fhb7* QTL combined with valuable 7e<sub>1</sub>L genes were isolated in BC<sub>1-2</sub> progenies to the Italian DW cv. Simeto of all cross combinations. Further BCs to the same DW yielded near-isogenic recombinant lines (NILRs, HOM+), whose spikes and seedlings were inoculated with *F. graminearum* and *F. culmorum*, respectively, for assessment of their FHB and FCR phenotypes compared with those of HOM– sibs. Following *F. graminearum* point inoculation, NILRs of both 7e<sub>1</sub>L+7e<sub>2</sub>L DW recombinant types, named R216 and R193 (same telomeric 7e<sub>2</sub>L portion with *Fhb7e<sub>2</sub>*, but inserted into the 7e<sub>1</sub>L segments of either R5 or R112, respectively), exhibited an average 75% reduction in FHB severity vs. HOM– controls (1). Similarly, 7e<sub>1</sub>L+7EL DW recombinants, possibly due to some contribution of the CS donor background, showed an even stronger resistance, with > 90% reduction of disease severity (3). Moreover, unlike the case of *Fusarium* spp. resistance QTL native to wheat, both *Fhb7e<sub>2</sub>* and *Fhb7E* showed to confer tolerance to FCR as well, with disease index reduced by over 50% (3).

The breeding potential of the various DW recombinant types equipped with either *Fhb7e<sub>2</sub>* or *Fhb7E* was preliminarily evaluated, on the basis of plant and spike traits, in small-scale field tests carried out during the 2018-19 and 2019-20 seasons at Viterbo experimental site (Central Italy). Natural disease pressure was negligible in both experimental years. Instead, weather conditions were quite different, with 2019-20 being much drier than 2018-19, characterized by a huge amount of rainfall and lower mean temperatures in coincidence with the critical phases of anthesis and grain filling. Whereas an overall absence of negative effects on yield and related traits was observed for all recombinant types (HOM+) vs. their controls (HOM–), the marked between-year difference was helpful at highlighting the best suited recombinant genotypes to the contrasting environmental conditions. Thus, between R216 and R193 (7e<sub>1</sub>L+7e<sub>2</sub>L), the 2018-19 season resulted more favourable to the latter, in which the 7e<sub>2</sub>L portion is part of the R112 longer 7e<sub>1</sub>L segment compared with R5. The better yield performance of R193 is in line with previous observations from multi-year/environment trials, which suggested R112 to carry in its most proximal 7e<sub>1</sub>L fraction (retained in R193) genes/QTL for morpho-physiological and agronomical attributes of the aerial and root plant portions that are best expressed in environments with optimal thermo-pluviometric patterns (5). On the other hand, R216 HOM+ had comparable or higher values than R216 HOM– for various yield and fertility traits in the hotter and drier 2019-20 season, thus mimicking the behaviour of its R5 parent (5). As to 7e<sub>1</sub>L+7EL recombinants, assessment of spike traits in R74-10/R112, R74-10/R5 and R69-9/R112 HOM+ genotypes and HOM– controls in the 2018-19 season, showed that presence of any of the three alien segments did not appreciably impair spike fertility and yield. However, R69-9/R112 was the best performing out of the three recombinants, and R74-10/R5 the least productive. This outcome might be associated with a different 7e<sub>1</sub>L/7EL ratio in the various recombinant types, with that of R74-10/R5 (longer 7EL segment than in R69-9, and shorter 7e<sub>1</sub>L segment than in R112) causing more disturbance to the recipient genome. Thus, the R69-9 derivatives appeared more appropriate for DW breeding, also because their 7EL portion does not replace the 7e<sub>1</sub>L allele of the *Yp* gene conferring higher semolina yellowness vs. the corresponding 7EL allele (2, 3). Consequently, subsequent work was focused on such recombinant types (R69-9/R5 and R69-9/R112), which exhibited a good performance at the plant and spike levels also in the drier 2019-20 season. Confirming their better adaptability to reduced rainfall, R69-9/R5 plants expressed higher values than their HOM– controls for a number of characters (mainly thousand grain weight and grain yield/spike), while R69-9/R112 was inferior to its HOM– controls for some spike traits. Based on 2019-20 dataset, an overall comparison of all DW-*Thinopyrum* spp. HOM+ recombinants, including R5 and R112 (7e<sub>1</sub>L only), as well as DW controls, Simeto and IDYT22 (an ICARDA line involved in

R216 and R193 pedigree), was carried out. ANOVA did not show statistically significant differences in grain yield/plant (GY). However, recombinants containing the 7e<sub>1</sub>L+7EL segment assembly, particularly R69-9/R5, turned out to be the best performing with respect to control varieties and to all other recombinant types. To a minor extent, also R216 and R193 (7e<sub>1</sub>L+7e<sub>2</sub>L) showed higher GY than R5/R112 and Simeto, while being comparable to IDYT22. These results indicate that, even disregarding the specific effects of the *Fhb7* QTL introgression, the presence of 7EL or 7e<sub>2</sub>L chromosomal portions onto 7e<sub>1</sub>L segments has a favorable impact on yield potential of the recipient DW, even improving the positive contribution known to be associated with the original 7e<sub>1</sub>L segments (5 and refs. therein).

An additional research activity enabled by the novel recombinant types was undertaken to get insights on the mechanisms underlying the *Fhb7*-mediated resistance. To this aim, the untargeted metabolomic profile of the rachis tissue sampled at 2-4 days following *F. graminearum* (*Fg*) inoculation of spikes of R69-9/R5 (*Fhb7E*) HOM+ NIRLs was recently compared with that of HOM- *Fg*-inoculated sibs and of mock-inoculated plants. Extracted metabolites from the 4 genotype x treatment combinations were analyzed by LC/MS. Preliminary evidence from MetPA (Metabolic Pathway Analysis) shows main changes between HOM+ and HOM- *Fg*-inoculated samples at the level of phenylalanine metabolism, phenylpropanoid and diterpenoid biosynthesis, known to be main routes the plant activates in response to *Fusarium* inoculation. Particular interest arouses the Vitamin B6 metabolism, specifically induced in *Fg*-inoculated *Fhb7E+* genotypes, which provides supporting evidence for B6 vitamers' role as potent antioxidants in plants subjected to abiotic and also biotic stresses. As a further contributor to the antioxidant capacity of stressed plants, the glutathione (GSH) metabolism was also up-regulated in *Fg*-inoculated *Fhb7E+* and, to a minor extent, *Fhb7E-* rachises. Of a particular GSH adduct, i.e. a de-epoxidated DON-GSH adduct, whose formation was recently associated with a peculiar, xenobiotic mechanism at the base of *Fhb7* resistance (4), clear proof of exclusive production in the rachis tissue of *Fhb7E+* plants was obtained by LC-MS/MS analyses. Whereas the GSH-mediated event appears to be a major determinant in DON detoxification brought about in the presence of *Fhb7* genes/QTL, additional detoxifying strategies, such as DON glycosylation, may contribute to an expected composite resistance response. In fact, the DON-3-glucoside (D3G) metabolite was solely detected in *Fhb7E+* *Fg*-inoculated rachises. In line with this, D3G was four times more abundant in seeds harvested from the latter plants than in *Fhb7E-* sibs. Combined with the nearly 800 times lower DON content found in HOM+ vs. HOM- seeds, these results confirm DW lines carrying *Fhb7E*, and *Fhb7* QTL in general, to be highly valuable also for the crop safety, thus enhancing its market/trade potential.

## ACKNOWLEDGEMENTS

Part of this work was carried out under the frame of the PRIMA programme supported by the European Union, Call 2018 – Farming Systems, Project “IMPRESA”, and in the context of the “Departments of excellence” initiative of the Italian Ministry of University and Research (law 232/216), whose financial contributions are gratefully acknowledged.

## REFERENCES

1. Forte, P., Virili, M. E., Kuzmanović, L., Moschetti, I., Gennaro, A., D'Ovidio, R., Ceoloni, C. (2014). A novel assembly of *Thinopyrum ponticum* genes into the durum wheat genome: pyramiding Fusarium head blight resistance onto recombinant lines previously engineered for other beneficial traits from the same alien species. *Mol. Breed.* 34:1701–1716, doi: 10.1007/s11032-014-0175-3
2. Ceoloni, C., Forte, P., Kuzmanović, L., Tundo, S., Moschetti, I., De Vita, P., et al. (2017). Cytogenetic mapping of a major locus for resistance to Fusarium head blight and crown rot of wheat on *Thinopyrum elongatum*

## *Durum Coordinated Project*

---

7EL and its pyramiding with valuable genes from a *Th. ponticum* homoeologous arm onto bread wheat 7DL. *Theor. Appl. Genet.* 130:2005–2024, doi: 10.1007/s00122-017-2939-8

3. Kuzmanović, L., Mandalà, G., Tundo, S., Ciorba, R., Frangella, M., Ruggeri, R., et al. (2019) Equipping durum wheat—*Thinopyrum ponticum* recombinant lines with a *Thinopyrum elongatum* major QTL for resistance to Fusarium diseases through a cytogenetic strategy. *Front. Plant Sci.* 10:1324, doi: 10.3389/fpls.2019.01324
4. Wan, H., Sun, S., Ge, W., Zhao, L., Hou, B, Wang, K., et al. (2020). Horizontal gene transfer of *Fhb7* from fungus underlies *Fusarium* head blight resistance in wheat. *Science* 368, doi: 10.1126/science.aba5435
5. Kuzmanović, L, Ruggeri, R., Able, J. A., Bassi, F. M., Maccaferri, M., Tuberosa, R., et al. (2018). Yield of chromosomally engineered durum wheat-*Thinopyrum ponticum* recombinant lines in a range of contrasting rain-fed environments. *Field Crops Res.* 228:147–157, doi: 10.1016/j.fcr.2018.08.014