

# Breeding for Global Resistance to FHB

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## Abstract

Fusarium head blight (FHB), a disease on several cereals, has been increasing over time due to a multitude of reasons which include: an extension of the global maize acreage in rotation with wheat (maize being a secondary host of the same fungus), the increasingly popular practice of reduced tillage with crop residue colonized by the fungus being maintained on or near the soil surface, the (desired) reduction in fungicide use, and the increased awareness of health issues related to FHB toxin production. We predict that global warming will further exacerbate the problem, as the disease thrives in high humidity, and warmer climates.

Since the mid 1980's CIMMYT has dedicated an intensive FHB resistance breeding program to the problem at the highly FHB-prone site of Toluca in the Mexican highlands with a mean rainfall of 800 mm during the cropping cycle, and relatively warm midday conditions. Annually we test 5-10,000 wheat and barley lines from around the world and our own breeding programs. Our inoculation, scoring and breeding methodologies have been fine-tuned over the years, widely published, conveyed to trainees and visiting scientists and adopted by many programs around the world. We measure all five types of resistance, which appear to some extent to be independently inherited, in a high-quality, labor-intensive, though resource-efficient approach.

While initially 20 years ago we emphasized the classical sources of resistance in wheat (e.g. Chinese, Latin American), we now have introgressed and accumulated those genes into high-yielding, durable rust resistant and high industrial quality genetic backgrounds that are much easier used by collaborators for crossing or direct release as varieties. In addition we have essentially expanded genetic diversity for resistance by in-house generation of novel synthetic hexaploid wheats exploiting *T. tauschii* derived resistance. This novel diversity single-handedly expands global recombinant diversity, and not just for FHB resistance, in a near exponential fashion. FHB resistant barley sources have likewise been identified by the ICARDA/CIMMYT program based at CIMMYT in close collaboration with CIMMYT scientists, and shared with partners. Novel combinations carrying multiple disease resistance and high quality have been developed, some in collaboration with private enterprise. The crossing strategy for all our crops conceptually aims to accumulate resistance mechanisms and underlying alleles. Markers are being applied on our parental stocks and this year for the first time will be applied to segregating populations. Haplotyping of about 100 elite FHB resistant CIMMYT wheats indicated that resistance existed beyond the classical 3BS Sumai#3 derived alleles, indicating potential novel genes. We expect oven resistance especially to be confirmed in the synthetic hexaploids.

During the past 20 years CIMMYT has expanded close collaboration with China, Uruguay, Brazil, Argentina, Mexico, Ethiopia, Romania, the USA, Canada, and Japan, with additional countries (e.g. France, Germany, Guatemala, India, Iran, Korea, Pakistan, Paraguay, Peru, Poland, Tanzania, and Ukraine)

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involved in evaluating our Scab Resistance Screening Nursery (SRSN), free-of-charge supplied upon request since the late 1980's. We are a full member of the United States Wheat and Barley Scab Initiative, a driving force behind modern research on FHB, based on our valued global genetic stocks (e.g. landraces, cultivars and wild relatives), including those in our Gene Bank collection, the single largest in the world, and because of our proven track record on breeding resistant genotypes. Cluster analysis of the SRSN shows that interaction does exist between genotypes and locations. Part of this is due to different scoring methodologies being used, but interaction is also evident when the same resistance type is measured in different locations on the same set of genotypes. Underlying reasons may be the presence of different *Fusarium* species, climate factors and associated differences in genotypic response/expression (e.g. temperature driven), or, and this is a controversial issue, actual specific race-by-genotype interaction. It is clear that selection in one location using certain resistance sources may not provide resistance in other locations and even result in genotypic rank changes between locations. The implications of this observation of genotype by location interaction are potentially large, with only a concerted international approach being capable of probing underlying mechanisms. Against this background we have, however, identified genotypes that are consistently resistant worldwide, and these are being shared with interested parties. Cultivars have been released based on such germplasm including in hotspots in China.

In the past most emphasis by almost all FHB resistance-breeding programs has been on reducing disease in the farmer's field (Types I and/or II), and we have made great strides in enhancing such resistance. Now the time has come, as global health awareness grows, to determine globally effective genetic sources of low toxin levels following infection. We are presently studying DH populations in which this character segregates.

The primary, secondary and tertiary gene pools are being exploited at CIMMYT to expand the genetic base of resistance. Using the ph-mutant system in which heterologous pairing is allowed to occur between genomes of distant wheat relatives, we are in the process of developing FHB resistant bread and durum wheats, the latter being a crop notoriously susceptible under FHB-prone conditions.

We are optimistic that our placement as an international FHB research program collaborating with partners will allow understanding of global genotype-by-location interactions, generate novel sources of resistance, increase probing of underlying mechanisms and contribute to providing resistant, high-quality, low-toxin cultivars for our farmers, processors, consumers and the global cereal trade.

## **Introduction**

*Fusarium* head blight (FHB), a disease on several cereals, has been increasing over time for a complexity of reasons which include: an extension of the global maize acreage in rotation with wheat (maize being a secondary host of the same fungus), the increasingly popular practice of reduced tillage with crop residue colonized by the fungus being maintained on or near the soil surface, the (desired) reduction in fungicide use, and the increased awareness of health issues related to FHB toxin production. We predict that global warming will further exacerbate the problem, as the disease thrives in high humidity, warmer climates.

## **Methodology**

Since the mid 1980's CIMMYT has dedicated an intensive FHB resistance breeding program to address the problem at the highly FHB-prone site of Toluca in the Mexican highlands experiencing 800 mm mean rainfall during the cropping cycle, and relatively warm midday conditions (van Ginkel *et al.*, 2003a, 2003b). Annually we test 5-10,000 wheat and barley lines from around the world and our own breeding programs. Our inoculation, scoring and breeding methodologies have been fine-tuned over the years, and have been widely published, conveyed to trainees and visiting scientists and adopted by many programs around the world. We measure all five types of resistance (Miller and Arnison, 1986; Mezterhazy, 1995; Schroeder and Christensen, 1963; Vivar, 1996), which appear to some extent to be

independently inherited, in a high-quality, labor-intensive, though resource-efficient approach.

## Genetic Resistance

The crossing strategy for all our crops conceptually aims to accumulate resistance mechanisms and underlying alleles (Singh and van Ginkel, 1997). Initially starting 20 years ago we emphasized the classical sources of resistance in wheat (e.g. Chinese, Latin American; Singh *et al.*, 1995; Van Ginkel *et al.* 1996). Now we have introgressed and accumulated those genes into high-yielding, durable rust resistant and high industrial quality genetic backgrounds that are much easier used by collaborators for crossing or direct release as varieties (van Ginkel and Gilchrist, 2002). See table 1 for two examples of how complementary cross combinations are designed based on their response as measured using the five resistance types.

**Table 1. Complementary wheat parental combinations 1x2 and 3x4 aimed to accumulate all FHB resistance Types. (Bold font = FHB resistant; normal font = FHB susceptible)**

Entry	Cross	RESISTANCE TYPE				
		I	II	III	IV	V
		Damage (%)	Damage (%)	Toxin (ppm)	Grain losses (%)	Grain (1-5)
1	Milan/Sha7	<b>0.00</b>	6.07	<b>0.14</b>	13.29	2
2	Bcn*2//Croc_1/ <i>Ae. squarrosa</i> (886)	11.56	<b>4.82</b>	0.38	<b>1.68</b>	<b>1*</b>
3	Mayoor//Tk Sn1081/ <i>Ae. squarrosa</i> (222)	<b>0.86</b>	7.26	0.49	<b>1.3</b>	<b>1*</b>
4	Gov/Az//Mus/3/Dodo/4/Bow (=Gondo)	2.51	<b>2.66</b>	<b>0.00</b>	21.16	2

(From: van Ginkel *et al.*, 2003b)

The primary, secondary and tertiary wheat gene pools are also being exploited at CIMMYT to expand the genetic base of resistance. We have greatly expanded the available genetic diversity for resistance by in-house generation of novel synthetic hexaploid wheats exploiting *T. tauschii* derived resistance. This novel diversity single-handedly expands global recombinant diversity, and not just for FHB resistance, in a near exponential fashion.

Also using the ph-mutant system in which heterologous pairing is allowed to occur between genomes of distant wheat relatives, we are in the process of developing FHB resistant bread and durum wheats, the latter being a crop notoriously susceptible under FHB-prone conditions.

FHB resistant barley sources have likewise been identified by the ICARDA/CIMMYT program based at CIMMYT in close collaboration with CIMMYT scientists, shared with partners. These novel combinations carry multiple disease resistance and high quality, with some having been developed in collaboration with private enterprises.

Markers are being applied on our parental stocks and for the first time will be applied to segregating populations. Haplotyping of about 100 elite FHB resistant CIMMYT wheats indicated that resistance existed beyond the classical 3BS Sumai#3 derived alleles, indicating potential novel genes. We expect novel resistance especially to be confirmed in the synthetic hexaploids.

**Table 2. Barley sources of FHB resistance identified by Mexico-based ICARDA/CIMMYT barley improvement program.**

Cross	Head Type	Cross	Head Type
Atahualpa	2	Gobernadora	2
Azafrán (Misc. Cal. 21)	2	Humai 10	2
Chamico	6	PFC 88209	6
Chevron	2	Shyri	2
CIho 4196	2	Svanhals	2
Fredrickson	2	Zhedar 1	2

(From: van Ginkel *et al.*, 2003b)

## International Cooperation

During the past 20 years CIMMYT has expanded close collaboration to include China, Uruguay, Brazil, Argentina, Mexico, Ethiopia, Romania, the USA, Canada, and Japan. Additional countries (e.g. France, Germany, Guatemala, India, Iran, Korea, Pakistan, Paraguay, Peru, Poland, Tanzania, and Ukraine) are also involved in evaluating our Scab Resistance Screening Nursery (SRSN), which was initiated in the late 1980's and is supplied free-of-charge upon request. Table 3 lists some of the most resistant genotypes worldwide from among the entries in the 1<sup>st</sup> until the 7<sup>th</sup> SRSN.

CIMMYT is also a full member of the United States Wheat and Barley Scab Initiative (USWBSI), a driving force behind modern research on FHB, based on our valued global genetic stocks (e.g. landraces, cultivars and wild relatives), including those in our Wheat Gene Bank collection, the single largest in the world, and because of our proven track record on breeding resistant genotypes.

**Table 3. Top Type II resistant wheat entries in global testing of Scab Resistance Screening Nursery (equal or better than Sumai#3 and Frontana; most resistant first)**

1 <sup>st</sup> SRSN	2 <sup>nd</sup> SRSN	3 <sup>rd</sup> SRSN	4 <sup>th</sup> SRSN	5 <sup>th</sup> /6 <sup>th</sup> SRSN	7 <sup>th</sup> SRSN
Shanghai #3	Ng82149/Kauz	Wuhan #3	Ng8675/Ng8645	Sha5/Weaver	Catbird
CMH78A.544	Ng8201/Kauz	China #7	Mayoor	Catbird	Gondo
Fan #1	Sha#3/Kauz	Ning7840	Ng8675/Cbrd	Chum18//Jup/Bjy	Shanghai
Ning7840		Shanghai #3	Lu 95	Gondo	Ng8675/Cbrd
Yangmai #6		F3.71/Trm//3383.20			Sha3/Cbrd
		Suzhoe #6			
		Ng82149			

(From: van Ginkel *et al.*, 2003b)

## Genotype-by-Location Interaction

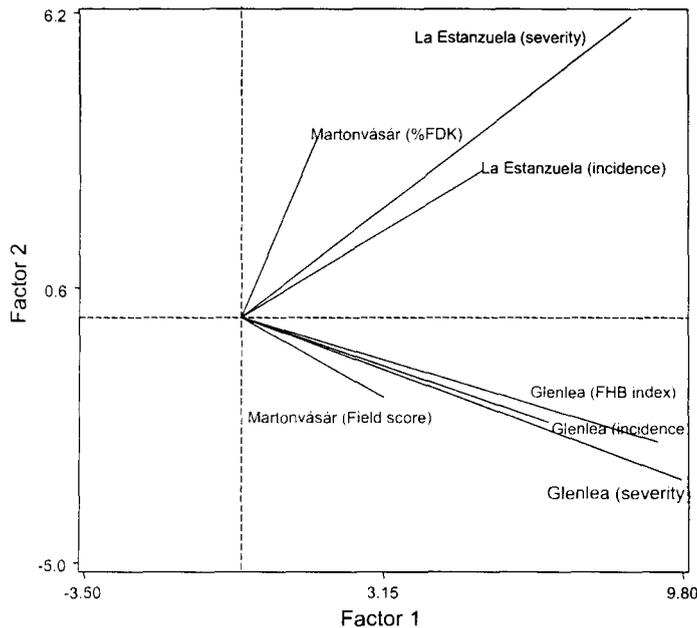
Cluster analysis of the SRSN shows that interaction does exist between genotypes and locations (See Figure 1). Although cooperators in La Estanzuela and Glenlea used the same evaluation methodologies (severity and incidence) to rank genotypes, their relative placement within the bi-plot is very distinct. Within La Estanzuela and within Glenlea, screening methodologies gave similar entry rankings, but within Martonvasar the two methodologies ranked entries differently.

The underlying reasons for this observation of genotype-by-location interaction may be various, including the presence of actually different *Fusarium* species encountering species-specific resistances, climate factors and associated differences in genotypic response/expression (e.g. temperature driven epidemics starting earlier or later than resistance mechanisms are able to engage), or, and this is a controversial issue, actual race-specific isolate-by-host genotypic interaction. It is clear that selection in one location using certain resistance sources may not always provide resistance in other locations and may even result in genotypic rank changes between locations.

The implications of this observation of genotype-by-location interaction are potentially large, with only a concerted international approach capable of probing underlying mechanisms. A global breeding enterprise such as CIMMYT's must address such potential interactions seriously with an eye to providing developing country farmers around the globe with varieties that provide stable long-term resistance under varying production conditions. Table 3 lists genotypes that contain effective resistance in various locations around the world, but these and genotypes like them should be studied in more depth as regards consistent global response to FHB.

## New Emphasis on Lowering Toxin Levels

In the past most emphasis by almost all FHB resistance-breeding programs has been on reducing disease in the farmer's field (Types I and/or II), and we have jointly made great strides in enhancing such resistance. In other words, our emphasis was on the plant and its visual affliction. Now the time has



**Fig. 1. Bi-plot analysis of wheat genotype response to FHB in the 6<sup>th</sup> SRSN, indicating some genotype-by-location interactions.**

come, as global health awareness grows, to determine globally effective genetic sources for low toxin levels associated with infection. This area is not well understood: sometimes grain toxin levels are surprisingly high following what was thought to be minor levels of visual infection or after an epidemic which started too late to be thought threatening. This emphasis on toxin levels will feature as one of the major reorientations in CIMMYT's research on FHB.

Some of the lines with the lowest levels of toxin after experiencing heavy FHB infection in China were: Sha#3/Cbrd, Ng8675/Cbrd, Milan/Sh7, Shanghai, and Mayo//Tk Sn1081/*Ae. squarrosa* (222). Their global effectiveness and the underlying genetics must be studied.

## Conclusions

CIMMYT with its international FHB research program collaborates with partners around the world both in advanced research institutes and with producers in developing countries. We are optimistic that this placement will allow a growing understanding of global genotype-by-location interactions, will generate novel sources of resistance, will increase probing of the underlying resistance mechanisms both at the tissue and genetical interface, will help re-orient our focus on genetically lowering toxin levels, and will contribute to providing resistant, high-quality, low-toxin cultivars to the farmers, processors, consumers and cereal trade of the world.

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