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Common quantitative resistance to four *Fusarium* species causing head blight in wheat and barley

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Abstract

Fusarium head blight (FHB) is one of the most noxious diseases affecting *Triticum* spp. and *Hordeum vulgare*. As several *Fusarium* pathogens are included in head blight, it is requested to explore whether *Fusarium* resistance has a common resistance to all *Fusarium* pathogens, or whether diverse genes regulate resistance to several pathogens. A common resistance is the consensus in the investigation, but only a few reports confirm this. We have therefore analyzed the presence of common resistance in a set of several bread and durum wheat and barley cultivars with diverse resistance levels under artificial infection with four *Fusariarn* species. Nine components obtained under *in vitro*, growth chamber and field conditions were assessed to better understand the nature of quantitative resistance to head blight. The scores of head blight intensity of *Triticum* spp. and *H. vulgare* cultivars to *F. culmorum*, *F. solani*, *F. verticillioides*, and *F. equiseli* were very similar, showing that the resistance to *F. culmorum* was identical to that for other *Fusarium* pathogens listed. This is a crucial singe to breeders as the resistance depends not only to any specific isolate of *F. culmorum*, but similarly to isolates of other *Fusarium* pathogens. This apply for all the components evaluated, FHB resistance covers common resistances to diverse head blight pathogens. It appears that resistance components are not independent variables but rather a series of components that follow epidemic and disease development; their genetic regulation may vary. This study presents the significance of assessing all quantitative features at the earliest and latest growth stages in the breeding and selection of resistant cultivars and germplasm. Resistance to several FHB pathogens appears to be connected; it is species non-specific, but further investigation is required. This is the first research which reports the presence of common resistance in durum wheat and barley against several *Fusarium* pathogens.

Keywords: *Hordeum vulgare*, *Fusarium* pathogens, quantitative resistance, *Triticum* spp.

1.Introduction

Wheat, involving bread (*Triticum aestivum*) and durum (*T. durum*), is proven as one of the most essential food crops which supplies daily nutrition to a board section of worldwide population. Barley (*Hordeum vulgare*) is one of the most principal widely planted cereal grain crops globally with multipurpose utilization as brewing material, animal feed, and human food. Annually, they are cultivated over an area of 270 million ha and yielding over 905 million metric tons [1]. Many studies have shown that worldwide *Triticum* spp. and *H. vulgare* production would request to be augmented by 60% to reach the food and feed necessities by 2050. This goal appears complicated to achieve in light of existent scenario of unpredictable meteorology change, scarcity of water resources, and reducing arable land [2]. In addition, frequent outbreaks of fungal species also causes drastic decrease in the wheat and barley yield as well as on quality seed production; around 21.5% of *Triticum* spp. and *H. vulgare* production is lost to these diseases yearly [3]. FHB is one of the most destructive diseases infecting wheat and barley. Disease symptoms involve spike bleaching, necrosis, and shriveled grains [4]. Grave epidemics can lead to very high production losses in individual fields, and large regions can be invaded where not only is the production decreased, but also the remaining production suffers grave quality damages due to

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toxins, i.e., deoxynivalenol (DON) [5, 6]. Consequently, DON contamination may lead to grave financial losses [7].

Surveillances of head blight species occurring in infected kernels or other parts of the spike led to the detection of a number of *Fusarium* pathogens [8, 9]. The pathogen nature of the head blight population is widely differing, from location to location and from year to year [10]. These result a large number of mycotoxins, differing largely in composition, several of which are responsible for the release of even 5-10 diverse toxins, encompassing masked forms [11]. In most fields of the globe, the dominant pathogens are principally *F. graminearum* and *F. culmorum*; thus, nearly all breeding programs concentrate on this. However, *F. equiseti*, *F. poae*, *F. sporotrichioides*, *F. avenaceum* and *Microdochium nivale* may play crucial functions in given areas [12]. The co-presence of several FHB pathogens in the same field is a normal situation. Many less aggressive species such as *F. verticillioides* and *F. solani*, can release highly toxic agents; resistance to them is consequently also significance [13]. The question is how far the issue of existence of multiple *Fusarium* pathogens included in head blight complex can be treated by breeding [7]. It is understandable that breeding efforts have been employed against these dominant or ruling pathogens, implicitly suggesting some art of common resistance against them [9].

Comprehensive reports have shown that no true vertical races exist within *F. culmorum* and *F. graminearum* [14, 15, 16]. Novel findings from the USA [17] confirm this. Several breeding programmers deal only with the ruling FHB pathogens such as *F. graminearum* or *F. culmorum*. Consequently, no detailed data is available as to whether the resistance to *F. graminearum* gives control in their breeding resource against other FHB pathogens or not. The response would infect the breeding methodology and policy, and the accuracy of resistance analyses in other regions with several compositions of FHB species. This non-specificity within *F. culmorum* and *F. graminearum* led to the idea that resistance to different *Fusarium* species might be common. The primary signal that resistance to *F. avenaceum* [14] could resemble that of the two principal pathogens dates from 1977, but convincing evidence has not yet been achieved. For *M. nivale* the situation is the same [15] as only one set of information was employed and the links were only moderate.

With the similar cultivars as utilized by van Eeuwijk *et al.* [15]. Mesterhazy [14] observed very similar resistance responses against *F. culmorum* and *F. gramineorum*; this held true for head blight, the level of DON contamination, *Fusarium* damaged kernels (FDK), production loss.

Limited researches have explored the resistance to several FHB pathogens. Klechkovskaya [18] analyzed the resistance to single strains of five diverse *Fusarium* species. The correlation coefficients changed between 0.50 and 0.65 for the infection intensity, and between 0.48 and 0.52 for the production, all significant at $P<0.05$, but not sufficiently close to confirm common resistance. Stack *et al.* [19] showed identical Type II resistance, resistance to pathogen spreading in the head, to seven *Fusarium* species on 5 genotypes of Sumai 3 origin in the greenhouse (FHB, FDK and DON findings). Resistance to *F. graminearurn* also provided protection against *F. poae*, *F. avenaceum* and *F. sporotrichioides*. *F. equiseti* and *F. acuminatum* were non-pathogenic. This referred only to the Sumai 3 resistance, and it is not known whether this result is of general significance as the number of genotypes was also moderate. The fact that the resistance of Sumai 3 is good in all the regions it was analyzed supports a working hypothesis that the resistance is maintained even when the pathogen composition is significantly diverse in *Triticum aestivum* production regions. Hollins *et al.* [20] showed one-season findings suggesting that the resistance to several *Fusarium* species might be common. Diamond and Cooke [21] found a close link between the resistance of wheat spikes to *F. culmorum* and the leaf resistance to *M. nivale*. In addition, Mesterhazy *et al.* [16] obtained very identical findings when analyzing wheat cultivars to *F. graminearum*, *F. avenaceum*, *F. sambucinum*, *F. sporotrichioides*, *F. verlicillioides*, *F. culmorum*, *M. nivale* and *F. poae*.

Empirical verification for species non-specificity originates mainly from experiments in which *M. nivale* or *Fusarium* spp. were represented by single isolates; in some cases only the findings for a single growing season were taken into account and often only head blight symptoms were tested. These findings permit an assumption of common resistance, but do involve experimental evidence. Therefore, a 5-year program was lunched in 1998 to verify the postulate for the common resistance of *Triticum aestivum* against several FHB species [16].

The experimental series was carried out under field conditions; spraying inoculation was employed. FHB, FDK, production performance and toxin contamination were analyzed [16]. The findings permit to conclusions regarding the resistance types described by Mesterhazy [14]. They are different from the resistance types presented by Browne and Cooke [22], Purahong *et al.* [23] and Shin *et al.* [24] as they analyzed, among others, latent period (LP) (time from inoculation to sporulation), area under disease progress curve (AUDPC) and coleoptile length reduction (CLR) which were not the case in the study conducted by Mesterhazy *et al.* [16]. LP, AUDPC, and CLR have been regarded as the most important *in vitro* components for testing both aggressiveness and quantitative resistance in the wheat/barley-FHB pathosystem [25]. These *in vitro* components evaluated on the scale of a given wheat/barley plant might mostly detected the rate of FHB outbreak development [25]. To better explore the background of quantitative resistance to head blight, the goal of the present research was to analyze whether FHB resistance has a common resistance to *Fusarium* pathogens in a set of diverse bread and durum wheat and barley cultivars with different resistance levels under artificial infection with four *Fusarium* species. Nine components obtained under *in vitro*, growth camber and field conditions at the earliest and latest growth stages were measured to test the existence of common resistance in wheat/barley-FHB pathosystem. Consequently, a clearer picture will be emerged on the relations between the resistances of cultivars to diverse *Fusarium* pathogens.

2. Materials and Methods

2.1. Wheat and barley cultivars

A set of eight cereal cultivars of Syrian origin covering a wide genetic and resistant variability including six *T. aestivum* and *T. durum* cultivars and two *H. vulgare* cultivars: Arabi Abiad (AB) and Arabi Aswad (AS) was chosen from previous *in vitro*, growth chamber and field experiments [25] to represent a range of quantitative resistance types to FHB infection. Wheat and barley cultivars AS and Bohoth10 (bread) moderately resistant, AB, Cham4 and Douma4 (bread) moderately susceptible, Cham7 and Cham9 (durum) susceptible to moderately susceptible, and Acsad65 (durum, susceptible) were utilized.

2.2. Fungal isolates

Sixteen single-spore derived cultures of four *Fusarium* species causing head blight, i.e. (*F. culmorum* (5 isolates), *F. solani* (6 isolates), *F. verticillioides* (synonym *F. moniliforme*) (4 isolates), and *F. equiseti* (one isolate)) chosen for their different aggressiveness levels (established on previous several experimental findings [25] were used. The isolates were collected through the 2015 growth season from naturally invaded wheat tissues in diseased heads in Ghab Plain with a FHB history, one of the principal Syrian wheat production areas. By using the keys of Leslie and Summerell [26], single spore cultures on Petri dishes with potato dextrose agar (PDA) with 13 mg/l kanamycin sulphate added after autoclaving, were classified morphologically to species level. By using random amplified polymorphic DNA markers, the 16 *Fusarium* species causing head blight isolates were recently analyzed [25]. The isolates were preserved by freezing at-16°C or in sterile distilled water at 4°C till use [27].

2.3. Inoculum preparation

FHB inoculum used for inoculation for the *in vitro*, growth chamber and field trials was normally performed as following: fungal suspension or four to six agar plugs out of each stored single-spore culture were put over the surface of Petri dishes PDA and incubated under continuous darkness at 22ºC for 10 days to allow sporulation and fungal development. Following incubation, isolates were covered with 10 ml of sterile distilled water and conidia were dislodged. Fungal suspensions were filtered through 2 layers of sterile cheesecloth to remove the pieces of mycelia and agar and directly quantified with a Neubauer chamber under an optical microscope and diluted to a desirable concentration as inoculum sources.

2.4. Quantitative components for resistance and aggressiveness

In order to test whether FHB resistance has a common resistance to *Fusarium* pathogens, nine pathogenic responses at the seedling and adult plant stages under *in vitro*, climatic growth chamber and field conditions of three bread cultivars, three durum cultivars and two barley cultivars with varying resistance levels to head blight to four *Fusarium* species was evaluated.

Pathogenic reactions of all cultivars infected with *Fusarium* fungi were previously evaluated according to methods described by Sakr [25] and shown in Table 1. Since no significant interaction year × fungus/cultivar was observed (climatic data for the station were somewhat similar during the three growing seasons [25]), field data were shown as the averages of the three growing seasons. Analysis of variance of bio-experiments revealed significant cultivar-by-isolate interactions for these nine quantitative components as revealed by Sakr [25].

Table 1. Nine pathogenic components obtained under in vitro, growth chamber and field conditions used in the present research as described by Sakr [25]

Pathogenic component	Experimental condition	Used technique
Latent period (LP)	*in vitro*	Detached leaf inoculation
Area under disease progress curve (AUDPC)	*in vitro*	Petri-dish inoculation
Coleoptile dwarfing (CD)	*in vitro*	Coleoptile infection
Disease incidence (DI, Type I)	*in vitro*	Detached head test (DHT)
Disease severity (DS, Type II)	*in vitro*	Detached head test (DHT)
Disease incidence (DI^{CC}, Type I)	Growth chamber	Head artificial inoculation
Disease severity (DS^{CC}, Type II)	Growth chamber	Floret artificial inoculation
Disease incidence (DI^{CC}, Type I)	Field	Head artificial inoculation
Disease severity (DS^{CC}, Type II)	Field	Floret artificial inoculation

2.5. Statistical analyses

The experimental data were subjected to analysis of variances (ANOVA) using DSAASTAT add-in version 2011. Before statistical analysis, the percentages were transformed using the angular transformation to stabilize variances. ANOVA incorporating the Fisher's LSD test at $P<0.05$ was used to compare the means of resistance of cultivars. The simple correlation (Pearson r) at $P<0.05$ between resistances of cultivars to different *Fusarium* species was used to evaluate the correlations.

3. Results and Discussion

The *Fusarium* pathogens causing FHB are numerous in countries where findings coming from a high number of pathogens were characterized [6, 12]. It is understandable that breeding efforts have been conducted against these dominant or ruling pathogens [7], implicitly suggesting some art of common resistance against them [11]. The question is whether resistance to these species is connected or not [8, 9]. In the latter case, we should breed for resistance against all separately and later pool them [28]. The issue is challenging and requests clarification [4]. In the current research, we showed that resistance in bread wheat, durum wheat and barley against four *Fusarium* species is common. To our best knowledge, this is the first report which documents the presence of common resistance in *T. durum* and *H. vulgare* against several *Fusarium* species.

Aggressiveness has been identified as the proportional intensity of disease [29]; it describes the general characteristic or quality of a pathogen species or genus capable to cause disease on a given host species [30]. In this context, we evaluated FHB disease causing ability of individual isolates of *Fusarium* pathogens (i.e., the 16 monosporic derived cultures were of the field-background natural population [25]). Results presented in Table 2 showed that the head blight scores revealed obvious resistance differences; however, the four FHB pathogens did not vary in their nine aggressiveness components on the eight tested wheat and barley cultivars. An overall homogeneous comparative was reported under several experimental conditions because of similarity in damage among the 16 fungal isolates. Aggressiveness of *F. graminearum* and *F. culmorum* isolates on *Triticum aestivum* was very close; suggesting an apparent lack of a difference in aggressiveness as reported by Browne and Cooke [22]. Our data did not confirm previous studies exhibiting that *Fusarium* pathogens were classified as weakly, moderately and highly pathogenic on barley and wheat plants [10, 11, 13]. *F. equiseti* and *F. culmorum*, invoved in the present work, was identified to be weakly and highly pathogenic, respectively, among several examined FHB species [5, 7]. The differences in these outputs may be attributable to the contrasting isolates and host cultivars used in this study and pervious work.

Sakr [25] postulated that the background of *Fusarium* pathogens may play a significance role in this pathogenic similarity. It appears that the fumonisins do not play any biological function in the pathogenesis of the analyzed four *Fusarium* species [6]; this supports our conclusion that there is not a single toxin that is responsible for the pathogenicity of all *Fusarium* pathogens.

Table 2. Resistance of three bread wheat, three durum wheat, and two barley cultivars to four Fusarium species, i.e., F. culmorum, F. solani, F. verticillioides and F. equiseti, under in vitro, growth chamber and field conditions

LP (days)				
Cultivars	***Fusarium* species**			
	F. culmorum	***F. solani***	***F. verticillioides***	***F. equiseti***
Acsad65, durum	5.5±1.0a	5.0±0.5a	4.0±2.0a	4.6±1.3a
Cham7, durum	6.2±1.5a	6.1±1.7a	4.1±1.7a	7.6±1.1a
Cham9, durum	4.2±0.8a	5.0±0.5a	3.3±1.7a	3.6±2.0a
Cham4, bread	4.7±1.2a	4.9±1.1a	4.1±1.7a	4.5±1.3a
Douma4, bread	6.9±0.7a	6.4±2.2a	5.1±2.0a	5.3±0.9a
Bohoth10, bread	4.6±1.1a	4.0±0.3a	3.4±1.8a	4.7±1.3a
Arabi Abiad, barley	6.3±2.1a	5.8±1.6a	3.9±1.7a	4.7±1.5a
Arabi Aswad, barley	6.2±1.4a	7.5±0.6a	4.7±2.5a	8.0±1.1a
AUDPC				
Cultivars	***Fusarium* species**			
	F. culmorum	***F. solani***	***F. verticillioides***	***F. equiseti***
Acsad65, durum	0.54±0.08a	0.49±0.04a	0.36±0.18a	0.41±0.05a
Cham7, durum	0.45±0.08a	0.48±0.04a	0.34±0.18a	0.48±0.06a
Cham9, durum	0.46±0.05a	0.45±0.06a	0.33±0.15a	0.41±0.03a
Cham4, bread	0.39±0.07a	0.50±0.12a	0.34±0.13a	0.49±0.07a
Douma4, bread	0.46±0.09a	0.45±0.10a	0.32±0.15a	0.48±0.09a
Bohoth10, bread	0.41±0.04a	0.39±0.02a	0.09±0.15a	0.45±0.06a
Arabi Abiad, barley	0.47±0.18a	0.42±0.11a	0.28±0.12a	0.33±0.07a
Arabi Aswad, barley	0.31±0.06a	0.38±0.03a	0.23±0.13a	0.40±0.08a
CD (%)				
Cultivars	***Fusarium* species**			
	F. culmorum	***F. solani***	***F. verticillioides***	***F. equiseti***
Acsad65, durum	51±17a	54±6a	50±25a	68±15a
Cham7, durum	57±18a	53±4a	54±30a	69±10a
Cham9, durum	52±16a	61±11a	50±25a	64±12a
Cham4, bread	62±10a	51±20a	56±22a	45±10a
Douma4, bread	62±12a	54±12a	53±24a	45±13a
Bohoth10, bread	61±9a	63±10a	54±25a	49±9a
Arabi Abiad, barley	50±18a	58±9a	59±29a	71±11a
Arabi Aswad, barley	71±7a	63±3a	57±31a	63±10a
DI (DHT) (%)				
Cultivars	***Fusarium* species**			
	F. culmorum	***F. solani***	***F. verticillioides***	***F. equiseti***
Acsad65, durum	59±8a	60±18a	47±17a	50±9a
Cham7, durum	50±14a	57±6a	38±19a	57±10a
Cham9, durum	49±12a	53±16a	42±16a	44±7a
Cham4, bread	44±14a	56±14a	32±10a	32±11a
Douma4, bread	49±16a	59±17a	37±17a	41±4a
Bohoth10, bread	44±12a	46±13a	37±15a	51±5a
Arabi Abiad, barley	51±20a	46±17a	25±8a	24±12a
Arabi Aswad, barley	28±5a	40±9a	25±12a	55±15a
DS (DHT) (%)				
Cultivars	***Fusarium* species**			
	F. culmorum	***F. solani***	***F. verticillioides***	***F. equiseti***
Acsad65, durum	61±14a	48±17a	40±15a	40±10a
Cham7, durum	49±19a	52±13a	31±14a	48±8a
Cham9, durum	52±18a	44±14a	31±11a	30±7a
Cham4, bread	48±21a	42±21a	33±9a	49±11a
Douma4, bread	39±15a	45±14a	31±15a	55±7a
Bohoth10, bread	41±15a	36±6a	25±17a	54±10a

Arabi Abiad, barley	46±19a	39±16a	23±5a	28±8a
Arabi Aswad, barley	34±5a	34±7a	21±8a	45±9a
DI (CC) (%)				
Cultivars	***Fusarium* species**			
	F. culmorum	***F. solani***	***F. verticillioides***	***F. equiseti***
Acsad65, durum	58±8a	58±18a	46±17a	45±10a
Cham7, durum	51±15a	59±6a	39±20a	55±8a
Cham9, durum	51±10	53±16a	41±15a	45±11a
Cham4, bread	45±12a	56±16a	32±9a	29±14a
Douma4, bread	47±14a	57±16a	39±18a	46±7a
Bohoth10, bread	45±8a	47±14a	38±14a	49±9a
Arabi Abiad, barley	53±21a	48±17a	27±9a	20±14a
Arabi Aswad, barley	29±4a	37±9a	27±12a	52±12a
DS (CC) (%)				
Cultivars	***Fusarium* species**			
	F. culmorum	***F. solani***	***F. verticillioides***	***F. equiseti***
Acsad65, durum	59±13a	49±21a	39±12a	36±9a
Cham7, durum	48±18a	51±13a	33±15a	42±8a
Cham9, durum	51±17a	43±13a	30±13a	36±7a
Cham4, bread	50±22a	42±18a	30±11a	53±11a
Douma4, bread	38±13a	45±10a	31±17a	52±9a
Bohoth10, bread	43±15a	36±4a	26±10a	63±20a
Arabi Abiad, barley	50±20a	40±20a	53±5a	36±11a
Arabi Aswad, barley	28±5a	32±18a	21±9a	66±26a
DI (FC) (%)				
Cultivars	***Fusarium* species**			
	F. culmorum	***F. solani***	***F. verticillioides***	***F. equiseti***
Acsad65, durum	62±10a	53±17a	42±16a	44±10a
Cham7, durum	46±10a	55±10a	40±21a	55±15a
Cham9, durum	49±11a	49±10a	36±15a	40±11a
Cham4, bread	41±14a	47±7a	30±14a	35±7a
Douma4, bread	43±12a	52±12a	34±17a	46±8a
Bohoth10, bread	43±10a	38±8a	30±13a	40±9a
Arabi Abiad, barley	49±13a	50±19a	35±12a	40±10a
Arabi Aswad, barley	33±8a	43±3a	25±13a	49±9a
DS (FC) (%)				
Cultivars	***Fusarium* species**			
	F. culmorum	***F. solani***	***F. verticillioides***	***F. equiseti***
Acsad65, durum	44±8a	42±13a	30±11a	34±4a
Cham7, durum	39±9a	44±5a	31±18a	45±11a
Cham9, durum	39±9a	40±8a	30±13a	33±10a
Cham4, bread	30±10a	35±5a	24±11a	29±8a
Douma4, bread	30±9a	40±10a	26±12a	37±7a
Bohoth10, bread	30±7a	28±6a	229±9a	27±11a
Arabi Abiad, barley	30±10a	39±15a	30±11a	36±6a
Arabi Aswad, barley	37±7a	31±2a	21±11a	35±8a

Values are means ± standard deviation. Values in same line with the same letter were not significantly different based on Fisher's LSD test at $P<0.05$. The identification of all abbreviations listed in this Table 2 was presented in Table 1. Pathogenic reactions of all cultivars infected with *Fusarium* fungi were previously evaluated according to methods described by Sakr [25].

Table 2. Correlation coefficients between cultivar reactions of wheat and barley to four *Fusarium* species

LP	***F. culmorum***	***F. solani***	***F. verticillioides***
F. culmorum	1.000		
F. solani	***	1.000	
F. verticillioides	***	**	1.000
F. equiseti	**	***	***
AUDPC			
F. culmorum	1.000		
F. solani	**	1.000	

F. verticillioides	**	***	
F. equiseti	***	*	**
CD			
F. culmorum	1.000		
F. solani	***	1.000	
F. verticillioides	***	*	1.000
F. equiseti	*	*	***
DI (DHT)			
F. culmorum	1.000		
F. solani	**	1.000	
F. verticillioides	***	***	1.000
F. equiseti	***	**	**
DS (DHT)			
F. culmorum	1.000		
F. solani	*	1.000	
F. verticillioides	**	**	1.000
F. equiseti	***	***	***
DI (CC)			
F. culmorum	1.000		
F. solani	***	1.000	
F. verticillioides	**	**	1.000
F. equiseti	***	**	**
DS (CC)			
F. culmorum	1.000		
F. solani	**	1.000	
F. verticillioides	***	***	1.000
F. equiseti	**	***	**
DI (FC)			
F. culmorum	1.000		
F. solani	*	1.000	
F. verticillioides	*	*	1.000
F. equiseti	***	***	**
DS (FC)			
F. culmorum	1.000		
F. solani	**	1.000	
F. verticillioides	**	**	1.000
F. equiseti	***	***	***

The identification of all abbreviations listed in this Table 2 was presented in Table 1. Pathogenic reactions of all cultivars infected with *Fusarium* fungi were previously evaluated according to methods described by Sakr [25]. (P<0.05)*, (P<0.01)**, (P<0.001)***.

Van der Plank [29] and Cowger and Brown [30] postulated that the quantitative resistance genes are equally effective for all pathogen pathogens. Our findings in the present research confirm this issue; Table 3 shows that the correlations between the pooled reactions for the nine tested trails at the earliest and latest growth stages conducted under *in vitro*, growth camber and field conditions to different *Fusarium* species were significant, suggesting very similar reactions to the different *Fusarium* species. Our observations lend strong confirmation to the theory that cultivar resistance in bread wheat, durum wheat and barley to any *Fusarium* species tested implies a similar level of resistance to other *Fusarium* species. The four *Fusarium* species, i.e., *F. culmorum*, *F. solani*, *F. verticillioides*, and *F. equiseti*, included in this work showed no exceptions. In harmoney with our findings, van Eeuwijk *et al.* [15], in a multilateral *Fusarium* trial working with isolates of *F. nivale* (*M. nivale*) (1), *F. graminearum* (6), and *F. culmorum* (9), on 25 European winter *Triticum aestivum* cultivars from the Netherlands, Hungary, France, Austria, and, Germany, reported no specificity within the European *F. culmorum* and *F. graminearum* population, and resistance to the two

FHB pathogens appears to have the same origin. Thus, it is not obligated to select shuttle breeding for head blight resistance to these two species. It seems that the resistance origin to *Microdochium nivale* is the same as that of *F. culmorum* or *F. graminearum*. It is remarkable that common resistance can present in fungal species that do not belong to the *Fusarium* genus. Mesterhazy *et al.* [16] obtained very similar dada when analyzing *Fusarium* pathogens and wheat cultivars; this experiment employed summarized findinds for 2–2 strains of *F. avenaceum*, *F. graminearum*, *F. sporotrichioides*, and *F. culmorum*, and one *F. sambucinum* strain was also included. The observations revealed common resistance to the diverse FHB pathogens [16]. Further, our large set of wheat and barley cultivars with highly differing genetically origins confirm the conclusion that common resistance to diverse *Fusarium* pathogens is a characteristic phenomenon in *Triticum* spp. and *H. vulgare*. For this reason, the probability is low that *Fusarium* spp. or wheat and barley cultivars not fitting into the system will be notified. The FHB resistance is race non-specific and probably species non-specific [8, 9, 11]. This predicts durable resistance for a prolonged duration [4, 7]. The only danger is the selection of more pathogenic strains in outbreak centers. In the Chinese Yangtze valley, an augmentation in the more aggressive strains from the *F. graminearum* clade was reported [6], which can jeopardize resistance and low toxin contamination. This requests confirmation in the FHB population.

It appears that resistance components tested in the present work are not independent variables but rather a series of components that follow epidemic and disease development as observed earlier in some studies [7, 9, 11, 13, 28]; their genetic regulation may change [8]. When we take into consideration the epidemic background and the disease development, the diverse resistance types are rather resistance components [5], not independent variables [4]. During FHB development, the several metabolic pathways build on each other, highly accounting on the environment and genetic background [6]. The several metabolic pathways participate to the finding we call resistance [30]. They interact with each other and there are additional genetic mechanisms [7], for example, in the specific resistance to DON accumulation [9].

Anther extrusion also belongs to this group, but a test is lacking for how this and other features are genetically related and regulated [12]. Our data show that a race non-specific resistance determines head blight resistance, and it appears that is also species non-specific. This suggests that higher resistance not only protects against *F. graminearum* but can also be efficient against *M. nivale* and the other *Fusarium* species [8, 9]. This is crucial because high susceptibility to *F. graminearum* would also mean a higher susceptibility to the other *Fusarium* spp. with lower pathogenicity [11]. Therefore, a breeding program is enough against *F. graminearum*, and this would also mean automatically higher resistance to the other *Fusarium* species [7].

It is significant that this non-specificity could be proven alike for latent period [22], area under disease progress curve [23], coleoptile dwarfing [24], disease incidence and disease severity [25] showing that resistance to FHB to a large extent determines also the other non tested components [9]. Quantitative trait loci responsible for the presence of these quantitative components should be characterized. These components in adult stage have nothing in common with the components in seedling stage of the quantitative disease resistance described by Browne and Cooke [22] as these relate to latent period which we did not measure by Mesterhazy *et al.* [16]. Quantitative disease resistance could also be clarified for head blight disease [6]. It seems that more resistance components can present than observed to date [11]. In spite of the cultivar/isolate interaction does not confirm significant in comment resistance [29]); a non-significant cultivar/isolate interaction is not a precondition for the confirmation of general resistance [30]. Analysis of variance of our bio-experiments showed significant cultivar-by-isolate interactions for these nine quantitative components [25]; however, resistance stability in cultivars to FHB infection was fulfilled over years as well as several experimental conditions, showing that QR of wheat and barley to *Fusarium* is mainly explained by major quantitative trait loci that confer resistance to all FHB isolates [25]. The stability of quantitative resistance evaluates of cultivars is in line with a postulate that wheat- and barley-*Fusarium* interactions for quantitative resistance were of decreased magnitude [8, 9, 11]. We therefore consider this to be the most powerful support yet for the common resistance of wheat and barley to *Fusarium* pathogens [4].

In our investigation, The scores of head blight intensity of *Triticum* spp. and *H. vulgare* cultivars to *F. culmorum*, *F. solani*, *F. verticillioides*, and *F. equiseli* were very similar, showing that the resistance to *F. culmorum* was identical to that for other *Fusarium* pathogens listed. This is a crucial singe to breeders as the resistance depends not only to any specific isolate of *F. culmorum*, but similarly to isolates of other *Fusarium* pathogens. This apply for all the components evaluated, FHB resistance covers common resistances to diverse head blight pathogens [7]. This holds true for all the components assesssed [28], FHB resistance covers common resistances to diverse *Fusarium* pathogens [6]. The common resistance reported against the *Fusarium* spp. demonstrates why highly-resistant cultivars resist infection in diverse parts of the world [11]. Thus, selection against a highly pathogenic isolate of the given FHB pathogen is sufficient and common resistance to the *Fusarium* species will be the output [12]. As *Fusarium* resistance is not specific, the resistance of cultivars is durable [28]. The principal issue is now to integrate *Fusarium* resistance with good agronomic criteria, quality, and resistance to other diseases [13]. Another task is to determine resistance values that vary from Sumai 3 and give similarly high resistance [5]. Our current understating permits the breeding of highly resistant resources, even though several scientific problems have not yet been solved. The most crucial task is to build a trustworthy selection system with artificial inoculation in all generations to permit for efficient screening. Such systems are already worked in many breeding companies and institutes.

4. Conclusion

As several *Fusarium* pathogens are included in head blight, it is requested to explore whether *Fusarium* resistance has a common resistance to all *Fusarium* pathogens, or whether diverse genes regulate resistance to several pathogens. A common resistance is the consensus in the investigation, but only a few reports confirm this. This is the first report which documents the presence of common resistance in durum wheat and barley against different *Fusarium* species, and is in harmony with data about bread wheat. This work shows the significance of assessing all quantitative traits at the earliest and latest growth stages in the breeding and selection of resistant cultivars and germplasm. Resistance to diverse FHB pathogens appears to be connected; it is species non-specific, but additional study is requested.

Compliance with Ethics Requirements. Authors declare that they respect the journal's ethics requirements. Authors declare that that they have no conflict of interest and all procedures involving human or animal subjects (if exist) respect the specific regulation and standards.

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