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Virulence analysis and effectiveness of new sources of resistance to barley powdery mildew (*Blumeria graminis* f. sp. *hordei*) in southwestern regions of Iran

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ABSTRACT

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Barley powdery mildew caused by the biotrophic obligate pathogen, *Blumeria graminis* f. sp. *hordei*, is one of the most important foliar diseases in major barley production areas in Iran. To determine the virulence spectrum of the powdery mildew pathogen in southwestern regions of the country and effectiveness of new sources of resistance, barley powdery mildew trap nurseries were established and evaluated under natural field conditions for disease development in three disease prone locations including Zarghan, Ahvaz, and Dezful during 2013-14 to 2017-18 cropping seasons. The trap nurseries consisted of a differential set including the barley cultivar Pallas and 18 near-isogenic 'Pallas' lines and a supplementary set including 34 barley cultivars carrying known or unknown resistance gene(s). Our results showed that there is virulence variation in the population of the pathogen in different locations. While the resistance genes *Mla6, Mla14, Mla7, Ml*(*No3*), *Mla12, Ml*(*Em2*), *Mla13* and *Ml*(*Ru3*) were effective across the years and locations, the *Mlk, Mlh, MlL*a and *Mlp* genes were ineffective in most years and locations. New virulence factors matching *Mla6, Mlp, Mlg+MlCP, Mla7* and *Mla3* genes were detected. Ineffectiveness of all resistance genes except the recessive *mlo* allele in Dezful and Zarghan over years indicating that the pathogen population in Dezful and Zarghan are more aggressive than Ahvaz. We concluded that the European *mlo* carrying barley cultivars and other sources of resistance with a combination of genes, such as Meltan and Escort could be considered as effective sources of powdery mildew resistance to be incorporated in the national barley breeding programs for the southwestern regions of Iran.

Keywords: barley, disease resistance, genetic variation, isogenic lines, pathogenicity factors

INTRODUCTION

Barley (*Hordeum vulgare* L. ssp. *vulgare*) is an important cereal crop that ranks fourth in world cereal production after maize, wheat and rice (Ullrich, 2011). Barely is the major staple crop and an important source of food for human, livestock feed and malting in brewing industries. With the annual cultivation area of 1.45 million hectares and total grain production of about 3.1 million tones (2017-2018), barley is the second important crops after wheat in Iran (Ahmadi *et al.*, 2019). Due to its wide ecological adaptability and tolerance to a range of biotic and abiotic stresses, barley is grown in most parts of the country, either as rainfed or irrigated crop.

Powdery mildew caused by the wind-borne biotrophic ascomycete fungal pathogen, *Blumeria graminis (D.C.) Golovin ex Speer* f.

sp. *hordei* Em. Marchal *(Bgh)*, is one of the most important foliar diseases of barley worldwide. This pathogen is present all over Iran including the major barley growing regions (Ershad, 2009). Barley powdery mildew pathogen overwinters as sexual fruiting bodies, called Chasmothecia (formerly Cleistothecia) in plant residues or as asexual conidia or mycelium on living host plants. The germinated ascospores released from the fruiting bodies or asexual conidia initiate primary infections on barley leaves. So in natural epidemics of disease under field conditions, the population of the pathogen is an admixture of different pathotypes, representing the genetic diversity of the local population of pathogen.

The use of host genetic resistance is known as the most effective, economic, and environmentally safe method to control barley powdery mildew. However, barley powdery mildew is considered as a high-risk pathogen for breaking down resistance genes, because it poses a mixture of sexual and asexual reproduction systems and a high potential for gene flow that support the rapid evolution of the pathogen population (McDonald and Linde, 2002).

Barley breeding for resistance to powdery mildew was traditionally based on the deployment of major genes. More than 85 race-specific resistance genes to powdery mildew have been identified in barley (Jørgensen, 1994; Chelkowski *et al*., 2003) and extensively used in breeding programs as sources of resistance. The mechanism of resistance of these genes is mainly based on a hypersensitivity response (HR) which is only elicited by particular avirulent pathogen isolates according to the gene-for-gene concept (Collins *et al*., 2002). However, the majority of these resistance genes were gradually overcome within a few years due to the appearance of new pathotypes of the pathogen (Hovmøller *et al*., 2000; Czembor and Czembor, 2000).

The monogenic non-hypersensitive type of resistance mediated by the recessive *mlo* allele of the *Mlo* locus is an exception. The *mlo* resistance is race-non-specific and effective against all known isolates of barley powdery mildew pathogen (Jørgensen, 1992; Büschges *et al.*, 1997) despite extensive cultivation of *mlo*-cultivars in Europe (Lyngkjær *et al.*, 2000). Identification of virulence patterns in the local population of the pathogen and monitoring of the utilized resistance genes in breeding programs is a prerequisite for efficient use of resistance sources in barley breeding programs. Recent studies showed that the majority of commercial barley cultivars grown in the southwestern regions of Iran are susceptible or moderately susceptible to powdery mildew (Aghnoum, 2018). Therefore, seeking for new sources of resistance is a high priority for the national barley breeding programs.

Several reports have been published about diversity of virulence factors matching resistance genes in the local populations of powdery mildew in different Asian countries (Dreiseitl, *et al.*, 2006; Dreiseitl and Wang, 2007; Rsaliyev *et al.*, 2017; Zeybek *et al.*, 2017). Analysis of barley powdery mildew virulence factors in four regions of China using 461 isolates during 2003-2004 showed that all isolated were avirulent for *Mla7, Mla6, Mla3, Mla1, Mla23, Mla22, Mla10, Mla9, Mlg, Mlat, Mlp1* and *Mlmw* resistance genes, however, virulence factors matching the majority of these genes are common in European populations of powdery mildew (Dreiseitl and Wang, 2007).

Powdery mildew virulence surveys in the central Asian country, Kazakhstan, during 2015-2016 showed that *Mla9*, (Mla1 + *MlaAl2*), (*Mla6* + *Mla14*), (*Mla13* + *MlRu3*), (*Mla7* + *MlNo3*), (*Mla10* + *MlDu2*), (*Mla13* + *MlRu3)* and *mlo-5* resistance genes are affective in this country (Rsaliyev *et al.*, 2017). A few studies have been carried out to identify the virulence factors of the pathogen in Iran. Based on a three-year virulence survey in ten powdery mildew hot spot areas during 1999-2002, virulence for *Mlk, Mla9* and *Ml (La)* were detected in most locations and *Mla16, Mlp, mlo, Mla13, Mla3, Mla6, Mla7+MLAb, Mlg+MICP*, and *Mla19* resistance genes were effective in all these locations (Patpour *et al*., 2005).

The main objectives of this research were to determine the virulence/avirulence patterns of the powdery mildew pathogen in barley-

growing areas of southwest regions of Iran, and to identify effective sources of resistance to be incorporated in the national barley breeding programs.

MATERIALS AND METHODS

Barley powdery mildew trap nurseries were evaluated against the disease under natural field conditions for disease development in three stations including Zarghan, Dezful and Ahvaz Agricultural Research Stations in Iran during 2013-14 to 2017-18 cropping seasons. THE nurseries comprised of a differential set including the barley cultivar Pallas and 18 'Pallas' near-isogenic lines (Table 1) that differ in their powdery mildew resistance genes (Kølster *et al.*, 1986) and a supplementary set including 34 cultivars carrying known or unknown resistance gene (s) (Table 2) along with the susceptible check Afzal.

Seed of differentials and supplementary set were kindly provided by Dr. Rients E. Niks from the Laboratory of Plant Breeding, Wageningen University and Research, Wageningen, The Netherlands. all these materials were sown in two row plots of one - meter length. Spreader rows of the susceptible check were sown after every 20 experimental lines and also around the nurseries.

powdery mildew scoring was visually recorded using the double-digit (00-99) scale (Eyal *et al.*, 1987) when the disease was fully developed on the spreader plots at the flowering stage. in this system, the first digit indicates the vertical progress of the disease from lower to higher leaves (Saari and Prescott, 1975), and the second digit represents the disease severity as a percentage of leaf area infected by powdery mildew clonies. for example; in score 53, 5 represents the moderately susceptible infection type based on the Saari and Prescott (1975) scale and 3 indicates 30% disease severity (30% of the infected leaf area is covered by the powdery mildew colonies).

RESULTS

Virulence pattern of barley powdery mildew pathogen

the reaction of Pallas differential lines to powdery mildew during 2013-2017 are presented in Table 1. in Dezful, the natural epidemic of powdery mildew disease appeared in all four years but in ahvaz and Zarghan disease developed only in two cropping seasons. The results of evaluation of Palls near-isogenic lines with well-known resistance genes in different locations showed that there was variation in virulence spectrum of the pathogen between years and locations.

Table 1. Reactions of Pallas differential lines used for monitoring the population of barley powdery mildew pathogen in southwest of Iran during 2014-2017 cropping seasons

		Dezful				Ahvaz		Zarghan	
Genotype	R gene(s)	2014	2015	2016	2017	2015	2016	2014	2017
Pallas	*Mla8*	53	0	71	71	0	0	0	83
P01	*Mla1, Ml(A12)*	71	0	73	0	0	0	0	82
P02	*Mla3*	51	0	52	0	0	0	0	72
P03	*Mla6, Mla14*	51	0	0	0	0	0	0	52
P04B	*Mla7, Ml(No3)*	0	0	51	0	0	0	0	72
P08B	*Mla9*	51	0	51	0	0	0	0	82
P09	*Mla10, Ml(Du2)*	51	0	51	0	0	0	21	82
P10	*Mla12, Ml(Em2)*	0	0	71	0	0	0	0	92
P11	*Mla13, Ml(Ru3)*	0	0	51	0	0	0	0	82
P12	*Mla22*	71	0	72	0	56	0	0	82
P13	*Mla23*	51	0	71	0	0	0	0	83
P16	*Mlk*	71	73	71	71	54	51	51	87
P17	*Mlk(1)*	71	71	71	72	0	0	0	87
P19	*Mlp*	51	51	53	52	54	33	31	76
P20	*Mlat*	71	71	51	71	53	0	35	74
P21	*Mlg, Ml(CP)*	72	0	71	0	0	0	0	73
P22	*mlo5*	0	0	0	0	0	0	0	0
P23	*MlLa*	53	51	73	72	53	33	32	42
P24	*Mlh*	71	72	71	73	53	0	53	73

Afzal	Susceptible check	75	75	72	73	79	65	99	85

Virulence factors for *Mlk, Mlh, MlL*a, and *Mlp* resistance genes appeared in most cropping cycles and locations. Virulence factors matching the *Mla22* and *Mlat* resistance genes were detected in all locations at least in one cropping season. Virulence for *Mla8*, *Mla1+Ml(A12)*, *Mla3*, *Mla6+Mla14*, *Mla7+Ml(No3)*, *Mla9*, *Mla10+Ml(Du2)*, *Mla12+ Ml(Em2)*, *Mla13+ Ml(Ru3)*, *Mla23* and*Mlg+Ml(CP)*was detected at least in one cropping season in Dezful and Zarghan, but not detected in Ahvaz.

The local population of the pathogen in dezful and zarghan showed to be more aggressive than ahvaz, since only the mlo gene remained effective in all cropping seasons in these locations. The *Mla6* and *Mla14*resistance genes were effective in all cropping seasons/locations except in Dezful in 2014 and in Zarghan in 2017. The *Mla7, Ml(No3), Mla12, Ml(Em2), Mla13,* and *Ml(Ru3)* resistance genes were effective in all cropping seasons/locations except in Dezful in 2016 and in Zarghan in 2017.

Reaction of different sources of resistance to powdery mildew

The reaction of the supplementary set carrying known or unknown resistance gene(s) to powdery mildew is presented in Table 2. Evaluation of the sources of resistance showed that all of the lines and cultivars were highly resistant in Ahvaz except Simon (*Mla9, Mlk*). In Zarghan only Escort (*Mlg, Mla7, Mlk, MlLa*), the *mlo* carrying cultivars/lines (Viskosa, Wren, L94, Alexis and Brenda) and two cultivars with unknown resistance gene(s), (Princess and Prisma) were resistant in both cropping cycles. In Dezful, most cultivars of the supplementary set showed different phenotypic reaction in different cropping seasons, except the *mlo* cultivars that were resistant in all cropping cycles.

Table 2. Reactions of the supplementary set carrying known or unknown resistance gene(s) to powdery mildew in the southwest of Iran during 2014-2017 cropping seasons

		Dezful				Ahvaz		Zarghan	
Genotype	R gene(s)	2014	2015	2016	2017	2015	2016	2014	2017
Digger	*Mla13, Ml(Ru3)*	51	0	0	0	0	0	0	62
Punto	*Mla3, Ml(Tu2), Ml(Im9), Ml(Hu4)*	53	51	71	0	0	0	0	73
Hennie	*Mla7, U*	0	0	71	0	0	0	0	82
Goldie	*Mla12, MlLa, U*	51	71	71	0	0	0	0	72
Tofta	*Mla13, Ml(Im9)*	0	0	51	0	0	0	0	72
Meltan	*Mla13, Ml(Im9), Ml(Hu4)*	0	51	51	0	0	0	0	42
Jarek	*MlLa, Ml(Kr)*	0	0	51	0	0	0	0	42
Steffi	*Ml(St1), Ml(St2)*	0	0	51	0	0	0	0	83
Optima	*U1*	0	0	51	0	0	0	0	82
Scarlett	*U2*	51	0	51	0	0	0	0	82
Tyra	*Mla1, Ml(Al2)*	52	0	71	83	0	0	0	71
Simon	*Mla9, Mlk*	52	72	71	53	54	0	0	72
Midas	*Mla6, Mla14*	0	51	71	42	0	0	0	71
Hassan	*Mla12, Ml(Em2)*	0	0	71	72	0	0	0	71
Hordeum 1063	*Mlk*	58	52	71	72	0	0	13	73
Lofa Abed	*MlLa*	71	71	b	62	0	0	33	71
Varunda	*MlLa*	53	71	71	86	0	0	32	71
Zephyr	*Mlg, Ml(CP)*	b	0	71	83	0	0	b	71
Vada	*MlLa*	51	72	0	72	0	0	0	72
Adele	*Mlg*	0	0	71	74	0	0	0	71
Escort	*Mlg, Mla7, Mlk, MlLa*	0	0	51	72	0	0	0	0
Ariel	*Mla12*	0	0	71	73	0	0	0	73
Viskosa	*mlo?*	11	11	11	0	0	0	0	0
Wren	*mlo?*	0	0	11	0	0	0	0	0
L94	*mlo 11*	0	0	11	0	0	0	0	0
Alexis	*mlo9*	0	0	11	0	0	0	0	0
Brenda	*mlo11*	0	0	11	0	0	0	0	0
Chalice	*mlo11*	11	11	11	0	0	0	0	0
Bond	*?*	0	31	31	74	0	0	0	71
Canut	*?*	0	0	51	62	0	0	0	72
Dialog	*?*	0	0	72	73	0	0	0	71
Fusion	*?*	0	0	51	73	0	0	0	72
Princess	*?*	0	0	51	74	0	0	0	0
Prisma	*?*	51	0	73	73	0	0	0	0
Afzal	Susceptible check	71	75	73	96	79	75	99	77

Simon (*Mla9, Mlk*), Hordeum 1063 (*Mlk*), Varunda, and Lofa Abed (*MlLa*) were susceptible in all cropping seasons. Virulence for some of the resistance genes that were incorporated in these cultivars including, *Mla9, Mlk, and MlLa* were also found in Dezful based on the reaction of Pallas near-isogenic lines. Viskosa, Wren, L94, Alexis, Brenda, and Chalice were resistant in all years and locations. All these genotypes are carrying an allele of the *mlo* gene. These genetic materials could be considered as effective sources of resistance to be incorporated in the barley breeding program for the southwest regions of Iran.

DISCUSSION

Since 1930 that the Iranian cereal breeding program was started, more than 37 high yielding adapted and abiotic tolerant barley cultivars have been released for different climate zones of the country including Northern Warm and Humid None (Zone I), Southern Warm and Dry Done (Zone II), Temperate Zone (Zone III) and Cold Zone (Zone IV), however, the biotic stresses including the barley powdery mildew disease still remain as a challenge for the Iranian barley breeders. Therefore, it is necessary to monitor the local population of the pathogen and use new sources of resistance.

Identification of the virulence factors matching the resistance genes of cereal rusts and powdery mildew commonly perform either through establishment of trap nurseries of differential lines under field conditions which rely on natural epidemic of the pathogen or using a collection of isolates under controlled conditions. Although the uniformity of artificial inoculation of the pathogen isolates under controlled conditions is an advantage but field trap nurseries provide a broader view of the pathogen race complexity for the breeders over a large area, therefore, field trap nurseries are more commonly used in breeding programs for monitoring the cereal rusts and powdery mildew pathogens at the national or international levels.

The results of evaluation of differential lines under the natural epidemics is highly dependent on the climatic conditions and other environment factors which is a disadvantage for this method. As can be seen in the Table 1 and Table 2, there is high levels of differences between the reactions of some genotypes in two different cropping seasons, although the reaction of the susceptible check indicated that disease pressure in the nursery was high during the scoring time. Although these differences could be partly due to different race composition of the pathogen population over years, the possibility of accidental disease escape should also be taken into account.

In a previous study (Patpour *et al.*, 2005), based on the reaction of field trap nurseries sown in ten hot spot locations in Iran during 2000-2002, no virulence was found for *Mla6, Mlg+MlCP, Mlp, Mla7+ MlAb, Mla3, Mla19, mlo, Mla13, Mla16,* and *Mla19* resistance genes, but virulence on *Mlk, Mla9,* and *Ml(La)* was common in all regions. However, in the present study, new virulence factors found for *Mla6, Mlp, Mlg+MlCP, Mla7* and *Mla3* genes was identified, but there was no virulence for *Mla9* in Ahvaz.

A few studies have been conducted to characterize the virulence structure of barley powdery mildew pathogen in the Middle East and Central Asian countries (e.g. Patpour 2005; Rsaliyev *et al.*, 2017; Zeybek *et al.*, 2017). A recent study showed that the populations of *Blumeria graminis* f. sp. *hordei* in Kazakhstan have low similarity with the European, African, Australian and South-East Asian populations of this pathogen. Out of one hundred and seven isolates collected from the South and Zhambyl region in Kazakhstan, all isolates were virulent on *Mla8* and avirulent on *Mla9, Mla1 + MlaAl2, Mla6 + Mla14, Mla13 + MlRu3, Mla7 + MlNo3, Mla10 + MlDu2* and *mlo*-5 resistance genes. (Rsaliyev *et al.*, 2017). In the present study, however, *Mla8* was ineffective in Dezful and Zarghan and there were virulence factors matching the *Mla1 + MlaAl2, Mla6 + Mla14, Mla13 + MlRu3, Mla7 + MlNo3, Mla10 + MlDu2, Mla13 + MlRu3* in Dezful in 2014 and 2016) and in Zarghan in 2017 (Table 3).

Table 3. Summary of effective and ineffective sources of powdery mildew resistance in the southwest regions of Iran

Location	Year	Effective genes	Ineffective genes
Dezful	2014	*Mla7, Ml(No3), Mla12, Ml(Em2), Mla13, Ml(Ru3), mlo5*	*Mla8, Mla1, Ml(A12), Mla3, Mla6, Mla14, Mla9, Mla10, Ml(Du2), Mla22, Mla23, Mlk, Mlk(1), Mlp ,Mlat, Mlg, Ml(CP), MlLa, Mlh*
	2015	*Mla8, Mla1, Ml(A12), Mla3, Mla6, Mla14, Mla7, Ml(No3), Mla9, Mla10, Ml(Du2), Mla12, Ml(Em2), Mla13, Ml(Ru3), Mla22, Mla23, Mlg, Ml(CP), mlo5*	*Mlk, Mlk(1),Mlp, Mlat, MlLa, Mlh*
	2016	*Mla6, Mla14, mlo5*	*Mla8, Mla1, Ml(A12), Mla3, Mla7, Ml(No3), Mla9, Mla10, Ml(Du2), Mla12, Ml(Em2), Mla13, Ml(Ru3), Mla22, Mla23, Mlk, Mlk(1), Mlp, Mlat, Mlg, Ml(CP), MlLa, Mlh*
	2017	*Mla8, Mla1, Ml(A12), Mla3, Mla6, Mla14, Mla7, Ml(No3), Mla9, Mla10, Ml(Du2), Mla12, Ml(Em2), Mla13, Ml(Ru3), Mla22, Mla23, Mlg, Ml(CP), mlo5*	*Mlk, Mlk(1), Mlp, Mlat, MlLa, Mlh*
Ahvaz	2015	*Mla8, Mla1, Ml(A12), Mla3, Mla6, Mla14, Mla7, Ml(No3), Mla9, Mla10, Ml(Du2), Mla12, Ml(Em2), Mla13, Ml(Ru3), Mla23, Mlk(1), Mlg, Ml(CP), mlo5*	*Mla22, Mlk, Mlp, Mlat, MlLa, Mlh*
	2016	*Mla8, Mla1, Ml(A12), Mla3, Mla6, Mla14, Mla7, Ml(No3), Mla9, Mla10, Ml(Du2), Mla12, Ml(Em2), Mla13, Ml(Ru3), Mla22, Mla23, Mlk(1), Mlat , Mlg, Ml(CP), mlo5, Mlh*	*Mlk, Mlp, MlLa,*
Zarghan	2014	*Mla8, Mla1, Ml(A12), Mla3, Mla6, Mla14, Mla7, Ml(No3), Mla9, Mla10, Ml(Du2), Mla12, Ml(Em2), Mla13, Ml(Ru3), Mla22, Mla23, Mlk(1), Mlp, Mlat, Mlg, Ml(CP), mlo5, MlLa*	*Mlk, Mlh*
	2017	*mlo5*	*Mla8, Mla1, Ml(A12), Mla3, Mla6, Mla14, Mla7, Ml(No3), Mla9, Mla10, Ml(Du2), Mla12, Ml(Em2), Mla13, Ml(Ru3), Mla22,Mla23, Mlk, Mlk(1), Mlp, Mlat, Mlg, Ml(CP), MlLa, Mlh*

Virulence for the powdery mildew race-specific resistance gene *MlLa*, present in the Pallas differential line, P23 and the barley cultivars, Lofa Abed, Varunda, and Vada were common in most /locations. Virulence for *MlLa* also reported Patpour *et al.* (2005) in different locations in Iran. The virulence factor matching the *MlLa* resistance gene also reported in many European countries (Hovmoller *et al.*, 2000; Aghnoum *et al.*, 2010; Kokina and Rashal, 2012) and many other countries including Tunisia and Morocco (Yahyaoui *et al.*, 1997), Australi (Dreiseitl, 2014), Kazakhstan (Rsaliyev *et al.*, 2017), China (Zhu *et al.*, 2010; Dreiseitl and Wang, 2007).

The *MlLa* gene, derived from the barley "*Hordeum laevigatum*" and is located on the long arm of chromosome 2H in a region carrying the 'Laevigatum' Quantitative Resistance Gene to Leaf Rust (*Rphq2*) and a barley leaf stripe (*Pyrenophora graminea*) resistance gene *Rdg1a* (Giese *et al.*, 1993; Arru *et al.*, 2002; Marcel *et al.*, 2007). *MlLa* confers an intermediate type of hypersensitive reaction to avirulent isolates of powdery mildew (Giese *et al.*, 1993; Marcel *et al.*, 2007). The barley cv. Vada and other European cultivars carrying the Laevigatum originated regions could be considered as a source of multiple disease resistance alone or in combination with the other resistance genes

Since 1979 when the first *mlo*-resistant barley cultivar was commercially released in Europe, many *mlo* cultivars have been grown extensively in several European countries (Jørgensen, 1992; Dreiseitl, 2012). However despite the widespread of spring barley cultivars carrying the *mlo* resistance gene in Europe, this type of resistance has remained effective over the last forty years, proving the durability of this resistance. In addition to the central and west European countries, the *mlo*-based resistance is reported to be effective in eastern Europe (Dreiseitl, 2003; Kokina and Rashal, 2012; Tratwal and Bocianowski, 2014; Dreiseitl, 2015), in North Africa (Yahyaoui *et al.*, 1997), in Western Asia (Dreiseitl, *et al.*, 2006), in central Asian country, Kazakhstan (Rsaliyev *et al.*, 2017), in Turkey (Zeybek *et al.*, 2017.), in Iran (Patpour *et al.*, 2005), in Australia (Hossain and Rahman 1993; Tucker *et al.*, 2013; Dreiseitl *et al.*, 2013;) and in China (Dreiseitl and Wang, 2007).

The results of a recent study in Central Europe showed that there was a gradual decrease in virulence frequencies of *Blumeria graminis* f. sp. *hordei* to some resistances genes resulting in a reduced average of virulence complexity in 2017, although over the same period, new virulence factors for previously effective resistance genes were detected (Dreiseitl, 2019). This emphasizes that monitoring of the powdery mildew pathogen for detecting new virulence and new effective sources of resistance should be carried out continuously. Based on our results we can conclude that in our national barley breeding program, deployment of the *mlo*-based non-race specific resistance gene(s) can be recommended in addition to exploiting sources of resistance gene combinations e. g. Meltan, and Escort. Sharing the powdery mildew national virulence survey data among the Middle East and Central Asian countries could help designing breeding strategies for durable control of barley powdery mildew on regional and international scales.

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