Sources of Resistance to Powdery Mildew in Wild Barley (*Hordeum vulgare* subsp. *spontaneum*) Collected in Jordan, Lebanon, and Libya

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Article

Sources of Resistance to Powdery Mildew in Wild Barley (*Hordeum vulgare* subsp. *spontaneum*) Collected in Jordan, Lebanon, and Libya

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Abstract: Barley powdery mildew (BPM) is caused by the pathogen *Blumeria graminis* f.sp. *hordei* (*Bgh*). It is an economically important disease and plant pathologists are looking for new sources of resistance to BPM. Barley genetic resources present in gene banks are often a rich source of disease resistance to be used by breeders. These new sources of resistance to BPM are often used in combination (pyramiding) with those that are already used in modern cultivars. Barley accessions, including the wild subspecies *Hordeum vulgare* subsp. *spontaneum (Hvs)*, are stored in many gene banks and often are a valuable source of economically important characteristics. This source of biodiversity should be more efficiently used to improve barley in the process of plant breeding. However, their proper characterization and availability are urgently needed. The resistance to BPM in 81 accessions of wild barley (*Hvs*) collected in Jordan (47), Lebanon (23), and Libya (11) was investigated. The seed samples of these accessions were obtained from the ICARDA gene bank and collected in 10 expeditions from 1981 to 1995. Twenty European differential isolates of BPM were used to select accessions with efficient resistance. Thirty-one resistant single plant lines were selected from 15 accessions from Jordan and Libya based on tests performed with the most avirulent isolate of *Bgh* available. These resistant single plant lines were tested for the presence of specific resistance genes using a differential set of *Bgh* isolates. After analysis of obtained results, it was concluded that all tested 31 single plant lines of wild barley have genes for resistance that are not represented in the Pallas isolines differential s. Twenty-six lines of *Hvs* selected from accessions originated in Jordan and Libya showed resistance reaction to all isolates used. Identified new sources of effective resistance to BPM in single plant lines of *Hvs* will be further tested and used in barley pre-breeding programs.

Keywords: *Blumeria graminis*; resistance genes; resistance; germplasm; gene bank; biodiversity; plant breeding; plant genetic resources; crop wild relatives; pre-breeding

1. Introduction

Among cereals, barley (*Hordeum vulgare* L.) is the fourth most important in the world. However, the importance of the crop in many areas of the world lies in the fact that it is often the only crop possible to grow in semi-arid areas and at elevations higher than other cereals. In the Near East and North Africa, barley is a typical crop in hostile environments. The importance of this crop is growing because of climate change and more unpredictable weather conditions in many regions of the world [1–3]. Barley is considered as one of the oldest domesticated crops. It is used for feed, malt, and food. In many areas, especially with arid and semi-arid climates, barley straw yield is the most important for farmers. Recently, more and more popular is the use of barley as food due to its health properties [3–6].

Barley's primary gene pool includes two subspecies: domesticated barley (*Hordeum vulgare* subsp. *vulgare*) and wild barley *(Hordeum vulgare* subsp. *spontaneum*) (*Hvs*). Wild barley differs from cultivated barley in several traits including a brittle rachis and it is considered a progenitor of cultivated barley [3,6]. *Hvs* occurs in Southwest Asia and, most probably due to human activities, populations of *Hvs* are present in Morocco, Ethiopia, and Tibet [3,6,7].

In the last century because of increasing crop erosion, many gene banks were established. The main goal of gene banks is to preserve key plant genetic resources in order to meet current and future needs concerning food production. It is achieved by introducing them into breeding programs to achieve biological progress and for use in direct production. To do this effectively there is a need for phenotyping and genotyping data for major gene bank collections [8–10]. There are relatively large collections of the genus *Hordeum* stored in many gene banks worldwide. It is estimated that about 485,000 accessions of this genus are stored at more than 200 institutions worldwide. These collections include *H. vulgare* ssp. *vulgare* (299 165 accessions), wild barley *Hvs* (32 385 accessions), and wild species of *Hordeum* (4 681 accessions). [3,6,11].

In West Asia and North Africa (WANA) including Jordan, Lebanon, and Libya are present diverse agroecological zones and different types and intensity of agriculture [12,13]. Wild barley is a widespread species in this region and genetically diverse populations of *Hvs* are reported to be collected [12–15]. Many studies showed that landraces and *Hvs* are very diverse and represent great value for breeding barley as the source of resistance to both abiotic and biotic stresses [16–18]. Recently there is also increasing interest in the study of both landraces and *Hvs* as a potential source of economically important characteristics to breed cultivars well adapted to changing climate conditions and more frequent weather anomalies [16,18].

Blumeria graminis (DC.) Golovin ex Speer f.sp. hordei Em. Marchal (Bgh) is a fungus that causes barley powdery mildew (BPM). It is considered as one of the most economically important pathogens on barley which can cause significant yield losses. Many studies have shown that Bgh is relatively rapidly developing many new races and that its spores are dispersed by wind over long distances in Europe [19–26]. It occurs in many barley growing regions of the world but it is especially important in Europe. This is due to the maritime climate in most of the Europe areas suitable for the development of BPM. In addition, barley is grown in Europe on relatively large areas and more than 60% of barley world production originates from this continent [21,25,26]. The average annual losses caused by this disease in barley production in Central Europe are estimated at about 10%. However, in many experiments, barley yield losses due to the occurrence of heavy infestation by BPM usually exceed 25%. The grain yield obtained from barley fields where BPM was present very often is characterized by lower quality characteristics important in malt production such as higher grain protein content and lack of proper grain size uniformity [27,30].

Chemical control and agronomic practices are used to reduce BPM incidence. However, these methods are often not effective, and in addition, there is a growing emergence of BPM resistance to fungicides [31,32]. A commonly used way to control BPM was the incorporation of new effective genes for powdery mildew resistance into barley cultivars [19,21,25]. It is the most effective and environmentally safe method to control this disease. Effective resistance not only protects the cultivated varieties but also reduces the production of inoculum and the spread of the pathogen to larger areas, leading to epiphytosis [24,25,33–35]. In most cases of growing cereals, including barley, in agricultural practice, the control against fungal pathogens is based on Integrated Pest Management (IPM) principles [36,37]. This approach to managing pests is based on combining biological, cultural, physical, and chemical methods to minimize economic, health, and environmental risks. Recently the use of genetic resistance as a component of IPM become more important due to the implementation of more environmentally friendly agricultural policies in many countries of the world [37,38].

From the very beginning of genetics studies of the resistance of barley to BPM, the Hvs was used. The very first study was conducted by Biffen in 1907 who analyzed the mode of inheritance of BPM resistance in progenies from crossing H. vulgare with Hvs [39]. Since that time race-specific resistance genes have been identified mainly in cultivated barley landraces [40–55] and wild barley [56–71] mostly originating from the WANA region [19,21,25]. Based on genetic studies many specific resistant genes were described in wild barley: Mla16-Mla21, Mla25-Mla29, Mla32, MlaLv, Mlf, Mlj, mlt, Ml(Ro), Ml(Ve) [25,58,59,65,66,68]. Barley breeders used many BPM resistance genes, especially in the Mla locus and Mlra, Mlk, MlLa, Mlg, Mlh [19,21,25]. However, many of these genes have lost their effectiveness as a result of pathogen adaptation and the emergence of virulent races to these genes [19–26]. In the last 40 years, only barley cultivars with Mlo resistance have been characterized

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as those with durable resistance to BPM because no known virulence for mlo genes was identified. This type of resistance to BPM was identified in barley mutants and in landraces, but not in Hvs [19,21,25,72–74].

Many studies proved that studies on the genetics of resistance to BPM using a differential set of BPM isolates can be successfully used for investigations to determine the presence of specific resistance genes in barley genetic resources [19,21,25,26]. The new efficient sources of resistance to BPM for proper crosses in breeding programs are crucial to conducting resistance breeding [25,33–35]. The use of seedlings in studies conducted to postulate specific BPM resistance genes using a differential set of Bgh isolates was proven to be an effective and sufficient method. This method is commonly used for the characterization of barley germplasm concerning its BPM resistance [26,40,43,50–52,54,55].

The presented investigation goal was to detect new sources of BPM resistance in accessions of Hvs collected in Jordan, Lebanon, and Libya.

1. Materials and method

1.1. Plant material

Eighty-one accessions of wild barley (H. vulgare subsp. spontaneum) (Hvs) collected in Jordan, Lebanon, and Libya were obtained from the ICARDA gene bank. These accessions were collected in 10 expeditions (LBY81, LBY82, LBY90, LBN92-2, LBN93, LBN94-1, JOR81-2, JOR85, JOR88-1, JOR95) during period 1981-1995. (Table 1).

1.2. Pathogen

Twenty *B. graminis* f. sp. *hordei* Em Marschal (*Bgh*) isolates were used to determine the resistance genes present in the tested accessions. These isolates possessed virulence genes corresponding to the most known resistance genes used in barley resistance programs (Table 2). Isolates originated from the collections in Risø National Laboratory, Roskilde, Denmark; Danish Institute for Plant and Soil Science, Lyngby, Denmark; Edigenossische Technische Hochschule – ETH, Zurich, Switzerland and Plant Breeding and Acclimatization Institute – National Research Institute (PBAI-NRI) IHAR-PIB Radzików, Poland. The isolates were chosen according to differences in virulence spectra that were observed on the Pallas isolines differential set [75] and on additional cultivars with resistance genes not present in Pallas isolines. Each of them represented a different pathotype, determined using the selected set of 20 Pallas isolines differential. Isolate Bgh 33 was the most avirulent isolate in the collection.

They were purified by single pustule isolation and were maintained and propagated on young seedlings of the powdery mildew susceptible cultivar Manchuria (CI 2330). Frequent virulence checks were made to ensure the purity of isolates throughout the experiment.

Table 1. Collection data of 81 accessions of wild barley (*H. vulgare* subsp. *spontaneum*) collected in Jordan, Lebanon, and Lybia.

ICARDA				OTHERNUMB (IHAR project No.)	COL_NO	COL CODE	SITE NO	COL_DATE	LON	LAT	ALT	PROVINCE	SITE
IG	CROP	CROP NO	ORI ID										
38616	ICWB	180007	JOR	1075	SY 27041	JOR81-2	7561	18.05.1981	E 35 55	N32 27	500	Irbid	27km before Jarash came from Ramtha
38617	ICWB	180008	JOR	1076	SY 27042	JOR81-2	7564	20.05.1981	E 36 17	N32 15	700	Mafraq	Road Zarqa-Mafraq; 22 km before junction Marfaq-Jarash
38618	ICWB	180009	JOR	1077	SY 27043	JOR81-2	7565	20.05.1981	E36 15	N32 17	700	Mafraq	Road Zarqa-Mafraq; 3km before junction Mafraq-Jarash
38619	ICWB	180010	JOR	1078	SY 27044	JOR81-2	7566	20.05.1981	E 36 10	N32 18	700	Mafraq	13 km after Mafraq (before Rihab) on the Mafraq-Jarash road
38620	ICWB	180011	JOR	1079	SY 27045	JOR81-2	7568	21.05.1981	E 35 52	N32 07	700	Balqa	26km S Jarash
38621	ICWB	180012	JOR	1080	SY 27046	JOR81-2	7569	21.05.1981	E 35 52	N32 10	500	Irbid	19km S Jarash
38622	ICWB	180013	JOR	1081	SY 27047	JOR81-2	7570	21.05.1981	E 35 52	N32 14	480	Irbid	3km Sjarash on the road to Amman
38623	ICWB	180014	JOR	1082	SY 27048	JOR81-2	7571	21.05.1981	E35 55	N32 20	1060	Irbid	11 km N Jarash on road to Irbid; top of hill
38624	ICWB	180015	JOR	1083	SY 27049	JOR81-2	7572	21.05.1981	E35 57	N32 23	900	Irbid	11 km S Jarash on the road to Amman
38625	ICWB	180016	JOR	1084	SY 27050	JOR81-2	7575	21.05.1981	E 36 00	N32 35	600	Irbid	3 km NW Ramtha
38626	ICWB	180017	JOR	1085	SY 27051	JOR81-2	7577	22.05.1981	E 35 45	N32 41	500	Irbid	Kufr Sum; 3 km S of Samar
38627	ICWB	180018	JOR	1086	SY 27053	JOR81-2	7580	22.05.1981	E 35 37	N32 40	-70	Irbid	Jordan Valley; 1.6 km S of left turn to Adesia (hot springs)
38628	ICWB	180019	JOR	1087	SY 27054	JOR81-2	7581	23.05.1981	E 35 42	N32 35	300	Irbid	Irbid-Esh Shuna road; 16 km W junction Irbid-Deir Abu Said
38629	ICWB	180020	JOR	1088	SY 27056	JOR81-2	7584	23.05.1981	E 35 45	N32 26	500	Irbid	8 km S of Deir Abu Said at Kufr Awan
38630	ICWB	180021	JOR	1089	SY 27057	JOR81-2	7586	23.05.1981	E 35 42	N32 22	600	Irbid	11 km S of Kufr Awn
38631	ICWB	180022	JOR	1090	SY 27058	JOR81-2	7588	23.05.1981	E35 49	N32 20	1100	Irbid	24 km S of Kufr Awn
38632	ICWB	180023	JOR	1091	SY 27059	JOR81-2	7594	25.05.1981	E35 47	N32 03	1000	Balqa	As Sarrouk; road Suweileh-Salt 8 km after junction
38633	ICWB	180024	JOR	1092	SY 27066	JOR81-2	7606	26.05.1981	E35 45	N31 32	800	Amman	29 km S Madaba; the southern slope of Wadi Wala valley
39398	ICWB	180789	JOR	1093	No.34	-	-	-	-	-	-	Tafila	King's Highway, 25 km south from mosque in Tafila; woodland
39821	ICWB	181212	JOR	1094	J-2-2	JOR85	2	18.05.1985	E35 57	N31 42	710	Amman	Madaba; Jiza 44 km S of Amman
39822	ICWB	181213	JOR	1095	J-5-4	JOR85	5	19.05.1985	E35 30	N30 30	1450	Ma'an	Shoubak; 10 km N Petra
39823	ICWB	181214	JOR	1096	J-7-3	JOR85	7	19.05.1985	E35 40	N30 47	1300	Tafila	Rashadiae 26 km N Shoubak towards Tafila
39824	ICWB	181215	JOR	1097	J-10-6	JOR85	10	20.05.1985	E35 54	N32 29	690	Irbid	Assarieh; Wadi Al. Gazira; 5 km E of Irbid-Amman highway
39825	ICWB	181216	JOR	1098	J-12	JOR85	12	21.05.1985	E36 04	N32 32	500	Irbid	Ramtha; perminout site of Y. university; 20 km E Irbid

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IG	CROP	CROP NO	ORI ID										
39826	ICWB	181217	JOR	1099	J-15-1	JOR85	15	21.05.1985	E36 12	N32 21	710	Mafraq	Mafraq 45 km E Irbid
39827	ICWB	181218	JOR	1100	J-16	JOR85	16	21.05.1985	E36 05	N32 20	850	Mafraq	Rahab; 3 km E Rahab; 10 km W Mafraq
39828	ICWB	181219	JOR	1101	J-18-2	JOR85	18	22.05.1985	E35 54	N31 47	800	Amman	Um el Amad; Madaba
39829	ICWB	181220	JOR	1102	J-19	JOR85	19	22.05.1985	E35 44	N32 06	900	Balqa	Um Jauza; 11 km N Salt
39850	ICWB	181241	JOR	1103	MSAJ 88026b	JOR88-1	16	24.05.1988	E36 01	N32 19	750	Mafraq	Hamama; on road Mafraq-Jarash
39851	ICWB	181242	JOR	1104	MSAJ 88032b	JOR88-1	21	25.05.1988	E35 42	N32 38	340	Irbid	Between El Mansoura and Kufr Asad
39877	ICWB	181268	JOR	1105	AE 1	-	-	09.05.1989	E35 55	N32 18	750	Irbid	Jarash
39933	ICWB	181324	LBY	1107	MSAZ 90028	LBY90	1	26.05.1990	E20 54	N32 33	320	Al Marj	Al. Marj station
39934	ICWB	181325	LBY	1108	MSAZ 90031	LBY90	4	26.05.1990	E21 08	N32 42	370	Al Marj	Sidi Ismel
39935	ICWB	181326	LBY	1109	MSAZ 90038	LBY90	7	26.05.1990	E21 38	N32 47	580	Al Bayda	2 km E Massah to El Beyda
39936	ICWB	181327	LBY	1110	MSAZ 90040	LBY90	8	26.05.1990	E21 52	N32 05	580	Al Bayda	20 km E El Beyda
39937	ICWB	181328	LBY	1111	MSAZ 90041	LBY90	9	27.05.1990	E22 03	N32 48	580	Al Qubbah	Saf Saf; just E El Bayda
39938	ICWB	181329	LBY	1112	MSAZ 90052	LBY90	14	27.05.1990	E22 50	N32 36	180	Darnah	Omer Zin; 23 km E Derna
39939	ICWB	181330	LBY	1113	MSAZ 90054	LBY90	16	28.05.1990	E21 55	N32 42	640	Shahhat	Arigha; 2 km S El Beyda
40156	ICWB	181547	LBN	1114	MSNSSH-92089	LBN92-2	4	28.07.1992	E35 19	N33 27	170	Zahle	15 km S Saida to Nabatiye; near Saksaniye
40168	ICWB	181559	LBN	1115	-	-	-	12.09.1992	E35 55	N33 50	1000	Zahle	
40177	ICWB	181568	LBN	1116	MSJVSK-93048	LBN93	1	21.06.1993	E35 52	N33 28	1150	Biqaa El	Biader El-Adas; below Sultan Ya'akoub village on the hill
40178	ICWB	181569	LBN	1117	MSJVSK-93049	LBN93	2	21.06.1993	E35 49	N33 37	1025	Biqaa El	Jeb-Janine; Izzi to Kend El-loz; 1 km W Izzi
40179	ICWB	181570	LBN	1118	MSJVSK-93057	LBN93	3	21.06.1993	E35 46	N33 37	1045	Biqaa El	2 km S Jeb-Janine; road to Lala
40180	ICWB	181571	LBN	1119	MSJVSK-93061	LBN93	4	21.06.1993	E35 43	N33 31	980	Biqaa El	Rashaya; 2 km from Sohmbr; E of Kafar Mechki
40181	ICWB	181572	LBN	1120	MSJVSK-93069	LBN93	5	21.06.1993	E35 46	N33 31	1050	Biqaa El	Rashaya; 1 km before Kantaba; on the road from Sahmor
40182	ICWB	181573	LBN	1121	MSJVSK-93070	LBN93	6	21.06.1996	E35 49	N33 27	1020	Biqaa El	Rashaya; 1 km before Ain Hircha; the road from Rashaya
40183	ICWB	181574	LBN	1122	MSJVSK-93075	LBN93	7	21.06.1993	E35 45	N33 26	1250	Biqaa El	Rashaya; 2 km from Ain Ata; on the road to Tefeir
40184	ICWB	181575	LBN	1124	MSJVSK-93082	LBN93	9	22.06.1993	E36 06	N33 56	1050	Biqaa El	Ba'labakk; 1 km before Talia; on the road from Zahle
40185	ICWB	181576	LBN	1125	MSJVSK-93091	LBN93	10	22.06.1993	E36 10	N34 02	1050	Biqaa El	Ba'labakk; 4 km W Ba'labakk; road to Bcharre; Iaat village

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IG	CROP	CROP NO	ORI ID										
40186	ICWB	181577	LBN	1126	MSJVSK-93100	LBN93	13	22.06.1993	E36 05	N34 12	1810	Biqaa El	Ba'lbakk; 3 km from Ain Ata; rad to Bcharre
40187	ICWB	181578	LBN	1127	MSJVSK-93104	LBN93	14	22.06.1993	E36 02	N34 08	1470	Biqaa El	Ba'lbakk; 2 km Yamouni coming from Ain Ata
40188	ICWB	181579	LBN	1128	MSJVSK-93109	LBN93	16	23.06.1993	E36 05	N34 01	1080	Biqaa El	500 m before the end of village Sa'ide; rad to Zahle
40189	ICWB	181580	LBN	1129	MSJVSK-93112	LBN93	17	23.06.1993	E35 49	N33 30	1100	Biqaa El	Rashaya; Dahr Al. Ahmar; 2 km NW Rashaya
40190	ICWB	181581	LBN	1130	MSJVSK-93120	LBN93	18	23.06.1993	E35 53	N33 31	1200	Biqaa El	Rashaya; Aiha; 3 km N road to Kfar Qoug
40191	ICWB	181582	LBN	1131	MSJVSK-93126	LBN93	19	23.06.1993	E35 54	N33 34	1470	Biqaa El	Rashaya; 6 km from Kfar Qoug towards Bakaa
40193	ICWB	181584	LBN	1132	MSJVSK-93135	LBN93	22	23.06.1993	E35 54	N33 38	1350	Biqaa El	Rashaya; 1 km E of Aita Al Foukhar
40181	ICWB	181572	LBN	1120	MSJVSK-93069	LBN93	5	21.06.1993	E35 46	N33 31	1050	Biqaa El	Rashaya; 1 km before Kantaba; on the road from Sahmor
40182	ICWB	181573	LBN	1121	MSJVSK-93070	LBN93	6	21.06.1996	E35 49	N33 27	1020	Biqaa El	Rashaya; 1 km before Ain Hircha; the road from Rashaya
40183	ICWB	181574	LBN	1122	MSJVSK-93075	LBN93	7	21.06.1993	E35 45	N33 26	1250	Biqaa El	Rashaya; 2 km from Ain Ata; on the road to Tefeir
40184	ICWB	181575	LBN	1124	MSJVSK-93082	LBN93	9	22.06.1993	E36 06	N33 56	1050	Biqaa El	Ba'labakk; 1 km before Talia; on the road from Zahle
40185	ICWB	181576	LBN	1125	MSJVSK-93091	LBN93	10	22.06.1993	E36 10	N34 02	1050	Biqaa El	Ba'labakk; 4 km W Ba'labakk; road to Bcharre; Iaat village
40186	ICWB	181577	LBN	1126	MSJVSK-93100	LBN93	13	22.06.1993	E36 05	N34 12	1810	Biqaa El	Ba'lbakk; 3 km from Ain Ata; rad to Bcharre
40187	ICWB	181578	LBN	1127	MSJVSK-93104	LBN93	14	22.06.1993	E36 02	N34 08	1470	Biqaa El	Ba'lbakk; 2 km Yamouni coming from Ain Ata
40188	ICWB	181579	LBN	1128	MSJVSK-93109	LBN93	16	23.06.1993	E36 05	N34 01	1080	Biqaa El	500 m before the end of village Sa'ide; rad to Zahle
40189	ICWB	181580	LBN	1129	MSJVSK-93112	LBN93	17	23.06.1993	E35 49	N33 30	1100	Biqaa El	Rashaya; Dahr Al. Ahmar; 2 km NW Rashaya
40190	ICWB	181581	LBN	1130	MSJVSK-93120	LBN93	18	23.06.1993	E35 53	N33 31	1200	Biqaa El	Rashaya; Aiha; 3 km N road to Kfar Qoug
40191	ICWB	181582	LBN	1131	MSJVSK-93126	LBN93	19	23.06.1993	E35 54	N33 34	1470	Biqaa El	Rashaya; 6 km from Kfar Qoug towards Bakaa
40193	ICWB	181584	LBN	1132	MSJVSK-93135	LBN93	22	23.06.1993	E35 54	N33 38	1350	Biqaa El	Rashaya; 1 km E of Aita Al Foukhar
40194	ICWB	181585	LBN	1133	MSJVSK-93139	LBN93	23	23.06.1993	E36 01	N33 48	1180	Biqaa El	Zahle; 2 km N Kosaya road to Deir El Ghazal
112846	ICWB	181657	LBY	1134	Z 16	LBY82	18	23.05.1982	E20 54	N32 30	-	Al Marj	Al. Marj, occasionally in the city area
112847	ICWB	181658	LBY	1135	Z 17	LBY82	19	24.05.1982	E24 14	N31 50	-	Tubruq	Safsaf, Al. Qarah district, roadsides

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IG	CROP	CROP NO	ORI ID										
110816	ICWB	181628	LBN	1136	2	LBN94-1	1	04.07.1994	E35 43	N33 34	1010	Biqaa El	Karaoun, 1 km from the main road to the lake
110819	ICWB	181629	LBN	1137	5	LBN94-1	3	04.07.1994	-	-	980	Biqaa El	Between Kafar Mishki and Jeb Farah; 20 km from site 1
110823	ICWB	181630	LBN	1138	9	LBN94-1	5	04.07.1994	E35 53	N33 31	1200	Biqaa El	1 km before Kafar Qouk; from Rashaya site road to east (site 18 in 1993)
110831	ICWB	181631	LBN	1139	17	LBN94-1	7	05.07.1994	E35 57	N33 38	1410	Biqaa El	2 km before Yanta; road from Aita Al Foukhar
110833	ICWB	181632	LBN	1140	19	LBN94-1	8	05.07.1994	E35 51	N33 35	1310	Biqaa El	2 km before Ain Arab; the road from Yanta
116004	ICWB	181639	LBY	1141	IDG 7373	LBY81	-	08.06.1981	E21 10	N32 22	450	Al Marj	4 km N main road Taknis-Marawah
116005	ICWB	181640	LBY	1142	IDG 7404	LBY81	-	12.06.1981	E21 43	N32 46	590	Al Bayda	Al Bayda, within the city on a road border
115780	ICWB	181660	JOR	1143	1	JOR95	1	31.05.1995	E36 01	N32 01	665	Zarqa	700 m before junction Mafraq-Zarqa and Khatlla road
115781	ICWB	181661	JOR	1144	10	JOR95	3	31.05.1995	E36 43	N32 18	960	Mafraq	Al Mniusa
115782	ICWB	181662	JOR	1145	14	JOR95	4	31.05.1995	E36 45	N32 15	1000	Mafraq	Al Thallag
115784	ICWB	181664	JOR	1146	19	JOR95	6	01.06.1995	E35 55	N32 25	760	Irbid	3 km W of En Nueima
115785	ICWB	181665	JOR	1147	21	JOR95	7	01.06.1995	E35 52	N32 26	810	Irbid	1 km after Shatana on road to Irbid
115786	ICWB	181666	JOR	1148	24	JOR95	8	01.06.1995	E35 50	N32 22	1030	Irbid	Samta Cross road with Ajlun
115787	ICWB	181667	JOR	1149	26	JOR95	9	01.06.1995	E35 49	N32 21	1020	Irbid	Ibben 1 km E
115788	ICWB	181668	JOR	1150	27	JOR95	10	02.06.1995	E35 52	N32 41	350	Irbid	1 km W Bereshda road to Habras bottom of the wadi
115789	ICWB	181669	JOR	1151	28	JOR95	11	02.06.1995	E35 43	N32 38	240	Irbid	Monsoura 2 km road to Kafr Asad
115790	ICWB	181670	JOR	1152	29	JOR95	12	02.06.1995	E35 42	N32 37	60	Irbid	Bottom of the valley; road Mansoura to Kafr Asad
115791	ICWB	181671	JOR	1153	32	JOR95	13	02.06.1995	E35 40	N32 35	30	Irbid	The road from Kafr Asad to N Shuneh wadi Al.-Arab
115792	ICWB	181672	JOR	1154	33	JOR95	14	02.06.1995	E35 40	N32 21	1020	Irbid	road Sakhra-Abben; 2 km from Sakhra
115793	ICWB	181673	JOR	1155	39	JOR95	17	03.06.1995	E35 41	N32 02	680	Balqa	
115795	ICWB	181674	JOR	1156	5	JOR95	2	31.05.1995	E36 32	N32 20	830	Mafraq	Manchiet Al.-Kabalan
115796	ICWB	181675	JOR	1157	50	JOR95	21	05.06.1995	E35 40	N30 24	1540	Ma'an	Al. Hisha 20 km NW Petra

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Table 2. *B. graminis* f. sp. *hordei* isolates used for artificial inoculation and their virulence spectra against resistance genes on the differential set of Pallas near-isogenic lines.

No.	Near isogenic lines / cultivars	Resistance genes	Isolates																			
			1	*2*	*3*	*4*	*5*	*6*	*7*	*8*	*9*	*10*	*11*	*12*	*13*	*14*	*15*	*16*	*17*	*18*	*19*	*20*
			Bgh 1	*Bgh 2*	*Bgh 3*	*Bgh 4*	*Bgh 8*	*Bgh 9*	*Bgh 11*	*Bgh 13*	*Bgh 14*	*Bgh 24*	*Bgh 28*	*Bgh 29*	*Bgh 31*	*Bgh 33*	*Bgh 36*	*Bgh 40*	*Bgh 48*	*Bgh 51*	*Bgh 57*	*Bgh 63*
1	Pallas	*Mla8*	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
2	P1	*Mla1*	0	0	4	4	4	0	0	0	0	0	0	4	0	0	4	0	0	4	0	0
3	P2	*Mla3*	1	0	0	0	0	0	0	0	0	0	0	4	0	0	4	4	0	0	0	0
4	P3	*Mla6, Mla14*	0	0	0	0	0	0	4	0	4	0	4	0	0	0	4	4	4	4	4	4
5	P4A	*Mla7, Mlk, +?*	2	2	2	2	2	2	2	2	2	2	4	2	4	0	2	2	2	4	4	2
6	P4B	*Mla7, +?*	4	4	4	1	0	2	2	4	4	0	2	4	4	1	4	4	1	4	4	4
7	P6	*Mla7, MlLG2*	4	4		0	0	2	1	2	4	0	2	2	4	0	4	2	0	4	4	4
8	P7	*Mla9, Mlk*	4	0	4	0	0	0	0	4	0	0	0	4	0	0	0	0	0	0	4	0
9	P8A	*Mla9, Mlk*	4	0	4	0	0	0	0	4	0	0	0	4	0	0	0	0	0	0	4	0
10	P8B	*Mla9*	4	0	4	0	0	0	0	4	0	4	0	4	0	0	0	0	0	0	4	0
11	P9	*Mla10, MlDu2*	4	4	4	0	1	4	0	4	0	2	0	4	4	4	4	0	0	4	4	4
12	P10	*Mla12*	0	0	4	0	0	4	0	0	4	0	0	4	4	0	4	4	0	4	0	4
13	P11	*Mla13, MlRu3*	4	0	4	0	0	0	0	0	4	4	0	0	4	0	0	0	0	4	0	4
14	P12	*Mla22*	4	4	0	4	4	0	4	0	4	4	4	4	4	0	0	4	4	4	0	0
15	P13	*Mla23*	1	1	2	1	2	1	2	1	1	1	1	2	1	1	1	1	1	1	1	1
16	P14	*Mlra*	4	4	4	0	4	4	4	4	0	4	4	4	4	4	4	4	4	4	4	4
17	P15	*Ml(Ru2)*	4	4	4	4	3	4	2	4	4	2	0	4	4	2	4	4	4	4	4	4
18	P17	*Mlk*	4	4	4	2	2	2	2	4	2	2	0	4	4	2	4	2	2	4	4	4
19	P18	*Mlnn*	4	4	4	4	4	2	4	4	4	2	2	4	4	4	4	4	4	4	2	2
20	P19	*Mlp*	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
21	P20	*Mlat*	2	2	2	4	2	2	2	4	2	2	2	2	2	2	2	4	2	4	2	2
22	P21	*Mlg, Ml(CP)*	4	4	4	0	0	0	4	0	4	0	4	4	4	4	4	4	0	4	0	4
23	P22	*mlo5*	0(4)	0(4)	0(4)	0(4)	0(4)	0(4)	3	0(4)	0(4)	0(4)	0(4)	0(4)	0(4)	0(4)	0(4)	0(4)	0(4)	0(4)	0(4)	0(4)
24	P23	*Ml(La)*	4	4	4	4	4	2	4	4	4	4	4	4	4	4	4	4	4	4	4	4
25	P24	*Mlh*	4	4	4	0	4	4	4	4	4	4	4	4	4	4	0	4	4	4	4	4
26	Benedicte	*Mla9,Ml(IM9)*	0	0	4	0	0	0	0	0	4	0	0	4	4	0	4	4	0	4	0	4
27	Lenka	*Mla13,Ml(Ab)*	4	0	4	0	0	0	0	0	4	0	0	0	4	0	0	0	0	4	0	4
28	Gunnar	*Mla3, Ml(Tu2)*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	Steffi	*Ml(St1), Ml(St2)*	2	2	2	0	0	0	0	0	4	0	0	2	3	0	4	2	0	2	0	4
30	Kredit	*Ml(Kr)*	4	2	4	0	2	0	0	2	4	4	4	2	4	0	4	2	2	4	4	4
31	Jarek	*Ml(Kr), +?*	4	4	4	4	4	2	4	4	4	4	4	4	4	4	4	2	4	4	2	4
32	Trumph	*Mla7, Ml(Ab)*	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4
33	Borwina	*Ml(Bw)*	4	3	3	0	4	0	4	4	4	2	2	3	4	4	4	3	4	4	2	2
34	Manchurian	-	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4

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2.3. Populations and single plant lines resistance tests

In the preliminary study thirty plants per accession were evaluated with the Bgh33 isolate. Next, the selected single plant lines were tested with 20 differential isolates of *Bgh*.

All these tests were conducted under controlled conditions with a 16/8 h day/night photoperiod and a 22/16°C temperature regime. In all tests, the cultivar Manchuria CI 2330 was used as a susceptible control.

Seedlings with a fully expanded first leaf were inoculated with *Bgh* by shaking conidia from the susceptible cv. Manchuria CI 2330. After 8-10 days, the reaction type (RT) of plants to infection by *Bgh* was scored. A five-point RT scale was used: 0, no visible symptoms; 1, minute necrotic flecks, no mycelial growth, and no sporulation; 2, frequent chlorosis, reduced mycelial growth and no or very scarce sporulation; 3, moderate mycelial growth, moderate sporulation, and occasional chlorosis; 4, profuse sporulation of well-developed colonies, 0(4) sparse small colonies originating from the stomatal subsidiary cells [42,76]. Plants with RT of 0, 0(4), and 1 were classified as highly resistant (R), plants that scored 2 as moderately resistant (M), and ratings of 3 and 4 as susceptible and very susceptible.

The postulation of the presence of resistant genes was based on a comparison of reaction spectra observed on tested accessions and the barley differential set (Table 2). This was done based on the gene-for-gene hypothesis [77]. The RT observed on each accession was compared with the *Bgh* virulence spectrum on the set of barley differential set.

3. Results

In the preliminary study, among 81 tested accessions of *H. vulgare* subsp. *spontaneum* collected in Jordan (47), Lebanon (23), and Libya (11) 15 expressed resistance to isolate Bgh33 of *B. graminis* f. sp. *hordei* (Table 3). Eleven of them originated from Jordan and 4 from Libya. None of the plants of accessions from Lebanon showed powdery mildew resistance in preliminary testing with isolate Bgh33. Twelve of the tested accessions in which plants were resistant to isolate Bgh33 showed heterogenous RT to powdery mildew: 3 of them showed only one type of reaction, 11 showed two different types and 1 showed 3 types (0, 2, 4).

Among scored resistance RT in tested lines with 20 differential isolates the most common reaction was 0 (immunity) (Table 4). It was observed in all tested lines with 65.5%. The rest of RT occurred with frequencies: 1 – 0.96%, 2 – 31.1%, and 4 – 2.4%. Reactions type 3 and 0(4) were not observed. In total 97.6 observed reactions represented resistance RT (0, 1, and 2).

The spectrum of RT of 31 tested lines to infection by 20 differential isolates was compared with results observed on a differential set of barley. Based on this analysis it was concluded that all of the tested lines have unknown gene or genes for resistance which are not represented in the differential set. Twenty-six of these lines (83,9%) showed resistance RT to all isolates used. After analysis of the obtained results, it was concluded that all selected 31 single plant lines of wild barley have unknown genes for resistance which are not represented in the Pallas isolines differential set.

Table 3. Resistance of lines selected from accessions *H. vulgare* subsp. *spontaneum* to *B. graminis* f. sp. *hordei* to isolate Bgh33 after inoculation at the seedling stage.

No.	ICARDA			OTHERN UMB (IHAR No.)	*Bgh 33*	No.	ICARDA			OTHERN UMB (IHAR No.)	*Bgh 33*
	IG	CROP NO	ORI ID				IG	Crop Nr	ORI ID		
1	38616	180007	JOR	1075	4	41	40177	181568	LBN	1116	4
2	38617	180008	JOR	1076	4	42	40178	181569	LBN	1117	4
3	38618	180009	JOR	1077	4	43	40179	181570	LBN	1118	4
4	38619	180010	JOR	1078	4	44	40180	181571	LBN	1119	4
5	38620	180011	JOR	1079	4	45	40181	181572	LBN	1120	4
6	38621	180012	JOR	1080	4	46	40182	181573	LBN	1121	4
7	38622	180013	JOR	1081	4	47	40183	181574	LBN	1122	4

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8	38623	180014	JOR	1082	4	48	40184	181575	LBN	1124	4
9	38624	180015	JOR	1083	0, 4	49	40185	181576	LBN	1125	4
10	38625	180016	JOR	1084	0, 4	50	40186	181577	LBN	1126	4
11	38626	180017	JOR	1085	4	51	40187	181578	LBN	1127	4
12	38627	180018	JOR	1086	0	52	40188	181579	LBN	1128	4
13	38628	180019	JOR	1087	4	53	40189	181580	LBN	1129	4
14	38629	180020	JOR	1088	4	54	40190	181581	LBN	1130	4
15	38630	180021	JOR	1089	0, 4	55	40191	181582	LBN	1131	4
16	38631	180022	JOR	1090	4	56	40193	181584	LBN	1132	4
17	38632	180023	JOR	1091	4	57	40194	181585	LBN	1133	4
18	38633	180024	JOR	1092	4	58	112846	181657	LBY	1134	0, 2, 4
19	39398	180789	JOR	1093	4	59	112847	181658	LBY	1135	4
20	39821	181212	JOR	1094	2, 4	60	110816	181628	LBN	1136	4
21	39822	181213	JOR	1095	4	61	110819	181629	LBN	1137	4
22	39823	181214	JOR	1096	4	62	110823	181630	LBN	1138	4
23	39824	181215	JOR	1097	4	63	110831	181631	LBN	1139	4
24	39825	181216	JOR	1098	4	64	110833	181632	LBN	1140	4
25	39826	181217	JOR	1099	4	65	116004	181639	LBY	1141	4
26	39827	181218	JOR	1100	4	66	116005	181640	LBY	1142	0, 4
27	39828	181219	JOR	1101	2, 4	67	115780	181660	JOR	1143	4
28	39829	181220	JOR	1102	4	68	115781	181661	JOR	1144	0, 4
29	39850	181241	JOR	1103	4	69	115782	181662	JOR	1145	4
30	39851	181242	JOR	1104	4	70	115784	181664	JOR	1146	0
31	39877	181268	JOR	1105	4	71	115785	181665	JOR	1147	4
32	39933	181324	LBY	1107	4	72	115786	181666	JOR	1148	2, 4
33	39934	181325	LBY	1108	3	73	115787	181667	JOR	1149	4
34	39935	181326	LBY	1109	0, 2	74	115788	181668	JOR	1150	4
35	39936	181327	LBY	1110	4	75	115789	181669	JOR	1151	4
36	39937	181328	LBY	1111	0, 4	76	115790	181670	JOR	1152	0

No.	ICARDA			OTHERNUMB (IHAR No.)		*Bgh 33**	No.	ICARDA		OTHERNUMB (IHAR No.)		*Bgh 33*
	IG	CROP NO	ORI ID					Crop Nr	ORI ID			
37		39938	181329	LBY	1112	4	77	115791	181671	JOR	1153	4
38		39939	181330	LBY	1113	4	78	115792	181672	JOR	1154	4
39		40156	181547	LBN	1114	4	79	115793	181673	JOR	1155	0, 2
40		40168	181559	LBN	1115	4	80	115795	181674	JOR	1156	4
							81	115796	181675	JOR	1157	4

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Table 4. Resistance of lines selected from accessions *H. vulgare* subsp. *spontaneum* to *B. graminis* f. sp. *hordei* isolates after inoculation at the seedling stage.

No.	ICARDA ICARDA IG	ICARDA IG line No.	CROP NO	ORI ID	OTHER NUMB (IHAR project No. - Line)	*Isolates* 1 Bgh 1	2 Bgh 2	3 Bgh 3	4 Bgh 4	5 Bgh 8	6 Bgh 9	7 Bgh 11	8 Bgh 13	9 Bgh 14	10 Bgh 24	11 Bgh 28	12 Bgh 29	13 Bgh 31	14 Bgh 33	15 Bgh 36	16 Bgh 40	17 Bgh 48	18 Bgh 51	19 Bgh 57	20 Bgh 63	***Postulated resistance alleles***
1	38624	1	180015	JOR	1083-1	0	0	0	0	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	*un*[*]
2	38625	1	180016	JOR	1084-1	0	0	0	0	2	0	2	0	0	0	0	0	0	0	0	0	0	2	0	0	*un*
3	38625	2	180016	JOR	1084-3	0	0	0	0	0	0	2	0	0	2	0	0	0	0	0	0	0	2	0	0	*un*
4	38625	3	180016	JOR	1084-4	0	0	0	0	0	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	*un*
5	38627	1	180018	JOR	1086-2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	*un*
6	38630	1	180021	JOR	1089-1	2	0	2	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	0	*un*
7	39821	1	181212	JOR	1094-1	4	0	4	0	0	0	2	0	0	2	2	4	0	2	0	0	0	2	2	0	*un*
8	39821	2	181212	JOR	1094-2	2	0	4	0	0	2	2	0	0	2	0	4	0	2	0	1	0	0	0	2	*un*
9	39828	1	181219	JOR	1101-1	2	0	2	-[**]	0	-	2	0	0	0	-	2	0	-	0	0	0	-	-	-	*un*
10	39828	2	181219	JOR	1101-2	0	0	0	-	0	2	2	0	0	2	0	2	0	-	0	0	0	-	-	0	*un*
11	39828	3	181219	JOR	1101-3	2	0	2	0	0	2	2	2	2	2	0	2	2	2	0	0	0	0	0	0	*un*
12	39935	1	181326	LBY	1109-1	0	0	0	0	0	0	2	0	0	2	0	0	0	0	0	0	0	2	0	0	*un*
13	39935	2	181326	LBY	1109-2	0	0	0	-	0	0	2	0	0	2	0	0	0	-	0	0	0	-	-	0	*un*
14	39935	3	181326	LBY	1109-3	0	0	0	2	2	2	2	2	0	2	2	2	0	2	2	0	0	0	2	0	*un*
15	39935	4	181326	LBY	1109-4	0	0	2	0	2	0	2	2	0	2	0	2	0	2	2	0	0	0	0	0	*un*
16	39937	1	181328	LBY	1111-1	0	0	0	0	2	0	2	2	0	4	0	2	0	0	2	0	0	2	2	0	*un*
17	39937	2	181328	LBY	1111-2	0	0	0	0	0	0	2	2	0	2	0	0	0	0	0	0	0	2	2	0	*un*
18	112846	1	181657	LBY	1134-1	0	0	2	1	0	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	*un*
19	112846	2	181657	LBY	1134-2	0	0	0	0	0	0	2	0	0	0	0	2	0	2	0	0	0	2	0	0	*un*
20	116005	1	181640	LBY	1142-1	0	0	2	0	0	0	2	2	0	2	0	0	0	0	2	0	0	2	2	0	*un*
21	115781	1	181661	JOR	1144-1	4	2	4	-	0	0	2	2	0	2	0	2	0	-	2	4	0	-	-	2	*un*
22	115781	2	181661	JOR	1144-2	0	0	0	0	0	0	2	0	0	2	0	0	0	0	2	0	0	0	0	0	*un*
23	115781	3	181661	JOR	1144-3	0	0	0	0	0	0	2	0	0	2	0	0	0	0	2	0	0	2	0	0	*un*
24	115784	1	181664	JOR	1146-1	0	0	0	0	0	-	0	0	0	0	-	0	0	0	0	0	0	0	0	-	*un*
25	115786	1	181666	JOR	1148-2	0	0	0	2	0	-	2	2	0	2	-	2	2	2	2	0	0	0	0	-	*un*
26	115790	1	181670	JOR	1152-1	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	*un*

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27	115790	2	181670	JOR	1152-2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	*un*
28	115793	1	181673	JOR	1155-1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	*un*
29	115793	2	181673	JOR	1155-3	0	0	0	0	0	0	2	0	2	0	0	0	0	0	1	0	0	2	0	*un*
30	115793	3	181673	JOR	1155-3	0	0	0	2	0	0	2	0	0	0	0	0	0	2	2	0	0	0	0	*un*
31	115793	2	181673	JOR	1155-2	0	0	0	0	0	0	2	0	0	4	2	2	0	0	2	0	0	0	0	*un*

* unknown resistance gene. ** no data.

4. Discussion

In Jordan, Lebanon, and Libya are many mountainous regions and different climate zones from relatively humid, with moderate temperature maritime to very dry and hot desert climates. Such conditions are favorable for the evolution of very diverse genotypes of plants including wild barley [12–15]. Powdery mildew occurs commonly in this area on barley and wild barley. Because the area of the Fertile Crescent is considered the center of origin and diversification of barley it is also the center of the presence of very diverse resistance genes to BPM [3,6,21,22]. This was confirmed in the present study in which were identified new sources of resistance to BPM in selections from accessions of *Hvs* from Jordan and Libya.

The Fertile Crescent area is considered the center of origin and diversification of barley Taking this fact into account, due to host-pathogen coevolution it is also the area of the very diverse Bgh population. Many studies have shown that this particular area is a very rich source od resistance to BPM [3,6,21,22]. This was confirmed in the present study in which were identified new sources of resistance to BPM in selections from accessions of *Hvs* from Jordan and Libya.

In the preliminary study, among 81 tested accessions of *Hvs* collected in Jordan (47), Lebanon (23), and Libya (11) in 15 was observed BPM resistance to isolate Bgh33. Eleven of them originated from Jordan, 4 from Libya, and none from Lebanon. Twelve tested accessions showed heterogenous resistance reactions to powdery mildew: 3 of them showed only one type of reaction, 11 showed two types and 1 showed 3 types (0,2,4). Heterogenous reactions of *Hvs* accessions to powdery mildew were also reported in other studies [70,71]. In populations of *Hvs*, BPM is not developing to levels that significantly damage plants. This is the result of both the stabilizing effect of the genetic heterogeneity within the populations of *Hvs* and the presence of resistance sufficient to control the limited disease development [69–71,76].

In tested lines with 20 differential BPM isolates the most common RT was 0 (immunity). This kind of RT was observed in all tested lines and with 65.5 % of all observed RT. The rest of RT occurred with frequencies: 1 – 0.96 %, 2 – 31.1%, and 4 – 2.4%. Reactions type 3 and 0(4) were not observed. In total 97.6 observed reactions represented resistance RT (0, 1, and 2). Such a relatively high percentage of resistance RT showed that *Hvs* collected in Jordan and Libya are valuable sources of resistance for European barley breeding which is in agreement with other studies [56,57,63,64,69,70].

Fungus *Bgh* is characterized by a high level of genetic variability. It can develop during a relatively short time a new races that can spread to long distances [19–26]. This resulted in a rapidly reduced number of resistance genes effectively controlling the occurrence and spread of *Bgh* to be available for barley breeders [25,26]. At the same time, modern barley cultivars which were grown in large areas across Europe often had no partial type of host resistance due to breeding for a race-specific type of BPM resistance in most modern breeding programs [21,25,33,34,85]. This fact was recognized a long time ago by plant pathologists and plant breeders and several ways to increase the durability of resistance genes were proposed. Major strategies were proposed and implemented: the use of multiline cultivars, the combining ('pyramiding') different resistance genes into one variety, and the deployment of many cultivars with different resistance genes in space (e.g. cultivar mixtures) or time (winter versus spring barley) [19,25,33–35]. However, for such BPM strategies of genetic control very useful is to introduce into breeding materials new effective sources of resistance. Such

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newly identified sources of BPM resistance are still being found in barley landraces and wild relatives [25,50–55,69–71]. There are many examples of successful use by barley breeders the new sources of resistance to BPM originating from *Hvs* populations to develop new resistant cultivars. In most cases, these new resistance genes were deployed in new cultivars under different strategies to prolong the time of their effectiveness against BPM [19,25,33–35].

The additional advantage of using germplasm from *Hvs* by barley breeders is the possibility to introduce other desirable agronomic traits e.g. tolerance to drought conditions and other biotic and abiotic stresses [16,18]. However, for many barley breeders, a heterogeneity of *Hvs* accessions is a problem because it complicates and prolongs the breeding process. Often pre-breeding activities resulting in well-characterized single plant lines of *Hvs* with many important economically traits including resistance to BPM are needed. Pre-breeding activities presented here provide breeders with new BPM sources of resistance. To be used in different breeding strategies [19,21,33–35]. The big advantage of the use of *Hvs* genetic resources in barley breeding is a lack of problems with sterility. Such problems are often present if *H. bulbosum* or mutants are used [19,21,25].

Two major strategies for BPM control are available. The first is to grow resistant cultivars and the second one is the application of fungicides [36–38]. However, in many countries, *Bgh* races resistant to commonly used fungicides have been described [31,32]. In addition, the cost of fungicides and concerns about the environment led many countries to restrict their use in disease control [36,38]. Taking this into account, the BPM control using effective resistance genes is increasingly important in IPM strategies. The understanding of BPM genetic control and how to properly use resistance genes resulted from many genetic studies of barley resistance to BPM and the relatively good characterization of the genetics of powdery mildew/barley interactions [19,21,25]. This is one of the best-described host-pathogen genetic interactions and more than 100 mildew resistance genes have been identified [21,25]. This kind of knowledge about well-characterized sources of BPM resistance resulted in many successful BPM resistance breeding programs using new sources of resistance to BPM [19,21,25,33–35]. Breeding for resistance as a strategy to control BPM is increasingly understood and acceptable by societies as ecologically safe.

In the presented study to identify new sources of resistance in wild barley accessions the test with a set of differential BPM isolates was used and the selection of single plant lines was conducted. This method was described in many studies to identify specific resistance genes in barley accessions and breeding lines [19,21,25,26]. In addition, it was successfully used in many studies to screen both landraces and wild barleys for new effective resistance genes [26,40,43,50–52,54,55,69–71]. However, for the description of the partial type of resistance to BPM, this kind of test is not sufficient. For the detection of this kind of resistance, there is a need to get, in addition to the RT, the measurements of resistance parameters in different stages of plant development (e.g. at the adult plant stage) [79–83]. Adult plant resistance of tested accessions should be investigated in additional specific tests because almost all wild barleys contain major specific resistance genes which very often mask minor resistance genes determining the partial resistance or the presence of adult resistance [19,21,25,79–85].

A very interesting genetic resource for the breeding of resistant barley is 31 single plant lines of wild barley which have genes for resistance not represented in the BPM differential set. These identified new sources of highly effective resistance to BPM in single plant lines of *Hvs* from Jordan and Libya will be used in the barley pre-breeding program.

Further studies are needed to determine the mode of action of resistance genes in identified new sources of BPM resistance described in the presented study based on results of testing of hybrids resulting from crosses among appropriate genotypes [40,45,52]. In the future, some other available methods for the characterization of resistant lines have to be used, especially those for the study of partial and adult resistance [79–85].

In addition, modern molecular methods have to be used for further characterization of identified resistance genes to be efficiently used in barley breeding [86–88].

5. Conclusions

The *Hvs* populations from Jordan and Libya are valuable sources of BPM resistance.

Selected single plant lines of *Hvs* may be used in pre-breeding programs to provide barley breeders with new well-characterised sources of BPM resistance.

Future studies will concentrate on determining the genetic basis of resistance occurring in 31 Hvs selections. They will include the crosses of investigated selections with well-chosen parents and the development of molecular markers.

To successfully introduce described new sources of BPM resistance into barley elite cultivars, pre-breeding work is needed in the creation of initial well-characterized plant materials. This a needed step to use barley germplasm from gene banks: first, to use it in breeding programs, and second, in agricultural practice as elite cultivars.

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References

1. Baik, B.K.; Ullrich S.E. Barley for food: characteristics, improvement, and renewed interest. *J. Cereal Sci*. **2008**, *48*, 233–242. http://dx.doi.org/10.1016/j.jcs.2008.02.002
2. FAOSTAT. Available online: https://www.fao.org/worldfoodsituation/csdb/en/ (accessed on 10 May 2023).
3. Badr, A.; Rabey, H.E.; Effgen, S.; Ibrahim, H.H.; Pozzi, C.; Rohde, W.; Salamini, F. On the origin and domestication history of barley (*Hordeum vulgare*). *Molecular biology and evolution* **2000**, *17*(4), 499-510.
4. https://doi.org/10.1093/oxfordjournals.molbev.a026330
5. Geng, L.; Li, M.; Zhang, G.; Ye, L. Barley: A Potential Cereal for Producing Healthy and Functional Foods. *Food Qual. Saf.* **2022**, *6*, 1–13. https://doi.org/10.1093/fqsafe/fyac012
6. Lukinac, J.; Jukić, M. Barley in the Production of Cereal-Based Products. *Plants* **2022**, *11*, 3519. https://doi.org/10.3390/plants11243519
7. Von Bothmer, R.; Sato, K.; Komatsuda, T.; Yasuda, S.; Fischbeck, G. The domestication of cultivated barley. In Diversity in barley *(Hordeum vulgare);* Von Bothmer, R., van Hintum, T., Knüpfer, H., Sato, K., Eds.; Elsevier Science, B.V.: Amsterdam, The Netherlands, 2003; Chapter 2; pp. 9–27. https://doi.org/10.1016/S0168-7972(03)80004-X
8. Molina-Cano, J.L.; Russell, J.R.; Moralejo, M.A.; Escacena, J.L.; Arias, G.; Powell, W. Chloroplast DNA microsatellite analysis supports a polyphyletic origin for barley. *Theoretical and Applied Genetics* **2005**, *110*, 613-619. https://doi.org/10.1007/s00122-004-1878-3
9. Newton, A.C.; Akar, T.; Baresel, J.P.; Bebeli, P.J.; Bettencourt, E.; Bladenopoulos, K.V.; Czembor, J.H.; Fasoula, D.A.; Katsiotis, A.;Koutis, K.; et al. Cereal landraces for sustainable agriculture. A review. *Agron. Sustain. Dev.* **2010**, *30*, 237–269.
10. https://doi.org/10.1051/agro/2009032
11. Khoury, C.K.; Brush, S.; Costich, D.E.; Curry, H.A.; Haan, S. De; Engels, J.M.M.; Guarino, L.; Hoban, S.; Mercer, K.L.; Miller, A.J.; Nabhan, G.P.; Perales, H.R.; Richards, C.; Riggins, C.; Thormann, I. Crop genetic erosion : understanding and responding to loss of crop diversity. *New Phytol.* **2022** *233(1)*, 84-118. https://doi.org/10.1111/nph.17733
12. Czembor, J.H.; Czembor, E.; Krystek, M.; Pukacki, J. AgroGenome: Interactive Genomic-Based Web Server Developed Based on Data Collected for Accessions Stored in Polish Genebank. *Agriculture* **2023**, *13*, 193. https://doi.org/10.3390/agriculture13010193
13. Knupfer, R. Triticeae genetic resources in ex situ genebank collections. In Genetic and Genomics of the Triticeae. Plant Genetics and Genomics: Crops and Models; Muelbauer, G.J., Feuillet, C., Eds.; Springer Science: New York, NY, USA, **2009**; Volume 7, pp. 31–80.
14. https://doi.org/10.1007/978-0-387-77489-3_2
15. Shakhatreh, Y.; Haddad, N.; Alrababah, M.; Grando, S.; Ceccarelli, S. Phenotypic diversity in wild barley (*Hordeum vulgare* L. ssp. *spontaneum* (C. Koch) Thell.) accessions collected in Jordan. *Genetic Res. Crop Evol.* **2010**, *57*, 131-146. https://doi.org/10.1007/s10722-009-9457-8

16. Thormann, I.; Reeves, P.; Reilley, A.; Engels, J.M.M.; Lohwasser, U.; Börner, A.; Pillen, K.; Richards, C.M.; Geography of genetic structure in barley wild relative *Hordeum vulgare* subsp. *spontaneum* in Jordan. *PLoS ONE* **2016**, *11*, e0160745. https://doi.org/10.1371/journal.pone.0160745
17. Al-Hajaj, N.; Grando, S.; Ababnah, M.; Alomari, N.; Albatianh, A.; Nesir, J.; Migdali, H.; Shakhatreh, Y.; Ceccarelli, S. Phenotypic evolution of the wild progenitor of cultivated barley (*Hordeum vulgare* L. subsp. *spontaneum* (K. Koch) Thell.) across bioclimatic regions in Jordan. *Genet. Resour. Crop Evol.* **2022**, *69*, 1485–1507. https://doi.org/10.1007/s10722-021-01314-1
18. Chang, C.W.; Fridman, E.; Mascher, M.; Himmelbach, A.; Schmid, K. Physical geography, isolation by distance and environmental variables shape genomic variation of wild barley (*Hordeum vulgare* L. ssp. *spontaneum*) in the Southern Levant. *Heredity* **2022**, *128*(2), 107-119. https://doi.org/10.1038/s41437-021-00494-x.
19. Rehman, S.; Amouzoune, M.; Hiddar, H.; Aberkane, H.; Benkirane, R.; Filali-Maltouf, A.; Al-Jaboobi, M.; Acqbouch, L.; Tsivelikas, A.; Verma, R.P.S.; Kehel, Z.; Birouk, A.; Amri, A.; Traits discovery in *Hordeum vulgare* sbsp. *spontaneum* accessions and in lines derived from interspecific crosses with wild *Hordeum* species for enhancing barley breeding efforts. *Crop Science*, **2020**, *61(1)*, 219–233. https://doi.org/10.1002/csc2.20360
20. Milner, S.G.; Jost, M.; Taketa, S.; Mazón, E.R.; Himmelbach, A.; Oppermann, M.; Weise, S.; Knüpffer, H.; Basterrechea, M.; König, P.; Schüler, D.; Sharma, R.; Pasam, R.K.; Rutten, T.; Guo, G.; Xu, D.; Zhang, J.; Herren, G.; Müller, T.; Krattinger, S.G.; Keller, B.; Jiang, Y.; González, M.Y.; Zhao, Y.; Habekuß, A.; Färber, S.; Ordon, F.; Lange, M.; Börner, A.; Graner, A.; Reif, J.C.; Scholz, U.; Mascher, M.; Stein, N. Genebank genomics highlights the diversity of a global barley collection. *Nat. Genet.* **2019**, *51*, 319–326. https://doi.org/10.1038/s41588-018-0266-x.
21. Capasso, G.; Santini, G.; Petraretti, M.; Esposito, S.; Landi, S. Wild and Traditional Barley Genomic Resources as a Tool for Abiotic Stress Tolerance and Biotic Relations. *Agriculture* **2021**, *11*, 1102. https://doi.org/10.3390/agriculture11111102
22. Jørgensen, J.H; Wolfe, M. Genetics of Powdery Mildew Resistance in Barley. *Crit. Rev. in Plant Sci.* **1994**, *13(1)*, 97-119. https://doi.org/10.1080/07352689409701910
23. Hovmoller, M.S.; Caffier, V.; Jalli, M.; Andersen, O.; Besenhofer, G.; Czembor, J.H.; Dreiseitl, A.; Flath, K.; Fleck, A.; Heinrics, F.; Jönsson, R.; Limpert, E.; Mercer, P.; Plesnik, S.; Rashal, I..; Skinnes, H.; Slater, S.; Vronska, O. The Eurpean barley powdery mildew virulence survey and disease nursery 1993-1999. *Agonomie* **2000**, *20(7)*, 729-744.
24. https://doi.org/10.1051/agro:2000172
25. Weibull, J.; Walther, U.; Sato, K.; Habekuß, A.; Kopahnke, D.; Proeseler, G. Diversity in resistance to biotic stresses. In Diversity in barley *(Hordeum vulgare);* Von Bothmer, R., van Hintum, T., Knüpfer, H., Sato, K., Eds.; Elsevier Science, B.V.: Amsterdam, The Netherlands, 2003; Chapter 8; pp. 143-178. https://doi.org/10.1016/S0168-7972(03)80010-5.
26. Dreiseitl, A. The *Hordeum vulgare* subsp. *spontaneum-Blumeria graminis* f. sp. *hordei* pathosystem: Its position in resistance research and breeding applications. *Eur. J. Plant Pathol.* **2014**, 138, 561–568.
27. Dreiseitl, A. Great pathotype diversity and reduced virulence complexity in a Central European population of *Blumeria graminis* f. sp. *hordei* in 2015–2017. *Eur. J. Plant Pathol.* **2019**, *53*, 801–811. https://doi.org/10.1007/s10658-018-1593-6
28. Kusch, S.; Qian, J.; Loos, A.; Kümmel, F.; Spanu, P.D.; Panstruga, R. Long-term and rapid evolution in powdery mildew fungi. *Mol Ecol.* **2023** *Mar 2*. https://doi.org/10.1111/mec.16909
29. Dreiseitl, A. Specific resistance of barley to powdery mildew, its use and beyond: a concise critical review. *Genes*, **2000**, *11*(9), 971. https://doi.org/10.3390/genes11090971
30. Dreiseitl, A. Powdery mildew resistance genes in European barley cultivars registered in the Czech Republic from 2016 to 2020. *Genes*, **2022**, *13*(7), 1274. https://doi.org/10.3390/genes13071274
31. Murray, G.M.; Brennan, J.P. Estimating Disease Losses to the Australian Barley Industry. *Australas. Plant Pathol.* **2010**, *39*, 85–96. https://doi.org/10.1071/AP09064
32. Kauppi, K.; Rajala, A.; Huusela, E.; Kaseva, J.; Ruuttunen, P.; Jalli, H.; Alakukku, L.; Jalli, M. Impact of Pests on Cereal Grain and Nutrient Yield in Boreal Growing Conditions. *Agronomy* **2021**, *11*, 592. https://doi.org/10.3390/agronomy11030592

33. Savary, S.; Ficke, A.; Aubertot, J.N.; Hollier, C. Crop losses due to diseases and their implications for global food production losses and food security. *Food Sec.* **2012**, 4, 519–537. https://doi.org/10.1007/s12571-012-0200-5
34. Hysing, S.C.; Rosenqvist, H.; Wiik, L. Agronomic and economic effect of host resistance vs. fungicide control of barley powdery mildew in southern Sweden. *Crop Protect.* **2012**, *41*, 122–127. https://doi.org/10.1016/j.cropro.2012.05.010
35. Hobbelen, P.H.F.; Paveley, N.D.; van den Bosch, F. The emergence of resistance to fungicides. *PLoS ONE* **2014**, *9*, e91910. https://doi.org/10.1371/journal.pone.0091910
36. Hollomon, D.W. Fungicide resistance: Facing the challenge. *Plant Protect. Sci.* **2015**, *51*, 170–176. https://doi.org/10.17221/42/2015-PPS
37. McDonald, B.A.; Linde, C. Pathogen population genetics, evolutionary potential, and durable resistance. *Annu. Rev. Phytopathol.* **2002**, *40*, 349–379. https://doi.org/10.1146/annurev.phyto.40.120501.101443
38. Burdon, J.J.; Barrett, L.G.; Rebetzke, G.; Thrall, P.H. Guiding deployment of resistance in cereals using evolutionary principles. *Evol. Appl.* **2014**, *7*, 609–624.
39. https://doi.org/10.1111/eva.12175
40. Mundt, C.H. Pyramiding for resistance durability: theory and practise. *Phytopathology* **2018**, *108*, 792–802. https://doi.org/10.1094/PHYTO-12-17-0426-RVW
41. Walters, D.R.; Avrova, A.; Bingham, I.J.; Burnett, F.J.; Fountaine, J.; Havis, N.D.; Hoad, S.P.; Hughes, G.; Looseley, M.; Oxley, S.J.P.; Renwick, A.; Topp, C.F.E; Newton, A.C. Control of foliar diseases in barley: Towards an integrated approach. *Eur. J. Plant Pathol.* **2012**, *133*, 33–73. https://doi.org/10.1007/s10658-012-9948-x
42. Jørgensen, L.N.; Hovmoller, M.; Hansen, J.G.; Lassen, P.; Clark, B.; Bayles, R.; Rodemann, B.; Flath, K.; Jahn, M.; Goral, T.; et al. IPM Strategies and Their Dilemmas Including an Introduction to www.eurowheat.org. *J. Integr. Agric.* **2014**, *13*, 265–281.
43. https://doi.org/10.1016/S2095-3119(13)60646-2
44. Lamichhane, J.R.; Arseniuk, E.; Boonekamp, P.; Czembor, J.H.; Decroocq, V.; Enjalbert, J.; Finckh, M. R.; Korbin, M.; Mati Koppel, M.; Kudsk, P.; Mesterhazy, A.; Sosnowska, D.; Zimnoch-Guzowska, E.; Messéan, A. Advocating a need for suitable breeding approaches to boost Integrated Pest Management: A European perspective. *Pest Management Science* **2018**, *74*, 1219-1227. https://doi.org/10.1002/ps.4818
45. Biffen, R.H. Studies in the inheritance of disease resistance. *J. Agric. Sci.* **1907**, 2, 109–128.
46. https://doi.org/10.1017/S0021859600001234
47. Czembor J.H.; Johnston M. R. Resistance to powdery mildew in selections from Tunisian barley landraces. *Plant breeding* **1999**, *118(6)*, 503-509. https://doi.org/10.1046/j.1439-0523.1999.00382.x
48. Czembor J.H.; Czembor H.J. Resistance to powdery mildew in barley landraces collected from Jordan. *Plant Breeding and Seed Science* **1999**, *43(2)*, 65-80.
49. Czembor J.H. Resistance to powdery mildew in barley (*Hordeum vulgare* L.) landraces from Egypt. *Plant Genetic Resources Newsletter* **2000**, *123*, 52-60.
50. Czembor J.H. Resistance to powdery mildew in populations of barley landraces from Morocco. Australasian Plant Pathology **2000**, *29*, 137-148. https://doi.org/10.1071/AP00022
51. Czembor J.H. Powdery mildew resistance in selections from barley landraces collected in Jordan, Egypt, Libya and Tunisia. *Scientia Agriculturae Bohemica* **2001**, *32(1)*, 43-65.
52. Czembor J.H.; Czembor H.J. Inheritance of resistance to powdery mildew (*Blumeria*
53. *graminis* f.sp. *hordei*) in selections from Moroccan landraces of barley. *Cereal Res.*
54. *Comm.* **2001**, *29(3-4)*, 281-288. https://doi.org/10.1007/BF03543672
55. Czembor J.H. Sources of resistance to powdery mildew (*Blumeria graminis* f. sp. *hordei*) in Moroccan barley landraces. *Canadian J Plant Path - Revue Canadienne de Phytopathol* **2001**, *23(1)*, 260-269. https://doi.org/10.1080/07060660109506939
56. Czembor J.H.; Czembor H.J. Selections from barley landrace collected in Libya as new sources of effective resistance to powdery mildew (*Blumeria graminis* f.sp. *hordei*). *Rostlinna Vyroba* **2002**, *48 (5)*, 217-223. https://doi.org/10.17221/4229-PSE
57. Czembor J.H. Resistance to powdery mildew in selections from Moroccan barley landraces. *Euphytica* **2002**, *125(3)*, 397-409. https://doi.org/10.1023/A:1016061508160
58. Czembor J.H.; Frese L. Powdery mildew resistance in selections from barley landraces collected from Turkey. *Die Bodenkultur* **2003**, *54(1)*, 35-40.

59. Silvar, C.; Flath, K.; Kopahnke, D.; Gracia, M.P.; Lasa, J.M.; Casas, A.M.; Igartua, E.; Ordon, F. Analysis of powdery mildew resistance in the Spanish barley core collection. *Plant Breed.* **2011**, *130*, 195–202. 10.1111/j.1439-0523.2010.01843.x
60. Surlan-Momirovic, G.; Flath, K.; Silvar, C.; Brankovic, G.; Kopahnke, D.; Knezevic, D.; Schliephake, E.; Ordon, F.; Perovic, D. Exploring the Serbian GenBank barley (*Hordeum vulgare* L. subsp *vulgare*) collection for powdery mildew resistance. *Genet. Resour. Crop. Evol.* **2016**, *63*, 275–287. https://doi.org/10.1007/s10722-015-0246-2
61. Piechota, U.; Czembor, P.C.; Słowacki, P.; Czembor, J.H. Identifying a novel powdery mildew resistance gene in a barley landrace from Morocco. *Journal of Applied Genetics* **2019**, *60(3)*, 243-254. https://doi.org/10.1007/s13353-019-00505-y
62. Piechota U.; Czembor P.C.; Czembor J.H. Evaluating barley landraces collected in North Africa and the Middle East for powdery mildew infection at seedling and adult plant stages. *Cereal Res Comm* **2020,** *48*, 179–185. https://doi.org/10.1007/s42976-020-00021-4
63. Czembor, J.H.; Czembor, E. Mlo resistance to powdery mildew (*Blumeria graminis* f.sp.
64. *hordei*) in barley landraces collected in Yemen. *Agronomy* **2021**, *11(8)*, 1582.
65. https://doi.org/10.3390/agronomy11081582
66. Czembor, J.H.; Czembor, E. Sources of Resistance to Powdery Mildew in Barley Landraces
67. from Turkey. *Agriculture* ***2021***, *11(10)*, 1017. https://doi.org/10.3390/agriculture11101017
68. Fischbeck, G.; Schwarzbach, E.; Sobel, Z.; Wahl, I. Mildew resistance in Israeli populations of 2-rowed wild barley (*Hordeum spontaneum*). *Z. Pflanz.* **1976**, *76*, 163–166.
69. Moseman, J.G.; Nevo, E.; Zohary, D. Resistance of *Hordeum spontaneum* collected in Israel to infection with *Erysiphe graminis hordei*. *Crop Sci.* **1983**, *23*, 1115–1119. https://doi.org/10.2135/cropsci1983.0011183X002300060022x
70. Jahoor, A.; Fischbeck, G. Identification of new genes for mildew resistance of barley at the Mla locus in lines derived from *Hordeum spontaneum*. *Plant Breed*. **1993**, *110*, 116–122. https://doi.org/10.1111/j.1439-0523.1993.tb01222.x
71. Kintzios, S.; Jahoor, A.; Fischbeck, G. Powdery-mildew-resistance genes *Mla29* and *Mla32* in *H. spontaneum* derived winter-barley lines. *Plant Breed*. **1995**, *114*, 265–266.
72. Kintzios, S.; Fischbeck, G. Identification of new sources for resistance to powdery mildew in *H. spontaneum* derived winter barley lines. *Genet. Resour. Crop. Evol*. **1996**, *43*, 25–31.
73. https://doi.org/10.1007/BF00126937
74. Mastebroek, H.D.; Balkema-Bomstra, A.G.; Gaj, M. Genetic analysis of powdery mildew (*Erysiphe graminis* f. sp. *hordei*) resistance derived from wild barley (*Hordeum vulgare* ssp. *spontaneum*). *Plant Breed.* **1995**, *114*, 121–125. https://doi.org/10.1111/j.1439-0523.1995.tb00775.x
75. Fetch, T.G.; Steffenson, B.J.; Nevok, E. Diversity and sources of multiple disease resistance in *Hordeum spontaneum*. *Plant Dis*. **2003**, *87*, 1439–1448. https://doi.org/10.1094/PDIS.2003.87.12.1439
76. Dreiseitl, A.; Bockelman, H.E. Sources of powdery mildew resistance in a wild barley collection. *Genet. Resour. Crop Evol.* **2003**, *50*, 345–350. https://doi.org/10.1023/A:1023953819787
77. Dreiseitl, A.; Dinoor, A. Phenotypic diversity of barley powdery mildew resistance sources. *Genet. Resour. Crop Evol*. **2004**, *51*, 251–258. https://doi.org/10.1023/B:GRES.0000024010.12369.b3
78. Dreiseitl, A.; Řepková, J.; Lízal, P. Genetic analysis of thirteen accessions of *Hordeum vulgare* ssp. *spontaneum* resistant to powdery mildew. *Cereal Res. Commun*. **2007**, *35*, 1449–1458. https://doi.org/10.1556/crc.35.2007.3.9
79. Řepková, J.; Teturová, K.; Dreiseitl, A.; Soldánová, M. Characterization and chromosomal location of powdery mildew resistance genes from wild barley PI282605. *J. Plant Dis. Protect*. **2009**, *116*, 257–259. https://doi.org/10.1007/BF03356319
80. Řepková, J.; Dreiseitl, A. Candidate markers for powdery mildew resistance genes from wild barley PI284752. *Euphytica* **2010**, *175*, 283–292. https://doi.org/10.1007/s10681-009-0096-0
81. Teturová, K.; Řepková, J.; Lízal, P.; Dreiseitl, A. Mapping of powdery mildew resistance genes in a newly determined accession of *Hordeum vulgare* ssp. *spontaneum*. *Ann. Appl. Biol*. **2010**, *156*, 157–165. https://doi.org/10.1111/j.1744-7348.2009.00375.x
82. Ames, N.; Dreiseitl, A.; Steffenson, B.J.; Muehlbauer, G.J. Mining wild barley for powdery mildew resistance. *Plant Pathol*. **2015**, *64*, 1396–1406. https://doi.org/10.1111/ppa.12384

83. Dreiseitl, A. High diversity of powdery mildew resistance in the ICARDA wild barley collection. *Crop Pasture Sci*. **2017**, *68*, 134–139. https://doi.org/10.1071/CP16221
84. Dreiseitl, A. Heterogeneity of powdery mildew resistance revealed in accessions of the ICARDA wild barley collection. *Front. Plant Sci*. **2017**, *8*, 202. https://doi.org/10.3389/fpls.2017.00202
85. Czembor, J.H.; Czembor, E. Mlo resistance of barley to powdery mildew *(Blumeria graminis* f.sp. *hordei*) Part II. Sources of resistance and their use in barley breeding. *Biul. IHAR* **2003**, *230*, 355-374.
86. Czembor, J.H.; Czembor, E. Mlo resistance of barley to powdery mildew (*Blumeria graminis* f.sp. *hordei*) Part III. Durability of resistance. *Biul. IHAR* **2003**, *230*, 375-386.
87. Reinstädler A.; Müller J.; Czembor J.H.; Piffanelli P.; Panstruga R. Novel induced *mlo* mutant alleles in 1 combination with site-directed mutagenesis reveal functionally important domains in the heptahelical barley Mlo protein. *BMC Plant Biology* **2010**, *10*, 31. http://www.biomedcentral.com/1471-2229/10/31
88. Kølster, P.; Munk, L.; Stølen, O.; Løhde, J. Near-Isogenic Barley Lines with Genes for Resistance to Powdery Mildew. *Crop Science*, **1986**, *26*(5), 903-907.
89. https://doi.org/10.2135/cropsci1986.0011183X002600050014x
90. Mains, E.B.; Dietz, S.M. Physiologic forms of barley mildew, *Erysiphe graminis hordei* Marchal. *Phytopathology* **1930**, *20*, 229–239.
91. Flor, H.H. Current status of the gene-for-gene concept. *Annu. Rev. Phytopathol*. **1971**, *9*, 275–296. https://doi.org/10.1146/annurev.py.09.090171.001423
92. Abdel-Ghani, A.H.; Parzies, H.K.; Omary, A.; Geiger, H.H. Estimating the outcrossing rate of barley landraces and wild barley populations collected from ecologically different regions of Jordan. *Theor Appl Genet*. **2004**, *109(3)*; 588-95. https://doi.org/10.1007/s00122-004-1657-1
93. Shtaya, M.J.Y.; Marcel, T.C.; Sillero, J.C.; Niks, R.E.; Rubiales, D. Identification of QTLs for powdery mildew and scald resistance in barley. *Euphytica*, **2006**, *151*, 421-429. https://doi.org/10.1007/s10681-006-9172-x
94. Spies, A.; Korzun, V.; Bayles, R.; Rajaraman, J.; Himmelbach, A.; Hedley, P.E., Schweizer, P. Allele mining in barley genetic resources reveals genes of race-non-specific powdery mildew resistance. *Frontiers in plant science*, **2012**, *2*, 113.
95. https://doi.org/10.3389/fpls.2011.00113
96. Hickey, L.T.; Lawson, W.; Platz, G.J.; Fowler, R.A.; Arief, V.; Dieters, M.; German, S.; Fletcher, S.; Park, R.F.; Singh, D.; et al. Mapping quantitative trait loci for partial resistance to powdery mildew in an Australian barley population. *Crop Sci*. **2012**, *52*, 1021–1032
97. https://doi.org/10.2135/cropsci2011.10.0535
98. Bengtsson, T.; Åhman, I.; Manninen, O.; Reitan, L.; Christerson T.; Due Jensen, J.; Krusell, L.; Jahoor, A.; Orabi, J.A. Novel QTL for Powdery Mildew Resistance in Nordic Spring Barley (*Hordeum vulgare* L. ssp. *vulgare*) Revealed by Genome-Wide Association Study. *Front Plant Sci.* **2017**, *8*, 1954. https://doi.org/10.3389/fpls.2017.01954
99. Cowger, C.; Brown, J.K. Durability of quantitative resistance in crops: greater than we know?. *Annual review of Phytopathology* **2019**, *57*, 253-277.
100. https://doi.org/10.1146/annurev-phyto-082718-100016
101. Gupta, S.; D'Antuono, M.; Bradley, J.; Li, C.; Loughman R. Identification and expression of adult plant resistance in barley to powdery mildew (*Blumeria graminis* f. sp. *hordei*) in Australia. *Euphytica* **2015**, 595–605. https://doi.org/10.1007/s10681-014-1280-4
102. Ge, C.; Wentzel, E.; Ellwood, S.R.; Souza, N.D.; Chen, K.; Oliver, R.P. Adult resistance genes to barley powdery mildew confer basal penetration resistance associated with broad-spectrum resistance. Plant Genome **2021**, *14(3)*, e20129, https://doi.org/10.1002/tpg2.20129
103. Czembor, J.H.; Czembor, E.; Suchecki, R.; Watson-Haigh, N.S. Genome-Wide Association Study for Powdery Mildew and Rusts Adult Plant Resistance in European Spring Barley from Polish Gene Bank. *Agronomy* **2022**, *12(1)*, 7. https://doi.org/10.3390/agronomy12010007

104. Singh, B.; Mehta, S.; Aggarwal, S. K.; Tiwari, M.; Bhuyan, S. I.; Bhatia, S.; Islam M. A. Barley, Disease Resistance, and Molecular Breeding Approaches. In Disease Resistance in Crop Plants. Wani, S.H. (ed.) Springer Nature Switzerland AG, 2019; Chapter 11; pp. 261-299. https://doi.org/10.1007/978-3-030-20728-1_11
105. Riaz, A.; Kanwal, F.; Börner, A.; Pillen, K.; Dai, F.; Alqudah, A.M. Advances in Genomics-Based Breeding of Barley: Molecular Tools and Genomic Databases. *Agronomy* **2021**, *11*, 894. https://doi.org/10.3390/agronomy11050894