

**SCREENING BARLEY GERMPLASM FOR RESISTANCE TO NET FORM NET
BLOTCH CAUSED BY *PYRENOPHORA TERES* F. *TERES* IN KAZAKHSTAN**

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Annotation. Net form net blotch, caused by *Pyrenophora teres* f. *teres*, is a major constraint to barley production worldwide, including in Kazakhstan, where information on resistance sources remains limited. This study aimed to evaluate the resistance of 106 spring barley accessions from different breeding programs in Kazakhstan at both seedling and adult plant stages. Seedling resistance was assessed under greenhouse conditions using two predominant pathogen races (100 and 500), while field resistance was evaluated under artificial infection using disease severity and area under the disease progress curve (AUDPC). A greater virulence of race 500 compared to race 100 was observed, with fewer accessions showing resistance at the seedling stage. A strong positive correlation between disease severity and AUDPC ($r = 0.885$) was observed. Differences between seedling and adult plant responses suggest the involvement of both race-specific and quantitative resistance mechanisms. This study provides the first systematic evaluation of resistance to predominant *P. teres* f. *teres* races in Kazakh barley germplasm.

Keywords: barley, net form net blotch, disease resistance, germplasm screening, race-specific resistance, field evaluation.

Introduction. Barley (*Hordeum vulgare*) is one of the most important cereal crops worldwide, ranking fourth in global grain production and being cultivated in more than 100 countries [1,2]. It is widely used for feed, malting, brewing, and human consumption [3]. Global production reached 145.9 million tonnes, while in Kazakhstan barley production exceeded 3.3 million tonnes, showing a significant increase compared to previous years [4,5]. Despite its importance, barley productivity is strongly affected by fungal diseases, which can result in average yield losses of up to 19.6% [6].

Net blotch is one of the most widespread and economically important diseases of barley and can cause yield losses of up to 40% under favorable conditions [7]. The disease is caused by the ascomycete *Pyrenophora teres*, which exists in two forms, the net form (*P. teres* f. *teres*, *Ptt*) and the spot form (*P. teres* f. *maculata*, *Ptm*). These forms are morphologically similar but differ genetically and in symptom expression [8,9]. The predominance of *P. teres* f. *teres* in the dry steppe regions of Kazakhstan creates a unique epidemiological scenario, where disease incidence can reach up to 90% in northern areas [10]. Population studies have shown that the net form predominates in Kazakhstan and neighboring regions, with most isolates identified as *P. teres* f. *teres* [11].

The pathogen is characterized by high genetic variability, which contributes to the emergence of numerous races differing in virulence [12–15]. Large-scale studies have identified extensive diversity within *P. teres* populations across different geographic regions, including Europe, North America, and Asia [14,16–20]. This high genetic variability underscores the necessity of region-specific phenotypic screening of barley germplasm [18].

Resistance to net blotch in barley can be expressed at different growth stages and is generally classified into race-specific resistance and adult plant resistance. Race-specific resistance is often controlled by major genes and is typically expressed at the seedling stage, whereas adult plant resistance is usually quantitative and influenced by multiple genes and environmental factors [8,14,21,22]. Several studies have identified quantitative trait loci associated with resistance at both seedling and adult plant stages, including loci on chromosome 6H [23–26]. These findings highlight the complexity of resistance mechanisms and the importance of evaluating resistance under both controlled and field conditions. Breeding for resistance remains one of the most effective strategies for managing net blotch. However, the success of breeding programs depends on the identification of resistant germplasm and an understanding of pathogen variability in specific regions. Despite the importance of barley production in Kazakhstan, information on resistance of domestically bred barley germplasm to predominant *P. teres* f. *teres* races under combined greenhouse and field conditions remains limited.

We hypothesized that domestically bred barley accessions differ in their resistance responses to predominant *P. teres* f. *teres* races at different growth stages. Specifically, resistance was assessed at the seedling stage using two predominant pathogen races and at the adult plant stage under field conditions, in order to identify potential sources of resistance for breeding programs in Kazakhstan.

Materials and methods. The plant material comprised barley accessions of domestic origin. The seedling and adult-plant resistance was evaluated in 106 spring barley accessions provided by six different breeding stations in Kazakhstan, namely Kazakh Research Institute of Agriculture and Plant Growing (KRIAPG), Aktobe Agricultural Experimental Station (Aktobe AES), Karabalyk Agricultural Experimental Station (Karabalyk AES), Kazakh Research Institute of Rice Breeding named after I. Zhakhayev (KRIRB), North-West Research and Development Center (NWRDC), Institute of Plant Biology and Biotechnology (IPBB).

Race-specific resistance of barley accessions was evaluated at the seedling stage under greenhouse conditions at the Research Institute for Biological Safety Problems (RIBSP, Gvardeisky, Zhambyl region, Kazakhstan). Barley seeds were sown in 200 mL plastic pots (5–6 seeds per pot) containing a mixture of field, soil, sand and compost (2:1:1, v/v/v). The experiment was conducted with two biological replicates. Seedlings were grown to the two-leaf stage at 20/18 °C (day/night) under a 16 h photoperiod ($180 \mu\text{mol m}^{-2} \text{s}^{-1}$). Seedling resistance was assessed using a modified detached leaf assay based on a previously published protocol [27]. Leaf segments were placed in trays containing 0.004% benzimidazole solution. Two predominant races of *Pyrenophora teres* f. *teres* (race 100 and race 500) were used for inoculation. Conidia were collected by flooding fungal cultures with sterile distilled water and gently scraping the surface with a sterile loop. The spore concentration was adjusted to 5×10^3 conidia mL^{-1} using a Goryaev counting chamber (hemocytometer equivalent). Inoculation was performed by applying 0.2 mL of conidial suspension onto each leaf segment. Tween 20 (Sigma-Aldrich, USA) was added (1 drop per 100 mL) to reduce surface tension. Inoculated samples were incubated under the same environmental conditions as described above.

To assess seedling resistance comprehensively the spring barley collections were inoculated with two races of *Pyrenophora teres* f. *teres* (race 100 and race 500) [11]. Symptom development of net blotch on barley accessions was assessed at 7–9 days post-inoculation with Ptt. Reaction types were classified as resistant (R), moderately resistant (MR), moderately susceptible (MS), susceptible (S), and very susceptible (VS) based on infection response using a 10-point numerical scale [28]. The main criteria for classification as resistant or moderately resistant were the presence of necrotic tissue and size restriction. The occurrence of distinct chlorotic zones that can merge with each other was the criteria for moderately susceptible to susceptible assessment. According to the

scale, accessions demonstrating an infection type (IT) response of ≤ 5 were considered resistant, and >5 were considered susceptible.

Field evaluation of adult plant resistance to net form net blotch (NFNB) was conducted at RIBSP (Gvardeisky, Zhambyl region, Kazakhstan) during the 2021–2022 growing seasons. Cultivars and lines were planted in the experimental field in plots with an area of 0.4 m². Plots contained two rows which were spaced 20 cm apart and 100–200 cm in length, with 50–60 seeds were sown in each row. Arna (spring barley) was seeded between the experimental plots as a susceptible spreader cultivar for the accumulation and spread of infection in the nursery. The phenotypic information provided in this study represents the mean values from two replicates. The infected plant segments were used as inoculum to establish artificial disease pressure. Disease evaluation was carried out three times and conducted first at the early booting stage (41–45 on the Zadoks scale), then during ear emergence (51–59 on the Zadoks scale), and finally during flowering (65–69 on the Zadoks scale) [29]. The disease severity score was assessed according to the 1–100 % scale based on the percentage of the necrotic and chlorotic areas, where ≤ 10 resistant (R), 11–20% moderately resistant (MR), 21–30% moderately susceptible (MS), and 31–100 % - susceptible (S) [30,31]. Disease intensity over a period of time was assessed by calculating the area under the disease progress curve (AUDPC) using the following formula [32],

$$AUDPC = \sum_{i=1}^{n-1} \left(\frac{y_i + y_{i+1}}{2} \right) \times (t_{i+1} - t_i), \quad (1)$$

where y_i is the disease severity percentage at time t_i ; $t_{i+1} - t_i$ is days between two disease percentage scores; n is the total number of observations

The correlation between the disease severity and the agronomic traits of the barley accessions was characterized by the 1000-grain weight (g) and grain yield per m². Plant height (PH) was measured in centimeters from the ground to the tip of the spike of 10–15 plants per plot (GS 90–99). Days to heading (DH) were measured as the number of days from planting to the period when about 50% of the plants had fully emerged spikes in GS 49–50 [29].

The correlation analysis and PCA were performed using GraphPad Prism 9.0.0 (GraphPad Software, San Diego, CA, USA). Variables with $p < 0.05$ were considered statistically significant.

Results and discussion. Evaluation of resistance to two predominant races of *Ptt* (race 100 and race 500) was assessed on 106 spring barley cultivars and lines from breeding stations in Kazakhstan (Table 1).

Table 1 – Seedling-stage infection response of barley lines and cultivars against net blotch races under greenhouse conditions

Origin of bred cultivars and lines	N	Race 100		Race 500		Both Races	
		R	S	R	S	R	S
KRIAPG	19	10	9	3	16	0	5
Aktobe AES	14	8	6	10	4	5	0
Karabalyk AES	43	33	10	17	26	14	7
KRIRB	28	19	9	8	20	7	8
NWRDC	1	1	0	0	1	1	0
IPBB + KRIAPG	1	1	0	0	1	1	0
Total	106	72	34	38	68	28	20

The choice of the *Ptt* races was based on the population analysis conducted in Kazakhstan, where the races 100 and 500 were among the most frequent in studied populations [11]. Seedling disease reaction was assessed in the greenhouse was performed using a Tekauz rating scale, based on lesion morphology and IT response [28]. Infection responses differed significantly between races Phenotypic data revealed significant differences between races (χ^2 test, $p < 0.0001$). The highest IT response was recorded for race 500 in 93/80–4, 3/95–13, 93/80–17 line and “Arna” cultivar.

Results of the seedling inoculation test showed that cultivars “Akzhol” (originated from IPBB and KRIAPG) and “Granal” (originated from NWRDC) exhibited moderately resistant-moderately susceptible (≤ 5) response to both *Ptt* races. Moreover, the same response was observed in five lines from Aktobe AES (154 (F6 4/80), 161 (10/80), 151 (10/83), 178 (44/87), 132 (4/85)), three cultivars (Rikotenze 2006; Tulpar; and Velikan) and eleven lines from Karabalyk AES, seven lines from KRIRB. Among the studied materials, seventy-two genotypes were resistant to race 100, while thirty-four were susceptible. Seedling resistance analysis to race 500 showed that thirty-eight genotypes were resistant and sixty-eight were susceptible. Twenty-eight genotypes showed resistance to both predominant races.

Disease severity for the same accessions, evaluated in the field conditions varied compared with seedling assessments in the greenhouse. The severity of the disease was assessed according to the 1-100 % scale, where ≤ 10 resistant (R), 11-20% moderately resistant (MR), 21-30% moderately susceptible (MS), and 31-100 % - susceptible (S). Mean disease severity values ranged from 0 to 40%. Of 106 studied barley samples (Table 2), the maximum % of disease severity was 40, where 47 lines and cultivars showed resistance (R, 0-10%), 45 were moderately resistant (MR, 11-20 %), 11 demonstrated moderately susceptible (MS, 30%), and 2 showed susceptible symptoms (S, 40%).

Table 2 – Classification of barley accessions according to their field reaction to net blotch

Origin	Immune	Resistant	Moderately resistant	Moderately susceptible	Susceptible
1	2	3	3	5	6
KRIRB	Inkar, Kaisar, 9/06-29K, 9/06-14K, 18/06-8K, 10/06-2K, 10/06-9K, 10/06-13K.	9/06-54K, 2/07-4K	Syr Aruy, Shakhristan, 28/98-3K, 9/06-74K, 13/06-132K, 13/06-177K, 13/06-167K, 13/06-171K, 13/06-153K, 13/06-67K, 13/06-165K, 6/06-8K.	13/06-175K, 13/06-131K, 13/06-124K, 13/06-166K, 10/06-14K.	15/06-5K
Karabalyk AES	Druzhnyi, 33-46-77, 43-12-13, 44-14-13, 47-47-13, 18-50-14, Azov x Orenburgskiy 17	Karabalykskii 115, 28-41-68, 93-306-12, 40-1-13, 16-46-14, Granal inerme x 17-24-79 nutans, Karabalykskii 5 nutans x Azov, Robust//Gloria-Bar/CopalCMB88 A.396-21M-1Y-1M-OY pallid x 43-99-56 nutans, 29220 Gusar medicum x Rannii nutans, 30821 Annabel nutans x Pastbishnyi hypiantchum, Raushan nutans x 30821 Annabel nutans, Ubagan.	Karabalykskii 110, Tulpar, Velikan, 16-29-6, 18-31-14, 22-35-27, 79-245-97, 52-149-12, 64-171-12, 66-175-12, 41-10-13, 42-11-13, 9-27-14, 17-48-14, 23-63-14, Azov x Orenburgskii 17, MSI d.6 x Karabalykskii 5 nutans, 30821 Annabel nutans x Pastbishnyi hypiantchum, 15 d. erectum x Ubagan medicum, Raushan nutans x 30821 Annabel nutans.	Rikotenze 2006, 25906 Camila nutans x Arna nutans	None

1	2	3	4	5	6
Aktobe AES	178 (44/87), 114 (31/83)	195 (49/86), 173 (182/83), 151 (10/ 83), 178 (F3 137/ 80), 123 (4/84), 132 (4/85)	196 (126/83), 194 (171/83), 163 (80/87), 154 (F6 4/80), 207 (156/80)	None	161 (10/80)
KRIAPG	None	93/80-4, 93/80-17, Sever-1, 3/95-13, 3/95-14, 3/95-12	93/80-14, 11/80-1, 3/95-14, 3/95-17, 3/95-19, 93/80-17, 5/98-20, 6/98-21	3/95-13, 93/80- 14, 59/87-30, 3/95-12	
IPBB + KRIAPG	Akzhol	None	None	None	None
NWRDC	None	None	Granal	None	None

To facilitate the interpretation of field resistance, disease severity scores were grouped into four resistance categories according to the corresponding AUDPC ranges (Table 3).

Table 3 – Overall ranges of disease severity scores with the AUDPC values among all the studied barley accessions in the field

Reaction type	Disease Score (%)	AUDPC
Resistant	≤ 10	0-175
Moderately Resistance	11-20	175-280
Moderately Susceptible	21-30	210-385
Susceptible	31-100	420-490

The classification demonstrated a clear relationship between disease severity and AUDPC values. Resistant accessions ($\leq 10\%$ disease severity) were characterized by AUDPC values ranging from 0 to 175, whereas moderately resistant and moderately susceptible accessions exhibited intermediate AUDPC values of 175–280 and 210–385, respectively. Susceptible accessions (31–100% disease severity) showed the highest disease development, with AUDPC values ranging from 420 to 490. These thresholds were subsequently used to classify all evaluated barley accessions according to their field resistance. Pearson's correlation coefficient between AUDPC and disease severity score was positively correlated ($r = 0.885$). The principal component analysis (PCA) was performed with the aim of understanding how disease severity, AUDPC, plant height, flag leaf area, and 1000-grain weight impact net blotch and incorporating these parameters as variables. As can be seen in Figure 1, both PC axes accounted for 69.91 % of the variation with PC1 and PC2 contributing to 38.85% and 31.06 % of variances respectively.

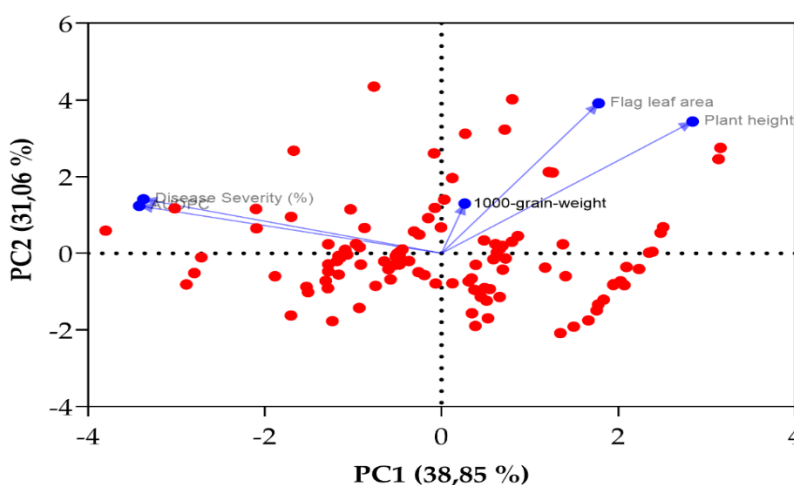


Figure 1 – Principal component analysis biplot depicting the contribution of several factors, including disease severity, AUDPC, plant height, flag leaf area, and 1000-grain-weight scores of barley cultivars and lines

Net blotch, caused by *Pyrenophora teres*, is one of the most economically important foliar diseases of barley and can result in substantial yield losses under favorable conditions [33]. The high genetic and pathogenic variability of *P. teres* populations complicates the development of durable resistance in barley cultivars [34,35]. In this context, the present study evaluated 106 barley accessions originating from Kazakhstan for resistance at both seedling and adult plant stages using two predominant pathogen races (100 and 500) previously identified in the region [11].

In the present study, only 35.8% of the accessions exhibited resistance to race 500 at the seedling stage, compared to 67.9% for race 100, indicating a markedly higher virulence of race 500 under controlled conditions. This finding is consistent with previous reports indicating differences in virulence spectra among *P. teres* populations [16]. The observed variability in infection types across accessions further supports the high genetic diversity of the pathogen, as reported in earlier studies [14,36–38].

Moreover, regional differences in pathogen populations, including those reported in Kazakhstan and neighboring regions, may contribute to the differential responses observed in this study [36,39]. A notable variation in resistance was also observed among accessions from different breeding institutions. Accessions originating from KRIAPG exhibited higher susceptibility, whereas those from Karabalyk AES showed comparatively higher resistance at the seedling stage. The higher frequency of resistant accessions from Karabalyk AES may reflect long-term selection under higher disease pressure in northern Kazakhstan, highlighting the importance of local adaptation in resistance breeding. A comparison between greenhouse and field evaluations revealed discrepancies in resistance expression across growth stages. In general, disease severity was lower under field conditions than in controlled greenhouse assays. This pattern has been reported previously and may be attributed to differences in environmental conditions, inoculum pressure, and host–pathogen interactions [22,40]. While greenhouse assays allow for controlled and reproducible evaluation of race-specific resistance, field conditions provide a more complex environment where quantitative resistance mechanisms may be expressed. This discrepancy was evident in several accessions that were susceptible at the seedling stage but showed low disease severity ($\leq 10\%$) and reduced AUDPC values under field conditions (Table S1), supporting the presence of adult plant resistance. Adult plant resistance (APR) is often quantitative and influenced by environmental factors such as temperature, humidity, and pathogen pressure [40,41]. Additionally, plants in field conditions are exposed to multiple biotic and abiotic factors, which may influence disease development and resistance expression [42].

The interaction between *P. teres* and barley is also influenced by the production of phytotoxins, which play a role in disease development and host susceptibility [43,44]. Previous studies have demonstrated that toxin production may contribute to differences in resistance responses, with resistant cultivars showing reduced sensitivity to pathogen-derived toxins [44–47]. Although toxin-mediated interactions were not evaluated in this study, the observed phenotypic responses suggest that additional mechanisms beyond toxin sensitivity may contribute to resistance [48].

Genetic studies have identified multiple quantitative trait loci (QTLs) associated with resistance to net blotch at both seedling and adult plant stages [22,24,25,33,49,50]. Notably, QTLs located on chromosome 6H have been shown to contribute to resistance at both growth stages [24,25]. Genome-wide association studies have further identified numerous loci associated with resistance, including those with stage-specific and shared effects [49]. The resistance observed in accessions showing consistent performance across growth stages may be associated with previously reported QTLs on chromosome 6H, although this hypothesis requires molecular validation, which may explain the variation observed between seedling and adult plant responses in this study [51].

It is important to acknowledge that the present study was confined to phenotypic evaluation and did not incorporate molecular or genomic analyses. Consequently, the genetic basis underlying the observed resistance in the studied barley accessions remains unresolved. Elucidating these mechanisms will require the integration of advanced approaches, including marker-assisted

selection and genome-wide analyses. Such strategies would enable the identification of resistance-associated loci and provide a deeper understanding of host–pathogen interactions, thereby accelerating the development of resistant cultivars.

To the best of our knowledge, this study represents the first comprehensive assessment of domestic introduced barley accessions in Kazakhstan, evaluating both seedling and adult plant resistance to the net form of net blotch caused by specific races of *Pyrenophora teres f. teres*. Unlike previous studies conducted in Kazakhstan, this work simultaneously evaluated resistance at seedling and adult plant stages using predominant pathogen races, providing an integrated phenotypic framework for resistance screening. The findings provide valuable insights into the resistance profiles of these accessions and highlight their potential as novel sources of resistance.

These genetic resources might be considered as potential candidates for incorporation into national breeding programs focused on improving disease resistance and barley productivity under local agroecological conditions.

Conclusion. This study has examined the seedling and adult plant resistance of barley accessions against the net form of net blotch. Field and greenhouse evaluation were performed on new 106 barley accessions originating from six breeding stations in Kazakhstan. The phenotypic analysis demonstrated high diversity and revealed various infection-type responses of the barley accessions from resistant to susceptible both in the field and in the greenhouse. In the current study, out of the 106 accessions, 72 were resistant to race 100, 38 to race 500, and 28 to both races in the seedling growth stages. Numerous cultivars, namely Akzhol (IPBB and KRIAPG), Granal (NWRDC), Rikotenze 2006, Tulpar, Velikan (Karabalyk AES) and lines originating from these stations including those from Aktobe AES displayed the resistance to both Ptt races (<5). Field studies showed that 47 lines and cultivars were resistant (R, 0–10%), 45 - moderate resistance (MR, 20%), 11 - moderate susceptibility (MS, 30%), and 2 - susceptible symptoms (S, 40%).

This study represents the first integrated phenotypic assessment of seedling and adult plant resistance to predominant *Pyrenophora teres f. teres* races in Kazakh barley germplasm. Future studies integrating molecular and genomic approaches will be essential to elucidate the genetic basis of the observed resistance and accelerate marker-assisted selection.

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References:

- [1] FAOSTAT [Электронный ресурс]. – Режим доступа: <https://www.fao.org/faostat/en/#home>. (Дата обращения: 19.11.2025.)
- [2] **Giraldo, P.**, Benavente E., Manzano-Agugliaro F., Gimenez E. Worldwide research trends on wheat and barley: a bibliometric comparative analysis // *Agronomy*, 2019. – Vol. 9. – Article 352. <https://doi.org/10.3390/agronomy9070352>.
- [3] **O'Boyle, P.D.**, Brooks W.S., Barnett A.H. Genetic characterization of barley net blotch resistance genes // *Plant Disease*, 2011. – Vol. 95. – № 1. – P. 19–23. <https://doi.org/10.1094/PDIS-02-10-0096>.
- [4] **Çağlar, Ö.**, Bulut S., Öztürk A. Determination of yield parameters of barley (*Hordeum vulgare* L.) inoculated with phosphorus-solubilizing and nitrogen-fixing bacteria // *Polish Journal of Environmental Studies*, 2024. – Vol. 33. – № 2. – P. 1033–1042. <https://doi.org/10.15244/pjoes/172036>.
- [5] Kazakhstan's wheat, barley production improves in 2022–23 [Электронный ресурс]. – Режим доступа: <https://www.world-grain.com/articles/18199-kazakhstans-wheat-barley-production-improves-in-2022-23>. (Дата обращения: 19.11.2025.)
- [6] **Murray, G.M.**, Brennan J.P. Estimating disease losses to the Australian barley industry // *Australasian Plant Pathology*, 2010. – Vol. 39. – № 1. – P. 85–96. <https://doi.org/10.1071/AP09064>.

- [7] **Jayasena, K.W.**, Van Burgel A., Tanaka K., Majewski J., Loughman R. Yield reduction in barley in relation to spot-type net blotch // Australasian Plant Pathology, 2007. – Vol. 36. – № 5. – P. 429–433. <https://doi.org/10.1071/AP07046>.
- [8] **Liu, Z.**, Ellwood S.R., Oliver R.P., Friesen T.L. *Pyrenophora teres*: profile of an increasingly damaging barley pathogen // Molecular Plant Pathology, 2011. – Vol. 12. – № 1. – P. 1–19. <https://doi.org/10.1111/j.1364-3703.2010.00649.x>.
- [9] **Tini, F.**, Covarelli L., Ricci G., Balducci E., Orfei M., Beccari G. Management of *Pyrenophora teres* f. *teres*, the causal agent of net form net blotch of barley, in a two-year field experiment in Central Italy // Pathogens, 2022. – Vol. 11. – Article 291. <https://doi.org/10.3390/pathogens11030291>.
- [10] **Рсалиев, А.С.**, Чудинов В.А., Амирханова Н.Т. Устойчивость селекционных материалов ячменя Карабалыкской сельскохозяйственной опытной станции к сетчатой пятнистости и мучнистой росе // Доклады Национальной академии наук Республики Казахстан. – 2016. – № 4 (308). – С. 79–87.
- [11] **Рсалиев, А.С.**, Амирханова Н.Т., Пахратдинова Ж.У. Внутривидовая дифференциация популяций *Pyrenophora teres* в Казахстане и Омской области России // Микология и фитопатология, 2018. – Т. 52. – № 1. – С. 55–65.
- [12] **Arabi, M.I.E.**, Al-Safadi B., Charbaji T. Pathogenic variation among isolates of *Pyrenophora teres*, the causal agent of barley net blotch // Journal of Phytopathology, 2003. – Vol. 151. – № 7–8. – P. 376–382. <https://doi.org/10.1046/j.1439-0434.2003.00734.x>.
- [13] **Cromey, M.G.**, Parkes R.A. Pathogenic variation in *Drechslera teres* in New Zealand // New Zealand Plant Protection, 2003. – Vol. 56. – P. 251–256. <https://doi.org/10.30843/nzpp.2003.56.6020>.
- [14] **Steffenson, B.J.**, Webster R.K. Pathotype diversity of *Pyrenophora teres* f. *teres* on barley // Phytopathology, 1992. – Vol. 82. – № 2. – P. 170–177.
- [15] **Wu, H.-L.**, Steffenson B.J., Li Y., Oleson A.E., Zhong S. Genetic variation for virulence and RFLP markers in *Pyrenophora teres* // Canadian Journal of Plant Pathology, 2003. – Vol. 25. – № 1. – P. 82–90. <https://doi.org/10.1080/07060660309507052>.
- [16] **Анисимова, А.В.**, Новикова Л.Ю., Новакази Ф., Копанке Д., Зубкович А.А., Афанасенко О.С. Полиморфизм по признаку вирулентности и особенности микроэволюции в популяциях возбудителя сетчатой пятнистости ячменя *Pyrenophora teres* f. *teres* // Микология и фитопатология, 2017. – Т. 51. – № 4. – С. 229–240.
- [17] **Lehmensiek, A.**, Bester-van der Merwe A.E., Sutherland M.W., Platz G., Kriel W.M., Potgieter G.F., Prins R. Population structure of South African and Australian *Pyrenophora teres* isolates // Plant Pathology, 2010. – Vol. 59. – № 3. – P. 504–515. <https://doi.org/10.1111/j.1365-3059.2009.02231.x>
- [18] **Peever, T.L.**, Milgroom M.G. Genetic structure of *Pyrenophora teres* populations determined with random amplified polymorphic DNA markers // Canadian Journal of Botany, 1994. – Vol. 72. – № 7. – P. 915–923. <https://doi.org/10.1139/b94-116>.
- [19] **Rau, D.**, Brown A.H.D., Brubaker C.L., Attene G., Balmas V., Saba E., Papa R. Population genetic structure of *Pyrenophora teres* Drechs., the causal agent of net blotch, in Sardinian landraces of barley (*Hordeum vulgare* L.) // Theoretical and Applied Genetics, 2003. – Vol. 106. – № 5. – P. 947–959. <https://doi.org/10.1007/s00122-002-1173-0>.
- [20] **Volkova, G.**, Yakhnik Y. *Pyrenophora teres*: population structure, virulence and aggressiveness in Southern Russia // Saudi Journal of Biological Sciences, 2022. – Vol. 29. – № 10. – Article 103401. <https://doi.org/10.1016/j.sjbs.2022.103401>.
- [21] **Gyawali, S.**, Chao S., Vaish S.S. et al. Seedling- and adult-plant-stage resistance of a world collection of barley genotypes to stripe rust // Journal of Phytopathology, 2018. – Vol. 166. – № 1. – P. 18–27. <https://doi.org/10.1111/jph.12630>.
- [22] **Steffenson, B.J.**, Hayes P.M., Kleinhofs A. Genetics of seedling and adult-plant resistance to net blotch (*Pyrenophora teres* f. *teres*) and spot blotch (*Cochliobolus sativus*) in barley // Theoretical and Applied Genetics, 1996. – Vol. 92. – № 5. – P. 552–558. <https://doi.org/10.1007/BF00224556>.
- [23] **Abu Qamar, M.**, Liu Z.H., Faris J.D. et al. A region of barley chromosome 6H harbors multiple major genes associated with net-type net blotch resistance // Theoretical and Applied Genetics, 2008. – Vol. 117. – № 8. – P. 1261–1270. <https://doi.org/10.1007/s00122-008-0852-2>.
- [24] **Cakir, M.**, Gupta S., Platz G.J. et al. Mapping and validation of the genes for resistance to *Pyrenophora teres* f. *teres* in barley (*Hordeum vulgare* L.) // Australian Journal of Agricultural Research, 2003. – Vol. 54. – № 12. – P. 1369–1377. <https://doi.org/10.1071/AR02226>.
- [25] **Grewal, T.S.**, Rosnagel B.G., Pozniak C.J., Scoles G.J. Mapping quantitative trait loci associated with barley net blotch resistance // Theoretical and Applied Genetics, 2008. – Vol. 116. – № 4. – P. 529–539. <https://doi.org/10.1007/s00122-007-0681-1>.

- [26] **Ho, K.M.**, Tekauz A., Choo T.M., Martin R.A. Genetic studies on net blotch resistance in a barley cross // Canadian Journal of Plant Science, 1996. – Vol. 76. – № 4. – P. 715–719. <https://doi.org/10.4141/cjps96-122>.
- [27] **Afanasenkov, O.S.**, Jalli M., Pinnschmidt H.O. et al. Development of an international standard set of barley differential genotypes for *Pyrenophora teres* f. *teres* // Plant Pathology, 2009. – Vol. 58. – № 4. – P. 665–676 <https://doi.org/10.1111/j.1365-3059.2008.02014.x>.
- [28] **Tekauz, A.** A numerical scale to classify reactions of barley to *Pyrenophora teres* // Canadian Journal of Plant Pathology. – 1985. – Vol. 7. – № 2. – P. 181–183. – DOI: <https://doi.org/10.1080/07060668509501673>.
- [29] **Zadoks, J.C.**, Chang T.T., Konzak C.F. A decimal code for the growth stages of cereals // Weed Research, 1974. – Vol. 14. – № 6. – P. 415–421. <https://doi.org/10.1111/j.1365-3180.1974.tb01084.x>.
- [30] **Kokhmetova, A.**, Sehgal D., Ali S. et al. Genome-wide association study of tan spot resistance in a hexaploid wheat collection from Kazakhstan // Frontiers in Genetics, 2021. – Vol. 11. – Article 581214. <https://doi.org/10.3389/fgene.2020.581214>.
- [31] **Eyal, Z.**, Scharen A.L., Prescott J.M., van Ginkel M. *The Septoria diseases of wheat: concepts and methods of disease management*. – Mexico, D.F.: International Maize and Wheat Improvement Center (CIMMYT), 1987. – 46 p.
- [32] **Simko, I.**, Piepho H.-P. The area under the disease progress stairs: calculation, advantage, and application // Phytopathology, 2012. – Vol. 102. – № 4. – P. 381–389. <https://doi.org/10.1094/PHYTO-07-11-0216>.
- [33] **Ma, Z.**, Lapitan N.L.V., Steffenson B.J. QTL mapping of net blotch resistance genes in a doubled-haploid population of six-rowed barley // Euphytica, 2004. – Vol. 137. – № 3. – P. 291–296. <https://doi.org/10.1023/B:EUPH.0000040474.95653.58>.
- [34] Compendium of barley diseases / ed. by D.E. Mathre. – 2nd ed. – St. Paul, Minnesota: APS Press, 1997. – 90 p.
- [35] **Shipton, W.A.**, Khan T.N., Boyd W.J.R. Net blotch of barley // Review of Plant Pathology, 1973. – Vol. 52. – P. 269–290.
- [36] **Çelik Oğuz, A.**, Karakaya A. Pathotypes of *Pyrenophora teres* on barley in Turkey // Phytopathologia Mediterranea, 2017. – Vol. 56. – № 2. – P. 224–234. https://doi.org/10.14601/Phytopathol_Mediterr-20267.
- [37] **Liu, Z.H.**, Zhong S., Stasko A.K., Edwards M.C., Friesen T.L. Virulence profile and genetic structure of a North Dakota population of *Pyrenophora teres* f. *teres*, the causal agent of net form net blotch of barley // Phytopathology, 2012. – Vol. 102. – № 5. – P. 539–546. <https://doi.org/10.1094/PHYTO-09-11-0243>.
- [38] **Tekauz, A.** Characterization and distribution of pathogenic variation in *Pyrenophora teres* f. *teres* and *P. teres* f. *maculata* from western Canada // Canadian Journal of Plant Pathology, 1990. – Vol. 12. – № 2. – P. 141–148. <https://doi.org/10.1080/07060669009501033>.
- [39] **Serenius, M.**, Mironenko N., Manninen O. Genetic differentiation in *Pyrenophora teres* populations measured with AFLP markers // Mycological Research, 2007. – Vol. 111. – № 2. – P. 213–223. <https://doi.org/10.1016/j.mycres.2006.11.008>.
- [40] **Rothwell, C.T.**, Singh D., van Ogtrop F., Sørensen C.K., Fowler R., Germán S., Park R.F., Dracatos P.M. Rapid phenotyping of adult-plant resistance in barley (*Hordeum vulgare*) to leaf rust under controlled conditions // Plant Breeding, 2019. – Vol. 138. – № 1. – P. 51–61. <https://doi.org/10.1111/pbr.12660>.
- [41] **Riaz, A.**, Periyannan S., Aitken E., Hickey L. A rapid phenotyping method for adult-plant resistance to leaf rust in wheat // Plant Methods, 2016. – Vol. 12. – Article 17. <https://doi.org/10.1186/s13007-016-0116-7>.
- [42] **Velásquez, A.C.**, Castroverde C.D.M., He S.Y. Plant–pathogen warfare under changing climate conditions // Current Biology, 2018. – Vol. 28. – № 10. – P. R619–R634. <https://doi.org/10.1016/j.cub.2018.03.054>.
- [43] **Backes, A.**, Guerriero G., Ait Barka E., Jacquard C. *Pyrenophora teres*: taxonomy, morphology, interaction with barley, and mode of control // Frontiers in Plant Science, 2021. – Vol. 12. – Article 614951. <https://doi.org/10.3389/fpls.2021.614951>.
- [44] **Smedegaard-Petersen, V.** Isolation of two toxins produced by *Pyrenophora teres* and their significance in disease development of net-spot blotch of barley // Physiological Plant Pathology, 1977. – Vol. 10. – № 3. – P. 203–211. [https://doi.org/10.1016/0048-4059\(77\)90027-5](https://doi.org/10.1016/0048-4059(77)90027-5).
- [45] **Mandahar, C.L.**, Garg I.D. Effect of net blotch infection on the physiology of barley:

respiration // Indian Journal of Mycology and Plant Pathology, 1980. – Vol. 10. – P. 12–16.

[46] **Sharma, H.S.S.** Assessment of the reaction of some spring barley cultivars to *Pyrenophora teres* using whole plants, detached leaves and toxin bioassay // Plant Pathology, 1984. – Vol. 33. – № 3. – P. 371–376. <https://doi.org/10.1111/j.1365-3059.1984.tb01332.x>.

[47] **Weiergang, I.**, Jørgensen H.J.L., Møller I.M., Friis P., Smedegaard-Petersen V. Correlation between sensitivity of barley to *Pyrenophora teres* toxins and susceptibility to the fungus // Physiological and Molecular Plant Pathology, 2002. – Vol. 60. – № 3. – P. 121–129. <https://doi.org/10.1006/pmpp.2002.0384>.

[48] **Sarpeleh, A.**, Wallwork H., Tate M.E., Catcheside D.E.A., Able A.J. Initial characterisation of phytotoxic proteins isolated from *Pyrenophora teres* // Physiological and Molecular Plant Pathology, 2008. – Vol. 72. – № 1–3. – P. 73–79. <https://doi.org/10.1016/j.pmpp.2008.05.003>.

[49] **Amezrou, R.**, Verma R.P.S., Chao S., Brueggeman R.S., Belqadi L., Arbaoui M., Rehman S., Gyawali S. Genome-wide association studies of net form of net blotch resistance at seedling and adult plant stages in spring barley collection // Molecular Breeding, 2018. – Vol. 38. – Article 58. <https://doi.org/10.1007/s11032-018-0813-2>.

[50] **Richter, K.**, Schondelmaier J., Jung C. Mapping of quantitative trait loci affecting *Drechslera teres* resistance in barley with molecular markers // Theoretical and Applied Genetics, 1998. – Vol. 97. – № 8. – P. 1225–1234. <https://doi.org/10.1007/s001220051014>.

[51] **Douiyssi, A.**, Rasmusson D.C., Roelfs A.P. Responses of barley cultivars and lines to isolates of *Pyrenophora teres* // Plant Disease, 1998. – Vol. 82. – № 3. – P. 316–321. <https://doi.org/10.1094/PDIS.1998.82.3.316>

References:

[1] FAOSTAT [Elektronnyj resurs]. – Rezhim dostupa: <https://www.fao.org/faostat/en/#home>. (Data obrashhenija: 19.11.2025.)

[2] **Giraldo, P.**, Benavente E., Manzano-Agugliaro F., Gimenez E. Worldwide research trends on wheat and barley: a bibliometric comparative analysis // Agronomy, 2019. – Vol. 9. – Article 352. <https://doi.org/10.3390/agronomy9070352>

[3] **O'Boyle, P.D.**, Brooks W.S., Barnett A.H. Genetic characterization of barley net blotch resistance genes // Plant Disease, 2011. – Vol. 95. – № 1. – P. 19–23. <https://doi.org/10.1094/PDIS-02-10-0096>

[4] **Çağlar, Ö.**, Bulut S., Öztürk A. Determination of yield parameters of barley (*Hordeum vulgare* L.) inoculated with phosphorus-solubilizing and nitrogen-fixing bacteria // Polish Journal of Environmental Studies, 2024. – Vol. 33. – № 2. – P. 1033–1042. <https://doi.org/10.15244/pjoes/172036>

[5] Kazakhstan's wheat, barley production improves in 2022–23 [Elektronnyj resurs]. – Rezhim dostupa: <https://www.world-grain.com/articles/18199-kazakhstans-wheat-barley-production-improves-in-2022-23>. (Data obrashhenija: 19.11.2025).

[6] **Murray, G.M.**, Brennan J.P. Estimating disease losses to the Australian barley industry // Australasian Plant Pathology, 2010. – Vol. 39. – № 1. – P. 85–96. <https://doi.org/10.1071/AP09064>.

[7] **Jayasena, K.W.**, Van Burgel A., Tanaka K., Majewski J., Loughman R. Yield reduction in barley in relation to spot-type net blotch // Australasian Plant Pathology, 2007. – Vol. 36. – № 5. – P. 429–433. <https://doi.org/10.1071/AP07046>

[8] **Liu, Z.**, Ellwood S.R., Oliver R.P., Friesen T.L. *Pyrenophora teres*: profile of an increasingly damaging barley pathogen // Molecular Plant Pathology, 2011. – Vol. 12. – № 1. – P. 1–19. <https://doi.org/10.1111/j.1364-3703.2010.00649.x>

[9] **Tini, F.**, Covarelli L., Ricci G., Balducci E., Orfei M., Beccari G. Management of *Pyrenophora teres* f. *teres*, the causal agent of net form net blotch of barley, in a two-year field experiment in Central Italy // Pathogens, 2022. – Vol. 11. – Article 291. <https://doi.org/10.3390/pathogens11030291>

[10] **Rsaliev, A.S.**, Chudinov V.A., Amirhanova N.T. Ustojchivost' selekcionnyh materialov jachmenja Karabalykskoj sel'skohozjajstvennoj opytnoj stancii k setchatoj pjatnistosti i muchnistoj rose // Doklady Nacional'noj akademii nauk Respubliki Kazahstan 2016. – № 4 (308). – S. 79–87. [in Russian]

[11] **Rsaliev, A.S.**, Amirhanova N.T., Pahratdinova Zh.U. Vnutrividovaja differenciacija populjacij *Pyrenophora teres* v Kazahstane i Omskoj oblasti Rossii // Mikologija i fitopatologija, 2018. – T. 52. – № 1. – S. 55–65. [in Russian]

[12] **Arabi, M.I.E.**, Al-Safadi B., Charbaji T. Pathogenic variation among isolates of *Pyrenophora teres*, the causal agent of barley net blotch // Journal of Phytopathology, 2003. – Vol. 151. – № 7–8. – P.

376–382. <https://doi.org/10.1046/j.1439-0434.2003.00734.x>

[13] **Cromey, M.G.**, Parkes R.A. Pathogenic variation in *Drechslera teres* in New Zealand // New Zealand Plant Protection, 2003. – Vol. 56. – P. 251–256. <https://doi.org/10.30843/nzpp.2003.56.6020>

[14] **Steffenson, B.J.**, Webster R.K. Pathotype diversity of *Pyrenophora teres* f. *teres* on barley // Phytopathology, 1992. – Vol. 82. – № 2. – P. 170–177.

[15] **Wu, H.-L.**, Steffenson B.J., Li Y., Oleson A.E., Zhong S. Genetic variation for virulence and RFLP markers in *Pyrenophora teres* // Canadian Journal of Plant Pathology, 2003. – Vol. 25. – № 1. – P. 82–90. <https://doi.org/10.1080/07060660309507052>

[16] **Anisimova, A.V.**, Novikova L.Ju., Novakazi F., Kopanke D., Zubkovich A.A., Afanasenko O.S. Polimorfizm po priznaku virulentnosti i osobennosti mikroevoljucii v populacijah vzbuditelja setchatoj pjatnistosti jachmenja *Pyrenophora teres* f. *teres* // Mikologija i fitopatologija, 2017. – T. 51. – № 4. – S. 229–240. [in Russian]

[17] **Lehmensiek, A.**, Bester-van der Merwe A.E., Sutherland M.W., Platz G., Kriel W.M., Potgieter G.F., Prins R. Population structure of South African and Australian *Pyrenophora teres* isolates // Plant Pathology, 2010. – Vol. 59. – № 3. – P. 504–515. <https://doi.org/10.1111/j.1365-3059.2009.02231.x>

[18] **Peever, T.L.**, Milgroom M.G. Genetic structure of *Pyrenophora teres* populations determined with random amplified polymorphic DNA markers // Canadian Journal of Botany, 1994. – Vol. 72. – № 7. – P. 915–923. <https://doi.org/10.1139/b94-116>

[19] **Rau, D.**, Brown A.H.D., Brubaker C.L., Attene G., Balmas V., Saba E., Papa R. Population genetic structure of *Pyrenophora teres* Drechs., the causal agent of net blotch, in Sardinian landraces of barley (*Hordeum vulgare* L.) // Theoretical and Applied Genetics, 2003. – Vol. 106. – № 5. – P. 947–959. <https://doi.org/10.1007/s00122-002-1173-0>

[20] **Volkova, G.**, Yakhnik Y. *Pyrenophora teres*: population structure, virulence and aggressiveness in Southern Russia // Saudi Journal of Biological Sciences, 2022. – Vol. 29. – № 10. – Article 103401. <https://doi.org/10.1016/j.sjbs.2022.103401>

[21] **Gyawali, S.**, Chao S., Vaish S.S. et al. Seedling- and adult-plant-stage resistance of a world collection of barley genotypes to stripe rust // Journal of Phytopathology, 2018. – Vol. 166. – № 1. – P. 18–27. <https://doi.org/10.1111/jph.12630>

[22] **Steffenson, B.J.**, Hayes P.M., Kleinhofs A. Genetics of seedling and adult-plant resistance to net blotch (*Pyrenophora teres* f. *teres*) and spot blotch (*Cochliobolus sativus*) in barley // Theoretical and Applied Genetics, 1996. – Vol. 92. – № 5. – P. 552–558. <https://doi.org/10.1007/BF00224556>

[23] **Abu Qamar, M.**, Liu Z.H., Faris J.D. et al. A region of barley chromosome 6H harbors multiple major genes associated with net-type net blotch resistance // Theoretical and Applied Genetics, 2008. – Vol. 117. – № 8. – P. 1261–1270. <https://doi.org/10.1007/s00122-008-0852-2>

[24] **Cakir, M.**, Gupta S., Platz G.J. et al. Mapping and validation of the genes for resistance to *Pyrenophora teres* f. *teres* in barley (*Hordeum vulgare* L.) // Australian Journal of Agricultural Research, 2003. – Vol. 54. – № 12. – P. 1369–1377. <https://doi.org/10.1071/AR02226>

[25] **Grewal, T.S.**, Rosnagel B.G., Pozniak C.J., Scoles G.J. Mapping quantitative trait loci associated with barley net blotch resistance // Theoretical and Applied Genetics, 2008. – Vol. 116. – № 4. – P. 529–539. <https://doi.org/10.1007/s00122-007-0681-1>

[26] **Ho, K.M.**, Tekauz A., Choo T.M., Martin R.A. Genetic studies on net blotch resistance in a barley cross // Canadian Journal of Plant Science, 1996. – Vol. 76. – № 4. – P. 715–719. <https://doi.org/10.4141/cjps96-122>

[27] **Afanasenko, O.S.**, Jalli M., Pinnschmidt H.O. et al. Development of an international standard set of barley differential genotypes for *Pyrenophora teres* f. *teres* // Plant Pathology, 2009. – Vol. 58. – № 4. – P. 665–676 <https://doi.org/10.1111/j.1365-3059.2008.02014.x>

[28] **Tekauz, A.** A numerical scale to classify reactions of barley to *Pyrenophora teres* // Canadian Journal of Plant Pathology. – 1985. – Vol. 7. – № 2. – P. 181–183. – DOI: <https://doi.org/10.1080/07060668509501673>

[29] **Zadoks, J.C.**, Chang T.T., Konzak C.F. A decimal code for the growth stages of cereals // Weed Research, 1974. – Vol. 14. – № 6. – P. 415–421. <https://doi.org/10.1111/j.1365-3180.1974.tb01084.x>

[30] **Kokhmetova, A.**, Sehgal D., Ali S. et al. Genome-wide association study of tan spot resistance in a hexaploid wheat collection from Kazakhstan // Frontiers in Genetics, 2021. – Vol. 11. – Article 581214. <https://doi.org/10.3389/fgene.2020.581214>

[31] **Eyal, Z.**, Scharen A.L., Prescott J.M., van Ginkel M. The Septoria diseases of wheat: concepts and methods of disease management. – Mexico, D.F.: International Maize and Wheat Improvement Center (CIMMYT), 1987. – 46 p.

- [32] **Simko, I.**, Piepho H.-P. The area under the disease progress stairs: calculation, advantage, and application // *Phytopathology*, 2012. – Vol. 102. – № 4. – P. 381–389. <https://doi.org/10.1094/PHYTO-07-11-0216>
- [33] **Ma, Z.**, Lapitan N.L.V., Steffenson B.J. QTL mapping of net blotch resistance genes in a doubled-haploid population of six-rowed barley // *Euphytica*, 2004. – Vol. 137. – № 3. – P. 291–296. <https://doi.org/10.1023/B:EUPH.0000040474.95653.58>.
- [34] Compendium of barley diseases / ed. by D.E. Mathre. – 2nd ed. – St. Paul, Minnesota: APS Press, 1997. – 90 p.
- [35] **Shipton, W.A.**, Khan T.N., Boyd W.J.R. Net blotch of barley // *Review of Plant Pathology*, 1973. – Vol. 52. – P. 269–290.
- [36] **Çelik Oğuz, A.**, Karakaya A. Pathotypes of *Pyrenophora teres* on barley in Turkey // *Phytopathologia Mediterranea*, 2017. – Vol. 56. – № 2. – P. 224–234. https://doi.org/10.14601/Phytopathol_Mediterr-20267.
- [37] **Liu, Z.H.**, Zhong S., Stasko A.K., Edwards M.C., Friesen T.L. Virulence profile and genetic structure of a North Dakota population of *Pyrenophora teres* f. *teres*, the causal agent of net form net blotch of barley // *Phytopathology*, 2012. – Vol. 102. – № 5. – P. 539–546. <https://doi.org/10.1094/PHYTO-09-11-0243>
- [38] **Tekauz, A.** Characterization and distribution of pathogenic variation in *Pyrenophora teres* f. *teres* and *P. teres* f. *maculata* from western Canada // *Canadian Journal of Plant Pathology*, 1990. – Vol. 12. – № 2. – P. 141–148. <https://doi.org/10.1080/07060669009501033>
- [39] **Serenius, M.**, Mironenko N., Manninen O. Genetic differentiation in *Pyrenophora teres* populations measured with AFLP markers // *Mycological Research*, 2007. – Vol. 111. – № 2. – P. 213–223. <https://doi.org/10.1016/j.mycres.2006.11.008>
- [40] **Rothwell, C.T.**, Singh D., van Ogtrop F., Sørensen C.K., Fowler R., Germán S., Park R.F., Dracatos P.M. Rapid phenotyping of adult-plant resistance in barley (*Hordeum vulgare*) to leaf rust under controlled conditions // *Plant Breeding*, 2019. – Vol. 138. – № 1. – P. 51–61. <https://doi.org/10.1111/pbr.12660>
- [41] **Riaz, A.**, Periyannan S., Aitken E., Hickey L. A rapid phenotyping method for adult-plant resistance to leaf rust in wheat // *Plant Methods*, 2016. – Vol. 12. – Article 17. <https://doi.org/10.1186/s13007-016-0116-7>
- [42] **Velásquez, A.C.**, Castroverde C.D.M., He S.Y. Plant–pathogen warfare under changing climate conditions // *Current Biology*, 2018. – Vol. 28. – № 10. – P. R619–R634. <https://doi.org/10.1016/j.cub.2018.03.054>
- [43] **Backes, A.**, Guerriero G., Ait Barka E., Jacquard C. *Pyrenophora teres*: taxonomy, morphology, interaction with barley, and mode of control // *Frontiers in Plant Science*, 2021. – Vol. 12. – Article 614951. <https://doi.org/10.3389/fpls.2021.614951>
- [44] **Smedegaard-Petersen, V.** Isolation of two toxins produced by *Pyrenophora teres* and their significance in disease development of net-spot blotch of barley // *Physiological Plant Pathology*, 1977. – Vol. 10. – № 3. – P. 203–211. [https://doi.org/10.1016/0048-4059\(77\)90027-5](https://doi.org/10.1016/0048-4059(77)90027-5)
- [45] **Mandahar, C.L.**, Garg I.D. Effect of net blotch infection on the physiology of barley: respiration // *Indian Journal of Mycology and Plant Pathology*, 1980. – Vol. 10. – P. 12–16.
- [46] **Sharma, H.S.S.** Assessment of the reaction of some spring barley cultivars to *Pyrenophora teres* using whole plants, detached leaves and toxin bioassay // *Plant Pathology*, 1984. – Vol. 33. – № 3. – P. 371–376. <https://doi.org/10.1111/j.1365-3059.1984.tb01332.x>
- [47] **Weiergang, I.**, Jørgensen H.J.L., Møller I.M., Friis P., Smedegaard-Petersen V. Correlation between sensitivity of barley to *Pyrenophora teres* toxins and susceptibility to the fungus // *Physiological and Molecular Plant Pathology*, 2002. – Vol. 60. – № 3. – P. 121–129. <https://doi.org/10.1006/pmpp.2002.0384>
- [48] **Sarpeleh, A.**, Wallwork H., Tate M.E., Catcheside D.E.A., Able A.J. Initial characterisation of phytotoxic proteins isolated from *Pyrenophora teres* // *Physiological and Molecular Plant Pathology*, 2008. – Vol. 72. – № 1–3. – P. 73–79. <https://doi.org/10.1016/j.pmpp.2008.05.003>
- [49] **Amezrou, R.**, Verma R.P.S., Chao S., Brueggeman R.S., Belqadi L., Arbaoui M., Rehman S., Gyawali S. Genome-wide association studies of net form of net blotch resistance at seedling and adult plant stages in spring barley collection // *Molecular Breeding*, 2018. – Vol. 38. – Article 58. <https://doi.org/10.1007/s11032-018-0813-2>
- [50] **Richter, K.**, Schondelmaier J., Jung C. Mapping of quantitative trait loci affecting Drechslera *teres* resistance in barley with molecular markers // *Theoretical and Applied Genetics*, 1998. – Vol. 97. – № 8. – P. 1225–1234. <https://doi.org/10.1007/s001220051014>

[51] Douiyssi, A., Rasmusson D.C., Roelfs A.P. Responses of barley cultivars and lines to isolates of *Pyrenophora teres* // Plant Disease, 1998. – Vol. 82. – № 3. – P. 316–321. <https://doi.org/10.1094/PDIS.1998.82.3.316>

ҚАЗАҚСТАНДАҒЫ АРПА ГЕНЕТИКАЛЫҚ ҚОРЫНЫҢ *PYRENOPHORA TERES* F. *TERES* ҚОЗДЫРҒЫШЫ ТУДЫРАТЫН ТОРЛЫ ДАҚ АУРУЫНА ТӨЗІМДІЛІГІН БАҒАЛАУ

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Аңдатпа. Арпаның торлы дақ ауруы (*Pyrenophora teres* f. *teres*) әлемнің көптеген аймақтарында, соның ішінде Қазақстанда да, арпа өнімділігін төмендететін аса қауіпті аурулардың бірі болып саналады. Алайда отандық селекциялық материалдардың осы патогенге төзімділігі жөніндегі мәліметтер жеткіліксіз. Зерттеудің мақсаты – Қазақстанның әртүрлі селекциялық мекемелерінен алынған 106 жаздық арпа үлгісінің *P. teres* f. *teres* қоздырғышына көктеу және ересек өсімдік кезеңдеріндегі төзімділігін кешенді бағалау. Көктеу кезеңіндегі төзімділік жылыжай жағдайында патогеннің басым 100 және 500 расаларын пайдалану арқылы анықталды. Ересек өсімдіктердің төзімділігі табиғи және жасанды инфекциялық аяда аурудың даму дәрежесі мен аурудың даму қисығы астындағы аудан (АДҚАА) көрсеткіштері бойынша бағаланды. Зерттеу нәтижелері 500 расаның 100 расаға қарағанда жоғары вируленттілікке ие екенін және оған төзімді үлгілер санының аз болғанын көрсетті. Сонымен қатар, аурудың даму дәрежесі мен АДҚАА арасында оң корреляция ($r = 0,885$) анықталды. Көктеу және ересек өсімдік кезеңдеріндегі төзімділік реакцияларының айырмашылығы расаға тән және сандық төзімділік механизмдерінің қатар әрекет ететіндігін көрсетті. Алынған нәтижелер Қазақстан селекциясында пайдаланылатын арпа генетикалық қорын *P. teres* f. *teres* қоздырғышының басым расаларына төзімділігі бойынша бағалауға мүмкіндік беріп, селекция бағдарламаларында құнды төзімділік көздерін іріктеу үшін ғылыми негіз қалыптастырады.

Тірек сөздер: арпа, торлы дақ ауруы, ауруға төзімділік, генетикалық қорды скринингтеу, расаға тән төзімділік, далалық бағалау.

КОМПЛЕКСНАЯ ОЦЕНКА УСТОЙЧИВОСТИ ГЕНОФОНДА ЯЧМЕНЯ К СЕТЧАТОЙ ПЯТНИСТОСТИ, ВЫЗЫВАЕМОЙ *PYRENOPHORA TERES* F. *TERES*, В КАЗАХСТАНЕ

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Аннотация. Сетчатая пятнистость ячменя, вызываемая *Pyrenophora teres* f. *teres*, является одной из наиболее распространенных и экономически значимых болезней культуры, приводящей к существенным потерям урожайности во многих странах мира, включая Казахстан. Несмотря на важность проблемы, сведения об источниках устойчивости отечественного селекционного материала к данному патогену остаются ограниченными. Целью настоящего исследования являлась комплексная оценка устойчивости 106 образцов ярового ячменя различных селекционных программ Казахстана к *P. teres* f. *teres* на стадиях проростков и взрослых растений. Оценка устойчивости проростков проводили в условиях теплицы с использованием двух преобладающих рас патогена (100 и 500), тогда как устойчивость взрослых растений изучали в полевых условиях при искусственном инфекционном фоне с использованием показателей степени развития болезни и площади под кривой развития болезни (ПКРБ). Установлено, что раса 500 обладала более высокой вирулентностью по сравнению с расой 100, что сопровождалось снижением числа устойчивых образцов на стадии проростков. Выявлена положительная корреляция между степенью развития болезни и значениями ПКРБ ($r = 0,885$). Различия в характере проявления устойчивости на стадиях проростков и взрослых растений свидетельствуют о сочетании расоспецифических и количественных механизмов устойчивости. Полученные результаты представляют собой первую комплексную фенотипическую оценку устойчивости казахстанского генофонда ярового ячменя к преобладающим расам *P. teres* f. *teres* и могут служить основой для отбора перспективных доноров устойчивости в селекционных программах.

Ключевые слова: ячмень, сетчатая пятнистость, устойчивость к болезням, скрининг генофонда, расоспецифическая устойчивость, полевая оценка.