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PECULIARITIES OF THE SUNFLOWER BREEDING FOR RESISTANCE TO BROOMRAPE (OROBANCHE CUMANA WALLR.)

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Since the beginning of the 20th century, the breeding for resistance to a parasitic plant, the broomrape, has been among the mainstreams of the world sunflower breeding. This scientific work has certain peculiarities due to biological features of the broomrape and its interactions with the host plant. The scientists' attention is focused on studying the genetic diversity and race composition of parasite populations; identifying and marking sunflower genes of resistance to the broomrape; evaluating effects of environmental conditions on the virulence of broomrape; elucidating 'the host plant–broomrape' interactions; detecting broomrape lesions during early stages of sunflower growth.

Keywords: *sunflower, breeding, resistance, broomrape, virulence, races, genes*

Introduction. The sunflower is an agricultural crop that is very picky about growing conditions' its yield is significantly affected by current climatic changes [1, 2], pests, diseases, weeds, and a parasitic plant, the broomrape (*Orobanche cumana* Wallr.). The latest progressive crop care measures do not give the expected results in the case of imperfect seed material from outdated hybrids. Therefore, the breeding of modern sunflower hybrids is aimed at combining valuable economic characteristics with resistance to abiotic and biotic factors, in particular to the broomrape [3].

Literature Review and Problem Articulation. The sunflower broomrape is a parasitic plant with a growing distribution area. There are many measures to control the broomrape: physical, chemical and biological methods, as well as certain requirements of cultivation technologies [4]. If farmers use the Clearfield®Plus technology to control the broomrape, they need imidazolinone herbicide-resistant hybrids [5, 6, 7]. However, the constant use of such herbicides has negative consequences: aftereffects on subsequent crops in crop rotation, ecological problems [8], herbicide resistance of target weeds [9]. The genetic resistance of sunflowers to the broomrape remains one of the main ways of controlling the spread of the parasite.

Currently, we are observing an aggravation of the broomrape problem due to an increase in the sunflower cultivation area [10]. The breeding for resistance to the broomrape is continuous because of the parasite evolution and emergence of more virulent races. The breeding constantly gives results – broomrape-resistant hybrids. The parasite evolves and overcomes achievements of breeders, who are forced to explore new levels of interactions between the parasite and the host plant. The race formation, various manifestations of the interactions between the domestic plant and the broomrape, complexity of genetic control of resistance to the latest virulent races - all these phenomena determine the peculiarities of the breeding for resistance to the broomrape.

Purpose and Objectives. Our purpose was to find available information on the sunflower breeding for resistance to the broomrape. To achieve this purpose, we solved following tasks: to review publications covering the history and current state of research into the subject; find out the specifics of such studies; and to highlight the main unresolved issues for the organization of further work.

Materials and Methods. Publications of Ukrainian and foreign scientists became the material for the study: articles in journals and conference abstracts.

Results and Discussion. The broomrape family (Orobanchaceae) consists of highly specialized parasitic angiosperm plants that switched to heterotrophic nutrition and metabolism, using representatives of other plant groups, and lost their own photosynthesis apparatus. The broomrape has no roots. Instead of them, there are specialized structures – haustoria, which absorb water and nutrients from the roots of host plants [11].

Changes in the broomrape race composition. Experiments and breeding of sunflowers for resistance to the broomrape were started in 1909-1913 by V.S. Pustovoyt in Krasnodar, Ye.M. Plachek in Saratov and V.B. Yenken in Kharkiv. At that time, there was only one – the first – broomrape race A. In 1912-1927, Kruglyk 7-15-163, Saratovskyi 169, Kruglyk 631, Kharkivska Zelenka and Kruglyk A-41 were created; these varieties showed high resistance to the broomrape (98-99%) [12]. Nevertheless, in 1925-1928, reports started coming from some southern regions that the varieties, which were considered resistant to the parasite, were affected [13-18]. It was concluded that another broomrape biotype, with higher virulence, had appeared. The new biotype of the parasite was designated by the letter Б (Cyrillic) and was called the "evil broomrape."

Later, it turned out that there were several races A and Б.V.S. Pustovoit noted: "The broomrape races B, depending on distribution areas, have different virulence, or more correctly, the race composition of what is united by the concept of broomrape Б, is not identical" [14]. Later, the same conclusion was drawn by well-known researchers I.G. Beylin [19, 20], A.M. Roshchyn [15] and L.A. Zhdanov [21, 22].

Features of resistant sunflower plants were also investigated. In particular, it was established that resistance to the broomrape could be visually detected due to characteristic thickening of roots, in the middle of which there were small dead broomrape shoots [23].

Before 1934, varieties that were resistant to broomrape race Б were created: Zhdanovskyi 8281, Zhdanovskyi 6432, Veydelevskyi 61, Veydelevskyi 62, Armavirskyi 762, and Armavirskyi 768. Subsequently, breeders created varieties that were better in resistance to the broomrape, oil content in seeds and other valuable economic characteristics. The yields of broomrape-resistant varieties upon strong contamination of the soil with race Б seeds was 2- –5-fold compared to the yields of susceptible varieties [24].

In 1963, all race Б-resistant varieties at Kaushany plots in Moldova were found to be affected by the broomrape [25]. In 1964–1966, a similar situation occurred in southwestern Romania [26]. This indicated the emergence of a new "Moldavian" virulent race of the broomrape [27]. To obtain new breeding material, which was supposed to be resistant to more aggressive broomrape races, G.V. Pustovoyt used interspecies hybridization. The obtained accessions had group immunity to such diseases and pests as downy mildew, broomrape, rust, Verticillium wilt and leaf mottle, leaf curling plum aphid, and sunflower moth [28–30]. In the late 1980s at the All-Union Scientific-Research Institute of Oil Crops, V.V. Tolmachyov analyzed the broomrape race composition [31] and concluded about the predominance of the Moldavian biotype, which was denoted by the Latin letter S. In Romania, as of 1980, A.V. Vranceanu et al. discovered and identified five broomrape races (A–E), resistance to which was determined by five dominant resistance genes (Or_1–Or_5) [32]. As race F was discovered in Spain, resistant genotypes with the Or6 gene, two recessive genes (or6 and or7) [33] or two partly dominant genes [34] were found. The new broomrape biotypes, which affected race F-resistant sunflowers, were designated as G and H [35]. In Spain, as early as the 1990s, resistant hybrids were affected by races D, E, and F, and in 2005, a new and more virulent race G appeared [36, 37].

During the last 20 years, the emergence of new broomrape races was observed in countries where this oil crop is grown in violated crop rotations. In Ukraine, highly virulent races were found in Odeska, Zaporizhska, Kharkivska, Donetska, and Dnipropetrovska Oblasts [38–40].

Having evaluated the broomrape occurrence challenge at the global level, Kaya Y. stated that in addition to the search for resistance genes, changes in the anatomy of broomrape-affected sunflower plants, their biochemical parameters as well as aspects of the parasite biology, such as reproductive systems and genetics of virulence, should be investigated [41].

Dr. Škorić et al. studied the dynamics of broomrape populations, focusing attention on certain dilemmas regarding the nomenclature of new races [42]. In 2014–2017, about 400 genotypes with different resistance to the broomrape were tested in 10 locations, and only one resistant genotype was selected. In different regions, new broomrape populations that could not be controlled by genes of resistance to race H were detected.

In 2018, F.I. Gorbachenko et al. assessed the possibility of deriving new sunflower genotypes that would be resistant to new broomrape populations [43]. Genetic resistance to races A, Б, C, D, E, and F was proven, and the lack of absolute certainty regarding resistance to new races G and H was emphasized. In 2014, Kaya Y. announced a two-fold acceleration of the appearance of new races [38].

In China, the broomrape was detected for the first time by a farmer in Heilongjiang (a province in northeast China) in 1959 [44]. The first report on the identification of broomrape races dates back to 1996 [45]. B.C. Dong, H.L. Sha used five sunflower lines – differentiators of broomrape races, which had been delivered from Spain to identify the race composition of broomrape specimens collected in three locations of Jilin (a province in northeastern China). Race A was identified in three specimens. In 2015, D.N. Ma, X.Z. Wan used the same lines - differentiators to determine the race composition of broomrape populations that were collected from different regions of China [46]. Races B, D, and F were identified in Inner Mongolia (northern China); races E and F – in Xinjiang (northwest China); A, B, E, and F – in Gansu (a province in the North of Central China); A, C, D, and E – in Jilin; A and E – in Heilongjiang. In 2019, Lu et al. used lines – differentiators from Romania and determined the race composition of broomrape populations collected in ten locations Xinjiang and Inner Mongolia [47]. Races D, E, F, and G were identified in the collected broomrape specimens. The discovery of two broomrape accessions that overcame the differentiator resistance to race G became the most impressive result. It should be noted that Inner Mongolia is the largest producer of the sunflower in China, with a total area sown with sunflower of about 400,000 hectares, which is 40.2% of the total area of this crop in China [48]. In 2020, B. Shi, J. Zhao highlighted progress in studies of the broomrape in China [49].

S. Clapco focused her research on evaluating the virulence and aggressiveness of different populations of the broomrape from countries such as China, Turkey, Bulgaria, Serbia, Spain, Ukraine, Romania, and Moldova [50]. The virulence of broomrape populations was evaluated in lines and commercial hybrids – differentiators of broomrape races with different resistance genes, including one genotype susceptible to all races, and four resistant genotypes (LC1003A, resistant to race E (Romania); LC1093A, resistant to race F (Romania); H_1E, resistant to race G (Romania); and H_2Lg, resistant to race H (Limagrain)). Populations were from Turkey, Romania, and Ukraine, one population from China (Inner Mongolia) and two populations from Moldova turned out to be the most virulent ones, affecting all sunflower genotypes, except for hybrid H_2Lg.

Therefore, studies of scientists from different countries regarding the evolvement of new physiological races of the broomrape demonstrate the annually growing threat from the parasite, the need for routine monitoring of broomrape populations and further investigations in this direction.

Genetic studies. Marking resistance genes of domestic plants and determining the molecular polymorphism of both host and parasitic plants are important problems of genetics, solving of which is aimed at the improvement of sunflowers in terms of resistance to the broomrape. By now, several genes responsible for resistance to the broomrape have been identified, and methods of their marking have been developed [51–53].

Studies in the genetics of resistance to *O. cumana* are limited by few relevant molecular markers. R. Pineda-Martos et al. developed a set of 79 SSR markers [54] that detect reproducible, high-quality amplicons that were polymorphic among 18 *O. Cumana* populations. In molecular studies, linkage analysis with a molecular marker is used to localize resistance genes. Molecular genetic maps of linkage groups with the Or7 resistance gene to race G were constructed [55, 56].

Genetic studies of the broomrape are mainly focused on the structure and genetic diversity of the parasite populations [57–63]. There were assumptions about evolutionary mechanisms of race formation, for example, mutation of one gene in local populations [58], genetic recombination of avirulence genes [59]. In particular, R. Pineda-Martos et al. [58] studied the genetic diversity of 50 broomrape populations from different regions of Spain, using 15 microsatellite markers, and revealed two remote gene pools of the parasite, within which the population variability was very low; on this basis, the conclusion about the emergence of new races as a result of mutations from the same genetic background was drawn.

Genetic linkage maps are important for studying the structure and organization of plant genomes. They are valuable resources in studies of parasitic plants to locate genes that control traits such as avirulence or host specificity. The objective of Á. Calderón-González et al. [64] was to construct genetic linkage maps using SSR and SNP markers and to map the Pg locus, which is involved in the pigmentation of broomrape plants. M.I. Rodríguez-Ojeda et al. used broomrape hybrids from crossing EK-A1 and EK-12 lines [65]. Line EK-A1 lacks pigments, resulting in yellow stems and white corollas, while line EK-12 has wild-type pigmentation, with bluish-violet stems and blue or pale-violet corollas. It was established that the pigmentation was partially controlled by dominant alleles at the Pg locus. SNP markers were used for genotyping broomrape lines EK-A1, EK-12, OS-94, EK-23, and SP [66, 67].

In 2020, Duca M. et al. analyzed the genetic diversity of the broomrape, using ISSR markers [68]. They used a collection consisting of 39 broomrape populations, seeds of which were harvested from three different geographical regions of the Republic of Moldova. These populations belong to different races and show remarkable genetic diversity [69, 70]. Fourteen ISSR primers were used, including those reported by Benharat et al. [71]. The study of the genetic polymorphism in broomrape populations allowed grouping them into different clusters according to geographical origins (south, north, center of the Republic of Moldova). In most cases, there was a clear distribution trend according to the geographical regions. This result is consistent with other scientists findings' [72, 73] based on other molecular markers.

Thus, the genes for resistance to the broomrape have been identified and methods of their marking have been developed; this ensures success in improving existing and developing new progressive approaches in the breeding for resistance to the broomrape. The issues of using inheritance patterns of sunflower resistance to new, virulent, common in Ukraine, broomrape races in the F_1 generation, which is important for the creation of commercial hybrids, have not been covered in the literature. Relationships between resistance to new, virulent, widespread in Ukraine races of the broomrape and valuable economic traits in F_1 hybrids also should be studies.

Influence of environmental conditions on the broomrape virulence. M. Duca et al. described the effects of environmental conditions on the virulence and spread of the broomrape in the Republic of Moldova [74]. The scientists collected 40 broomrape populations from different regions of the country, concurrently sampling soil and indicating the geographic coordinates of the sampling point. The daily temperatures at the soil surface and air humidity from May to July were analyzed. The broomrape populations collected in the central part of Moldova were less virulent and mainly belonged to race E or less virulent races (about 65% of the populations). At the same time, the populations from southern and northern regions were characterized by increased virulence; more than 60% of the populations were identified as races G and H [69]. More intensive broomrape-induced damage in the southern and central parts of the Republic of Moldova may be due to increased temperature in these regions compared to the northern parts.

For another representatives of the Orobanchaceae family (Phelipanche sp.), it was established that its spread on tobacco (*Nicotiana tabacum* L.) plants was facilitated by high content of humus and pH from weakly acidic to neutral, but high concentrations of potassium negatively affected Phelipanche sp. Spread [75].

Aggressiveness of broomrapes significantly depends on weather and climate [76, 77]; therefore, an increase in temperature and lack of precipitation may lead to their spread over large areas [78, 79, 80]. Taking into account the recent climatic changes, specifically temperature rise and consequences of this global process, one can predict an increase in the intensity of damage by the parasite, which prompts breeders to combine resistance to adverse abiotic factors and resistance to the broomrape.

Mechanisms of resistance to the broomrape. Resistant hybrid growing is the most effective method of fighting against the broomrape. In most cases, genetic resistance to the broomrape is vertical and controlled by the main dominant Or genes [81]. L. Velasco et al. reported in detail that resistance to race G, which had been transferred to domestic sunflowers from the wild species *Helianthus debilis* subsp. *tardiforus*, was determined by the single dominant Or_{Deb2} gene [82]. At the same time, there are studies showing that resistance to race G was determined by one recessive gene [83, 84].

M. Fernández Aparicio et al. provided genetic and physiological characteristics of resistance to highly virulent broomrape races, which is determined by the Or_{Deb2} gene [85]. In their experiment, they used line DEB2, which carries the resistance gene (Or_{Deb2}). The main Or_{Deb2} gene determines a new physiological response in sunflower that blocks broomrapes. This gene confers resistance to race G from Turkey, Spain, and Eastern Europe [86].

To develop long-term protection strategies, it is important to understand the genetic principles of host-parasite interactions. Biological features of the parasite require pre-cultivation at certain temperatures and humidity as well as stimulation with nutrients from sunflower roots for the germination of broomrape seeds [87].

F.L. He et al. harvested root exudates from sunflower seedling grown by hydroponic method to analyze and identify root exudate components [88]. They revealed that some chemicals, in particular dehydrochloride, could cause the germination of broomrape seeds. When the dehydrochloride concentration around the rhizosphere of the host plant roots reached a certain level and the environmental conditions, such as temperature and soil moisture, were suitable, broomrape seeds germinated during all stages of sunflower growth.

Molecular mechanisms of the ‘broomrape–domestic plant’ interactions were described by Y. Zhang [89]. Plants were found to be able to alter related physiological and biochemical metabolic pathways and regulate gene expression during broomrape-induced stress.

Therefore, the studies demonstrated the specificity of control of resistance to the broomrape, which is conferred by genetic factors. This confirms that genetic methods are the best ones to fight against the broomrape.

Methods of evaluation for resistance to the broomrape. Breeders constantly improve methods for assessing resistance. Scientists strive to adapt the phytotron test [90] to modern equipment, developing certain methodological subtleties [91]. In addition, new methods of evaluation are developed: histological [92] and molecular genetic [93] assessments.

In their experiments, Ortiz-Bustos C.M. et al. investigated blue-green fluorescence (BGF) of sunflower leaves for early detection of broomrape lesions [94]. They analyzed leaf fluorescence readings during early growth phases of healthy plants to determine appropriate areas and times for BGF imaging, to evaluate the use of BGF imaging as an indicator of broomrape infestation during initial subterranean development of the parasite, to compare BGF information with leaf pigment concentrations, and to asses the impact of subterranean broomrape infestation during the early stages of sunflower growth. They proved that, using BGF, it was possible not only to detect the beginning of broomrape-induced stress to domestic plants, but also to monitor its development over time, which will ensure rapid phenotyping of sunflower lines.

A. Le Ru et al. worked on image analysis for automatic phenotyping of broomrape nodules on sunflower roots [95]. Sunflower seedlings that had been inoculated with the broomrape were grown in a rhizotron consisting of a transparent plexiglass box with a layer of rock wool and fiberglass paper wetted with nutrient solution. Resistance of seedlings can be characterized at the stage of attachment of broomrape sprouts (compatible/incompatible) and at the stage of nodule formation of the parasite (quantification of the nodule number and necrosis) [96, 97]. The monitoring device was named RhizOSun. It will facilitate further research into the influence of various physicochemical parameters of the ‘sunflower–broomrape’ interactions in the early stages.

Sunflower plants with various resistances to the broomrape have different activity of enzymes such as oxyreductase, polyphenol oxidase, peroxidase, catalase. Enzymatic activities characterize resistance to this parasite regardless of race. Enzymatic activities in different parts of the sunflower plant (leaves and roots) and in genotypes differing in resistance were studied [98-101]. Genotypic differences in enzymatic activities were observed.

This direction of research remains imperfect because there is no convenient, rapid and simple method of breeding evaluation of sunflower accessions for resistance to the broomrape.

Conclusions. The sunflower broomrape is one of the main biotic factors that harm the crop fileds. The peculiarity of the breeding for resistance is associated with continuous formation of new races of the parasite. Studies by scientists from different countries on the formation of new physiological races of the broomrape indicate the annually growing threat from the parasite, the need for constant monitoring of broomrape populations and the continuous development of research in this direction. Several genes of resistance to the broomrape have been identified; methods of their marking have been developed; this ensures success in improving the existing and developing new progressive approaches in the sunflower breeding for resistance to the parasite.

The specificity of control of resistance to the broomrape, which is determined by genetic factors, was established. This confirms that genetic methods are the best ones to fight against the broomrape. However, inheritance patterns of resistance to new, virulent, widespread in Ukraine broomrape races are not described in the literature, though it is important for the creation of commercial hybrids.

The relationships between resistance to new virulent broomrape races, which are common in Ukraine, and valuable economic characteristics in F_1 hybrids should be also studied. Taking into account the recent climatic changes, in particular a rise in air temperatures and consequences of this global process, one can predict an increase in the intensity of damage to sunflowers by the parasite, which prompts breeders of the crop to combine resistance to adverse abiotic factors and resistance to the broomrape.

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PECULIARITIES OF THE SUNFLOWER BREEDING FOR RESISTANCE TO BROOMRAPE (OROBANCHE CUMANA WALLR.)

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Purpose and Objectives. Our purpose was to find available information on the sunflower breeding for resistance to the broomrape. To achieve this purpose, we solved following tasks: to review publications covering the history and current state of research into the subject; find out the specifics of such studies; and to highlight the main unresolved issues for the organization of further work.

Materials and Methods. Publications of Ukrainian and foreign scientists became the material for the study: articles in journals and conference abstracts.

Results and Discussion. In the article, publications covering domestic and foreign studies of the peculiarities of sunflower breeding for resistance to the parasitic plant *Orobanche cumana Wallr*. are collected and reviewed. The changes in the race composition of the parasite since the beginning of the 19th century, which have accelerated in recent years, are described. Experiments and breeding for resistance to the broomrape began in 1909-1913, when there was only one (the first) broomrape race A. Currently, the existence of the seventh race (G) and the broomrape biotypes affecting race G-resistant sunflower accessions has been recognized in the world. During the last 20 years, the appearance of new broomrape races was observed in the countries where sunflowers are grown with violations of crop rotation requirements. Marking resistance genes of domestic plants and determining the molecular polymorphism of both host and parasitic plants are important problems of genetics, solving of which is aimed at the improvement of sunflowers in terms of resistance to the broomrape. The identification of genes of resistance to the broomrape and the development of methods for their marking are discussed. Studies in the genetics of resistance to *O. cumana* are limited by few relevant molecular markers. Scientists announced that they had onstructed a molecular genetic map of linkage groups with the Or7 gene of resistance to race G. Genetic studies of the broomrape as a plant are mainly focused on the structure and genetic diversity of parasite populations. The broomrape aggressiveness depends on weather and climate, so an increase in temperatures and lack of precipitation can lead to the broomrape spread over large areas. Scientists adapt the phytotron test for resistance to the broomrape to modern equipment, developing certain methodological subtleties. In addition, new methods of evaluation are developed: histological and molecular genetic assessments

Conclusions. The sunflower broomrape is one of the main biotic factors that harm the crop fields. The peculiarity of the breeding for resistance is associated with continuous formation of new races of the parasite. Studies by scientists from different countries on the formation of new physiological races of the broomrape indicate the annually growing threat from the parasite, the need for constant monitoring of broomrape populations and the continuous development of research in this direction. Several genes of resistance to the broomrape have been identified; methods of their marking have been developed; this ensures success in improving the existing and developing new progressive approaches in the sunflower breeding for resistance to the parasite. The specificity of control of resistance to the broomrape, which is determined by genetic factors, was established. Thus, genetic methods are the best ones to fight against the broomrape. However, inheritance patterns of resistance to new, virulent, widespread in Ukraine broomrape races are not described in the literature, though it is important for the creation of commercial hybrids. The relationships between resistance to new virulent broomrape races, which are common in Ukraine, and valuable economic characteristics in F_1 hybrids should be also studied. Taking into account the recent climatic

changes, in particular a rise in air temperatures and consequences of this global process, one can predict an increase in the intensity of damage to sunflowers by the parasite, which prompts breeders of the crop to combine resistance to adverse abiotic factors and resistance to the broomrape.

Key words: *sunflower, breeding, resistance, broomrape, virulence, races, genes*

ОСОБЛИВОСТІ СЕЛЕКЦІЇ СОНЯШНИКУ НА СТІЙКІСТЬ ДО ВОВЧКА (OROBANCHE CUMANA WALLR.)

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Мета і задачі досліджень. Метою досліджень став пошук відкритої інформації щодо селекції соняшнику на стійкість до вовчка. Для досягнення мети вирішували задачі: розглянути публікації, в яких висвітлено історію та сучасний стан досліджень за тематикою; з’ясувати особливості даного напряму досліджень; виділити основні невирішені питання для організації подальшої роботи.

Матеріали та методи. Матеріалом для досліджень стали публікації українських й іноземних науковців: статті в наукових виданнях і тези конференцій.

Обговорення результатів. У статті зібрано і проаналізовано літературні джерела, в яких вітчизняні та зарубіжні науковці висвітлили свої дослідження стосовно особливостей селекції соняшнику на стійкість до рослини-паразита – вовчка *Orobanche cumana* Wallr. Виявлено зміну расового складу паразита починаючи з початку XIX століття, яка пришвидшилася останніми роками. Досліди та селекцію на стійкість до вовчка розпочато в 1909–1913 рр., коли існувала єдина – перша – раса вовчка A. Зараз у світі визнано наявність сьомої раси G і біотипів вовчка, що уражують зразки соняшнику, стійкі до раси G. Протягом останніх 20 років появу нових рас вовчка спостерігали в країнах, де соняшник вирощують з порушенням сівозміни. Маркування генів стійкості культурної рослини й визначення молекулярного поліморфізму як рослини-хазяїна, так і паразитичної рослини є важливою проблемою генетики та спрямовано на поліпшення соняшнику за стійкістю до вовчка. Розглянуто ідентифікацію генів стійкості до вовчка, розроблення методів їх маркування. Розвиток досліджень з генетики стійкості до *O. cumana* стримує обмеженість відповідних молекулярних маркерів. Науковцями заявлено про складення молекулярно-генетичної карти груп зчеплення з геном стійкості Or_7 до раси G.Генетичні дослідження вовчка як рослини головним чином зосереджено на структурі популяцій паразита, визначенні їх генетичного різноманіття. Агресивність вовчка залежить від погодно-кліматичних умов, отже підвищення температури та відсутність опадів може призвести до поширення вовчка на великі території. Методику випробування стійкості соняшнику в умовах фітотрону науковці пристосовують під сучасне обладнання, розвивають окремі методичні тонкощі, а також розробляють нові методи оцінювання: гістологічні, молекулярно-генетичні.

Висновки. Вовчок соняшниковий є одним з головних біотичних чинників, що шкодить посівам культури. Особливість селекції на стійкість пов’язана з постійним процесом утворення нових рас паразита. Дослідження науковців різних країн щодо утворення нових фізіологічних рас вовчка демонструють щорічно зростаючу загрозу з боку паразита, необхідність постійного моніторингу популяцій вовчка та безперервного розвитку досліджень у цьому напрямі. Ідентифіковано окремі гени стійкості до вовчка, розроблено методи їх маркування, що забезпечує успіх у вдосконаленні існуючих і розробку нових прогресивних методів селекції соняшнику на стійкість до паразита.

Установлено специфічність контролю стійкості до вовчка, що визначено наявністю генетичних факторів. Отже найкращим методом боротьби з вовчком є генетичний метод. Але в літературі не висвітлено закономірностей успадкування стійкості до нових вірулентних рас вовчка, поширених в Україні, що важливе для створення комерційних гібридів. Також потребують розвитку дослідження зв'язку між стійкістю до нових вірулентних рас вовчка, які поширені в Україні, та цінними господарськими ознаками в гібридів першого покоління. Враховуючи зафіксовані останніми роками зміни клімату в напрямі підвищення температури повітря та інші наслідки цього глобального процесу, можна передбачити зростання інтенсивності ураження соняшнику паразитом, що спрямовує селекцію культури на поєднання стійкості до несприятливих абіотичних чинників зі стійкістю до вовчка.

***Ключові слова**: соняшник, селекція, стійкість, вовчок, вірулентність, раси, гени*

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VALUABLE REPRESENTATIVE OF TRITICUM POLONICUM L. FOR GROWING IN UKRAINE

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The article presents the botanical and agronomic characteristics of *Triticum polonicum var. pseudocompactum* studied in the eastern forest-steppe zone of Ukraine.

***Keywords:** Triticum polonicum*, *performance, biometric and technological parameters, chemical composition, pasta quality*

Introduction. *Triticum polonicum* (also known as the Polish wheat, which is a confusing name, because it did not originate or was not cultivated on an industrial scale in Poland) is spring wheat. It is an allotetraploid (genome formulae *AABB*) species with 28 chromosomes [1]. *T. polonicum* was traditionally grown in small areas of the Mediterranean region, Ethiopia, Russia and in other parts of Asia. [2] S. Maysoun [3] even mentioned that this species was cultivated in Ukraine. This species is characterized by longer glumes and grains in comparison with other wheat species [1, 4].

Literature review and problem articulation. Nowadays when agrarians reopen neglected and underutilized wheat species, *T. polonicum* is in the focus of researchers and breeders. Popular sites even call it 'grain of hope'. It is seldom cultivated as an independent food crop; it is rather considered as material for breeding. Polish wheat can be a source of resistance to Fusarium head blight [5] and a material for the biofortification of wheat with essential

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