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Searching for diseases resistance sources in old cultivars, landraces and wild relatives of cereals. A review

Poszukiwanie źródeł odporności na choroby w odmianach dawnych i miejscowych oraz dzikich gatunkach pokrewnych zbóż. Praca przeglądowa

Summary. Modern plant production is focused on the cultivation of cultivars combining many traits such as partial or long-term resistance to the most common cereal diseases and tolerance to abiotic factors. Nowadays there is a growing interest in the return to the cultivars of old varieties and local populations (landraces), especially in organic farming. Due to their adaptability to marginal environments, higher resistance to pathogens, as well as being easily accessible as genetic resources for breeders, they can contribute to ensuring food security. Crops wild relatives and landraces are extremely valuable research material in scientific and breeding works. The aim of this paper is to summarize the issue of old cultivars, landraces and wild cereal related species as sources of stable and durable resistance to biotic stresses.

Key words: old cultivars, wild related species, resistance genes, resistance breeding, genetic diversity, sources of resistance

INTRODUCTION

Cereals are the most important plants used for nutritional purposes [http://www.fao.org/faostat/en/]. Known and cultivated for thousands of years around the world, they are the basic source of food. Among cereal crops, wheat, rice, corn, rye, oats, barley, millet and sorghum are in the world's leading crop area. Corn, wheat and rice cover 30% of the caloric demand of 4.5 billion people in more than 100 developing countries [Hellin et al. 2012]. In Poland, there is an upward trend in the share of cereals in the general area of sowing. In 2018, the sown area of cereals was 74% of all crops [GUS 2018]. It is estimated that global demand for grain will increase by 70% by 2050 [Semenov et al. 2014]. Achieving this level requires doubling the yield. Meeting the growing demand for cereals brings the need for high yielding cultivars resistant to increasing pressures from biotic (diseases and pests) and abiotic stress (drought, salinity, weather anomalies) [Cairns et al. 2013]. Depletion of the gene pool of modern cereal cultivars results in the interest of scientists and breeders in other potential sources of resistance to stress genes. This pool of resources are old and local cultivars as well as wild species related to crop plants.

THE MOST IMPORTANT FUNGAL DISEASES OF CEREALS

One of the most important factors affecting the size and quality of grain yield are common diseases caused by pathogenic fungi. During the vegetation period, the largest infection is caused by fungi causing, among others, powdery mildew (*Blumeria graminis*), brown rust (*Puccinia recondita* f. sp. *tritici*), as well as head blight (*Fusarium* spp.). With favorable climatic conditions for fungal growth, its rapid development causes death of plant tissues, leading to a reduction in the assimilation area of green plant parts. The limitation of photosynthetically active surface with intensified transpiration causes active evaporation of water from above-ground parts of plants, thus worsening their development. These factors negatively influence the number and mass of the seeds. Losses caused by pathogenic fungi occur each year in varying intensity both in conventional (extensive, intensive) and organic crops.

Powdery mildew of cereals and grasses is one of the most dangerous diseases of wheat and barley. It is less important in oat and rye crops. Until recently, triticale was considered resistant to this disease. However, in recent years, more and more reports have been announced about *Blumeria graminis* infection of this species [Kryczyński and Weber 2011, own observations]. Species such as: millet, sorghum, maize do not get infested by *B. graminis* [Fiedorow et al. 2006]. Within *B. graminis* species, special forms are distinguished, which are adapted to specific host species. The pathogen is usually genus specific and therefore, the disease does not spread between cereal species. Powdery mildew of cereals and grasses occurs all over Poland, causing the greatest damage in the coastal regions and south-eastern and central parts of the country. In conditions particularly favorable for the development of *B. graminis*, the yield reduction of winter wheat grain may reach even 30% [Kochman and Węgorek 1997, Tratwal and Jakubowska 2004, Jańczak and Pawlak 2006]. Infection of ears of wheat, and of flag and sub-flag leaves in barley causes the greatest yield losses. Cultivated winter forms of barley infected in early spring by the pathogen causing powdery mildew of cereals and grasses (*B. graminis* f. sp. *hordei*) show less developed shoots and poorly developed root system. This phenotype results in a decreased yield. Factors affecting the spread and development of this disease include wintering mycelium on winter crops, perennial grasses, and self-seeding in living plant tissues. At the humidity of 50 to 100% during the rainfall or persistent dew, appropriate sunshine and a wide range of temperatures, optimal conditions for pathogen development from germination of spores to the generation of conidia, are created.

Brown rust of cereals and grasses is one of the most serious diseases of winter wheat, winter triticale and spring barley leaves. In 2018, it was also the most frequently occurring fungal disease in rye. Particularly high pressure was observed on extensive crops (http://www.farmer.pl/produkcja-roslinna/zboza/rdza-brunatna-szaleje-w-zycie,78829.html).

Brown rust of cereals and grasses is a common disease in all areas of spring and winter cultivation. The greatest losses are caused by the cultivation of winter wheat. It is observed in all phases of plant development. In case of severe infection, the losses caused by this disease range from 40 to 50% [http://plony.eu/choroby-zboz/]. In Poland, average yield losses are estimated at around 5 to 10%. Favorable weather conditions for development of this pathogen are longer periods of sunny and dry weather in spring and early summer. Its occurrence is also favored by high intensity of crops, at the same time, high nitrogen fertilization and large amount of dew accumulating on the plants. Spores of *P. recondita* spread due to the wind over very long distances, therefore early and effective detection of this disease outbreaks is important.

Head blight of cereals is a disease caused by several species of fungi *Fusarium culmorum*, *Gibberella avenacea*, *Gibberella zeae* and *Microdochium nivale*. It is common in wheat, rye, triticale, barley and oat crops. The most severely infected are crops of winter crops, less spring ones, while on oats occurs rather sporadically.

Head blight of maize is a disease caused by fungi of the genus *Fusarium*. Disease symptoms begin to be visible in the stage of milk and wax maturity; mycelium with a characteristic salmon or reddish color is visible on the top layer of leaves covering the cob and on the seeds. Infected kernels usually die. Maize diseases caused by fungi of the genus *Fusarium* are currently the most dangerous diseases of this plant in Poland. The consequence of both the scales of the stalk base as well as the head blight of cobs is often a decrease in the quantity and quality of the crop [Mesterhazy et al. 2012]. In the early stage of growth, the seedling scales caused by *Pythium* and *Fusarium* fungi is particularly dangerous. Symptoms of this disease are brown and dying sprouts. When the disease is mastered by seedlings, they die at the point of contact with the ground. The disease most often attacks during a cold and rainy spring [Metodyka integrowanej ochrony kukurydzy dla producentów 2013].

The root rotting and stem base scales (stem fusariosis) are diseases of maize, the source of infection of which are fungi of the genus *Fusarium* living in the soil and post-harvest residue. The infection occurs through the penetration of spores into the plant, and plant damage caused by feeding of pests (e.g. corn borer) facilitates this. Under favorable conditions (warm and humid weather), the tissues rot inside the stem, which makes the plants unable to support their own weight and break in places of infestation. The infected tissues inside the stems are reddish or salmon-colored. A characteristic symptom is also sagging of cobs. Fungi being the perpetrators of this disease also have the ability to produce mycotoxins harmful to humans and animals [Prończuk et al. 2007].

RESISTANCE BREEDING

Breeding of cultivars with increased resistance to biotic and abiotic factors is called the resistance breeding. Its main goal is to obtain cultivars resistant or tolerant to a given stress factor by means of traditional or modern breeding methods. The search for effective sources of resistance or tolerance to adverse abiotic and biotic factors promotes the development of immune culture [Pietrusińska and Czembor 2015].

Development of various breeding directions leading to obtaining resistant plants gave rise to pyramidization, i.e. accumulation of effective resistance genes. The introduction of several resistance genes to one genotype allows for a comprehensive resistance to various types of pathogens or pests. Effective genes used in breeding programs should condition stable and long-lasting resistance to important abiotic and biotic stress factors. The basic problem of resistance breeding is the emergence of new virulent pathotypes for previously resistant cultivars. The appearance of new physiological pathogens influences the overcoming of immunity [Pietrusińska et al. 2011]. Another problem in the resistance breeding is heterozygosity in the second generation of open-pollinated species (e.g. rye) and disappearance of the heterosis effect occurring in the first generation, i.e. beneficial interaction of allelic and non-allelic genes. This problem does not occur in self-pollinating plants, i.e. wheat and barley.

Using the achievements of resistance breeding in practice is considered one of the effective and economical methods of plant protection. It carries a number of benefits, the most important of which are: the release of the yield potential of a cultivar and reduction of negative impact of pesticides on the environment.

PLANT GENETIC RESOURCES AND THEIR USE IN BREEDING

Currently cultivated species were created as a result of a long-term process of plant domestication, the beginnings of which are estimated at 20,000 years BC. Species of arable crops, which are the most important source of food for the world, arose through domestication or a long-term selection based on phenotypic traits. Selected plants were well yielding and possessing favorable phenotypic traits. Based on the available literature, it can be estimated that out of 400,000 plant species, about 200 were domesticated. It is estimated that only 12 species provide more than 75% of the food consumed in the whole of this pool of plants worldwide. With the intensification of cultivation, there has been a growth of plant breeding aimed at obtaining high and stable yields in various environments [Gracz et al. 2015].

Biodiversity is the sum of genetic traits considered within a given taxonomic unit [Rao and Hodgkin 2002]. This variability is the result of mutation, selective pressure and genetic drift. The basic source of biological diversity is genetic variability, most often expressed as the mean number and relative frequency of the alleles per *locus* [Hughes et al. 2008]. All commonly grown plant species arose as a result of domestication and long-term introduction of changes in both quantitative and qualitative traits through natural selection and anthropopressure. Local cultivars are traditional, regional ecotypes that have adapted to their natural environment due to the isolation from other populations of the same species [Jones et al. 2008]. Local and old cultivars come from regions with traditional cultivation and primitive agrotechnical system, where systematic improvement of cultivars was not applied. They are heterogeneous, dynamic populations undergoing natural selection pressure, adapted to the local climate. Long-term co-evolution with pathogens of different virulence contributed to the accumulation of resistance alleles. Wild related species were not subjected to strong breeding selection, and heterogeneity and environmental pressure influenced the consolidation of many desirable immune alleles [Villa et al. 2005]. Local cultivars of crops, often having unique traits, have been replaced by modern elite species representing a narrow genetic pool. In this way, their diversity disappeared with the local cultivars. Continuous selection towards agronomically important features narrowed the gene pool of cultivated species [Buckler et al. 2001, Gacek et al. 2016]. The effectiveness of selection depends to a large extent on the genetic diversity that ensures the proper development of a population while maintaining resistance to abiotic and biotic stresses.

Local forms are often population cultivars. In population cultivars, the spread of diseases is limited by collective resistance. Both vulnerable and resistant genotypes are found in heterozygous and inhomogeneous populations. This leads to less infection and slows down the epiphytoses. The presence of susceptible genotypes reduces the selective pressure on the pathogen. Population cultivars of the open-pollinated species, like rye, are more likely to acquire the resistance genes through natural crossbreeding and selection [Geiger et al. 1988, Mirdita 2006]. Resistance of population cultivars can also be increased through the use of recurrent selection [Ferwerda 1956]. In the case of hybrid cultivars, the possibilities of resistance breeding depend on the availability of genetically diverse inbred lines and the possibility of introducing genes by backcrossing.

However, local forms and wild related species are often characterized by a wide spectrum of unfavorable features, i.e. low fertility, susceptibility to lodging or low winter hardiness, and many others. Conducting the research upon the usefulness of simple rye hybrids with *Secale kuprijanovii* and *S. montanum* in terms of introducing resistance to powdery mildew of cereals and grasses, lines were selected that were subjected to 5-fold backcrossing [Rzepka-Plevneš et al. 1995]. The obtained hybrids were characterized by a reduced number and weight of grains and ear, as well as lower weight of 1000 grains compared to the reference cultivar [Rzepka-Plevneš et al. 1995]. With the widespread use of diverse genetic resources in resistance breeding, the problem may be difficult acclimatization of cultivars not adapted to local conditions, as in the case of rye. Pleiotropy, epistasis, as well as the joint coupling of desired and negative traits may hinder direct use of local cultivars as sources of genetic variation [Haussmann et al. 2004].

Modern pro-ecological plant production is focused on the cultivation of cultivars characterized by resistance to the most common cereal diseases and insensitive to abiotic factors that reduce the quality and size of the crop. At present, there is a growing interest in the return to the cultivation of old cultivars and local populations, especially in organic cereal crops. In addition, they are a source of gene resources important for sustainable agriculture in the context of climate change. *In situ* protection of plants helps to preserve the genetic identity of areas of natural occurrence, enabling adaptation to local conditions. Therefore, gene banks that protect these valuable resources against extinction play an extremely important role in protecting the cultivars/populations of local crop plants [Bellucci et al. 2013].

USE OF WILD CEREAL SPECIES IN BREEDING

The use of wild species of related crops and local cultivars may contribute to increasing the genetic diversity of cultivated cultivars. Wild and cultivated forms are distant evolutionary, often represent different level of ploidy and lack of chromosomal homology, which may result in low cross-breeding efficiency and difficulty in direct introduction of traits to elite cultivars.

Plant genetic resources within a given genus are divided into gene pools of a given order, in terms of relatedness at the genetic level, i.e. sexual compatibility of plants [Harlan and de Wet 1971, Gepts 2000]. Based on studies on gene pools made by the Harlan and de Wet team [1971], followed by Gepts and Papa [2003], a total of four orders of gene pools can be identified.

The primary gene pool includes crop species and their cultivars as well as wild species and cultivars that generate completely fertile hybrids. Genotypes belonging to this gene pool have homologous chromosomes. This pool is very diverse and is a source of many useful alleles that have been lost in the breeding selection process. Free crossing of individuals with different genotypes within this pool enables the direct transfer of genetic material and obtaining fertile offspring. This pool is still little known and relatively little used in the process of resistance breeding of the elite cultivars of many crop species [Tanksley and McCouch 1997].

The primary gene pool of the genus *Triticum* consists of species belonging to the original cultivars of local and old wheat and wild species [Jiang and Gill 1994]. Among them, there are ancestors of common wheat (*Triticum aestivum* L.) containing at least two genomes homologous to *T. aestivum* (AABBDD), i.e. tetraploid *T. turgidum* (AABB), diploid *T. tauschii* (DD) and *T. monococcum* (AA) [Mujeeb-Kazi 2006, Feuillet et al. 2007, Qi et al. 2007]. Transfer of genetic material through crossings coinciding with elite cultivars is widely used in modern breeding programs. *Triticum dicoccoides* (AABB) is the ancestor of almost all currently grown wheat, including *T. aestivum*, *T. dicoccum* (AABB) and *T. durum* (AABB). Genes for specific resistance to powdery mildew *Pm16*, *Pm26*, *Pm36*, *MlZec1*, *Pm3k* were identified in *T. dicoccoides* [Yahiaoui et al. 2009]. The gene for resistance to powdery mildew of cereals and grasses *Pm30* also originating from *T. dicoccoides*, determined the resistance to all tested isolates of *B. graminis* in studies conducted by Chen et al. [2005]. Research upon the resistance to brown rust of cereals and grasses as well as stripe rust of cereals and grasses at the seedling stage and adult plants among 742 objects of *T. dicoccoides* conducted by Anikster et al. [2005] enabled the identification of genotypes characterized by partial or permanent immunity. Fu et al. [2009] described the *Yr36* gene (*Stripe rust – Yr* genes), which confers resistance to the broad spectrum of *P. striiformis* isolates. The *Yr36* gene may provide a new source of resistance to yellow rust of grain and grass for *T. durum* and *T. aestivum*. Modern durum wheat cultivars are often susceptible to head blight. Searching for the source of resistance led to the identification of partially resistant lines of wild *T. dicoccoides* [Oliver et al. 2007].

For barley (*Hordeum vulgare* L.), the primary gene pool includes very diverse material of local cultivars of barley and diploid ancestor of the cultivated form *H. vulgare* ssp. *spontaneum* [von Bothmer et al. 2003]. Primary gene pool is a donor of important resistance genes. The available literature does not describe the total tolerance for yellow barley dwarf disease caused by three viruses so far: *barley yellow dwarf virus*-MAV (BYDV–MAV), *barley yellow dwarf virus*-PAV (BYDV–PAV) and *cereal yellow dwarf virus*-RPV (CYDV–RPV). Genes of tolerance to BYDV were identified in local cultivars originating from Ethiopia, *Ryd2* and *Ryd3* [Niks et al. 2004]. In the cultivar Egypt 4 and hybrid lines derived after crossing with *H. spontaneum*, genes for resistance to barley dwarf rust (*Rph*) were identified. *Rph1* and *Rph2* genes are found in numerous allelic forms [Niekerk et al., 2001]. Primitive local cultivars based on dynamic populations are a valuable source of mildew resistance genes for cereals and grasses (*B. graminis* f. sp. *hordei*). An example is the work carried out by Czembor [2000, 2001], in which new sources of resistance to powdery mildew of cereals and grasses have been identified among local cultivars originating from the Mediterranean basin. Valuable disease resistance alleles contained in the primary gene pool can be easily introduced into breeding programs by means of crossbreeding convergent with elite cultivars [Yun et al. 2006]. However, barley hybrid lines rarely outgrow the elite cultivars in terms of productivity. Multiple backcrossing should be performed to restore the recipient's traits [Inostroza et al. 2009].

For rye (*Secale cerale* L.), the primary gene pool includes species that can be crossed between each other, i.e. *Secale vavilovii*, *Secale strictum* and *Secale montanum*. Rye is intensively used in wheat farming as a valuable source of disease resistance genes, increasing the yields and improving adaptability to adverse environmental conditions [Friebe et al. 1996]. It is a significant part of genetic diversity stored in the form of local cultivars [Matos et al. 2001, Gailīte et al. 2013] and wild forms [Burger et al. 2006, Jenabi et al. 2011]. These forms contain many useful traits like resistance to diseases or to abiotic factors [Santos et al. 2018]. Wild forms of rye related to rye are *S. vavilovii* originating in southwestern Asia, and *S. strictum* occurring in the Mediterranean, southwestern Asia, Central Asia and the Caucasus [Frederiksen and Petersen 2008, Sencer and Hawkes 2008]. Wild rye species, especially *S. vavilovii*, may be crossed with *S. cereale* [Sencer and Hawkes 2008]. Genotypes resistant to brown rust of rye can be found among wild forms (*S. montanum* Guss.) and cultivars grown in eastern and central Europe, as well as in Canada and Russia [Kobylyanskii and Solodukhina 1996]. In addition, *S. montanum* is a valuable source of resistance to powdery mildew of cereals and grasses and rye brown rust, whereas *S. vavilovii* is used for growing cultivars resistant to lodging and fouling [Rzepka 1993].

In the case of maize (*Zea mays* L.), sources of resistance to diseases are sought in the area of present Mexico, in the area of this plant domestication. There are wild forms considered as the ancestors of maize, constituting the primary gene pool of this species - teosinte and its subspecies: *Zea mays* ssp. *parviglumis* and *Zea mays* ssp. *mexicana*. Teosinte is considered resistant to diseases that threaten maize. Resistance to many diseases, including gray leaf spot (GLS) (*Cercospora sorghi Ellis & Everh.*), southern corn leaf blight (SCLB) (*Cochliobolus heterostrophus* Drechs.), southern corn rust (SCR) (*Puccinia polysora* Underw.), maize streak virus (MSV) derived from teosinte has been incorporated into several tropical populations of maize [Warburton et al. 2017]. The *Htn1* gene, that determines the resistance of maize to northern corn leaf blight (NCLB) (*Exserohilum turcicum*), has been identified in a cultivar of local maize from Mexico in the 1970s and is successfully used in breeding programs [Hurni et al. 2015]. Currently, about 60 local cultivars are grown in Mexico. Mexican local cultivars are a genetic reservoir of desirable resistance traits to biotic and abiotic factors [Arteaga et al. 2016]. Also in populations of local maize in India, sources of resistance to one of the most dangerous diseases of this species have been identified, yellow leaf spot (*Helmintosporium turcicum*), which can be used to increase the resistance of new cultivars [Yousuf et al. 2018]. Sources of resistance to the most important diseases of maize are also sought in the materials collected in gene banks. Research conducted by Qureshi et al. [2015] over 50 maize plants gathered at The Maize and Millet Research Institute (Pakistan), allowed to isolate 11 objects highly resistant to stem fusariosis.

The secondary pool is constituted by all related species of crops, between which the crossing barriers occur.

For wheat, the secondary gene pool are polyploid species that have at least one genome homologous for crop forms. Genome D plays particular role in crossbreeding with hexaploid wheat, thus eliminating difficulties in obtaining seeds of hybrid plants obtained through heterosis. In this pool, we include, among others, *T. timopheevii* (AAGG), *T. crassum* (DDMM), *T. cylindricum* (CCDD). *T. timopheevii* tetraploid species (AAGG) is a donor of the stem rust resistance gene *Sr36* and the powdery mildew resistance gene *Pm37* [Perugini et al. 2008]. Three tested wheat lines of *T. cylindricum*: Acy1, Acy9 and Acy22 were found to be resistant to virulent isolates of *P. recondita* and *P. graminis* [Bai et al. 1995]. Selected lines served as sources of resistance to brown rust of wheat and stem rust of cereals and grasses for common wheat. This pool also includes *Aegilops crassa* (DDM) [McIntosh et al. 1995, Feuillet et al. 2007].

Wild species of the genus *Aegilops* are also used in the resistance breeding of triticale. The intergeneric hybrids, i.e. *Aegilops* × *Secale* and *Aegilops cylindrica* (CD) × *Triticum aestivum* are commonly obtained in breeding programs [Morrison et al. 2002]. Hybrids of triticale (*Aegilops crassa* Boiss × *Triticosecale*) obtained by Strzembicka et al. [2007] were characterized by resistance to brown rust of triticale with simultaneous tolerance to high concentration of aluminum ions in the soil [Strzembicka et al. 2007].

The secondary gene pool for barley includes di- and tetraploid *H. bulbosum* and tetra- and hexaploid *Elymus* ssp. (SSHHYY). Transfer of genetic material from a secondary gene pool is problematic. After pollination with compatible pollen (female sterility), the lack of seed production is often observed, as well as their low viability and recombination disorders [Ogbonnaya et al. 2013]. Pickering [2000] described the method of distant crossing (bulbous method), thus enabling breaking the distant crossing barriers and introducing of *H. bulbosum* genome (pollen donor) fragments to *H. vulgare*. For the first time, this type of crossing was used 30 years ago and is used to obtain haploids in barley [Pickering and Johnston 2005]. Gene resources from secondary pool are a valuable source of resistance to viruses, as well as many diseases of fungal origin, such as powdery mildew of cereals and grasses or barley rust (*P. hordei*). An example is *H. bulbosum*, as a donor of two dominant genes *Rym14Hb* and *Rym16Hb*, that determine the resistance to barley mosaic virus (BaMMV) located on 6HS and 2HL chromosomes [Ruge et al. 2003, Ruge-Wehling et al. 2006] as well as *Ryd4Hb* gene that was introduced into the genome of cultivated barley [Scholz et al. 2009]. The dominant character of virus resistance genes is unique in barley [Kai et al. 2012]. *MlHb* is a mildew resistance gene identified in *H. bulbosum* and introduced into barley (Pickering et al. 1995]. This gene is conjugated to the *Rph20Hb* barley rust gene [Pickering et al. 1998]. In general, *H. bulbosum* is a source of resistance to diseases of fungal origin, such as cereal rhinchosporiosis (*Rynchosporium secalis*) [Pickering et al. 2006], barley dwarf rust (*P. hordei*) [Walther et al. 2000] as well as pests and viruses [Ruge-Wehling et al. 2006].

The secondary pool for rye is *S. silvestre*. Detailed analysis of hybrids belonging to several *Secale* species showed that *S. cereale* genome differs from that of *S. silvestre* in three translocations [Singh 1977]. Based on research performed by Rzepka [1993], *S. silvestre* can be used in breeding the cultivars resistant to lodging and fouling [Rzepka 1993, Broda et al. 2008].

The tertiary gene pool includes a group of distantly related species that do not share common genomes with crop species and homologous recombination cannot be used in the introgression of new genes. Transfer of genetic material in the process of a direct crossing with crop cultivars is practically impossible [Feuillet et al. 2007]. Genetic material can be introduced into cultivated forms through chromosome and genetic engineering. Tertiary gene pool includes species that constitute valuable gene resources carrying important functional traits [Mujeeb-Kazi 2006].

The tertiary gene pool covers majority of *Triticeae* species that do not belong to the primary and secondary gene pool. This pool is a donor of several genes resistant e.g. to stalk rust *Sr24* from *Thinopyrum ponticum* ($JJJ^{s}J^{s}$) or *Sr38* from *Triticum ventricosa* (DN) [McIntosh et al. 1995]. Combination of resistance genes (*Sr24, Sr25, Sr26, Sr32, Sr39, Sr43, Sr47, Sr51*) was introduced into wheat from wild related species belonging to the tertiary gene pool i.e. *Th. ponticum*, *T. speltoides* (SS) and *Ae. searsii* (Ss), to build the resistance to the stalk rust *Ug99* [Hajjar and Hodgkin 2007, Singh et al. 2007]. In addition, the resistance genes *Yr17*, *Lr37* (leaf rust) and *Sr38* were introduced into the wheat cultivars by translocation from *T. ventricosa* [Ambrozková et al. 2002].

The literature data show that about 50 translocations introduced into the genome of cultivated wheat are known [Chełkowski et al. 2003]. The *Pm21* gene was first transferred from *Haynaldia villosa* (syn. *Dasypyrum villosum*) (VV) to *T. durum* in the 1980s by Chen et al. [1995] through the translocation T6AL·6VS. It has been introduced into many cultivars of wheat grown both in Europe and Asia. Based on the available literature and own observations, the *Pm21* gene is considered to be highly effective. Yr26, that determines the resistance to yellow rust of cereals and grasses, comes from the same species [Chen et al. 1995, Yildirim et al. 2000].

Genes engineering, from wild or related species, have transferred genes to arable wheat such as: *Lr9* (*Aegilops umbellulata*) (U), *Lr19*, *Lr24* oraz *Lr29* (*Agropyron elongatum*), *Lr21* (*Aegilops tauschii*), *Lr28* (*Agropyron intermedium*) [McIntosch et al. 1995, Górny 2004].

In hybrid wheats, of which one of parents was a tertiary pool species, new features of resistance to diseases, insects and nematodes were observed [Ogbonnaya et al. 2013], e.g. resistance to brown leaf spot (*Pyrenophora tritici – repentis*) in the hybrid population of *T. turgidum* and *Ae. tauschii* [Tadesse et al. 2007].

In the case of barley, the tertiary gene pool consists of wild *Hordeum* species. *H. bogdanii* is the source of genes responsible for the maturation of grain (*Hinb-A* oraz *Hinb-B*) [Terasawa et al. 2012].

In the case of rye, the tertiary gene pool includes *Triticum* and *Aegilops* (UM, US, UMN, SU, UC, U). The 1R, 2R, 3R, 5R and 6R rye chromosomes are practically homologous to the wheat 1, 2, 3, 5 and 6 chromosomes groups, while 4R and 7R chromosomes are partially homologous to groups 4 and 7 in wheat [Bauer et al. 2017]. Significant similarity allows to use rye as a source of resistance genes for wheat. The aphid resistance genes were introduced: *Dnr1-Dnr4* and *Dn7* (*Dnr – dissimilatory nitrite reductase*) localized respectively on chromosomes 1RL, 3RS, 4R, 7R and 1RS from rye to wheat [Łukaszewski et al. 2001, Smith et al. 2004, Marais et al. 2018]. Chromosome 1R from the Petkus cv. has been the most frequently used source of resistance since the 1960s. This allowed the transfer of resistance to many important wheat diseases [Crespo-Herrera et al. 2017]. The Petkus and Insave cultivars are, respectively the translocation sources of 1BL.1RS and 1AL.1RS. They carry, among others, genes of resistance to brown rust of cereals and grasses – *Lr26*, yellow rust of cereals and grasses – *Yr9*, stalk rust of cereals and grasses – *Sr31* and powdery mildew of cereals and grasses – *Pm8* [Friebe et al. 1996, Rabinovich 1998]. 2R chromosome is a source of *Lr25* and *Pm7* resistance genes [Heun and Friebe 1990], the same gene for resistance to powdery mildew of cereals and grasses other than *Pm7* was also identified on the same chromosome [An et al. 2006], and the Imperial cv. carries the *Sr27* gene on the 3R chromosome [Crespo-Herrera et al. 2017]. Introduction of resistance genes from rye to wheat is not limited to cultivars of *S. cereale* as gene donors. Introgressive lines of *S. africanum* are also used. Yang et al. [2009] introduced translocation of 1BL.1RaS to the line L9-15, which ensured high resistance to yellow rust of cereals and grasses.

The quaternary gene pool covers all synthetic forms that do not occur in the natural environment, resulting from genetic transformation [Hammer 1998, Gepts i Pape 2003].

SUMMARY

Wild forms of cultivated plants, primitive or local cultivars are extremely diverse and valuable genetic material used in resistance breeding to improve the forms of crops. Wild and related forms are unique sources of resistance to diseases important from the point of view of a breeder. However, it should be remembered that the same genotypes may be carriers of negative traits. Creation, breeding and cultivation of resistant cultivars has a positive effect on ecosystems by limiting the use of chemical plant protection products. Introduction of primitive forms to breeding programs allows to preserve the

biodiversity and genetic diversity. Research on the search for effective sources of resistance in ancient, local cultivars and wild cereal related species is justified.

Genetic resources, including wild related species and forms of local crops, constitute national and global heritage. Gene banks located around the world play an important role in this process. By collecting and storing genetic material, they influence the preservation of biodiversity. Deposited material is a potential source of important functional features, such as disease resistance. *In situ* protection ensures the maintenance of dynamic populations in natural ecosystems. With narrow genetic basis of currently cultivated elite cultivars, preserving the biodiversity can be crucial to the food security of future generations.

REFERENCES

Ambrozková M., Dedryver F., Dumalasová V., Hanzalová A., Bartoš P., 2002. Determination on the custer on wheat rust resistance genes *Yr17*, *Lr37* and *Sr38* by a molecular marker. Plant Prot. Sci. 38(2), 41–45.

An D.G., Li J.M., Zhu Y., Li L.H., Li H., 2006. Introgression of resistance to powdery mildew conferred by chromosome 2R by crossing wheat nullisomic 2D with rye. J. Integr. Plant Biol. 48(7), 838–47, https://doi.org/10.1111/j.1744-7909.2006.00275.x.

Anikster Y., Manisterski J., Long D.L., Leonard K.J., 2005. Leaf rust and stem rust resistance in *Triticum dicoccoides* populations in Israel. Plant Dis. 89, 55–62, https://doi.org/10.1094/PD--89-0055

Arteaga M.C., Moreno-Letelier A., Mastretta-Yanes A., Vazquez-Lobo A., Brena-Ochoa A., Moreno-Estrada A., Equiarte L.E., Pinero D., 2016. Genomic variation in recently collected maize landraces from Mexico. Genomics Data 7, 38–45, https://doi.org/10.1016/j.gdata.2015.11.002.

Bai D., Scoles G.J., Knott D.R., 1995. Rust resistance in *Triticum cylindricum* Ces. (4x, CCDD) and its transfer into durum and hexaploid wheats. Genome 38(1), 8–16.

Bauer E., Schmutzer T., Barilar I., Bauer E., Schmutzer T., Barilar I., Mascher M., Gundlach H., Martis M.M., Twardziok S.O., Hackauf B., Gordillo A., Wilde P., Schmidt M., Korzun V., Mayer K.F.X., Schmid K., Schön C.C., Scholz U., 2017. Towards a whole-genome sequence for rye (*Secale cereal* L.). Plant J. 89, 853–869, https://doi.org/10.1111/tpj.13436.

Bellucci E., Bitocchi E., Rau D., Nanni L., Ferradini N., Giardini A., Rodriguez M., Attene G., Papa R., 2013. Population structure of barley landrace populations and gene- flow with modern varieties. Plos One 8(12), 1–11, https://doi.org/10.1371/journal.pone.0083891.

Broda Z., Kurasiak-Popowska D., Kowalska A., Ćwiklińska A., 2008. Analiza podobieństwa genetycznego wybranych gatunków w rodzaju *Secale* [Analysis of genetic similarity of selected species in *Secale* genus]. Biul. IHAR 247, 65–71.

Buckler E.S., Thornsberry J.M., Kresovich S., 2001. Molecular diversity, structure and domestication of grasses. Genet. Res. 77, 213–218.

Burger J.C., Lee S, Ellstrand N.C., 2006. Origin and genetic structure of feral rye in the western United States. Mol. Ecol. 15(9), 2527–2539, https://doi.org/10.1111/j.1365-294X.2006.02938.x.

Cairns J. E., Hellin J., Sonder K., Araus J. L., MacRobert J. F., Thierfelder Ch., Prasanna B. M., 2013. Adapting maize production to climate change in sub-Saharan Africa. Food Sec. 5, 345–360, https://doi.org/10.1007/s12571-013-0256-x.

Chełkowski J., Golka L., Stępień Ł., 2003. Appication of STS markers for leaf rust resistance genes in near-isogenic lines of spring wheat cv. Thatcher. J. Appl. Genet. 44(3), 323–338.

Chen P.D., Qi L.L., Zhou B., Zhang S.Z., Liu D.J., 1995. Development and molecular cytogenetic analysis of wheat-*Haynaldia villosa* 6VS/6AL translocation lines specifying resistance to powdery mildew. Theor. Appl. Genet., 91, 1125–1128, https://doi.org/10.1007/BF00223930.

Chen X.M., Luo Y.H., Xia X.C., Xia L.Q., Chen X., Ren Z.L., He A.H., Jia J.Z., 2005. Chromosomal location of powdery mildew resistance gene *Pm16* in wheat using SSR marker analysis. Plant Breed. 124, 225–228, https://doi.org/10.1111/j.1439-0523.2005.01094.x.

Crespo-Herrera L.A., Garkava-Gustavsson L., Åhman I., 2017. A Systematic review of rye (*Secale cereale* L.) as a source of resistance to pathogens and pests in wheat (*Triticum aestivum* L.). Hereditas 154, 14, https://doi.org /10.1186%2Fs41065-017-0033-5.

Czembor H.J., 2000. Resistance to powdery mildew in barley (*Hordeum vulgare* L.) landraces from Egypt. Plant Genet. Resour. Newsl. 123, 52–60.

Czembor H.J., 2001. Sources of resistance to powdery mildew (*Blumeria graminis* f.sp. *hordei*) in Moroccan barley landraces. Can. J. Plant Pathol. 23, 260–269, https://doi.org/10.1080/07060660109506939.

Ferwerda F.P., 1956. Recurrent selection as a breeding procedure for ray and other cross-fertilized plants. Euphytica 5, 175–184.

Feuillet C., Langridge P., Waugh R., 2007. Cereal breeding takes a walk on the wild side. Trends Genet. 24, 24–32, https://doi.org/10.1016/j.tig.2007.11.001.

Fiedorow Z., Gołębniak B., Weber Z., 2006. Ogólne wiadomości w fitopatologii [General news in phytopathology]. Wyd. AR, Poznań.

Frederiksen S., Petersen G., 2008. Morphometrical analyses of secale (*Triticeae*, *Poaceae*). Nord. J. Bot. 17(2), 185–198, https://doi.org/10.1111/j.1756-1051.1997.tb00309.x.

Friebe B., Jiang J., Raupp W., Mcintosh R., Gill B.S., 1996. Characterization of wheat-alien translocations conferring resistance to diseases and pests. Euphytica 91(1), 59–87.

Fu D., Uauy C., Distelfeld A., Blechl A., Epstein L., Chen X., Sela H., Fahima T., Dubcovsky J., 2009. A kinase-START gene confers temperature-dependent resistance to wheat stripe rust. Science 323, 1357–1360, https://doi.org/10.1126/science.1166289.

Gacek E., Głazek M., Matyjaszczyk E., Pruszyński G., Pruszyński S., Stobiecki S., 2016. Metody ochrony w integrowanej ochronie roślin [Methods of protection in integrated plant protection]. Centrum Doradztwa Rolniczego w Brwinowie, Oddział w Poznaniu, s. 81, https://www.cdr.gov.pl/images/wydawnictwa/2016/2016-METODY-OCHRONY-W-INTEGROWANEJ-OCHRONIE-ROSLIN.pdf.

Gailīte A., Gaile A., Gaile I., Voronova A., Veinberga I., Kokare A., Rungis D., 2013. Genotypic assessment of the Latvian rye (*Secale cereale* L.) collection. Proc. Latvian Acad. Sci. 3(684), 264–267.

Geiger H.H., Schuhmacher A.E., Billenkamp N., 1988. Frequencies of vertical resistances and virulences in the rye-powdery mildew pathosystem. Plant Breed. 100(2), 97–103.

Gepts P., 2000. A phylogenetic and genomic analysis of crop germplasm: A necessary condition for its rational conservation and utilization. In: Proc. Stadler Genetics Symposium, June 8–10, 1998, New York, 163–181.

Gepts P., Papa R., 2003. Possible effects of (trans)gene flow from crops on the genetic diversity from landraces and wild relatives. Environ. Biosafety Res. 2, 89–103.

Górny A.G., 2004. Zarys genetyki zbóż. Tom 1. Jęczmień, pszenica i żyto [Barley, wheat and rye]. Wyd. Instytut Genetyki Roślin PAN, Poznań, 181–327.

Gracz J., Tyczewska A., Twardowski T., 2015. Perspektywy i wyzwania hodowli roślin w erze postgenomowej [Prospects and challenges of plant breeding in the postgenomic era]. Nauka 2, 109–126.

GUS, 2018. Rocznik Statystyczny 2018 [Statistical Yearbook 2018]. Główny Urząd Statystyczny, Warszawa.

Hajjar R., Hodgkin T., 2007. The use of wild relatives in crop improvement: a survey of developments over the last 20 years. Euphytica 156, 1–13, https://doi.org/10.1007/s10681-007-9363-0.

Hammer K., 1998. Genepools – structure, availability and elaboration for breeding (German, Engl. Summary). Schriften Gen. Res. 8, 4–14.

Harlan J.R., de Wet J.M.J., 1971. Towards a rational classification of cultivated plants. Taxon 20, 509–517, https://doi.org/10.2307/1218252.

Haussmann B.I.G., Parzies H.K., Presterl T., Miedaner T., 2004. Plant genetic resources in crop improvement. Plant Genet. Resour., C, 2(1), 3–21.

Hellin J., Shiferaw B., Cairns J. E., Reynolds M., Ortiz-Monasterio I., Banziger M., Sonder K., La Rovere R., 2012. Climate change and food security in the developing world: Potential of maize and wheat research to expand options for adaptation and mitigation. J. Develop. Agric. Econ.. 4(12), 311–321, https://doi.org/10.5897/JDAE11.112

Heun M., Friebe B., 1990. Introgression of powdery mildew resistance from rye into wheat. Phytopathology 80(3), 242–245.

http://plony.eu/choroby-zboz/ [dostęp 09.2018].

http://www.fao.org/faostat/en/ [dostęp 09.2018].

http://www.farmer.pl/produkcja-roslinna/zboza/rdza-brunatna-szaleje-w-zycie,78829.html_[dostęp 09.2018].

Hughes A.R., Inouye B.D., Johnson M.T.J., Underwood N., Vellend M., 2008. Ecological consequences of genetic diversity. Ecol. Lett. 11, 609–623, https://doi.org/10.1111/j.1461-0248.2008.01179.x.

Hurni S., Scheuermann D., Krattinger S. G., Kessel B., Wicker T., Herren G., Fitze M. N., Breen J., Presteri T., Ouzunova M., Keller B., 2015. The maize disease resistance gene Htn1 against northern corn leaf blight encodes a wall-associated receptor-like kinase. Proc Natl Acad Sci USA 112(28), 8780–8785, https://doi.org/10.1073/pnas.1502522112.

Inostroza L., Pozo A., Matus I., Castillo D., Hayes P., Machado S., Corey A., 2009. Association mapping of plant height, yield, and yield stability in recombinant chromosome substitution lines (RCSLs) using *Hordeum vulgare* subsp. *spontaneum* as a source of donor alleles in a *Hordeum vulgare* subsp. *vulgare* background. Mol. Breed. 23, 365–376, https://doi.org/ 10.1007/ s11032-008-9239-6.

Jańczak C., Pawlak A., 2006. Występowanie i szkodliwość mączniaka prawdziwego (*Blumeria graminis*) w pszenicy ozimej w latach 2003–2005 [Occurrence and harmfulness of powdery mildew (*Blumeria graminis*) in winter wheat in 2003-2005]. Post. Ochr. Rośl. 46(2), 582–542.

Jenabi T., Saeid H.,Rahiminejad M.R., 2011. Biodiversity of *Secale strictum* in Iran measured using microsatellites. Genet. Resur. Crop. Ev. 58(4), 497–505, https://doi.org/10.1007/ s10722-010-9593-1.

Jiang J., Gill B.S., 1994. Different species-specific chromosome translocations in *Triticum timopheevii* and *T. turgidum* diphyletic origin of polyploid wheats. Chromosome Res. 2, 59–64.

Jones H., Lister D.L., Bower M.A., Leigh F.J., Smith L.M., Jones M.K., 2008. Approaches and constraints of using existing landrace material to understand agricultural spread in prehistory. Plant Genet. Resour-C. 6(2), 98–112, https://doi.org/10.1017/S1479262108993138.

Kai H., Takata K., Tsukazaki M., Furusho M., Bana T., 2012. Molecular mapping of *Rym17*, a dominant and *rym18* a recessive barley yellow mosaic virus (BaYMV) resistance genes derived from *Hordeum vulgare* L. Theor. Appl. Genet. 124, 577–583, https://doi.org/10.1007/ s00122-011-1730-5.

Kobylyanskii V.D., Solodukhina O.V., 1996. Genetic bases and breeding utilization of heterogeneous resistance of rye to brown rust. International symposium on rye breeding and genetics. EUCARPIA. Vortrage Fuer Pflanzenzuchtung, Stuttgart, 155–163.

Kochman J., Węgorek W., 1997. Ochrona roślin. Choroby infekcyjne [Plant protection. Infectious diseases]. Wyd. 5, Plantpress, Kraków, . 445–447.

Kryczyński S., Weber Z., 2011. Fitopatologia. T. 2. Choroby roślin uprawnych [Diseases of cultivated plants]. PWRiL, Poznań, 350-352, ISBN 978-83-09-01077-7.

Łukaszewski A.J., Porter D.R., Baker C.A., Rybka K., 2001. Attempts to transfer russian wheat aphid resistance from a rye chromosome in russian triticales to wheat. Crop Sci. 41, 1743––1749, https://doi.org/10.2135/cropsci2001.1743.

Marais G.F., Horn M., Torr F., 2018. Intergeneric transfer (rye to wheat) of a gene(s) for russian wheat aphid resistance. Plant Breed. 113(4), 265–71, https://doi.org/10.1111/j.1439-0523.1994.tb00735.x.

Matos M., Pinto-Carnide O., Benit C., 2001. Phylogenetic relationships among portuguese rye based on isozyme, RAPD and ISSR markers. Hereditas 134, 229–36, https://doi.org/10.1111/j.1601-5223.2001.00229.x.

McIntosh R.A., Wellings C.R., Park R.F., 1995. Wheat rusts: An atlas of resistance genes. CSIRO Publications, East Melbourne.

Mesterhazy A., Lemmens M., Reid L.M., 2012. Breeding for resistance to ear rots caused by *Fusarium* spp. in maize – a review. Plant Breed. 131, 1–19, https://doi.org/10.1111/j.1439-0523.2011.01936.x.

Metodyka integrowanej ochrony kukurydzy dla producentów, 2013. [Methodology of Integrated Corn Protection for Producers]. IOR – PIB, Poznań.

Mirdita V., 2006. Genetische Variation for Resistenz gegen Mutterkorn (*Claviceps purpurea* [Fr.] Tul.) bei selbstinkompatiblen und selbstfertilen Roggenpopulationen. Rozprawa doktorska. Stuttgart, Univ. Hohenheim, http://opus.uni-hohenheim.de/volltexte/2006/148/.

Morrison L.A., Riera-Lizarazu O., Crémieux L., Mallory-Smith C.A., 2002. Jointed goatgrass (*Aegilops cylindrica* Host) × wheat (*Triticum aestivum* L.) hybrids. Crop Sci. 42, 1863–1872.

Mujeeb-Kazi A., 2006. Utilization of genetic resources for bread wheat improvement. Genet. Resour. Chromosome Eng. Crop Improv. 2, 61–97.

Niekerk van B.D., Pretorius Z.A., Boshoff W.H.P., 2001. Occurrence and pathogenicity of *Puccinia hordei* on barley in South Africa. Plant Dis. 85, 713–717, https://doi.org/10.1094/PDIS.2001.85.7.713.

Niks R.E., Habekuß A., Bekele B., Ordon F., 2004. A novel major gene on chromosome 6H for resistance to barley against the barley yellow dwarf virus. Theor. Appl. Genet. 109, 1536–1543, https://doi.org/10.1007/s00122-004-1777-7.

Ogbonnaya F.C., Abdalla O., Mujeeb-Kazi A., Kazi A.G., Gosnian N., Lagudah E.S., 2013. Synthetic hexaploids: harnessing species of the primary gene pool for wheat improvement. Plant Breed. Rev. 37, 35–122.

Oliver R.E., Stack R.W., Miller J.D., Cai X., 2007. Reaction of wild emmer wheat accessions to *Fusarium* head blight. Crop Sci. 47, 893–899, https://doi.org/10.2135/cropsci2006.08.0531.

Perugini L.D., Murphy J.P., Marshall D., Brown-Guedira G., 2008. *Pm37*, a new broadly effective powdery mildew resistance gene from *Triticum timophevii*. Theor. Appl. Genet. 116(3), 417–425, https://doi.org/10.1007/s00122-007-0679-x.

Pickering R., 2000. Do the wild relatives of cultivated barley have a place in barley improvement? In: S. Logue (ed), Barley genetics. Proceedings of the 8th international barley genetics symposium, vol. 1. Department of Plant Science, Waite Campus, Adelaide University, s. 223–230.

Pickering R., Johnston P.A., 2005. Recent progress in barley improvement using wild species of *Hordeum*. Cytogenet. Genome. Res. 109, 344–349.

Pickering R.A., Hill A.M., Michel M., Timmerman-Vaughan G.M., 1995. The transfer of a powdery mildew resistance gene from *Hordeum bulbosum* L. to barley (*H. vulgare* L.) chromosome 2 (2I). Theor. Appl. Genet. 91, 1288–1292, https://doi.org/10.1159/000082418.

Pickering R.A., Ruge-Wehling B., Johnston P.A., Schweizer G., Ackermann P., Wehling P., 2006. The transfer of a gene conferring resistance to scald (*Rhynchosporium secalis*) from *Hordeum bulbosum* into *H. vulgare* chromosome 4HS. Plant Breed. 125(6), 576–579, https://doi.org/10.1111/j.1439-0523.2006.01253.x.

Pickering R.A., Steffenson B.J., Hill A.M., Borovka I., 1998. Association of leaf rust and powdery mildew resistance in a recombinant derived from a *Hordeum vulgare* × *Hordeum bulbosum* hybrid. Plant Breed. 117, 83–84.

Pietrusińska A., Czembor J.H., 2015. Piramidyzacja genów – powszechne narzędzie używane w programach hodowlanych [Pyramidization of genes – a common tool used in breeding programs]. Biul. IHAR 278, 3–16.

Pietrusińska A., Czembor J.H., Czembor P.C., 2011. Pyramiding of two resistance genes for leaf rust and powdery mildew resistance in common wheat. Cereal Res. Comm. 39(4), 577–588, https://doi.org/10.14199/ppp-2017-006.

Prończuk M., Bojanowski J., Warzecha R., Laudański Z., 2007. Badania nad odpornością kukurydzy na zgorzel podstawy łodyg. Cz. I. Ocena podatności odmian mieszańcowych w warunkach infekcji naturalnej [Research on the resistance of maize to stalk base scales. Part I. Evaluation of susceptibility of hybrid cultivars in conditions of natural infection]. Biul. IHAR 245, 155–169.

Qi L., Friebe B., Zhang P., Gill B.S., 2007. Homoeologous recombination, chromosome engineering and crop improvement. Chromosome Res. 15, 3–19, https://doi.org/10.1007/s10577-006-1108-8.

Qureshi S. H., Qayyum A., Fiers W., 2015. Sources of genetic resistance in maize to Fusarium stalk rot and their variations in molecular level. Turk. J. Agric. Forest. 39, 503-513, https://doi.org/10.3906/tar-1409-76.

Rabinovich S.V., 1998. Importance of wheat-rye translocations for breeding modern cultivar of *Triticum aestivum* L. Euphytica 100(1), 323–40.

Rao V.R., Hodgkin T., 2002. Genetic diversity and conservation and utilization of plant genetic resources. Plant Cell Tiss. Org. 68, 1–19, http://doi.org/10.1023/A%3A1013359015812.

Ruge B., Linz A., Proeseler G., Pickering G., Greif P., Wehling P., 2003. Mapping of *Rym14Hb*, a gene introgressed from *Hordeum bulbosum* and conferring resistance to BaMMV and BaYMV in barley. Theor. Appl. Genet. 107, 965–971, https://doi.org/10.1007/s00122-003-1339-4.

Ruge-Wehling B., Linz A., Habekuss A., Wehling P., 2006. Mapping of *Rym16(Hb)*, the second soil-borne virus-resistance gene introgressed from *Hordeum bulbosum*. Theor. Appl. Genet. 113, 867–873, https://doi.org/10.1007/s00122-006-0345-8.

Rzepka D., 1993. Badania nad mieszańcami *S. cereale* × *S. vavilovii* Gross. w aspekcie ich przydatności w hodowli odmian żyta odpornych na porastanie. Cz. I. Ocena odporności na porastanie mieszańców międzygatunkowych żyta [Studies on hybrids of *S. cereale* × *S. vavilovii* Gross. in terms of their suitability in growing the rye cultivars resistant to fouling. Part I. Evaluation of resistance to crossbreeding of interspecific rye hybrids]. Hod. Rośl. Aklim. 37(5/6), 69–79.

Rzepka-Plevneš D., Tomczak P., Pławska M., 1995. Możliwość wykorzystania mieszańców międzygatunkowych żyta w hodowli odmian plennych i odpornych na mączniaka prawdziwego (*Erysiphe graminis* D.C f.sp. *secalis marchal*) [Possibility to use the rye inter-species hybrids in breeding of fertile cultivars resistant to powdery mildew (*Erysiphe graminis* D.C f. sp. *secalis marchal*)]. Hod. Rośl. Aklim. 39(6), 68–80.

Santos E., Benito C., Silva-Navas J., Gallego F.J., Figueiras A.M., Pinto-Carnide O., Matos M., 2018. Characterization, genetic diversity, phylogenetic relationships, and expression of the aluminum tolerance *MATE1* gene in *Secale species*. Biol. Plant. 62(1), 109–120, https://doi.org/10.1007/s10535-017-0749-0.

Scholz M., Ruge-Wehling B., Habekuss A., Schrader O., Pendinen G., Fischer K., Wehling P., 2009. Ryd4Hb: a novel resistance gene introgressed from *Hordeum bulbosum* into barley and conferring complete and dominant resistance to the barley yellow dwarf virus. Theor. Appl. Genet. 119, 837–849, https://doi.org/10.1007/s00122-009-1093-3.

Semenov M. A., Stratonivitch P., Alghabari F., Gooding M.J., 2014. Adapting wheat in Europe for climate change. Journal of cereal science 59, 245–256 https://doi.org/10.1016/j.jsc.2014.01.006.

Sencer H.A., Hawkes J.G., 2008. On the origin of cultivated rye. Biol. J. Linn. Soc. 13(4), 299–313, https://doi.org/10.1111/j.1095-8312.1980.tb00089.x.

Singh R., 1977. Cross compatibility meiotic pairing and fertility in 5 Secale species and their interspecific hybrids cereale. Res. Comminic 5, 67–75.

Singh R.P., Huerta-Espino J., Sharma R., Joshi A.K., Trethowan R., 2007. High yielding spring bread wheat germplasm for global irrigated and rainfed production systems. Euphytica 157, 351–363, https://doi.org/10.1007/s10681-006-9346-6.

Smith C.M., Belay T., Stauffer C., Stary P., Kubeckova I., Starkey S., 2004. Identification of russian wheat aphid (Homoptera: Aphididae) populations virulent to the *Dn4* resistance gene. J. Econ. Entomol. 97(3), 1112–1117.

Strzembicka A., Gruszecka D., Grądzielewska A., 2007. Odporność mieszańców pszenżyta z kozieńcami i pszenperzem na rdzę brunatną i żółtą oraz mącznika prawdziwego [Resistance of triticale hybrids with phasmatops and wheatgrass to brown and yellow rust as well as powdery mildew]. Zesz. Probl. Post. Nauk Rol. 517, 711–719.

Tadesse W., Schmolke M., Mohler V., Wenzel G., Hsam S.L.K., Zeller F.J., 2007. Molecular mapping of resistance genes to tan spot (*Pyrenophora tritici*-repentis race 1) in synthetic wheat lines. Theor. Appl. Genet. 114, 855–862, https://doi.org/10.1007/s00122-006-0484-y.

Tanksley S.D., McCouch S.R., 1997. Seed banks and molecular maps: unlocking genetic potential from the wild. Science 277, 1063–1066.

Terasawa Y., Rahman S.M., Takata K., Ikeda T.M., 2012. Distribution of Hordoindoline in the genus Hordeum. Theor. Appl. Genet. 124(1), 143–151, https://doi.org/10.1007/s00122-011-1693-6.

Tratwal A., Jakubowska M., 2004. Ocena przydatności systemów wspomagania decyzji o ochronie pszenicy ozimej przed mączniakiem prawdziwym na terenie Wielkopolski [The assessment of the usefulness of decision support systems for winter wheat protection against powdery mildew in Wielkopolska]. Post. Ochr. Rośl. 44, 1169–1172.

Villa T.C.C., Maxted N., Scholten M., Ford-Lloyd B., 2005. Defining and identifying crop landraces. Plant Genet. Resour-C 3(3), 373–384, https://doi.org/10.1079/PGR200591.

von Bothmer R., Sato K., Komatsuda T., Yasuda S., Fischbeck G., 2003. The domestication of cultivated barley. In: von Bothmer R., van Hintum T., Knuüpffer H., Sato K. (ed.) Diversity in barley (*Hordeum vulgare*). Elsevier Science B.V., Amsterdam, 9–27.

Walther U., Rapke H., Proeseler G., Szigat G., 2000. *Hordeum bulbosum* – a new source of disease resistance-transfer of disease resistance to leaf rust and mosaic viruses from *H. bulbosum* into winter barley. Plant Breed. 199, 215–218.

Warburton M.L., Rauf S., Marek L., Hussain M., Ogunola O., Sanchez Gonzalez J.J., 2017. The use of crop wild relatives in maize and sunflower breeding. Crop Sci. 57, 1–14, https://doi.org/10.2135/cropsci2016.10.0855.

Yahiaoui N., Kaur N., Keller B., 2009. Independent evolution of functional *Pm3* resistance genes in wild tetraploid wheat and domesticated bread wheat. Plant J. 57, 846–856, https://doi.org/10.1111/j.1365-313X.2008.03731.x.

Yang Z., Li G.R., Jia J.Q., Zeng X., Lei M.P., Zeng Z.X., Zhang T., Ren Z.L., 2009. Molecular cytogenetic characterization of wheat– *Secale africanum* amphiploids and derived introgression lines with stripe rust resistance. Euphytica 167(2), 197–202, https://doi.org/10.1007/s12041-011-0081-y.

Yildirim A., Jones S.S., Murray T.D., Line R.F., 2000. Evaluation of *Dasypyrum villosum* populations for resistance to cereal eyespot and stripe rust pathogens. Plant Dis. 84(1), 40–44, https://doi.org /10.1094/PDIS.2000.84.1.40.

Yousuf N., Dar S.A., Lone A.A., Ahanger M.A., Dar Z.A., Bhat M.A., Shikari A., Sofi P. A., Bhat Z.A., Gulzar S., 2018. Field screening of maize (*Zea mays* L.) landraces for resistance against turcicum leaf blight (TLB) under temperate conditions. Int. J. Chem. Stud. 6(1), 333–337.

Yun S.J., Gyenis L., Bossolini E., Hayes P.M., Matus I., Smith K.P., Steffenson B.J., Tuberosa R., Muehlbauer G.J., 2006. Validation of quantitative trait loci for multiple disease resistance in barley using advanced backcross lines developed with a wild barley. Crop Sci. 46, 1179–1186, https://doi.org/10.2135/cropsci2005.08-0293.

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Streszczenie. Nowoczesna produkcja roślinna ukierunkowana jest na uprawę odmian łączących w sobie częściową lub trwałą w czasie odporność na najczęściej występujące choroby zbóż z tolerancją na abiotyczne czynniki stresowe. Obecnie obserwowany jest wzrost zainteresowania dawnymi i lokalnymi odmianami, zwłaszcza w ekologicznych uprawach zbóż. Duże zdolności adaptacyjne do środowisk marginalnych i odporność na patogeny tych genotypów, a także łatwy dostęp hodowców do zasobów genowych mogą przyczynić się do zwiększenia bezpieczeństwa żywnościowego. Dzikie gatunki pokrewne zbóż oraz odmiany lokalne stanowią niezwykle cenny materiał badawczy i aplikacyjny w pracach naukowych oraz hodowlanych. Celem niniejszej publikacji jest przybliżenie zakresu i możliwości wykorzystywania w programach hodowlanych odmian dawnych, miejscowych i dzikich gatunków pokrewnych zbóż jako potencjalnych dawców stabilnej i trwałej odporności na stresy biotyczne.

Słowa kluczowe: dawne odmiany, dzikie gatunki pokrewne, geny odporności, hodowla odpornościowa, różnorodność genetyczna, źródła odporności

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