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

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
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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 re-
stance 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 epiphytotic. 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 kaprijanovii* 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-Plevenš 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 geneitic 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, Feillet 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, MIZec1, 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 cereale* 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 [Fribe 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]. Hy-
bridges of tritcale (Aegilops crassa Boiss × Triticeae) obtained by Strzembicka et al. [2007] were characterized by resistance to brown rust of tritcale 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 RyeHb 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 rhinchoriosis (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 Ss24 from Thinopyrum ponticum (JJJJJ) or Ss38 from Triticum ventricosa (DN) [McIntosh et al. 1995]. Combination of resistance genes (Ss24, Ss25, Ss26, Ss32, Ss39, Ss43, Ss47, Ss51) 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 Ss38 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 [Chelkovski et al. 2003]. The Pm21 gene was first transferred from Haynaldia villosa (syn. Dasyopyrum villosum) (VV) to T. durum in the 1980s by Chen et al. [1995] through the translocation T6A-L6V5. It has been introduced into many cultivars of wheat grown both in Europe and Asia. Based on the available litera-
ture 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), $Lr19$, $Lr24$ or $Lr29$ ($Agropyron elongatum$), $Lr21$ ($Aegilops tauschii$), $Lr28$ ($Agropyron intermedium$) [McIntosh et al. 1995, Görny 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 maturat $Hinb$ion 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.

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


Source of funding: Ministry of Agriculture and Rural Development (Poland), Multiannual Programme, Area 1 Protection of crop genetic resources.

**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 patogene tych genotypów, a także łatwy dostęp hodowców do zasobów genowych mogą przyczynić się do zwiększenia bezpieczeństwa żywnościowego. Dzikie gatunki pokrewnie 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 trwalej odporności na stresy biotyczne.

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

Received: 3.10.2018
Accepted: 3.12.2018