Characteristics of immunity to leaf diseases of winter wheat samples under the conditions of the north-east forest steppe of Ukraine

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To realize the genetic potential of the productivity of bread winter wheat varieties, it is necessary to maintain a certain level of plant resistance to disease. Resistance donors may lose this property as a result of changes in the virulence of the pathogen and defeat of the genetic systems of plant resistance. This makes it necessary to search for new resistance sources and donors to leaf diseases. Our researches were conducted using field, laboratory and mathematical-statistical methods. Phenological observations, accounting, evaluation and harvesting were conducted according to currently accepted methods. 86 bread winter wheat samples from the 4th WWSRRN CIMMYT were studied for resistance to leaf diseases in our research during 2014–2016. The manifestation of variability depended significantly on the genotype for three diseases. The highest genotype influence was observed in resistance to septoria disease, where it was 81%. On average the highest indicator of resistance (7.7) to powdery mildew during the three years of research was observed in the mid-late ripening samples. The mid-early ripening group was considered to be the most adapted to the powdery mildew pathogen in the Northeastern Forest-Steppe. The highest average indicator of resistance (7.5) to brown rust for the three years of research was found in the early ripening group. The samples of the mid-ripening group were most adapted to the brown rust pathogen. The highest average resistance to septoria disease was also found in the early ripening group. The best adaptation to septoria disease was observed in mid-late ripening samples. 36% of the samples were resistant to three diseases. As a result of the research, a number of CIMMYT samples were isolated from the 4th WWSRRN, which exceeded the standard in resistance to powdery mildew, brown rust and septoria disease. They were characterized by better performance. Valuable forms for breeding work that can be resistance donors to leaf diseases were identified among them.

Keywords: resistance; powdery mildew; brown rust; septoria disease; pathogen; yield capacity.

Introduction
Global climatic changes have a negative impact on global trends in crop production, which undoubtedly affects our country. Every year winter wheat crops are affected by extremely low or high temperatures and they suffer from disease and pests. A significant proportion of domestic and foreign wheat breeding varieties have not been adapted to the new global climate warming and drought, which have recently been observed during the vegetation period in the natural and climatic zones of Ukraine. As a result, wheat yield capacity is unstable and individual farms suffer from significant economic losses (Morgun et al., 2014). The problem of crop protection against disease does not lose its relevance in modern grain production. The need of the world market for environmentally friendly agricultural products leads to the tendency to reduce the use of chemical plant protection products against pathogens (Brygadyrenko & Nazimov, 2015; Reshetniak et al., 2017). An alternative to pesticide use is the cultivation of resistant varieties. They reduce the usage of pesticides which are hazardous to humans, animals and the environment (Mukha & Zayima, 2013).

Modern world and advanced domestic developments in genetics and breeding, connected with creation of new plant varieties, are characterized by wide application of both classic methods and the latest molecular and genetic developments in this branch (Kovalyshyna et al., 2017). Vlasenko et al. (2012) conducted an analysis of the genealogy of wheat varieties, which determined a very high level of successful application of the distant hybridization method by scientists in many countries (the USA, England, Sweden, Germany, Italy, France, etc.). The results prove the great effectiveness of this method, and it allows radical changes to be made in the heredity of important economic features of the plant organism and the creation of new valuable forms and plant varieties that provide the expansion of genetic wheat diversity. The combination of varied innovative genetic and molecular technologies with traditional breeding allows us to obtain new high-yielding, high-tech varieties of crops adapted to modern climatic challenges (Morgun et al., 2014).

Yachevskya (1990) made a thorough review of foreign studies of using the distant hybridization method in wheat breeding.

The main conclusion is that many species and genera related to bread wheat are the carriers of inexhaustible genetic properties. They are introduced by many breeders of the world into the wheat genome, increasing its resistance against various diseases, pests and stressful environmental conditions. So they increase the yield capacity, the grain quality and achieve their higher stability.

Worldwide, powdery mildew caused by the fungus Blumeria graminis f. sp. tritici is a major wheat disease. The pathogen can cause significant crop losses in epiphytotics. The use of genetic resistance is the most effective approach to control the disease. To identify the genomic regions responsible for the US winter wheat resistance and to identify DNA markers in these regions, Lu Liu et al. (2017) conducted studies on the associated genomic set of 185 winter wheat samples. They identified markers associated with the nine quantitative loci characteristic and simple sequence markers (SSR) associated with three loci responsible for powdery mildew...
dew resistance. Most of the loci in the US winter wheat population have been reported before, but loci on 1A, 6A, and 1B chromosomes are probably new. Germplasm with immunity to powdery mildew is a good resistance source and it can be used in further breeding work.

The N0324 wheat line obtained from *Triticum dicoccoides* Thell as a result of 5055/Shaan 253 crossing provides effective protection against powdery mildew. The analysis of 205 samples in F2 created by crossing N0324 with the susceptible variety Shanyi 255 determined that in Russia resistance of N0324 line was controlled by a single recessive gene, temporarily identified as Pm5055. Four SSR markers, such as Xwmc441, Xbarc7, Xbarc13, and Xbarc55, were connected with the gene at a distance of 10.6, 23, 23, and 23.9 microns, respectively. Chinese Spring null-tetrasomic and ditelosomic lines were used to determine chromosomal marker locations. The results showed that this gene can be located on chromosome 2B. Pm5055 can be used to diversify sources of resistance to powdery mildew in future breeding programs for wheat varieties (Marnoudou et al., 2016).

The creation of wheat lines with alien translocations facilitated the practical use of distant species in wheat improvement. The Robertson translocation of *Triticum aestivum* / *Thinopyrum bessarabicum* in 6D wheat chromosome from 6Eb *Thinopyrum bessarabicum* (2n = 2x = 14, Eeb) occurred through a chromosomal rearrangement – fusion. The F2 population was obtained from the plant crossing between the DS6Eb (6D) line and the Roushan bread wheat variety (2n = 6x = 42, AABBDD). Three PCR-based markers that were characteristic for chromosomes 6D and 6Eb were used for screening F2 plants. A homoygous line with complete fertility was detected among F3 families and tested by genomic line in situ hybridization (Ardalani et al., 2016).

In wheat breeding programs the accurate and rapid detection of 6RL chromatin in the wheat genotype is essential for the effective use of elite genes on the long arm of 6 (6RL arm) rye chromosome. PCR-specific 6RL markers can foster the detection of elite 6RL genes in wheat breeding. A limited number of 6RL-specific markers were developed. 300 of new PCR-specific 6RL-specific markers were detected in the research. SLAF-seq fragment sequencing technology was used. The fragments were additionally physically mapped in four areas on 6RL arms using 6R and 6RL lines. In addition, 95 of 300 markers demonstrate polymorphisms that can be used to investigate the diversification of the 6RL rye genome. The markers developed in this research can be used to identify predetermined 6R introgression and to accelerate the use of elite 6RL genes in wheat breeding (Li et al., 2016).

Allelic resistance genes of Pm3 to wheat give specific resistance to powdery mildew (*Blumeria graminis* f. sp. *tritici* Bgt) and encode nucleotide-binding domains rich in leucine-rich repeated (NLR) receptors. The N0324 wheat variety and tested in field studies. They showed various degrees of resistance to powdery mildew. Scientists from China tested by genomic line in situ hybridization (Ardalani et al., 2016).

Aegilops tauschii is an excellent source of disease resistance that is transferable to *T. aestivum*. The source TA1662 (2n = 2x = DD) was crossed with the powdery mildew susceptible line KS05H14 (2n = 6x = AABBDD) followed by backcrossing to develop a population of 96 BC2F4 introgression lines (Wiersma et al., 2017). Genotyping by sequencing was used to develop a genetic map of the entire genome that was linked to *Ae. tauschii* reference genome. Bgt analysis with peeling was used to select the introgression lines and it was found that the resistance was as a separate locus (χ2 = 2.0, P = 0.157). The resistance Pm58 gene is mapped on the 2DS chromosome. Pm58 was evaluated under the field condition in replication experiments in 2015 and 2016. It was detected in one of the Pm58 loci that reduced the powdery mildew prevalence and explained 21% of changes in the field (P < 0.01). Kaspar analyses were developed from closely related GBS-SNP markers, a genetic map was refined, and four markers identified by Pm58 were determined. This new source of resistance will help to originate wheat varieties resistant to powdery mildew.

The worldwide distribution of rye 1RS translocations contained in wheat varieties for commercial purposes is largely explained by the fact that they carry disease and pest resistance genes. The 1BU/1RS translo-
cation contains Pm8 – the resistance gene to powdery mildew (pathogen – Blumeria graminis), Sr31 – the resistance gene to stem rust (pathogen – Puccinia striformis) (McIntosh et al., 1998). The 1AL/1RS translocation of the Amigo variety carries the resistance gene to aiphas B and C 682, Acreia toxicohelia (Ketler) Cm3 rate, a powdery mildew resistance gene Pm17, a gene for resistance to stem rust SrA1R (McIntosh et al., 1998, 2005). Genes containing wheat-rye translocations under the Northeast Forest-Steppe conditions provide resistance to varieties. According to the productivity elements the translocation carriers are characterized by high combining ability, they form higher and more stable grain yields (Bakumenko & Vlasenko, 2018).

Rye (Secale cereale L.) chromosome-specific markers can contribute to the effective utilization of elite genes of rye in wheat (Triticum aestivum L.) breeding programs. Qiu (2016) developed 578 new rye-specific markers using specific length amplified fragment sequencing (SLAF-seq) technology, and 76 markers displayed different polymorphism among Kustro, Imperial, and King II rye. A total of 427 and 387 markers were, respectively, located on individual chromosomes and chromosome arms of Kustro by using a set of wheat-rye monosomic addition lines and 13 monotelosomic addition lines, which were derived from T. aestivum L. ‘Mianyang11’ × S. cereale L. ‘Kustro’. In addition, two sets of wheat-rye disomic addition lines, which were derived from T. aestivum L. var. Chinese Spring × S. cereale L. var. Imperial and T. aestivum L. ‘Holdfast’ × S. cereale L. var. King II, were used to test the chromosomal specificity of the 427 markers. The chromosomal locations of 281 markers were consecutive among the three sets of wheat-rye addition lines. The markers developed in this study can be used to identify a given segment of rye chromosomes in wheat background and accelerate the utilization of elite genes on rye chromosomes in wheat breeding programs.

The genomic sequence based on the Chinese Spring wheat chromosome scheme allows development of large-scale markers of polymere chain reaction (PCR) specific to homoeologues (Zeng et al., 2016). Based on the Chinese Spring genes, Zeng et al. (2016) developed 183 homoeologous-specific markers for 4B and 7B chromosomes. These markers were used in PCR tests for nullisomes 4B and 7B and their line of euploid synthetic hexaploid wheat (SHW) generated from hybridization between Triticum turgidum (AABB) and wild diploid species. Aegilops tauschii (DD). These studies confirmed that up to 64% of markers for chromosomes 4B or 7B against the SHW background are homoeologous-specific. Thus, these markers had a very good ability to be transferred between bread Chinese Spring wheat and SHW lines. Homoeologous-specific markers developed using genes with known functions may be useful for genetic studies, including home-based chromosome tracking and homoeologous expression and interaction analysis. Aegilops speltoides Robertson translocation includes all Ae. speltoides chromosomal arms, except the long arm of the homologous group of 4 chromosomes (Liu et al., 2016). Aegilops speltoides of the genus Poaceae is the most likely donor to the genomes of the B and G polyploid species of Triticum, as well as an important source of wheat resistance to diseases and pests. Most RObTs were fully fertile and they facilitated gene mapping and accelerated the introgression of agronomically useful traits into wheat by homologous recombination. The agent of powdery mildew – Puccinia recondita L. sp. tritici Rob. Et Desm. (syn. P. triticum Erkiss.) is adapted to different climatic regions, so it is observed in all of the areas in the world in wheat cultivation. This is a specific disease of wheat, which causes large scale crop failure, especially in the Forest-Steppe and Polissya of Ukraine. Brown rust epiphytotes occurred 2–3 times every 5 years in Ukraine (Vozhzhova, 2018).

One of the priority directions for winter wheat breeding is to provide resistance to brown rust. Gene Lr34 provides wheat resistance by type of slow pace of development. The results of identification work in 646 samples of the gene Lr34 bread winter wheat and its allelic condition are presented. The alleles of the Lr34 gene were evaluated by the codominance of the molecular SNS marker csl V34 by the polymerase chain reaction method. 238 samples that carry the brown rust resistance gene Lr34 in the dominant allelic condition were identified (Kovalyshyna & Dmytryenko, 2017; Kovalyshyna, 2018). Scientists from the National University of Life and Environmental Sciences of Ukraine, the Institute of Plant Protection of the NAAS of Ukraine and the V. M. Remeslo Mironivka Institute of Wheat identified the allelic condition of the Lr34 gene among the 15 studied varieties (Kovalyshyna & Dmytryenko 2017; Kovalyshyna, 2018). Only three cultivars – Berehynia Myronivska, Dragopilka MIP and Balada Myronivska – contain the Lr34 (+) allele, which is only 20% of the studied varieties. The Lr34 gene is known to be non-specific. It provides overall resistance to various brown rust pathotypes in adult plants. Therefore, the results show that when creating new wheat varieties resistant to brown rust, it is necessary to use varieties with the identified “resistant” allele of the Lr34 gene, as the resistant source in breeding.

Kenya wheat Kenya Kongoni (Triticum aestivum L.) has a high level of plant resistance to leaf rust and yellow rust (Calvo-Salazar, 2015). Kenyan scientists identified genomic regions associated with rust resistance in a population of 148 recombinant inbred lines generated from crossing between Avocet-YR and Kenya Kongoni. Field experiments to characterize the plant resistance to leaf rust and yellow rust were conducted in Mexican and Uruguayan environments. A connection map with technology of 438 different arrays and 16 simple sequence repetition markers was built using JoinMap 4.1. Genetic analyses showed that resistance to both diseases under study was determined by four to five genes, including Lr46/Yr29 and Sr2/Lr27/Yr30. Quantitative loci analyses of traits showed that pleiotropic loci of APR Ylcr.ism-1BL, corresponding to Lr46/Yr29 and the predicted new Ylcr.ism-7BL, are 5–57% and 12–35% of the phenotypic variation for resistance. These loci, in combination with other three LR QTLs and two YR QTLs, respectively, provided high levels of resistance to both leaf rust and yellow rust in wheat in Mexican and Uruguayan environments. Other identified QTLs, Ylcr.ism-1DS, Ylcr.ism-2BL, and Ylcr.ism-7BL may be new loci for both rust forms in common wheat (Calvo-Salazar, 2015).

Twenty-six wheat genotypes were evaluated for the level of plant resistance to leaf rust in two different locations (Shybin El-Kom and Ita-El-Barrow) during two consecutive growing seasons 2011–2013 (Fahmi et al., 2015). Wheat varieties Sids 12, Sids 13, Misor 1 and Misor 2, Shandweel 1, Beni Sweif 4 and Beni Sweif 5 have specific resistance. Meanwhile the genotypes of wheat with Lr 34 (Giza 165, Giza 168, Sakha 8, Sakha 94, Sakha 95, Gemmeiza 5, Gemmeiza 7, Gemmeiza 9, Gemmeiza 10, Gemmeiza 11) showed high level of resistance to brown rust. Other tested varieties were highly susceptible to this pathogen: Giza 160, Giza 163, Giza 164, Sakha 69, Sakha 93, Sids 1 and Giza 139. To confirm the presence of the Lr resistance gene of 34 adult plants, the SSR marker, i.e. the csLv34 allele was used in the tested genotypes (150 bp).

The Chikheti (2016) study was planned to detect resistance to three rust diseases (leaf, stem and yellow) in new varieties under field conditions. The RIL population was evaluated for 2012–2013 and genotyped with DARtSeq. The map link was constructed using 3439 DARtSeq markers with an average density of 2.7 cm. The composite display interval identified three QTLs for stem rust, and leaf rust W195/BTSS RIL. Two consecutive QTLs for stem rust, YQR.sun-3DS and YQR.sun-4DL were introduced by W195 and one incompatible QTL, YQR.sun-7AS, BTSS, for leaf rust QLR.sun-2BS and QLR.sun-3BS was made by BTSS and QLR.sun-4DL using W195. It was demonstrated that QLR.sun-2BS Lr25.BTSS restrained the QTL stem rust; QLR.sun-4DL restrained the QTL leaf rust; QYr.sun-2BS and QYr.sun-3BS restrained the QTL yellow rust. Located QTL for all three rust diseases in 4D chromosome corresponded to the Sr8a resistance gene, which is a BTSS carrier. Located QTL for all three rust diseases in 4D chromosome corresponded to the Sr8a resistance gene, which is a BTSS carrier. Located QTL for all three rust diseases in 4D chromosome corresponded to the Sr8a resistance gene, which is a BTSS carrier. Located QTL for all three rust diseases in 4D chromosome corresponded to the Sr8a resistance gene, which is a BTSS carrier.
phytopathological test (up to three isolates of the fungus with virulence to TcL9, TcLr19, TcL26) and with PCR analysis using 10 molecular markers Lr1, Lr3, L9, Lr10, Lr19, L20, L24, L26, Lr34 and L37. The research showed that among the studied varieties there were no universal ones resistant to all three clones. 11 varieties showed resistance to three clones, but in the germination phase they were affected by pathogens. In the researched varieties the resistance genes L9, Lr10, L24, L26 were also not detected with the PCR analysis. Of the 37 researched varieties, 29 contained Lr34 gene and 20 had an ineffective Lr3 gene that could not protect plants from brown rust in the field. It indicates that the resistant varieties carry additional unidentified Lr genes. Two resistance genes were determined in some varieties. The Khipchak cultivar had Lr1 gene, which lost its effectiveness. The difference between the degree of damage of some varieties under the conditions of Rostov region and St. Petersburg indicates the difference between the North Caucasian and Northwestern populations in resistance to the pathogen of brown rust.

The most common and harmful pathogen of wheat grain is Septoria leaf (Septoria tritici) Rob. et Desn. (Suhormal, 2013). The harvest lost from septorirosis depends on the degree of disease development. Its share in the complex of the most common winter wheat diseases is from 7% to 25% in different regions of Ukraine. The disease is widespread in almost all wheat growing areas. Currently, several resistance genes to S. tritici were identified and named Sb. According to the data of scientists of the Plant Growing Institute (Kryuchenko et al., 2012), the first three genes – Sb1–Sb3 are – are defined by Wilson (1985). Sb4 – Somasco (1990). Arnaïno (2001) reported about Sb5 gene, a genetic source of its resistance as Ae. tauschii, and information of Brading et al., about the detection of Sb6. Genes with the constant symbols of Sb7–Sb12 and Sb6Ac1 and Sb6Ac2 was also identified (McIntosh, 2008). Sources of the cultivated wheat resistance to the septoria disease pathogen are its related species (Triticale, Triticum timopheevii, T. fungidichum, T. monococcum, T. boeoticum, T. kiharae, T. urartii, T. zhukerskii, T. tauschii, etc.) and wild varieties (Agropyron elongatum, Aegilops searsrooa, Ae. speltoides, Ae. sharonensis), from which the resistance is transferred to cultivated varieties by interspecific and distant hybridization.

Winter wheat varieties originated and regionalized in Ukraine are generally not highly resistant to leaf diseases (Kryuchenko et al., 2012). Therefore, it is necessary to carry out deliberate work to originate varieties resistant to the studied diseases and to introduce them into breeding. It will reduce the infection and prevent the emergence of new pathogen races.

After literature source processing it became clear that the potential of foreign translocations to originate new varieties is not exhausted, since their manifestation is largely determined by the genotypic environment. So the searching for donors of leaf disease resistance among varieties and hybrids of domestic and foreign breeding, in particular among the samples of CIMMYT breeding-ground (International Center for Wheat and Corn Improvement), is relevant at this time. More than 140,000 unique wheat seed collections were collected at CIMMYT. According to its programs, this organization annually sends half a million packages of seeds to 600 partners in 100 countries. CIMMYT programs are aimed at improving the agricultural productivity in the countries of the world. The wheat specialist in the program, Nobel laureate Norman Borlaug worked with Mexican researchers and farmers to develop wheat genotypes that were disease resistant and showed much higher yield capacity than traditional varieties. New wheat lines are originated and selected under different climatic conditions (Khondoker et al., 2019).

From the world-renowned organization – International Center for Wheat and Corn Improvement (CIMMYT), we obtained the fourth winter wheat breeding ground resistant to stem rust (4th WWSRRN). They began to create this breeding-ground in early 2004–2005, when a race of stem rust Ug99 appeared. It affected about 90% of the world wheat area. For this reason, it was decided to create such a breeding-ground in CIMMYT (Khondoker et al., 2019).

As a rule, foreign translocations contain resistance genes to stem rust. The wide distribution of rye 1RS translocations in commercial wheat varieties is largely due to the fact that they carry disease and pest resistance genes. The 1BL/1RS translocation contains Pm8 – powdery mildew resistance gene (pathogen – Blumeria graminis), Sr31 the resistance gene to stem rust (pathogen – Puccinia graminis), Lr26 – the resistance gene to brown rust (pathogen – Ycc9c) and the yellow rust resistance gene (pathogen Puccinia striiformis) (McIntosh et al., 1998). 1AL/1RS translocation from the Amigo variety carries the resistance gene to aphids B and C Gb2, Aecia tosicheilla (Keifer) Cn3 rate, to resistance powdery mildew PM17, the resistance gene to stem rust SrAIR (Kozub et al., 2005; Khondoker et al., 2019). Virtually to the end of the XX century, the rye resistance gene of Sr31 1LL/1RS translocation was effective against all known rusted stem races. The situation changed with the emergence of the Ug99 (TTKSK) race in Uganda, then in Kenya and with the threat of its further spread. The presence of rye 1BL/1RS translocation and Sr31 gene is not a reliable protection against stem rust, since TTKSK and related isolates are virulent to Sr31 (Pretorius, 2000). One of the genes that provide resistance to the TTKSK race of stem rust is the SrAIR gene, which is on the rye 1AL/1RS translocation from Amigo. It is designated Sr1RSAmigo (Kozub et al., 2010; Olson et al., 2010; Bakumenko et al., 2015). It is this translocation that contains the resistance gene to powdery mildew PM17, which made it possible to hypothesize the resistance of the obtained samples simultaneously to two diseases of stem rust and powdery mildew. We decided to check the samples resistant to stem rust from CIMMYT breeding-ground for resistance to powdery mildew, brown rust and septorirosis disease, to select sources for further breeding work.

The aim of the study: to find out the immunological properties of the 4th WWSRRN CIMMYT samples for resistance to leaf diseases (powdery mildew, rust, septoria) in the northeastern forest-steppe of Ukraine and to identify the sources of resistance of the studied trait.

Materials and methods

The material was 86 CIMMYT samples from the 4th WWSRRN nursery (winter wheat stem rust resistant nursery). The laying out of research and phenological observations were conducted according to standard methods (Volkodav, 2003). The seeds of the collectable samples were sown with a manual seeder MS-1 in triplicate with a plot area of 1.2 m². Plot placement was systematic. Sowing of the samples was carried out within the time limits allowed for the Northeastern Forest-steppe of Ukraine (from September 20 to October 2). Seed rate was at 5 million pieces/ha. The mineral fertilizers of Superagro N15P15K15 with norm of 100 kg/ha and early spring fertilization with ammonium nitrate (100 kg/ha) were applied. The harvesting was done manually. The crop was converted to standard humidity.

The evaluation of the wheat resistance to leaf diseases was performed on a natural infectious background using varieties of infection carriers (Agassiz – powdery mildew; Sel/Egin – brown rust; Borovii – septoria disease). Resistance to powdery mildew and septoria disease was determined according to the modified Saari and Prescott scale from the tube exit phase to milky-wax maturity several times. The manifestation of resistance to brown rust was evaluated three times according to the 9-point integrated scale for cereal resistance assessment. The main consideration was the maximum disease manifestation, which was usually observed during the period of grain formation (Kryuchenko et al., 2012). Structural analysis of the bundle material was conducted to identify the yield properties of the varieties and the dependence of the yield elements on the pathogen damage was determined. The length of the stem, the mass of 1000 grains and the yield capacity were ascertainment during the analysis. Biometric data processing was performed by mathematical and statistical methods (Dospehov, 1985).

The area under the research is characterized by a temperate continental climate with warm summers and not very cold winters with thaws. Weather conditions were analyzed according to the weather report of the Institute of Agriculture of the North-East of NAAS of Ukraine, which is located at a distance of 6 km from the experimental field. The highest rainfall over the years of research was in 2016 – 792 mm and the lowest rainfall was in 2014 – 553 mm. The average annual air temperature over the years varied +8.8…+ 9.5 °C. The highest sum of active temperatures was recorded during the growing season 2015/2016 – 3,489 °C, the lowest in 2014/2015 – 3,242 °C. In general, the contrasting weather conditions over the years of research promoted the compre-
Results

We found a different norm of genotype response to hydrothermal conditions changes (Table 1) during the years of research (ecogradient).

Table 1

<table>
<thead>
<tr>
<th>The source of variability</th>
<th>Powdery mildew</th>
<th>Brown rust</th>
<th>Septoria disease</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genotype</td>
<td>F</td>
<td>%</td>
<td>F</td>
</tr>
<tr>
<td>Conditions of the year</td>
<td>12</td>
<td>0.1%</td>
<td>12</td>
</tr>
<tr>
<td>Interaction genotype/year</td>
<td>12</td>
<td>0.8%</td>
<td>12</td>
</tr>
<tr>
<td>Random</td>
<td>-</td>
<td>5.2%</td>
<td>-</td>
</tr>
<tr>
<td>General</td>
<td>100</td>
<td>100%</td>
<td>100</td>
</tr>
</tbody>
</table>

Note: F – Fisher value; % – the fraction of the factor influence.

The confidence level was less than 0.1% of significance on both factors for the three diseases. Therefore, different genotypes and conditions of the year have a statistically significant effect on resistance to powdery mildew, brown rust and septoria disease. Genotype was found to account for 65.4% of resistance powdery mildew in bread wheat, with 0.1% of resistance due to eco-gradient, 28.7% due to interaction of both factors, and about 5.8% due to random factors. As for the resistance to brown rust, the impact of the genotype was equal to 41.3%, impact of the eco-gradient – 22.7%, the interaction of both factors – 27.9%, and random factors – about 8.1%. As a result, the variability manifestation of the analyzed trait according to all three diseases significantly depended on the variety genotype and much less on the eco-gradient and the interaction of these sources.

The first group includes early ripening varieties in which the average resistance reached the highest value (6.83) in 2014 (Table 2).

Table 2

<table>
<thead>
<tr>
<th>The group of samples ripeness (number of days from spring awakening to earing)</th>
<th>Amounts of samples in the group, pcs.</th>
<th>Resistance to powdery mildew over the years, by points</th>
<th>x ± SD, n = 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Early ripening (58–60)</td>
<td>6</td>
<td>6.83 ± 4.17</td>
<td>4.52 ± 5.17</td>
</tr>
<tr>
<td>Mid-early ripening (61–63)</td>
<td>6</td>
<td>6.53 ± 7.81</td>
<td>7.86 ± 7.40</td>
</tr>
<tr>
<td>Mid ripening (64–66)</td>
<td>61</td>
<td>7.10 ± 7.13</td>
<td>6.89 ± 7.04</td>
</tr>
<tr>
<td>Mid-late ripening (67–70)</td>
<td>13</td>
<td>7.20 ± 7.69</td>
<td>8.00 ± 7.70</td>
</tr>
</tbody>
</table>

Note: different letters indicate values which reliably differ from one another within one column of the table according to the results of comparison using Tukey test with Bonferroni correction.

But the maximum score was only 9.0 (the cultivar Afina), the minimum score was 4.67 (the cultivar Seri). Over the years of research the lowest average indicator of resistance (4.17) to powdery mildew was in 2015, with a maximum of 9.0 (the cultivar Afina) and a minimum score 2.5. In 2016, the average resistance indicator was slightly higher (4.52), the maximum (9.0) – the cultivar Afina, the minimum (1.27). On average, over three years of research, the indicator of early maturing samples was 5.17. Compared to other groups, this score was the lowest with a variation of 2.66. The highest resistance rate was observed over three years in the cultivar Afina.

In the mid-early ripening group in 2014, the average resistance was at the lowest value (6.53), the maximum – 7.2 (samples Trakia/ Mag74/MON3/SHAHI4/EBV/D99–1), and the minimum – 5.0. In the 2015 growing season, the average resistance indicator reached 7.81, the maximum – 9.0, the minimum – 6.0. In 2016, the maximum score was 9.0. It was also fixed in MCCORMICK/Trego. Over three years of the research, the average indicator of the analyzed trait was 7.4 with a variation range of 1.33. MCCORMICK/Trego showed the highest resistance over the three years. RINA-6/4/BEZ/NAD/ZN/ESS53/24/3P900K, TAM200/KAUZ/BEZ/NAD/KZM/ESS5/24/3P900K, TAM 302/KS93U450 had higher resistance among the varieties of this group.

Mid-ripening morphotypes were included to the third group. In 2013/2014 the average resistance indicator of these varieties reached 7.1 points, the maximum – 8.8 (Cv. roldina/Ae. speltoides (10 KR)), the minimum – 4.7. The average stability indicator in 2014/2015 was the highest – 7.13, the maximum – 9.0 (1744/7C/SU/RLD3/CROW/4/ MILAN5/TOR, X84W063-9-18/U1324-25-1–4–K/92/3/L62531, and others), the minimum 1.0. In 2015/2016, the average stability indicator was 6.89, the maximum – 9.0 (RAN 96/GANUS3-3, CMH72-48/ Morocco3/BDPN/4/Terna31, and others), the minimum – 1.3. Over three years, the average stability score was 7.04 and the variation rate was 0.24. Over three years among the varieties of this group Se1.1B*Z3/KAUZ2/BOW/Kauz4/Burhot-45/Boema, Rana96/GA GSU-3, OK8136/Mercan-2, Rina-6/4/BEZ/NAD/KZM/ESS524/3/ F900K, Cv. roldina/Ae. speltoides (10 KR), Cv. Lada/K-62903, and others showed consistently higher resistance.

In 2014 in the group of mid-late varieties the average resistance to powdery mildew was the highest among all maturity groups – the score 7.2, but the lowest over the years of research, the maximum – 9.0 (Simano), the minimum – 5.3. The average resistance indicator in 2015 was also the highest among the previous groups – the score 7.89, the maximum – 9.0 (EC-P, Fiorina, Simano), the minimum – 3.3. For the growing season 2015/2016, the average indicator was 8.0 and was the highest among the years of research, the maximum – 9.0 (T0804, EC-P, SD29107-2/S99 W042, Fiorina, Simano), the minimum – 3.2. Over three years of research, the average late samples had the highest stability score of 7.7 points among all groups, with a variation score 1.2. Among the varieties of this group over three years the following were characterized by high resistance – ID800994/W/VEE/Piopio3/MNCH4/4FDL4/ Kauz, TAM107/T21, (KS95U522/TX95V/A0011)/F1/JAGGIER, CH111.14422, Simano.

Table 3

<table>
<thead>
<tr>
<th>The group of samples ripeness (number of days from spring awakening to earing)</th>
<th>Amounts of samples in the group, pcs.</th>
<th>Resistance to brown rust over the years, by points</th>
<th>x ± SD, n = 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Early ripening (58–60)</td>
<td>6</td>
<td>8.11 ± 5.22</td>
<td>6.01 ± 7.48</td>
</tr>
<tr>
<td>Mid-early ripening (61–63)</td>
<td>6</td>
<td>7.67 ± 5.66</td>
<td>6.09 ± 7.14</td>
</tr>
<tr>
<td>Mid ripening (64–66)</td>
<td>61</td>
<td>7.29 ± 5.72</td>
<td>6.87 ± 7.58</td>
</tr>
<tr>
<td>Mid-late ripening (67–70)</td>
<td>13</td>
<td>7.98 ± 5.01</td>
<td>7.06 ± 5.20</td>
</tr>
</tbody>
</table>

Note: see Table 2.
In 2014/2015, the average resistance was the highest as for eco-
gradents and other groups – 8.32, maximum – 9.0 (Afina, HB/FO290/
X84W063-9-392//ARH/3/LE 2301), minimum – 3.0. In 2016 the maxi-
num resistance indicator was 8.8 (HB/FO290/X84W063-9-392/ARH/
3/LE 2301), the minimum – 2.5. For three years, the average resistance of
early ripening samples was 7.48 and it was the highest in comparison
with other groups, with a variation range of 2.31. Over three years the
varieties Afina, HB/FO290/X84W063-9-392//ARH/3/LE 2301 were
among the varieties of this group with stable resistance.

In the group of mid-early ripening samples in the 2013/2014 growing
season, the average was 7.67, the maximum – 8.7, and the
minimum – 6.3. In 2014/2015, the maximum resistance indicator was 9.0
(TAM302/KS93U450, MCCORMICK/TREGO), the minimum – 4.6.
In 2015/2016, the average indicator was the lowest over the years of
research and the highest among the groups – 6.01, the maximum –
7.4 (MCCORMICK/TREGO), and the minimum – 3.0. For three years of
research, the average indicator in this group was 7.14. The range of
variation in the group (over years) was 1.58 points. Rina-6/4/BEZ/
NAD/KZM/ES85.24//3/F900K, TAM302/KS93U450, MCCORMICK/
Trego showed the consistently higher resistance among the varieties of
this group.

In 2014, the average resistance indicator to brown rust in the mid-
ripening group was the lowest among the studied groups and the ave-
gage over the years of research – 7.29 points, the maximum – 9.0 (Ca-
et/PEHLIVAN, B10/B.ARRIERO, 1//CHAM6//13/D1/LMT/3/
SH7414//CROW, TAM200/KAUZ/GOLDMARK/3/BETTY,
and others), the minimum – 4.1. In 2015 the average resistance indicator was
7.17 points, the highest – 9.0 (Dalger-1//Vorona/BAJ, Caket/Pehlivan,
B10/B.Arriero, OK81306//MERCAN-2, Santa, 06395GP1, and others),
minimum – 3.0. In 2015–2016, the maximum resistance indicator was
8.8 points (Caket/Pehlivan), the minimum – 2.1. This group of varieties,
compared to others, had the lowest average resistance (5.87 points) over
three years of the study. The variation range for the analyzed trait was 1.42.
The following samples had consistently higher resistance: T08/02, Afina,
KZM/ES85.24//3/F900K, MCCORMICK/Trego, Caket/Pehlivan,
FL9547/NC00-14622, FL9547/TX00D1626.

In 2014, the average resistance indicator to brown rust in mid-
late ripening samples was 7.98 points, the maximum – 9.0 (SD29107-2/SD99
W042, Simano, ID800944/WVE/PIPIPO35/MNCH/4/DFDL4/Kauz,
and others), and the minimum was 5.0. In 2015 the samples T08/04,
SD29107-2/SD99W042, (KS95U522/TX95VA0011)F1/JAGGER, Si-
mano showed the maximum resistance indicator (9 points). In 2015–
2016 growing year the average indicator was the lowest over the years
and groups of research – 5.2 points, the maximum – 7.9 (CH111
14422), minimum – 3.2. Over three years of research, the average resis-
tance indicator was 7.06 and the variation range was 2.81, T08/02 and
Fiorina showed the highest resistance among the varieties of this group.

In the 2013–2014 growing season the average resistance indicator in
early ripening samples over the years and groups of research was
highest – 7.3, maximum – 8.43 (NCOO-14622/2137), minimum – 1.5
(64)

Note: see Table 2.

Table 4

<table>
<thead>
<tr>
<th>The group of sample</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
</tr>
<tr>
<td>Amounts</td>
</tr>
<tr>
<td>(number of days from spring</td>
</tr>
<tr>
<td>days from flowering to curation)</td>
</tr>
<tr>
<td>Early ripening</td>
</tr>
<tr>
<td>Mid-early ripening</td>
</tr>
<tr>
<td>Mid-late ripening</td>
</tr>
<tr>
<td>Late ripening</td>
</tr>
</tbody>
</table>

Note: see Table 2.
Dulger-1/Vorona/BAU, HBF0290/X4W063-9-329/ARH/3/LE2381, Dulger-1/Vorona/BAU1/4/1D13.1/MLT/3/SIH414/CRW, 2/MV. MAGDALENA/3/TX96/2427, K920709-B-5-1/1-BURB10, NCOO-14622/2137. Thirty-one samples (36%) were resistant to three diseases. We identified samples that were significantly higher than the standard and were characterized by better productivity (Table 5).

Table 5

Characteristics of group disease resistance of the 4th WWSRRN CIMMYT winter wheat samples, average 2014-2016, (x ± SD, n=8)

<table>
<thead>
<tr>
<th>Sample</th>
<th>Resistance to points</th>
<th>Plant height, cm</th>
<th>Seed weight, 1000 g</th>
<th>Yield capacity, g/m²</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Powdery mildew</td>
<td>Brown rust</td>
<td>Septoria disease</td>
<td></td>
</tr>
<tr>
<td>Podolianka St</td>
<td>6.10 ± 0.15^d</td>
<td>6.10 ± 0.31^e</td>
<td>5.90 ± 0.09e</td>
<td>93.0 ± 2.2 ± 0.32^f</td>
</tr>
<tr>
<td></td>
<td>6.90 ± 0.09e</td>
<td>7.16 ± 0.03^c</td>
<td>7.76 ± 0.32^d</td>
<td>75.9 ± 1.50 ± 0.28^g</td>
</tr>
<tr>
<td>Fiorina</td>
<td>± 0.21^e</td>
<td>± 0.25^f</td>
<td>± 3.2^h</td>
<td>± 1.00 ± 0.39^i</td>
</tr>
<tr>
<td>Rina-6/4/BEZ/</td>
<td>8.68 ± 0.26^a</td>
<td>8.09 ± 0.15j</td>
<td>8.1 ± 1.2 ± 0.12^k</td>
<td>75.4 ± 28.0 ± 28.0^l</td>
</tr>
<tr>
<td>NAD/KZM(ES8524)/3/F900K</td>
<td>8.02 ± 0.33^m</td>
<td>7.80 ± 0.17^n</td>
<td>8.2 ± 2.60 ± 1.25^o</td>
<td>75.2 ± 58.0 ± 58.0^p</td>
</tr>
<tr>
<td>6E693/3PI</td>
<td>7.17 ± 0.28^b</td>
<td>7.43 ± 0.07^c</td>
<td>7.23 ± 1.5 ± 1.61^d</td>
<td>51.23 ± 19.2 ± 19.2^e</td>
</tr>
<tr>
<td>Cv. rodina/ae.</td>
<td>8.83 ± 0.23^c</td>
<td>6.88 ± 0.20^b</td>
<td>10.50 ± 2.5 ± 1.73^d</td>
<td>53.00 ± 23.2 ± 23.2^e</td>
</tr>
<tr>
<td>spectoides(10KR)</td>
<td>8.07 ± 0.23^c</td>
<td>6.87 ± 0.20^b</td>
<td>7.59 ± 2.5 ± 1.73^d</td>
<td>52.43 ± 23.2 ± 23.2^e</td>
</tr>
<tr>
<td>FL9547/NCOO</td>
<td>7.62 ± 0.17^d</td>
<td>7.80 ± 0.17^d</td>
<td>8.07 ± 2.8 ± 3.5±</td>
<td>58.23 ± 57.0 ± 57.0^g</td>
</tr>
<tr>
<td>14622</td>
<td>0.45 ± 0.29^a</td>
<td>0.12 ± 0.12^d</td>
<td>1.7 ± 2.00 ± 2.00^j</td>
<td>72.37 ± 27.9 ± 27.9^l</td>
</tr>
<tr>
<td>MCCORMICK/2</td>
<td>0.28 ± 0.48 ± 0.14^f</td>
<td>0.28 ± 2.8 ± 17.3 ± 17.3 ± 27.6^g</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tegio</td>
<td>0.29 ± 0.48 ± 0.14^f</td>
<td>0.28 ± 2.8 ± 17.3 ± 17.3 ± 27.6^g</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Note: see Table 2.

Among these genotypes, the highest resistance to powdery mildew was 8.83 points in sample C. rodina/ae. spectoides (10 KR), and to brown rust 8.67 points (FL9547/NCOO-14622), to septoria disease Rina-6/4/BEZ/NAD/KZM(ES8524)/3/F900K, FL9547/NCOO-14622 – 8.3 points. Four dwarf and three medium-grown samples were selected among the resistant samples to the three diseases. All were characterized by a large mass of 1000 seeds. Three samples (Rina-6/4/BEZ/NAD/KZM(ES85824)/3/F900K, Cv. rodina/ae. spectoides (10 KR), FL9547/NCOO-14622), which were distinguished by group resistance, exceeded the standard cultivar Podolianka by yield.

Discussion

An important role in problem solving in modern agriculture is the creation and widespread use of bread wheat that meets the requirements of production (Morhun et al., 2014). It means that the plants of these varieties must successfully withstand the adverse effects of external factors and use favourable environmental conditions with maximum efficiency. Now the new high-yielding, high-quality variety has a genetic yield capacity potential of more than 10 t/ha, but its production under production conditions does not exceed 30-50% (Kolomiates et al., 2018). It is explained by the irregularities in cultivation procedure, the lack of mineral nutrients in plants during the vegetation period, as well as the lack of adaptability of new varieties to global climate change.

The main guarantee for the creation of modern high-productive, adaptive varieties, of course, is the base line. Breeding practice confirms the need for focused search for valuable parental forms among the world’s plant diversity (Bakumenko et al., 2015). The historical experience of mankind has shown that a prerequisite for the effective development of agriculture, science and education in any country is the wide utilization and testing of valuable samples of foreign plant genes (Lytvynenko & Topal, 2015).

Prevalence of winter wheat with pathogens is a significant negative factor that reduces the quantitative and qualitative characteristics of the obtained grain harvest (Leonov et al., 2016). The main way to solve the problem of reducing the harmfulness of disease is the creation and introduction of resistant varieties. To do this the prerequisite is the selection of resistance sources, the study of the genetic basis of resistance and the nature of the trait inheritance. Kovalyshyn & Dmytrenko (2017) studied the resistance to brown rust in hybrid populations of F2 winter wheat under artificial inoculation with a pathogen in a field infestation nursery. The results of studies of 39 second-generation hybrid combinations determined that the resistance to brown rust was inherited as both a dominant and recessive trait. It was proved that the tested donors had different resistance genes to brown rust. Resistance of the donor T901 v 4511 is controlled with two recessive genes, T902 v 4511 – with one recessive gene, HBE 0331 156 and HBE 0425-156 – with one dominant gene in each. Samples NYE 0140-119 and NBE 208-120 have common (identical) genes – one dominant and one recessive. All donors of this trait have resistance genes independent of the known effective ones. The availability of new donors makes it possible to enrich the bank of resistance genes to the disease and based on them to create new, non-uniform, bread wheat varieties.

In Uman National University of Horticulture, resistance of winter wheat varieties was studied, which revealed the phases of the highest crop damage by septoria disease (Subromud, 2013). The damage to winter wheat with septoria leaf disease, which was dependent on the weather conditions, the phases of the crop vegetation period and the variety, was determined. The highest prevalence and extent of damage to wheat with septoria disease was found in the tube exit phase. Under conditions favourable for the pathogen development, the varieties Pyvna, Shestopolyanka, Dykanka, Vasylyna and Tronka were less affected.

Khomenko & Sandetska (2018) conducted research in the fields of the Institute of Plant Physiology and Genetics, NAS of Ukraine. As a result, the sources of complex resistance to unfavourable factors and pathogens (powdery mildew, brown rust and yellow leaf spot) were identified among the following winter wheat varieties: Natalka, Pereyaslavka, Podolynka, Darynka, Kyivska, Zbruch, Kyivska Ostytsa, Smushlianka, Snitudka and Favorytyka. The studied varieties are involved in breeding programs for the creation of a high yield capacity and highly adaptive winter wheat base line.

The susceptibility of newly developed varieties to the brown rust and powdery mildew pathogens was studied according to the results of joint research conducted by scientists of the National University of Life and Environmental Sciences of Ukraine, the Institute of Plant Protection of the NAAS and the V. M. Remeslo Mironivska Institute of Wheat (Kovalyshyn et al., 2018). During the three years of the research, the damage was within 0.1-10% and 1-20%, respectively. Damage to Podolianka (the standard) with the powdery mildew pathogen over the years of research (2015, 2016, 2017) was 10%, 15% and 10%, respectively, and with brown rust pathogen – 10%, 15%, 0%. The damage of the cultivar Keprok susceptible to the powdery mildew pathogen was at the level of 15%, 35%, 15%. Brown rust developed on the susceptible cultivar Mironovskaya 10 at the level of 15%, 30%, and in 2017 the disease on wheat plants was not shown at all. According to the results of identification of the allelic condition of the Lr34 gene, among the 15 studied varieties, only 3 varieties – Berehnyina Mironovska, MIP Dniproanka and Balada Mironivska – have the Lr34 (+) allele, which is only 20% of the tested varieties. The Lr34 gene is known to be non-specific. It provides overall resistance to various brown rust pathotypes in adult plants. Therefore, the obtained results show that when creating new varieties of wheat resistant to brown rust, it is necessary to use varieties with the identified “resistant” allele of the gene Lr34, as a source of stability in breeding.

Resistance of bread spring wheat varieties to leaf fungal diseases was investigated in two ecological zones – Forest-Steppe and Polissya of Ukraine (Blyzniuk et al., 2019). The cultivar with complex resistance to pathogens – Zlata, Legyan; as for resistance to powdery mildew and brown rust – Heroinia, Paniunka, Simkodka Mironivska, Yasnar, as for resistance to powdery mildew and septoria – Koksia was allocated for the Forest-Steppe zone. For the Polissya zone varieties found to have complex resistance to pathogens were Zlata and Paniunka, varieties with resistance to powdery mildew and brown rust were Simkodka Mironivska. It was found that the most valuable varieties were characterized by the combination of a high index of complex resistance with individual resistance to some leaf fungal diseases. In the research of Lytvynenko & Topal (2015), a collection nursery was formed, which included breeding ma-
terial of different genetic and environmental origin from 1T/1RS – 5
lines of the Genetic Breeding Institute (Er.3252/09, Er.3381/09,
Er.352/11, Er.139/09, Er.167/11) and 27 cultivars, including Kniha
noya Olha and Vykhovanka from Odessa, as well as from 1VL/1RS – 11
varieties including Schedrist odeska (SGI). DNA analysis showed that
that all varieties with 1BL/1RS translocation carry the same transloca-
have resistance genes to powdery mildew and brown rust. The presence
of wheat-rye translocations 1AL/1RS, 1BL/1RS in bread wheat wheats
varieties can have a negative effect on the grain quality and its baking
properties of flour, due to the increased amount of water-soluble pro-
teins – albumin and scelins (allel-1 allele) from rye (Kim et al., 2004;
Litvinenko & Topal, 2015). However, varieties with translocations 1AL/1RS, 1BL/1RS observed improvements of the flour baking prop-
erties while reducing protein gluten and increasing protein gliadin. It
contributed to the better dough elasticity, ability to rise and improvement
in the bread-baking properties.

The Department of Plant Genetic Improvement of the Institute of
Plant Physiology and Genetics (IFRG) of the NAS of Ukraine conducts
focused breeding aimed at high productivity in combination with high
baking quality and a range of other economically valuable characteris-
tics (Morgan et al., 2014).

Kozub et al. (2018) examined 20 varieties of bread wheat from
competitive testing for reserve protein loci. Particular attention was
paid to new varieties Syntetyk and Bohdanka with rye material, which
were also studied using cytogenetic analysis. Among the studied group
of varieties, rye material at gladiol encoding loci was found in three
cultivars – Syntetyk, Kryzhynka and Bohdanka. Syntetyk and Kryzhyn-
ka were found to have rye translocation 1BL/1RS, and Bohdanka
cultivar – 1AL/1RS. These facts were confirmed cytologically. The allel-
cide condition form mode of the Gluiadin Gl-1 (Gld) and HMW loci of the
glutelin Gln-1 subunits in the studied set of varieties was determined.
Genealogy of the first bread wheat variety of winter breeding in the Rus-
sian Federation with translocation 1AL/1RS – Bohdanka is specified.

Over the years, scientists from Ukraine, countries from the CIS and
non-CIS have conducted a number of studies in this field and obtained
significant results as for the identification of resistance genes to brown
rust, powdery mildew, septoria, pyrenophorosis (Leonov et al., 2016).
In practical terms, winter wheat lines were created using distant and
intraspesc hybridization, which had value as a base line for creating
resistant varieties. Since the loss of resistance varieties is a natural pro-
duce due to changes in the populations of pathogens, the variability of
environmental conditions, so the search for new sources of disease re-
sistance, expanding the genetic diversity of existing winter wheat varie-
ties, the study of the composition of pathogens and identification of new
resistance genes could be a permanent and constant selection process
for any crop, and in particular wheat.

Based on our research during 2014–2016 on resistance to leaf dis-
ases of the 4th WWSRRN CIMMYT samples, 36% out of all studied
samples resistant to three diseases were identified. Genotypes which ex-
ceeded the standard as for resistance and were characterized by better
performance were identified. Among them were valuable forms for
breeding work which can be donors of resistance to leaf diseases.

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