EVALUATION OF GENETIC SOURCES OF TOLERANCE OF COMMON WHEAT AGAINST BYDV AND CYDV

HODNOCENÍ GENETICKÝCH ZDROJŮ PŠENICE SETÉ NA ODOLNOST VŮČI BYDV A CYDV

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The article is concerned with the evaluation of genetic sources of common wheat (*Triticum aestivum* L.) with respect to barley yellow dwarf disease (BYD), which is caused by BYDV and CYDV viruses. The BYDV-PAV serotype prevails in the Czech Republic. Individual genotypes were characterised by means of 3 DNA markers to confirm the presence of 2 resistance genes designated *Bdv2* and *Bdv3*, originating from *Thinopyrum intermedium* (Host) Barkworth & D. R. Dewey Detection of presence of rusts resistance genes *Lr34* and *Yr18*, which are believed to be tightly linked to resistance gene *Bdv1*, was carried out. 76 common wheat genotypes, arranged into 3 collections, were also tested for tolerance against BYDV-PAV in the field trials in 2005, 2006 and 2008.

Results of the analysis showed that wheat lines carrying translocation originating from *T. intermedium* manifested a higher level of the BYDV-PAV infection compared to lines without the translocation. No significant difference in tolerance against the BYDV-PAV was found between the collection involving genotypes with a presumed presence of the *Bdv1* gene and the collection of wheat lines where the genetic basis of tolerance is unknown. Wheat lines, which positively tested for *Lr34/Yr18* presence, exhibited a higher level of the BYDV-PAV infection compared to the collection of lines lacking both rusts resistance genes. The hypothesis that the presence of the *Lr34/Yr18/Bdv1* increases tolerance of common wheat against BYD was not confirmed. Higher levels of tolerance of wheat lines lacking *Lr34/Yr18/Bdv1* genes and translocation from *T. intermedium* has probably a polygenic character.

Key words: common wheat, resistance, BYD, DNA markers, field trials

Barley yellow dwarf virus (BYDV), is vectored by more than 20 aphid species, and represents one of the most significant viral pathogens of cereals. It attacks almost all *Triticeae* species, including the major crops, *i.e.*, wheat, barley and oat. Five serotypes were described by Rochow et al. (1971) according to the prevailing vector – RPV (vectored by *Rhopalosiphum padi* L.), RMV (vectored by *Rhopalosiphum maidi* Fith), MAV (vectored by *Sitobion*

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avenae F.), SGV (vectored by *Schizapsis graminis* Rond.) and PAV serotype which is vectored by *R. padi, S. avenae* and other aphids. The PAV serotype prevails in the Czech Republic. The particular strains of BYDV differ in virulence, host range and vector specifity. Vector specifity does not always correspond with serotype and this statement is supported by numerous examples (Halbert et al. 1992).

Due to the cytopathological and genome organisational differences, the BYDV group was reclassified into two different genera. The PAV, MAV and SGV serotypes now belong to BYDV, whereas the RMV, RPV and isolates that resemble them belong to Cereal Yellow Dwarf Virus – CYDV (Miller and Rasochová 1997). BYDV belongs to the genus of Luteovirus, while CYDV into the genus of Polerovirus.

The disease is often called Barley Yellow Dwarf (BYD) (Chain et al. 2006). Symptoms of BYD are variable and can be confused with nutrient deficiency, environmental stress or other diseases. Generally, BYD causes dwarfism of plants, inhibition of root formation and leaf yellowing, but symptoms in wheat are not always obvious. Seedling infection usually results in reduced plant growth, and discoloration appears first on the older leaves. The severity of infection also depends on plant age. The favourable weather conditions for the spread of the disease are cold and moist seasons and therefore autumn and early spring infections are believed to be more significant for yield losses in wheat.

Control of the disease can be partially achieved through cultural practices, *e.g.*, by sowing wheat at the optimum date and application of insecticides, but the best control is achieved by the cultivation of tolerant or resistant germplasm (Henry and Plumb 2002). Tolerant plants present attenuated symptoms and lower yield losses even though they multiply virus. In resistant plants, virus multiplication and spread are inhibited or reduced, and disease symptoms are usually highly localised or are not visible (Kang et al. 2005).

No true BYD resistance has been found in wheat varieties except one gene in some cultivars. The gene *Bdv1* was reported by Singh et al. (1993), who described the tolerance of particular lines to BYD as a single-gene resistance. This partially dominant gene is closely linked with genes *Lr34* and *Yr18*, which confer tolerance to leaf rust and stripe rust and are located on the short arm of chromosome 7DL (Spielmeyer et al. 2005). The major effect of *Bdv1* gene is slowing symptoms of the BYD in adult plants and is believed to originate from the Brazilian cultivar Frontana. The *Bdv1* gene was widely employed in wheat breeding programs in CIMMYT, Mexico.

Because the *Bdv1* gene does not provide real resistance, breeders have continued to search for other resistance genes among *Poaceae* species. Some wild grasses show a very high level of tolerance to BYD infection and *Thinopyrum intermedium* (Host) Barkworth et Dewey was chosen to be the most perspective donor of resistance. The resistance genes are located on the long arm of the chromosome 7 (so called *Ti* translocation) and were designated *Bdv2* and *Bdv3*, respectively. The mechanism of BYD resistance is a malfunction of viral multiplication or reduced viral movement (Ayala et al. 2001). Both dominant genes are present in many translocated wheat lines conferring different levels of tolerance to BYD infection. Several QTLs associated with BYD tolerance were identified (Ayala et al. 2002).

The main aim of this paper was to evaluate different common wheat lines according to their field resistance against BYDV-PAV infection and presence of specific markers of *Lr34/Yr18*, *Bdv2* and *Bdv3* resistance genes.

MATERIAL AND METHOD

Plant material

Seventy six common wheat lines were kindly provided by the Crop Research Institute in Prague and by the breeding station Stupice Selgen Inc. Seventy six wheat lines were arranged into three collections – collection A including wheat lines with putative presence of the *Bdv1* gene (Table 2), collection B including wheat lines with putative presence of *Bdv2* and *Bdv3* genes (Table 3) and collection C including wheat lines with unknown basis of BYD tolerance (Table 4).

PCR assays

DNA was isolated by the commercial isola-

tion kit GenElute Plant Genomic DNA Miniprep Kit according to the manufacturer's instructions (Sigma). Three markers were used to detect presence of the *Bdv2* and *Bdv3* genes originating from *T. intermedium* (Table 1).

PCR profile of *BYAgi* and *SCGpl* markers were as following: 25 ml PCR reaction containing 25 ng.ml^{-1} DNA, 0.4 mM of each primer, 1 × PCR buffer, 2.5 mM $MgCl_2$, 280 mM dNTP, 1U Taq polymerase (Fermentas, Latvia). Amplification of *BYAgi* marker was performed as following: 1 × (94°C, 30 s); 35 × (94°C, 30 s; 60°C, 30 s; 72°C, 45 s); 1 × (72°C, 45 s). Amplification of *SCGpl* marker was as following: 1 × (72°C, 60 s; 96°C, 60 s); 35 × (94°C, 60 s; 65°C, 60 s; 72°C, 120 s); 1 × (72°C, 600 s). PCR profile for *Bdv3* marker was as following: 25 ml PCR reaction containing 50 ng.ml^{-1} DNA, 0.2 mM of each primer, 280 mM dNTP, 1 × PCR buffer, 2.5 mM $MgCl_2$, 0,75U Taq polymerase (Fermentas, Latvia). Amplification of *Bdv3* marker was performed as following: 35 × (94°C, 30s; 58°C, 45 s; 72°C, 60 s).

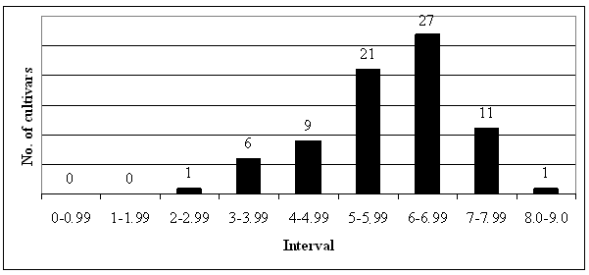

Fig. 1. Histogram of wheat cultivars tested in field conditions according their average resistance against BYD

Marker *WMS130* according to Suenaga et al. (2003) was used to detect presence of the *Lr34/Yr18* genes (Table 1). PCR profile for *WMS130* marker was as following: 25 ml PCR reaction containing 25 ng.ml^{-1} DNA, 0.4 mM of each primer, 280 mM dNTP, 1x PCR buffer, 2.5 mM $MgCl_2$, 1U Taq polymerase (Fermentas, Latvia). Amplification of *WMS130* marker was performed as following: 40 × (94°C, 30s; 52°C, 45 s; 72°C, 60 s).

Field infection tests

Field infection trials were carried out in 2005, 2006 and 2008. Trials consisted of two blocks of small plots separated by a protective belt. One of the blocks represented the infection variant and the other is the control, the uninfected variants. Plants were grown on 2 row plots 1m long with 3 replications. At the beginning of the tillering stage infection with BYDV-PAV was carried out by means of *Rhopalosiphum padi* aphids obtained from greenhouse rearing. The inoculation suction was from 5 to 7 days and then the aphids were killed by an insecticide. Applications of fungicides and insecticides were carried out during the vegetation period in order to protect plants against undesirable viral and fungal diseases. Symptomatic reactions to the virus infection were recorded three times during the vegetation period in infected plants till the stage of full flowering using 0–9 scale developed by Schaller and Qualset (1980).

Statistical analysis were carried out by means of Statistica software.

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List of markers used for PCR assays

Primer	Sequence	Author	Detected gene	Character
BYAgi-R BYAgi-F	5´- CTG AAC ACG AAT TTG CTG AGG TTG - 3´ 5´- CAT GGA TAA TTC AGG GAG CAT TCT G - 3´	Stoutjesdijk et al. (2001)	*Bdv2*	D
SCGpl-R SCGpl-F	5´CAG GAC AAG TGA AAG CAC CTA AGC 3´ 5´GTC CAC AAG TCA TAT GGG GAC AC 3´	Zhang et al. (2004)	*Bdv2*	D
Bdv3-R Bdv3-F	5'- CGA CGA ATT CCC AGC TAA ACT AGA CT -3' 5'- CTT AAC TTC ATT GTT GAT CTT A -3'	Ohm and Kong (2006)	*Bdv2/Bdv3*	C
WMS130-R WMS130-F	5'- CTC CTC TTT ATA TCG CGT CCC -3' 5'- AGC TCT GCT TCA CGA GGA AG -3'	Suenaga et al. (2003)	*Lr34/Yr18*	C

D = dominant marker, C = codominant marker

RESULTS AND DISCUSSION

High molecular weight DNA was used for PCR assays. Three markers were used to detect the *Ti* translocation in common wheat lines. The *BYAgi* primers amplified fragment of 566 bp, the *SCGpl* primers amplified fragment of 330 bp, which is in correspondence with previously

T a b l e 2

Collection A – average values of symptom scoring and presence of markers

Line/Cultivar	Vegetation type, line (l), cultivar (c)	Marker BYAgi	Marker SCGpl	Marker Bdv3	Marker WMS130	Symptom score – average value 2005–2008**
Sandra	*S, l	–**	–	–	+**	6.8
Leguan	S, l	–	–	–	+	5.5
Anza	S, l	–	–	–	+	4.6
Jara	S, l	–	–	–	+	6.5
Maringá Rht+	S, l	–	–	–	–	3.6

* – S = spring growth habit, W = winter growth habit,
** – (+) indicates presence of the marker, (–) indicates absence of the marker,
*** – 0–9, 0 = no symptoms

T a b l e 3

Collection B - average values of symptom scoring and presence of markers

Line/Cultivar	Vegetation type, line (l), cultivar (c)	Marker BYAgi	Marker SCGpl	Marker Bdv3	Marker WMS130	Symptom score – average value 2005–2008**
CIMMYT126	S, l	+	+	+	+	7.8
CIMMYT287	S, l	+	+	+	+	7.7
CIMMYT289	S, l	+	+	+	+	7.9
CIMMYT290	S, l	+	+	+	+	7.5
CIMMYT291	S, l	+	+	+	+	6.7
CIMMYT292	S, l	+	+	+	+	6.9
CIMMYT293	S, l	+	+	+	+	7.5
CIMMYT294	S, l	+	+	+	+	6.9
CIMMYT295	S, l	+	+	+	+	6.9
CIMMYT296	S, l	+	+	+	+	6.5
CIMMYT297	S, l	+	+	+	+	6.2
CIMMYT299	S, l	+	+	+	+	6.4
CIMMYT344	S, l	+	+	+	+	6.8
CIMMYT345	S, l	+	+	+	+	7.0
CIMMYT349	S, l	+	+	+	+	6.9
CIMMYT350	S, l	+	+	–	+	5.9
CIMMYT351	S, l	+	+	+	+	6.5
CIMMYT352	S, l	+	+	+	–	7.4
P961341	W, c	+	+	+*	–	5.3
TC14-290E	S, c	+	+	+	–	5.8
TC14-290J	S, c	+	+	+	–	6.5
TC7	S, c	+	+	+	+	7.6
Z2	S, c	–	–	–	–	6.8
Z6	S, c	–	–	–	–	7.0**
TC5	S, c	+	+	+	+	7.5
TC9	S, c	+	+	–	–	8.1

* – alleles for *Bdv2* and *Bdv3* genes
** – average value from 2005-2006

Others symbols are identical with the Table 2.

reported results by Stoutjesdijk et al. (2001) and Zhang et al. (2004). The SSR marker *Bdv3* is codominant – fragment of 170 bp is specific to wheat, fragments of 198 bp and 290 bp are specific to the 7E chromosome segment carrying *Bdv2* and *Bdv3* resistance genes (Rochow and Muller 1971). The presence of the markers in individual lines is stated in Tables 2, 3 and 4. The *WMS130* primers amplified fragment of 130 bp in wheat lines carrying the *Lr34/Yr18* genes while fragment of 135 bp was amplified in genotypes lacking both rusts resistance genes.

Collection A (Table 2) involves wheat cultivars with assumed presence of the *Bdv1* gene and absence of *Bdv2* and *Bdv3* genes. All cultivars except cultivar Maringá *Rht+* were positively tested for the presence of the *Lr34/Yr18* genes, but no marker for resistance genes derived from *T. intermedium* was detected. According to Mařík et al. (2003) symptom value 5 can be applied to distinguish resistant and susceptible plants. Cultivars Anza and Maringá *Rht+* can be considered resistant, while other cultivars from collection A as susceptible. The presumed effect of the *Bdv1* gene is slowing of disease symptoms in adult plants (Singh et al. 1993). Cultivar Anza is considered to be a referential cultivar for the *Bdv1* gene. Higher level of tolerance against BYD of cultivars Maringá *Rht 1+2* and Anza was confirmed in study of Bartoš et al. (2002), while cultivar Jara was shown to be more susceptible. Ayala et al. (2002) suppose that the effect of the *Bdv1* gene is not as high as expected in the previous study by Singh et al. (1993). Results of the field trials support this hypothesis. Higher level of tolerance against BYD of cultivars Maringá *Rht+* and Anza is probably polygenic (Tola and Kronstad 1984).

Collection B involves cultivars with a presumed presence of *Bdv2* and *Bdv3* genes. The presence of these genes translocated from *T. intermedium* into wheat genome results in lower virus titer in infected plants (Chain et al. 2005). The presence of all three markers for *Ti* translocation was detected in all CIMMYT lines except line CIMMYT350, where only the presence of both dominant genes was confirmed. This can be the result of a different translocation size. All CIMMYT lines are derived from the original TC14 line carrying the smallest *Ti* translocation from the group of TC lines. TC lines have the *Ti* translocation located on the 7DL chromosome. Lines originating from TC14 line are considered as suitable genetic sources of resistance against PAV, MAV and RPV serotypes (Henry 1997). Despite the presence of resistance genes most of the CIMMYT lines exhibited high susceptibility to BYDV-PAV infection, which is in accordance with previously reported results by Henry and Plumb (2002) and Henry (1997). Only line CIMMYT350 can be considered as moderately resistant. Lines TC14-290E and TC14-290J were also developed from the TC14 line and presence of *Ti* translocation was confirmed by all three markers. The TC14-290J line exhibited higher level of BYDV-PAV infection compared to TC14-290E line.

Lines TC5, TC7 and TC9 also belong to the group of TC lines and presence of all three markers for *Ti* translocation was detected in TC5 and TC7 lines. These lines exhibited high level of BYD infection during the field trials and can be considered as highly susceptible.

Lines Z2 and Z6 were developed from Zhong5 line carrying the *Ti* translocation of chromosome 2 (Barloy et al. 2003). No marker for *Bdv2* and *Bdv3* genes were detected in these lines, which is a consequence of different *Ti* translocation.

Cultivar P961341 was developed from cultivar P29, one of the first winter wheats carrying both *Bdv2* and *Bdv3* resistance genes on chromosome 7. P961341 is the only line from all collections where presence of the *Bdv3* gene was detected. The presence of BYD resistance genes results in lower virus titer compared to susceptible lines (Ohm and Kong 2006). P961341 can be considered as moderately resistant to BYDV-PAV infection and this result is in accordance with previously reported results by Anderson et al. (1998).

Chain et al. (2006) studied changes in virus titer in resistant and susceptible cultivar under different infection pressure, but no significant difference between resistant and susceptible plants was observed. According to the authors of the study the high level of BYD infection pressure can result in the suppression of the resistance genes. Wianjung and Anderson (2004) studied course of CYDV infection in cultivar P29. According to their study, resistance against

CYDV is not based on the inhibition of virus replication, but on the localisation of the virus spread at the site of attack. This mechanism inhibits virus spread in the infected plant. Resistance controlled by *Bdv2* and *Bdv3* resistance genes was overcome in case, if plants were inoculated by higher number of aphids in early developmental stages. Jiang et al. (2004)

T a b l e 4

Collection C – average values of symptom scoring and presence of markers

Line/Cultivar	Vegetation type, line (l), cultivar (c)	Marker BYAgi	Marker SCGpl	Marker Bdv3	Marker WMS130	Symptom score – average value 2005–2006
Sulamit	W, c	–	–	–	–	4.00
Rialto	W, c	–	–	–	–	4.80
Estica	W, c	–	–	–	–	6.00
Siria	W, c	–	–	–	–	6.50
Vlasta	W, c	–	–	–	+	4.20
Batis	W, c	–	–	–	–	6.00
Bruncka	S, c	–	–	–	+	6.15*
Zuzana	S, c	–	–	–	–	5.75*
Vinjett	S, c	–	–	–	+	6.05*
Munk	S, c	–	–	–	–	7.20
Saxana	S, c	–	–	–	–	6.00
Ludwig	W, c	–	–	–	–	5.80
Hana	W, c	–	–	–	–	5.10
Clarus	W, c	–	–	–	–	5.00
Cubus	W, c	–	–	–	+	6.00
Globus	W, c	–	–	–	+	5.30
Solara	W, c	–	–	–	–	6.30
Linda	S, c	–	–	–	–	6.40
Akteur	W, c	–	–	–	–	5.80
Versailles	W, c	–	–	–	–	3.80
Caphorn	W, c	–	–	–	–	5.00
WKL91-138	S, c	–	–	–	+	2.70
Bingo-Baer	S, c	–	–	–	–	6.40*
Q.G 22.24	S, c	–	–	–	+	4.50
Costero B	S, c	–	–	–	–	6.10*
Q.G 100	S, c	–	–	–	+	4.50
CHD 125/02	S, c	–	–	–	–	5.30
Swedjet	S, c	–	–	–	–	6.80
Soa 217/02	S, c	–	–	–	–	4.00
Q.G 4.37	S, c	–	–	–	–	3.70
CHD 287/01	S, c	–	–	–	–	5.20
Bombonia	S, c	–	–	–	–	4.60*
Quino-Banes	S, c	–	–	–	–	5.00*
Q.G 2.1	S, c	–	–	–	–	3.20
Kivu 85	S, c	–	–	–	+	3.00
Remeslivna	W, c	–	–	–	–	5.20
CIT925080	S, c	–	–	–	+	5.13*
Sisson	S, c	–	–	–	–	5.80
Roane	S, c	–	–	–	–	3.75*
CIT90004	S, c	–	–	–	–	5.65*
Kněžna	S, c	–	–	–	+	5.20
Avalanche	W, c	–	–	–	–	4.90*
F201R	S, c	–	–	–	–	6.20
Tribute	S, c	–	–	–	–	5.00
Marton Vasáry 8	W, c	–	–	–	–	5.60*

* = average values from 2005, 2006 and 2008
Others symbols are identical with the Table 2

compared level of resistance at translocated line TAI-27, which exhibited higher tolerance against BYD compared to susceptible wheat lines, but the level of tolerance expressed by TAI-27 was lower compared to *T. intermedium*. This finding led authors to hypothesise that not all genes responsible for resistance to BYD were translocated into wheat genome from *T. intermedium* and it is therefore likely that most of the present wheat lines carrying the *Ti* translocation contain only several genes of resistance. It is possible that symptom manifestation at translocated wheat cultivars is a result of lacking other resistance genes from *T. intermedium*.

Collection C involves common wheat cultivars with different levels of tolerance against BYD infection without resistance induced by *Ti* translocation. The genetic substance of tolerance of these cultivars is ambiguous. No marker for *Bdv2* or *Bdv3* resistance genes was detected, which is accordance with presumed expectation. Cultivars from collection C reached an average value of 5.4, which is the least value from all evaluated collections (Table 5). Cultivars WKL91-138 and Kivu 85 exhibited the lowest level of BYD symptoms and both lines are widely employed in breeding programs at the breeding station Stupice Selgen Inc. Many of the cultivars from the collection can be considered resistant. It is likely that resistance of these lines has a polygenic character. Statistical features of all three collections are stated in Table 5.

Most of the tested lines exhibited symptoms between 6–6.99 points of the symptom scale (Fig. 1). Only 16 lines from all collections can be considered resistant as they exhibited symptoms up to value 4.99 of the symptom scale. Cultivars evaluated in the interval 5–5.99 can be considered as moderately resistant, others as susceptible.

Table 5

Statistic characteristics of symptom scoring of collections A, B and C

Collection	$\bar{x}$	s	v
A	5.40	1.33	1.54
B	6.92	0.69	0.47
C	5.21	1.04	1.07

$\bar{x}$ – average value for collection, s – standard deviation, v - variance

Table 6

Statistical evaluation of symptom scoring of collections by means of F-test and t-test

Collection	F-test value	t-test value
A × B	0.032	0.061
B × C	0.03	$5.2.10^{-12}$
A × C	0.36	0.77

Significance level $\alpha = 0.05$

Statistically significant differences between collections B and C were observed (Table 6). Average values of symptom score between collections A × C and A × B are not different on the significance level $\alpha = 0.05$. Wheat lines from collection B, involving cultivars with *Ti* translocation, exhibited the highest susceptibility to BYD infection out of all collections tested (Table 5).

Marker *WMS130* detects presence of the *Lr34/Yr18* rust resistance genes in the wheat genome. According to Singh et al. (1993) these genes are closely linked to the *Bdv1* gene, and

Table 7

Statistical characteristics of wheat collections with presence or absence of marker *WMS130*, respectively

Cultivars	$\bar{x}$	s	v	F-test value	t-test value
Cultivars without WMS130 marker	5.53	1.11	1.24	P = 0.31	P = 0.032
Cultivars with WMS130 marker	6.15	1.31	1.73		

Significance level $\alpha = 0.05$

$\bar{x}$ – average value for collection, s – standard deviation, v – variance

therefore presence of the marker *WMS130* could indicate increased tolerance against BYD infection. In present study, cultivars carrying the *WMS130* marker exhibited higher susceptibility to BYDV-PAV infection compared to the group of cultivars not carrying the marker (Table 7). The presence of the rust resistance genes *Lr34/Yr18* in wheat genome does not contribute to the higher level of tolerance against BYD.

CONCLUSION

Results of PCR analysis and field trials indicate the following conclusions:

The presence of the *Bdv2* resistance gene was confirmed by means of 3 DNA markers in the most of the wheat cultivars carrying the translocation from *Thinopyrum intermedium*. Only cultivar P961341, developed from P29 line, has both *Bdv2* and *Bdv3* resistance genes.

Not all tested markers for the *Ti* translocation were detected in particular translocated wheat lines, which can be the result of a different translocation size in the plant genome.

Seventy six wheat cultivars, arranged into three collections, were tested for tolerance against BYD in the field trials in 2005, 2006 and 2008.

Collection of wheat genotypes carrying the *Ti* translocation exhibited the highest level of susceptibility to BYDV-PAV infection. The presence of the chromosome segment from *Thinopyrum intermedium* in wheat genome affects titer of virus, but obviously has very little effect on manifestation of disease symptoms.

The presence of the rust resistance genes *Lr34/Yr18*, which are believed to be linked with the *Bdv1* gene, does not affect the level of tolerance against BYDV-PAV infection. Wheat cultivars without marker for *Lr34/Yr18* exhibited statistically higher levels of tolerance compared to cultivars carrying the marker.

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SOUHRN

Článek se věnuje hodnocení vybraných genetických zdrojů pšenice seté (*Triticum aestivum L.*) na odolnost vůči žluté virové zakrslosti (BYD), způsobené viry BYDV a CYDV. V České republice je sledován výskyt zejména sérotypu BYDV-PAV. Jednotlivé genotypy byly charakterizovány pomocí tří DNA markerů z hlediska přítomnosti translokace části genomu *Thinopyrum intermedium* (Host) Barkworth & D. R. Dewey), kterou byly do genomu pšenice seté přeneseny nejméně dva geny rezistence vůči BYD nazvané *Bdv2* a *Bdv3*. Rovněž byla zkoumána přítomnost genů *Lr34* a *Yr18*, které jsou podle některých studií v těsné vazbě s částečně dominantním genem rezistence *Bdv1*. Soubor genotypů, rozdělený do tří kolekcí, byl testován na odolnost vůči BYDV-PAV v polních podmínkách v letech 2005, 2006 a 2008.

Z výsledků analýz je patrné, že genotypy nesoucí translokaci části genomu *T. intermedium* vykazují průměrně vyšší stupeň napadení virem BYDV než rostliny bez této translokace. Nebyl prokázán statisticky průkazný rozdíl v odolnosti vůči BYDV mezi genotypy s předpokládanou přítomností genu *Bdv1* a ostatními genotypy, u nichž není známo genetické založení odolnosti. Genotypy, které byly pozitivně testovány na přítomnost genů *Lr34/Yr18*, vykázaly vyšší stupeň napadení než genotypy, u kterých přítomnost obou genů nebyla prokázána. Nebyla tedy potvrzena hypotéza, že přítomnost genů *Lr34/Yr18/Bdv1* zvyšuje odolnost pšenice seté vůči BYD. Je pravděpodobné, že zvýšená odolnost některých genotypů bez přítomnosti genů *Lr34/Yr18* a translokace části genomu *T. intermedium* je řízena polygenně.

Klíčová slova: pšenice setá, rezistence, BYD, DNA markery, polní hodnocení