MARKERING OF SOME BARLEY TRAITS BY MEANS OF HORDEIN SIGNAL GENES

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The method of approximative determination of constant occurrence of individual allelic blocks of signal hordein genes and expression classes of some quantitative barley characters in the collection of 61 varieties and new breeds of spring and winter barley forms was used for the evaluation in 1992–1995. Vertical electrophoresis in starch gel columns was used for the manifestation of hordein signal genes. Allelic hordein blocks were separated from the electrophoretic spectra according to the published catalogues. The dependence between the occurrence of hordein genes and selected agronomical characters of barley was evaluated by χ^2 test. The strength of dependence was expressed by the coefficient of association. Orientation marker values were determined for the evaluated varieties and new breeds of barley on the basis of the determined values of association coefficients between the frequency of individual alleles of hordein loci and the expression class agronomically important characters.

1. The probable markers of the high value of thousand seed weight were the alleles A23, B17* and F3. On the other hand, the alleles A32, B21 and B8 became evident as the markers of a low expression of this character.
2. The alleles B47 and B17 appeared to be the markers of a high portion of grains above the 2.5 mm sieve.
3. The high extract content in malt dry matter was markered by the B47 allele, while BN allele appeared to be a marker of the low content.
4. The markering ability of powdery mildew resistance showed the alleles A12 and B(17), the alleles B17 and BN were markers of susceptibility.
5. The alleles A12, AN, B(17), B52 and BN1 had the ability of markering resistance to the leaf rust of barley, on contrary to the alleles B8 and B19 marker susceptibility.

6. The allele AN was angled to marker a higher plant length in spring barley; A3, A14, B3 and BN1 showed the analogic ability in winter barley.
7. The markering of winterhardiness was not proved reliably due to the low representation of winter varieties in experimental collection. However, the alleles A12, A3 and BN1 were not found in springs forms.

barley; electrophoresis; hordeins; genetic markers

INTRODUCTION

Hordeins – prolamine proteins of barley grain present genetic protein markers, suitable for markering of some economically important barley characters. Markering effects of barley protein signal genes can be determined by the approximative determination of constant occurrence of individual allelic blocks of signal genes and individual markered characters. The precondition for successfulness of this estimate is the genotypic variability of evaluated collections and their sufficient quantity.

MATERIAL AND METHODS

The aim of this work is the approximative determination of association between individual hordein alleles and qualitative classes of agronomically important characters of barley. Agronomical characters and the occurrence of hordein genes were tested in 61 varieties and advanced breeding lines of spring barley (*Hordeum vulgare* L. convar. *distichum* L. Alef. var. *nutans* Vib.) and winter barley forms (*Hordeum vulgare* L. convar. *hexastictum* L. Alef., convar. *distichum* L. Alef. var. *hybernum* Vib., respectively) of domestic and foreign origin. The outline of tested varieties is shown in Table IA, B.

In the official trials of the Institute for Supervising and Testing in Agriculture (ISTA) in Brno the domestic spring varieties were tested in three years tests (1993–1995) and the winter ones in 1992 and 1993. Experiments testing the foreign spring varieties started at the Breeding Station (BS) Stupice in 1992 and the spring varieties were tested at the Czech University of Agriculture (CUA) in Prague in 1995.

For the separation of hordein proteins the vertical electrophoretic method in starch gel columns was used according to Sozinov and Poperelja (1978) partly modified by Šašek and Černý (1983).

The developed zones of electrophoretic spectrum were evaluated according to the catalogues, published by Pomorcev et al. (1985) and Šašek et al. (1990a, b).

IA. Mean values of studied characters – set A

Character	Grain portion	Thousand seed weight	Extract in malt dry matter
	%	g	%
Akcent	78.7	49.3	81.0
Alexis	64.0	48.6	80.4
Amazone	82.5	47.1	79.9
Amulet	93.1	48.9	80.6
Apex	95.0	53.5	80.1
Bienheim	66.0	51.8	77.9
Ditta	54.5	43.6	78.6
Forum	67.2	45.4	82.6
Grif	44.0	48.0	76.7
Grosso	76.0	53.4	77.7
Hard	56.0	52.0	76.8
Cheri	74.5	50.1	80.5
Jarek	76.4	51.6	81.4
Jaspis	63.9	46.9	80.0
Jubilant	86.6	48.4	81.5
Kompakt	80.6	47.5	81.0
Krona	81.0	47.1	79.9
Ladik	88.4	49.4	80.5
Magda	85.0	52.8	77.2
Malvaz	88.9	50.5	78.7
Novum	59.9	45.9	80.5
Orbit	63.5	46.7	80.3
Primus	87.0	51.9	79.4
Prisma	70.5	51.0	79.4
Profit	74.2	50.4	78.9
Regatta	67.0	52.1	77.2
Rubín	72.6	48.6	81.7
Signal	69.7	49.2	78.4
Sladko	85.2	47.4	80.9
Stabil	83.9	45.8	81.4
Steffi	94.0	51.2	80.8
Svit	86.2	51.9	81.9
Terno	86.4	50.9	80.2

IB. Mean values of studied characters – set B

Variety	Plant length	Powdery mildew resistence	Leaf rust of barley resistance	Extract in malt dry matter
	cm	9 till 1	9 till 1	%
Spring varieties				
Akcent	70.1	7.4	7.8	81.2
Alexis	72.5	7.0	3.3	80.4
Amazone	71.0	8.0	3.5	79.9
Apex	0*	9.0	7.0	80.1
Blenheim	67.0	5.0	4.0	77.9
BR-4118	71.5	5.2	5.5	82.0
BR-4415	74.5	6.8	6.4	82.7
CE-431	69.0	8.2	5.1	81.8
CE-590	65.0	7.2	6.0	80.3
CE-685	74.0	6.2	6.4	81.0
CE-686	75.0	5.6	5.9	81.5
Ditta	77.5	7.9	7.9	80.2
Donum	58.0	5.9	5.0	82.6
Forum	65.0	8.6	4.9	82.8
Grif	74.0	5.0	4.0	76.7
Grosso	73.0	7.0	7.0	77.7
Hard	75.0	6.0	8.0	76.8
HE-4809	55.0	3.9	5.2	80.7
HE-5038	71.0	7.0	5.6	81.4
HE-5237	71.0	6.3	5.5	80.4
HE-6124	73.5	6.4	6.5	81.6
Heran	50.0	3.4	5.0	0*
Cheri	68.0	6.5	7.5	80.5
Jarek	0*	0*	0*	81.4
Jaspis	0*	0*	0*	80.0
Jubilant	0*	0*	0*	81.5
KM-1220	74.0	6.1	7.4	80.2
KM-1252	70.5	6.5	6.5	81.3
KM-974	55.0	5.0	5.8	81.7
Krona	74.5	7.8	6.9	81.1
Ladik	62.0	6.1	7.4	80.5

Continuation of Tab. IB

Variety	Plant length	Powdery mildew resistence	Leaf rust of barley resistance	Extract in malt dry matter
	cm	9 till 1	9 till 1	%
Spring varieties				
Magda	68.0	8.0	8.5	77.2
Malvaz	0*	0*	0*	78.7
Novum	63.0	6.0	6.2	81.1
Orbit	70.3	5.1	6.5	80.5
Prisma	71.0	5.0	4.0	79.4
Profit	0*	0*	0*	78.9
Regatta	72.0	5.5	6.0	77.2
Reggae	74.0	8.1	6.9	81.7
Riff	74.0	8.0	7.5	80.2
Rubín	70.0	7.8	4.3	81.9
SG-S-159	66.5	6.4	6.4	81.1
SG-S-160	68.5	6.0	5.6	81.3
SG-S-167	75.0	8.1	5.7	81.7
Signal	77.8	6.8	6.6	79.1
SK-3084	61.0	4.8	5.0	81.3
SK-3212	69.0	5.4	5.6	81.3
SK-3214	62.0	5.0	5.3	81.2
SK-3247	65.0	5.7	6.4	82.2
SK-3507	67.0	5.6	6.8	81.7
SK-3662	69.0	5.5	5.6	81.8
Sladko	64.0	6.5	6.0	81.1
Stabil	62.0	6.1	7.2	81.2
Steffi	0*	9.0	4.0	80.8
Svit	65.0	6.6	5.8	81.9
Terno	0*	0*	0*	80.2
Winter varieties				
Kamil	96	5.6	7.0	0*
Kromoz	94	6.2	6.9	0*
Lunet	95	5.9	6.1	0*
Marinka	96	7.5	6.2	0*
Okál	92.0	5.45	6.95	0*

The dependence between the occurrence of different hordein gene alleles and selected agronomical characters, their classes of expressions respectively, was evaluated by χ^2 test. The testing criterion of χ^2 test enables the evaluation of difference between real and expected frequency of both variables, i.e. allele frequency and expression classes of agronomically important characters.

For the calculation of χ^2 value the following formula was used:

$$\chi^2 = \sum i \sum j \frac{n_{ij}^2 . n}{(n_i . n_j)} - n$$

where: i – columns of contingent table
j – rows of contingent table
n – sum total of contingent table
n_i – sum of column individuals
n_j – sum of row individuals

Number of degrees of freedom was calculated according to the formula:

$$f = (k - 1) . (m - 1)$$

where: k – alteration number of character one
m – alteration number of the second character

The expected dependence of both parameters (k, m) was estimated in probability 100 – α (α = level of significance).

The strength of dependence was expressed by the coefficient of association V.

$$V = \sqrt{\frac{\chi^2}{n}}$$

where: V – coefficient of association
χ^2 – value of χ^2 test
n – sum total of frequencies

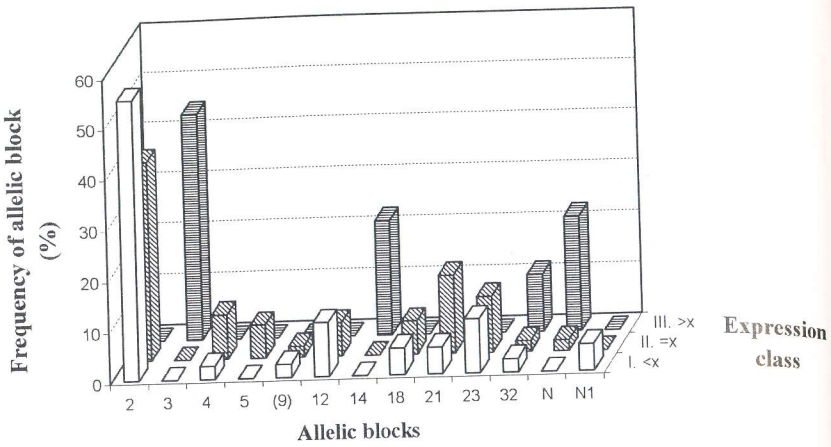
The used method of the determination of dependence of both parameters and the strength of determined dependence can be illustrated by the example of plant length.

The frequencies of allelic blocks – locus Hrd A in three classes of character expression – plant length are shown in Fig. 1. The foundation data, illustrated in Fig. 1, were used for formation the contingent table (Table IA, B). Evaluation of χ^2 is demonstrated in Table II. The values of coefficients of association of individual alleles – locus Hrd A and the classes of plant length expression are characterized in Fig. 2 and Table III. Fig. 3 then shows the general assessment of the coefficients of association, determined for the alleles of studied loci Hrd A, Hrd B and Hrd F.

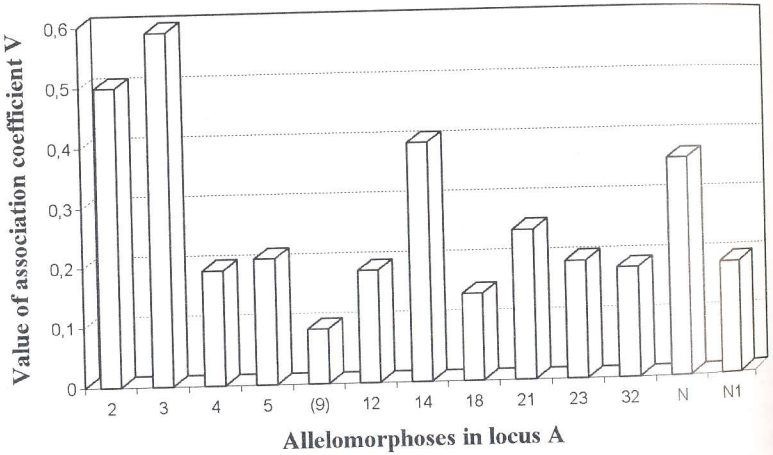
II. Plant length – locus A. Design of contingent table m x n

Allele	I	II	III	Sum
2	55.2	39	0	94.2
3	0	0	44.4	44.4
4	2.6	8.7	0	11.3
5	0	6.5	0	6.5
(9)	2.6	2.2	0	4.8
12	10.5	6.5	0	17
14	0	0	22.2	22.2
18	5.2	6.5	0	11.7
21	5.2	15.2	0	20.4
23	10.5	10.9	0	21.4
32	2.6	2.2	11.1	15.9
N	0	2.2	22.2	24.4
N1	5.2	0	0	5.2
Sum	99.6	99.9	99.9	299.4
Allele	Inter-result			Sum
2	97.23	48.39	0.00	145.63
3	0.00	0.00	133.07	133.37
4	1.80	20.07	0.00	21.87
5	0.00	19.48	0.00	19.48
(9)	4.23	3.02	0.00	7.26
12	6.51	7.45	0.00	13.95
14	0.00	0.00	66.53	66.53
18	6.95	10.82	0.00	17.77
21	3.98	33.94	0.00	37.93
23	15.49	16.64	0.00	32.13
32	1.28	0.91	23.22	25.41
N	0.00	0.59	60.53	61.13
N1	15.63	0.00	0.00	15.63
Sum	153.10	161.30	283.40	597.80

Statistical parametr	Value
χ^2 square	298.4
Inter-result	0.99665999
Association coefficient V	0.9983286
Inter-result	0.4991636
Coefficient of contingency according to Pearson	0.70651511



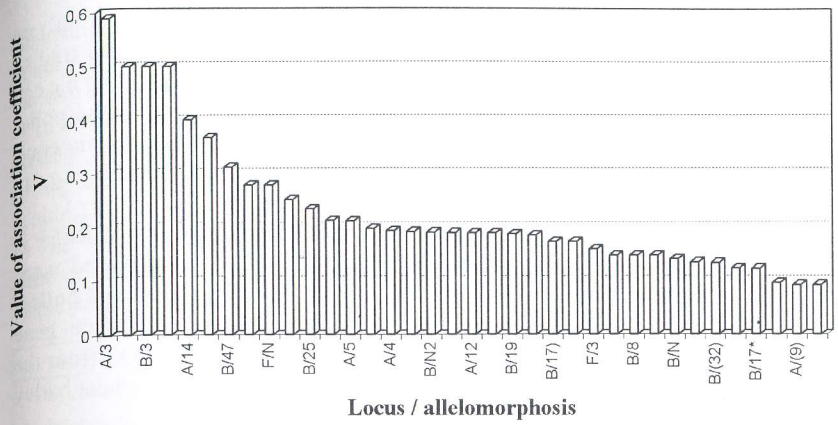
1. Plant length – frequency of allelic blocks in locus A



2. Plant length – association coefficients in locus A

RESULTS AND DISCUSSION

Genetic markers represent an intensive factor in plant breeding (Sax, 1923). They enable oligogene mapping, for example disease resistance genes and polygene mapping, conditioning quantitative trait loci (QTL). At present



3. Plant length – general outline of association coefficients

III. Plant length – locus A. Evaluation of χ^2 square

Statistical parameter (allelomorphis in locus)	χ^2 square	Association coefficient *V*	Coefficient of contingency *C*	Significance level alpha
A/2	74.751	0.499	0.447	< 0.01
A/3	104.225	0.589	0.508	< 0.01
A/4	11.004	0.192	0.188	< 0.01
A/5	13.288	0.21	0.206	< 0.01
A/(9)	2.489	0.091	0.091	0.30–0.20
A/12	10.507	0.187	0.184	< 0.01
A/14	47.948	0.399	0.371	< 0.01
A/18	6.313	0.145	0.144	0.05–0.02
A/21	18.835	0.25	0.243	< 0.01
A/23	11.534	0.196	0.192	< 0.01
A/32	10.07	0.183	0.18	< 0.01
A/N	40.047	0.365	0.343	< 0.01
A/N1	10.583	0.188	0.185	< 0.01

the molecular markers on DNA level (e.g. Soller, Beckmann, 1993; Asins, Carbonell, 1988; Melchinger, 1990) have been used for these purposes.

Methodology of QTL mapping usually comes from the segregation rate analysis in F2, BC generation of progenies alternating in the studied trait or from the utilization of called near isogenic lines (NIL) (Melchinger, 1988). In markering polygene quantitative properties it is usually the population exploitation (F2, BC, synthetic population) which is in a genetic equilibrium of linked genes and genes out of linkage groups (Melchinger, 1988; Soller, Beckmann, 1983).

The prerequisite for markering traits and properties by means of RFLP is the chromosomes map construction. Heun et al. (1991) constructed maps of 7 barley chromosomes by localisation of 155 RFLP markers and hulless gene, determining hulless grains, and powdery mildew resistance gene (Mla 12). Jahoor et al. (1991) developed by means of NIL PO2 from the variety Pallas, having the gene Mla 3 and by the help of additive wheat barley lines an analogical system of RFLP markers for barley.

For the evaluation of the heredity of leaf rust resistance at recombined lines from the cross *H. vulgare* x *H. bulbosum*, Pickering et al. (1998) used RFLP markers.

For routine breeding of winter barley for Barley mild mosaic virus (Barley yellow mosaic) virus (BaMMV/BaYMV) resistance controlled by ym4 gene, Tuvesson et al. (1998) developed a method, based on DNA markers (PCR).

Baar et al. (1998) localised a newly discovered gene of cereal nematode resistance (*Heterodera avenae* Woll.) by means of RFLP analysis.

Jahoor et al. (1996) used RFLP markers also for markering QTL such as lodging resistance, stem breakage, plant height, period of ear formation, some grain parameters and grain yield. Oziel et al. (1996) also studied two quantitative barley traits, i.e. malting quality and winterhardiness by means of some morphological, enzyme, STS (Sequence Tagged Site) and RFLP markers. Their studies proved the possibility of contemporary selection for a higher malting quality and a higher winterhardiness.

Financial costs, connected with the RFLP marker use are significantly higher in comparison with the protein markers. Beckmann and Soller (1983) suggest in most cases their compensation by gained scientific or economic value. Our markering method of some barley traits and properties by means of approximative dependence of allelic hordein gene frequency on the qualitative class of agronomic trait enables obtaining orientation data about the markering of evaluated traits with significantly lower costs and considerable time saving.

Two sets of varieties and new breeds were evaluated for the markering of some barley characters. Set A contained Czech and foreign spring barley varieties, which were evaluated in field experiments at BS Stupice and in the

experimental field CUA in Prague. The following characters were evaluated in set A: thousand seed weight, portion of grains above the 2,5 mm sieve and the extract content in malt dry matter (Table IV).

In set B were determined: extract in malt dry matter, resistance to powdery mildew and to leaf rust of barley and the length. The set was increased by spring and winter varieties evaluated in the official trials of the ISTA in Brno (Table IV).

The varieties and advanced breeding lines were separated for the evaluation of characters studied into three classes according to the expression level of particular characters or properties.

Thousand seed weight		
In class I	low	under 48.30 g
In class II	medium	48.31–50.33 g
In class III	high	above 50.34 g

Portion of grain 2.5 mm		
In class I	low	under 70.81%
In class II	medium	70.82–80.78%
In class III	high	above 80.79%

Extract content in malt dry matter – set A		
In class I	low	under 79.18%
In class II	medium	79.19–80.42%
In class III	high	above 80.43%

Extract content in malt dry matter – set B		
In class I	low	under 80.00%
In class II	medium	80.01–81.19
In class III	high	above 81.20%

Powdery mildew resistance		
In class I	susceptible	under 5.88
In class II	medium resistant to poor susceptibility	5.89–6.58
In class III	resistant	above 6.59

Barley leaf rust resistance		
In class I	susceptible	under 5.55
In class II	medium resistant to poor susceptibility	5.56–6.49
In class III	resistant	above 6.50

IV. Plant length. Numerical specification locus/allelomorphosis

Locus/allelomorphosis	Allele	Association coefficient *V*
A/2	2	0.499
A/3	3	0.589
A/4	4	0.192
A/5	5	0.210
A/12	12	0.187
A/14	14	0.399
A/18	18	0.145
A/21	21	0.250
A/23	23	0.196
A/32	32	0.183
A/(9)	(9)	0.091
A/N	N	0.365
A/N1	N1	0.188
B/3	3	0.499
B/8	8	0.145
B/17	17	0.187
B/19	19	0.185
B/21	21	0.095
B/23	23	0.277
B/25	25	0.233
B/43	43	0.122
B/45	45	0.145
B/47	47	0.31
B/52	52	0.171
B/(17)	(17)	0.171
B/(32)	(32)	0.132
B/17*	17*	0.121
B/N	N	0.139
B/N1	N1	0.499
B/N2	N2	0.189
F/0	0	0.091
F/1	1	0.133
F/2	2	0.19
F/3	3	0.157
F/N	N	0.277

The determined hordein blocks of electrophoretic spectrum zones, the occurrence of hordein gene alleles, respectively, are shown in Table V. The alleles described as N have not been catalogized yet, alleles in brackets or with a little asterisk present modified blocks. About 49% of the evaluated varieties represent hordein homogenic lines.

Thousand kernel weight

The strong dependence between the genes for high TKW and the occurrence of hordein blocks was found at the allele A23, B17 and F3. The high frequency of alleles A32, B21 and B8 in the first class showed the tendency for markering a low manifestation of the character. Allele F2 with the frequency in extreme values and allele A–N with the high representation of the character with an average manifestation is not significant for the mapping of linkage interactions (Table VI).

These results are completely different in comparison with S o z i n o v' s (1985) information. The cause of this difference is evidently due to the different genotype of steppe barley, used by Ukrainian authors.

Portion of grain above 2.5 mm

Alleles B47 and B117 are responsible for the high portion of grain above the sieve, with allele B–N, A32, A18 respectively, marker of a higher portion of grain under the sieve. The rest of evaluated alleles did not show the markering ability in this character (Table VI).

Content of extract in malt dry matter

According to the results obtained in set A, it is evident that the extractability is markered by four alleles – A21, B17, B47 and B–N. Allele B47 is evidently responsible for the higher extract content, while allele B–N was found in the class with the lowest expression of this character in a very high frequency. Alleles A21 and B17 were present in the second class with an average character value in the highest frequency, but the extreme values of the character were zero.

According to the results in set B the alleles A4, B47, B45 were to marker a high extract content. Alleles B–N, B29 and A23, present in the first class in a high frequency, or a very low frequency in the second and third class, could marker the genes for a low grain extractivity in barley genotypes (Table VI).

Comparison of results of the both sets evaluated proved relations between allele B47 occurrence and a high extract content in malt dry matter.

V. HRD allelic blocks, separated from electrophoretic spectra of tested varieties and new breeds of spring and winter barley

Variety	Line	HRD – locus and allele		
		A	B	F
Akcent	A	12	21	1
Alexis	A	2	19	1
Amazone	A	2	8	2
	B	21	21	0
Apex	A	2	17*	3
	B	2	17*	2
Blenhelm	A	23	29	3
	C	18	N	1
	D	18	17	2
	B	2	N	1
BR-4148	A	5	17	2
BR-4415	A	4	21	1
	B	5	17	2
	(C)	5	17	3
C-590	A	12	25	1
C-685	A	2	47	1
	B	2	47	1
CE-431	A	2	47	1
	B	2	47	1
CE-686	A	2	47	1
	(B)	21	47	1
	C	2	47	1
Ditta	A	32	21	1
Donum	A	4	45	3
	B	2	29	3
	C	2	45	3
Forum	A	N1	8	2
Grif	A	32	21	1
	B	2	8	2
Grosso	A	23	29	3
Hard	A	23	29	3
HE-1728	A	18	52	1
	B	32	11	0
	C	2	47	1

Continuation of Tab. V

Variety	Line	HRD – locus and allele		
		A	B	F
HE-4809	A	2	47	1
	B	2	47	1
	C	2	N2	2
	D	2	N2	2
	(E)	23	29	3
HE-5038	A	(9)	25	1
	B	2	25	1
	(C)	2	47	1
Heran	A	2	47	1
	B	2	47	1
Cheri	A	2	N	1
Jaspis	A	21	25	1
Jarek	A	2	19	1
Jubilant	A	N2	29	3
	(B)	23	29	3
KM-1220	A	2	43	2
KM-1252	A	4	52	1
	B	18	52	1
	C	4	45	3
	D	18	45	3
KM-974	A	2	17	3
	B	(9)	17	3
	C	2	17	3
	(D)	23	21	1
Kompakt	A	2	19	2
	B	2	8	2
	(C)	2	(32)	1
Krona	A	N	29	3
Ladík	A	23	21	1
Magda	A	23	29	3
	B	12	29	3
Malvaz	A	2	17	3
Novam	A	32	21	0
Orbit	A	21	25	1
Primus	A	21	25	1

Continuation of Tab. V

Variety	Line	HRD – locus and allele		
		A	B	F
Primus	B	2	25	1
	(C)	23	8	2
Prisma	A	23	29	3
Profit	A	2	25	1
Regatta	A	2	N	1
	B	2	N	1
Reggae	A	2	(17)	3
	B	2	(17)	3
Riff	A	N	(17)	3
	B	N	(17)	3
Rubia	A	4	45	3
SG-S-159	A	12	21	1
SG-S-160	A	12	47	1
SG-S-167	A	21	25	1
Signal	A	N	N	N
	B	N	23	3
SK-3084	A	21	19	1
SK-3212	A	21	25	1
	(B)	18	17	2
SK-3214	A	2	19	1
SK-3247	A	2	47	1
	B	2	47	1
SK-3662	A	21	17*	2
Sladko	A	12	21	1
	B	12	21	1
Stabil	A	2	47	1
	B	N1	47	1
	C	21	25	1
	D	2	25	1
Stelli	A	21	19	1
	B	2	(8)	2
Svit	A	2	47	1
	B	2	47	1
Terno	A	21	17*	2
	B	2	17*	2

Allele B–N was found in the class with low extractivity in a high frequency. In all classes of the character expression, allele B17 was found in high representation for the average level of extract content.

Oziel et al. (1996) localised genes in the contrary to our results, influencing the percentage of malt extract and some other traits of malting quality, on chromosome 7.

Powdery mildew

Genes for resistance to powdery mildew were present on 4 and 5 (Nilan, Wettstein, 1984; Tsuchiya, 1984), or on chromosome 1, 4, 5, 6 and 7 (Jahoor, Fischbeck, 1987). The obtained results proved the ability of hordein alleles A12 and B (17) for markering genes controlling the resistance to powdery mildew, localized on chromosome 5. Also a significant relation between the hordein alleles B17 and B–N and the susceptibility to powdery mildew was proved (Table VI).

Our results widen the knowledge of foreign authors about the markering of powdery mildew resistance by hordein genes (Sozinov, 1985). The main cause of some differences is evidently caused by use of ecologically and genetically different varieties.

Leaf rust of barley

Nine genes for race specific resistance control the resistance to leaf rust of barley. They are identified as Pa–Pa 9, localized on 3rd and 5th chromozomes (Hraška et al., 1989) or on chromosome 2, 3 and 5 (Tsuchiya, 1984). Our results show the allele ability A–N and B(17), B52, B–N1 to markering the resistance (Table VI).

The alleles B8 and B19 significantly marker the susceptibility to this disease.

Plant length

The winter varieties showed an extraordinary plant length. The high frequency of alleles A3, A14 and B3, B–N1 occurring only in winter varieties, in the third class for the higher plant length, could indicate a markering ability of this character expression. The occurrence of A–N allele in the third class with the extraordinary character expression, which is typical for spring varieties and is in correlation with the plant length. The alleles A2 and B47 seem to be the markers of a shorter plant length (Table III).

Above mentioned alleles can marker winter character at the same time, which is genetically determined by the chromosomes 4, 5 and 7 (Tsuchiya, 1984).

VI. Associantin coefficients

Locus/ /allelamorphosis	Association coefficient *V* Thousand seed weight	Association coefficient *V* Grain portion 2.5 mm
A/2	0.254	0.325
A/4	0.277	0.277
A/12	0.152	0.224
A/18	0.234	0.277
A/21	0.266	0.255
A/23	0.302	0.066
A/32	0.324	0.343
A/N	0.331	0.213
A/N1	0.263	0.134
A/N2	0.277	0.158
B/8	0.319	0.058
B/17	0.234	0.134
B/19	0.092	0.271
B/21	0.405	0.067
B/23	0.277	0.195
B/25	0.266	0.053
B/29	0.228	0.087
B/45	0.277	0.277
B/47	0.043	0.363
B/(32)	0.184	0.277
B/(8)	0.164	0.158
B/17*	0.337	0.322
B/N	0.281	0.34
F/0	0.263	0.134
F/1	0.149	0.064
F/2	0.313	0.064
F/3	0.37	0.041
F/N	0.277	0.195

Locus/ /allelamorphosis	Association coefficient *V* Extract in malt dry matter – set A	Association coefficient *V* Extract in malt dry matter – set A
A/2	0.076	0.15
A/4	0.171	0.271
A/5	–	0.207
A/12	0.27	0.156
A/18	0.286	0.182
A/21	0.128	0.045

Continuation of Tab. VI

Locus/ /allelamorphosis	Association coefficient *V* Extract in malt dry matter – set A	Association coefficient *V* Extract in malt dry matter – set A
A/23	0.169	0.26
A/32	0.216	0.147
A/(9)	–	0.169
A/N	0.199	0.202
A/N1	0.244	0.169
A/N2	0.171	0.118
B/8	0.117	0.127
B/17	0.287	0.225
B/19	0.212	0.167
B/21	0.177	0.176
B/23	0.2	0.184
B/25	0.285	0.044
B/29	0.227	0.315
B/43	–	0.149
B/45	0.17	0.271
B/47	0.394	0.293
B/(32)	0.207	–
B/52	–	0.169
B/(8)	0.171	–
B/(17)	–	0.169
B/N	0.411	–
B/(32)	–	0.118
B/(8)	–	0.149
B/17*	0.459	0.265
B/N	0.411	0.379
B/N2	–	0.202
F/0	0.153	0.127
F/1	0.257	0.217
F/2	0.248	0.142
F/3	0.272	0.281
F/N	0.2	0.184

Locus/ /allelamorphosis	Association coefficient *V* Powdery mildew	Association coefficient *V* Leaf rust of barley
A/2	0.228	0.291
A/3	0.075	0.199
A/4	0.219	0.18

Continuation of Tab. VI

Locus/ /allelamorphosis	Association coefficient *V* Powdery mildew	Association coefficient *V* Leaf rust of barley
A/5	0.151	0.152
A/12	0.229	0.251
A/14	0.097	0.104
A/18	0.155	0.167
A/21	0.101	0.107
A/23	0.014	0.148
A/32	0.044	0.011
A/(9)	0.119	0.209
A/N	0.14	0.259
A/N1	0.117	0.102
B/3	0.044	0.148
B/8	0.104	0.223
B/17	0.237	0.05
B/19	0.17	0.223
B/21	0.217	0.136
B/23	0.142	0.147
B/25	0.161	0.06
B/29	0.196	0.234
B/43	0.142	0.137
B/45	0.154	0.167
B/47	0.104	0.302
B/52	0.202	0.209
B/(17)	0.244	0.209
B/(32)	0.127	0.147
B/(8)	0.171	0.137
B/17*	0.194	0.148
B/N	0.179	0.014
B/N1	0.149	0.259
B/N2	0.182	0.197
F/0	0.117	0.102
F/1	0.194	0.227
F/2	0.133	0.232
F/3	0.149	0.286
F/N	0.142	0.147

References

ASINS, M. J. – CARBONELL, E. A.: Detection of linkage restriction fragment length polymorphism markers and quantitative traits. Theor. Appl. Genet., *76*, 1988: 623–626.

BARR, A. R. – CHALMERS, K. J. – KARAKOUSIS, A. – KRETSCHMER, J. M. – MANNING, S. – LANCE, R. C. M. – LEWIS, J. – JEFFRIES, S. P. – LANGRIDGE, P.: RFLP mapping of a new cereal cyst nematode resistance locus in barley. Plant Breeding, *117*, 1998: 185–187.

BECKMANN, J. S. – SOLLER, M.: Restriction fragment length polymorphisms in genetic improvement: methodologies, mapping and costs. Theor. Appl. Genet., *67*, 1983: 35–43.

ČERNÝ, J. – ŠAŠEK, A. – DOSTÁL, J. – BRADOVÁ, J. – HANIŠOVÁ, A. – KUBÁNEK, J. – KURZOVÁ, E.: Selection of homozygous genotypes in wheat B.c. 1–F2 generations by means of gliadin markers. Scientia Agric. bohemoslov., *17*, 1985: 153–162.

ELLIS, R. P.: Electrophoresis of grain proteins: Detection of rye proteins in wheat x rye hybrids. J. Nat. Inst. of Agric. Bot., *12*, 1971: 236–241.

HEUN, M. – KENNEDY, A. E. – ANDERSON, J. A. – LÁPITAN, N. L. V. – SORRELLS, M. E. – TANSKLEY, S. D.: Construction of a restriction fragment length polymorphism map for barley (*Hordeum vulgare*). Genome, *34*, 1991: 437–447.

HRAŠKA, Š. et al.: Špeciálna genetika poľnohospodárskych rastlín. Bratislava, Príroda 1989.

JAHOOR, A. – FISCHBECK, G.: Genetical studies of resistance of powdery mildew in barley lines derived from *Hordeum spontaneum* collected from Israel. Plant Breeding, *99*, 1987: 265–273.

JAHOOR, A. – BACKES, G. – GRANER, A. – HERRMANN, R. G. – FISCHBECK, G.: Development of RFLP markers for barley. Plant Breeding, *107*, 1991: 73–76.

JAHOOR, A. – SCHÖNFELD, M. – BACKE, G. – MOHLER, V. – WENZEL, G.: Využití molekulárních markerů ve šlechtění obilovin. Perspektiva některých nových směrů ve šlechtění obilovin (Use of molecular markers in cereal breeding. Prospects of some new trends in cereal breeding). In: Obilnářský seminář 96, ČSSA, VÚRV, Praha, 1996: 4–6.

LEKEŠ, J. et al.: Ječmen (Barley). Praha, SZN 1985.

MELCHINGER, A. E.: Locating quantitative trait loci by means of molecular markers. Biometrics in plant breeding. In: Proc. Seventh Meet. Eucarpia, Section Biometrics in Plant Breeding, Norway, August 2nd–5th, 1988.

MELCHINGER, A. E.: Use of melecular markers in breeding for oligogenic disease resistance. Plant Breeding, *104*, 1990: 1–19.

NILAN, R.A. – WETTSTEIN, D.: Masterlist of barley genetic stocks. Program in genetics and cell biology. Washington State Univ., Contribution to BGN, Vol. 15, 1984.

OZIEL, A. – HAYES, P. M. – CHEN, F. Q. – JONES, B.: Application of quantitative trait locus mapping to the development of winter-habit malting barley. Plant Breeding, *115*, 1996: 43–51.

PICKERING, R. A. – STEFFENSON, B. J. – HILL, A. M. – BOROVKOVA, I.: Association of leaf rust and powdery mildew resistance in recombinant derived from a *Hordeum vulgare* x Hordeum bulbosum hybrid. Plant Breeding, 1998, 117, 93–84.

POMORCEV, A. A. – NECVETAJEV, V. P. – SOZINOV, A. A.: Polimorfizm kulturnogo jačmeňa (*Hordeum vulgare* L.) po gordeinam. Genetika, *21*, 1985: 629–639.

PRUGAR, J. – HRAŠKA, Š.: Kvalita jačmeňa (Barley quality). Bratislava, Príroda 1989.

SAX, K.: The association of size differences with seed coat pattern and pigmentation in *Phaseolus vulgarus*. Genetics, *8*, 1923: 552–560.

SOLLER, M. – BECKMANN, J. S.: Genetic polymorpism in varietal identification and genetic improvement. Theor. Appl. Genet., *67*, 1983: 25–33.
SOZINOV, A. A.: Polimorfizm belkov i jego značenie v genetike i selekcii. Moskva, Nauka 1985.
SOZINOV, A. A. – POPERELJA, F. A.: Metodika vertikalnogo elektroforeza v krachmalnom gele i genetičeskij princip. Oděsa, VSGI 1978.
ŠAŠEK, A. – ČERNÝ. J.: Improving the identification of allelic gliadin blocks. Scientia Agric. bohemoslov., *15*, 1983: 103–109.
ŠAŠEK, A. – ČERNÝ, J. – BRADOVÁ, J.: Kontrola odrůdové pravosti genetických zdrojů ječmene setého elektroforézou hordeinů (Control of varietal purity of genetic barley sources by hordein electrophoresis). Rostl. Výr., *37*, 1991: 565–574.
ŠAŠEK, A. – ČERNÝ, J. – DOSTÁL, J. – HANIŠOVÁ, A.: Autorské osvědčení č. 255259/1989 na vynález: Způsob získávání genotypů embryí pšenice (Author's certification No. 255259/1989 for patent: Way of obtaining of genotypes of wheat embryos). Úřad pro vynálezy a objevy v Praze, 15. 3. 1989.
ŠAŠEK, A. – ČERNÝ, J. – NECVETAJEV, V. P. – BRADOVÁ, J.: A catalogue of electrophoretic hordein spectra of Czechoslovak certified spring barley varieties. Scientia Agric. bohemoslov., *22*, 1990: 1–10.
ŠAŠEK, A. – BRADOVÁ, J. – ČERNÝ, J. – NECVETAJEV, V. P.: A catalogue of electrophoretic hordein spectra in the assortment of winter barley varieties and new varieties. Scientia Agric. bohemoslov., *22*, 1990: 11–21.
ŠAŠEK, A. – SÝKOROVÁ, S. – BRADOVÁ, J. – ČERNÝ, J.: Využití elektroforézy bílkovinných genetických markerů pšenice a ječmene v kontrole odrůd a osiv (Use of electrophoresis of protein genetic wheat and barley markers in the control of varieties and seeds). Praha, 1994.
TSUCHIYA, T.: Linkage maps of barley (*Hordeum vulgare* L.). In: O'BRIEN, S. J. (ed.): Genetic maps 1984. Volume 3. Cold Spring Harbor Laboratory: 508–521.
TUVESSON, S. – POST, L. – ÖHLUND, R. – HAGBERG, P. – GRANER, A. – SVITASHEV, S. – SCHEHR, M. – ELOVSSON, R.: Molecular breeding for the BaMMV/BaYMV resistance gene ym4 in winter barley. Plant Breeding, *117*, 1998: 19–22.

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Markerování některých znaků ječmene setého pomocí hordeinových signálních genů.

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Metodou aproximativního stanovení souhlasného výskytu jednotlivých alelických bloků signálních hordeinových genů a tříd exprese některých kvantitativních znaků ječmene byl v letech 1992 až 1995 hodnocen soubor 61 odrůd a nového šlechtění ječmene setého, jarní a ozimé formy.

K manifestaci hordeinových signálních genů bylo použito vertikální elektroforézy ve sloupcích škrobového gelu. Alelické hordeinové bloky byly vyčleněny z elektroforetických spekter podle publikovaných katalogů.

Závislost mezi výskytem alel hordeinových genů a zvolenými agronomickými znaky ječmene byla hodnocena χ^2-testem. Těsnost závislosti byla vyjádřena koeficientem asociace *V*.

Na základě zjištěných hodnot koeficientu asociace mezi četností jednotlivých alel-hordeinových lokusů a třídou exprese posuzovaných agronomicky významných znaků byly stanoveny pro použitý soubor odrůd a nových šlechtění ječmene setého orientační markerovací hodnoty.

1. Pravděpodobnými markery vysoké hodnoty hmotnosti tisíce semen jsou alely A23, B17* a F3. Naproti tomu alely A32, B21 a B8 se jeví jako markery nízkého projevu tohoto znaku.
2. Alely B47 a B17* se jeví jako markery vysokého podílu zrna nad sítem 2,5 mm.
3. Vysoký obsah extraktu v sušině sladu markeruje alela B47, zatímco alela B–N se jeví jako marker nízkého obsahu v sušině sladu.
4. Schopnost markerovat rezistenci k padlí travnímu projevují alely A12 a B(17). Alely B17 a B–N se jeví jako markery k náchylnosti k padlí travnímu.
5. Alely A12, A–N, B(17), B52 a B–N1 projevují schopnost markerovat rezistenci ke rzi ječné. Naproti tomu alely B8 a B19 markerují náchylnost k této chorobě.
6. Pro jarní ječmeny projevuje tendenci markerovat vyšší délku rostlin alela A–N. U ozimých ječmenů prokázaly analogickou markerovací schopnost A3, A14, B3 a BN1.
7. Markerování ozimosti, resp. jarovosti je problematické vzhledem k nízkému zastoupení ozimých odrůd v pokusných souborech. Alely A14 a A3, B3, B–N1 nebyly zjištěny u jarních forem.

ječmen; elektroforéza; hordeiny; genetické markery

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