PROTEIN COMPOSITION OF BARLEY SEEDS AND EVALUATION OF THEIR GERMINATION ENERGY AND SEEDLING VIGOUR UNDER CONTROL AND WATER STRESS CONDITIONS

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ABSTRACT

Parental genotypes, cv. Aramir and line R567, as well as selected doubled haploid (DH) barley lines differed in the main protein fraction content in seeds. Paternal form R567 and DH line C55 were characterized by the highest protein content, while the seed of the line C23 as compared to other genotypes had the lowest content of main protein fractions. Quantitative and qualitative differences were also found in electrophoretic patterns of albumins and globulins and in polypeptide composition of hordein B and C subfractions. Spectra of these proteins were found to have more bands in the parental form R567 and DH line C55. Electrophoretic albumin + globulin patterns in the DH line C23 differed from that of the remaining barley genotypes; that type of genotype was observed to have recombination with regard to polypeptide composition of hordein B and C subfractions.

The water stress delayed the seed germination into normal seedlings in all genotypes. The highest germination energy under stress conditions was characteristic of seeds from the parental form R567 and DH line C55. Seedlings of these two genotypes, as compared to the others, distinguished by the longest plumule both in control and under water stress conditions.

Stress effect on the seedling vigour was expressed in a significant reduction of the seedling length, the plumule being more sensitive to drought than roots. A smaller reduction of the plumule length was caused by the stress in the parental form R567 and DH line C55, whereas root response to water stress was similar in all studied genotypes.

KEY WORDS: barley, germination, protein composition, water stress, seeds, seedling vigour

INTRODUCTION

The ability of seeds to produce healthy seedlings capable of optimum development as well as plants effected by a wide range of environmental factors is an important character from the agricultural point of view. Seeds with a higher germination energy usually have a higher vigour and are of a large sowing value (Grzesiuk and Kulka 1988). Proteins both storage and growth-regulating, contained in the seed fulfil an important function in germination. Embryo developmental and seedling growth under different environmental conditions to a large degree depend on activity of proteins in seeds (Grzesiuk and Górecki 1991).

Proteins contained in barley seeds differ in biochemical structure (Ivanko 1971; Kapała 1979; Kapała and Patyna 1986). Significant polymorphism of these proteins both among wild species and cultivated varieties was found on the basis of electrophoretic separations (Przybylska and Kapała 1974; Kapała 1979; Kapała 1981). A number of studies are devoted to interpretation of electrophoretic patterns (Przy-

bylska 1972; Heisel et al. 1986; Drzewiecki 1993; Kapała and Patyna 1993) and to location on chromosomes of genes encoding seed proteins (Drzewiecki 1997). It has been found that genes encoding storage barley proteins are associated with genes determining useful traits (Adamski et al. 1995) and resistance (Jensen et al. 1980, Waga and Grzywa 1995).

There are communications that seeds of various cereal cultivars and seeds within a cultivar differ by their germination ability and vigour both under optimum conditions for germination and under conditions of water stress (Akalehiyot and Bewley 1977; El-Sharkawi and Springuel 1977; Blum et al. 1980; Leszczyńska 1988; Gawrońska and Grzelak 1991, 1993). There is, however, no data concerning relationship between quantitative and qualitative protein composition of seeds and germination energy and seeds vigour under optimal germination and water stress conditions.

Earlier studies on the response of two barley genotypes, cv. Aramir and collection line R567, to soil drought showed that seeds of these genotypes differed by quantitative and qualitative composition of seed proteins (Gniazdowska-Skoczek and Kapała 1997). It was also found that seeds of the cv. Aramir, line R567 and selected DH lines derived from the F₁ (Aramir x R567) differed in germination speed (unpublished data).

Abbreviations used

DH – doubled haploid, PEG – polyethylene glycol

Our intention was to determine is there a relationship between quantitative and qualitative protein composition in the grain of the parental genotypes (cv. Aramir and line R567) and selected DH lines (C23, C41, C47/1 and C55) and seed germination energy and vigour under optimal germination and water stress conditions.

MATERIAL AND METHODS

Plant material. Seeds harvested in 1995 of the parental genotypes, cv. Aramir and line R567, as well as selected DH lines were used in the studies. The cv. Aramir is a European genotype, while the line R567 is African derived from the cross Burea x Brown (Barbacki et al. 1978). The selected DH lines C23, C41, C47/1 and C55 were obtained from the F_1 hybrids (cv. Aramir x R567) by *H. bulbosum* method at the Institute of Plant Genetics, Polish Academy of Sciences in Poznań (Kasha and Kao 1970; Adamski 1979). Details concerning cultivation of barley in soil crops are given in Skoczek et al. (1990).

Extraction of the main protein fraction. The procedure leading to separation of the main protein fraction from barley seeds was taken from Ingversen and Koie (1973). Details are given in Kapała and Patyna (1986).

Determination of protein content. The contents of particular protein fractions were determined quantitatively according on colour intensity as a result of Coomassie Brilliant Blue bond with standard protein extracts (chromatography-paper test). Stained protein spots were cut out and the dye was eluted with sodium dodecyl sulphate solution. The absorbance of the dyed eluate was recorded by a spectrophotometer (Kapała 1994). The studied samples were analysed in four replications.

Electrophoresis: Albumins and globulins were analyzed in polyacrylamide gel plates in the basic buffer system as described by Kapała (1979). Hordein electrophoresis was performed according to the method by Kapała (1981).

Seed germination was carried out in Petri dishes of 9 cm diameter. Seeds (25 per dish) were transferred on two sheets of blotter moistened with 10 cm³ of distilled water (control) or with PEG solution with a relevant osmotic potential. Three osmotic potentials of -0.3, -0.6 and -0.9 MPa were used. PEG 600 solution with a suitable osmotic potential was prepared according to Premachandra and Shimada (1987). To prevent seeds from microflora development they were rinsed prior to sowing with 5% CaOCl₂ followed by distilled water and then were blotted dry. Petri dishes with seeds were kept in an air-conditioned chamber at 20°C in the dark. Seeds germination into normal seedlings was scored 4 days after sowing. The experiment was performed in 4 replications.

Seed vigour evaluated by growth test was based on biometrical measurements of seedling plumules (coleoptile with the first leaf) and seminal roots (Perry 1977). Seeds were germinated on filter paper covering glass plates, the upper part of which had hollows for seed made at 1 cm intervals, each plate having about 15 seeds. The plates covered with filter paper wetted with distilled water or PEG solution of a relevant osmotic potential were placed in glass containers which had distilled water or PEG solution on the bottom.

The glass containers were kept in an air-conditioned chamber at 20°C in the dark. Seeds for each genotype and each level of drought stress were sown in 6 replications with 15 seeds per plate. The length plumule and seminal roots were biometrically measured 8 days after sowing. The number of

seed germinating into normal seedlings were also counted. The obtained results were subjected to a statistical analysis.

RESULTS

The parental forms, cv. Aramir and line R567, as well as the selected DH lines differed in main protein fraction content in seeds (Table 1). Among the studied genotypes, the parental form R567 and DH line C55 distinguished by the highest protein content. In the maternal form of Aramir and DH line C41 the protein fraction content in seed was similar and significantly lower than in the paternal line R567. The DH line C47/1 had an intermediate protein content in comparison to its parents, whereas the DH line C23 was found to have the lowest main protein fraction content in seed (Table 1).

TABLE 1. Seed protein composition of the parental genotypes (cv. Aramir and line R567) and selected DH lines.

Genotypes	Main protein fraction content (% of dry matter)		
	albumins + globulins	glutelins	hordein
Aramir	4.1	4.6	7.3
R567	4.6	5.2	8.3
C23	3.9	4.4	7.1
C41	4.1	4.6	7.2
C47/1	4.3	4.9	7.9
C55	4.6	5.3	8.4
LSD			
	0.05	0.195	0.217
	0.01	0.267	0.297

Electrophoretic patterns of albumins and globulins of the cv. Aramir and line R567 showed significant quantitative and qualitative differences. Spectra of these proteins were found to be richer in the parental form R567 (Fig. 1). The DH lines C41 and C47/1 were observed to have the same type of albumin + globulin spectrum as the parental form Aramir. The DH line C55 had the same electrophoretic patterns of albumins + globulins as the parental line R567. The electrophoretic spectrum of albumins + globulins of the DH line C23 differed from that of other analysed barley forms.

The parental forms, cv. Aramir and line R567, significantly differed in polypeptide composition of hordein B and C subfractions. A richer polypeptide spectrum of the both hordein protein subfractions was revealed in the line R567. The DH lines C41 and C47/1 showed the same type of polypeptide spectrum of hordein proteins as the cv. Aramir. The DH line C55 was found to have the same electrophoretic hordein patterns as the paternal form R567. Polypeptide composition of hordein C subfraction in the line C23 was the same as that in the initial cv. Aramir whereas polypeptide spectrum of B subfraction conformed to the electrophoretic patterns of that hordein subfraction in the paternal form R567. The DH line C23, therefore, was observed to have recombination with regard to polypeptide composition of hordein B and C subfractions.

Seeds of parental forms, and DH lines differed in germination energy and the length of seedlings (Table 2 and Fig. 3A, B, C, D). Under control conditions, the studied genotypes

Fig. 1. Electrophoretic patterns of salt-soluble seed proteins (albumins + globulins) of the parental genotypes (cv. Aramir and line R567) and selected DH lines of barley.
a – photographic presentation,
b – diagrammatic presentation.

TABLE 2. Percent normal seedlings of the parental genotypes (cv. Aramir and line R567) and selected DH lines of barley 4 days after sowing as influenced by osmotic stress.

Genotypes	Percent seeds germinated into normal seedlings			
	control	-0.3 MPa	-0.6 MPa	-0.9 MPa
Aramir	97.8	80.4	12.3	0
R567	90.7	85.3	72.6	56.5
C23	97.3	82.9	30.7	0
C41	100	82.8	10.9	0
C47/1	100	90.0	26.4	0
C55	100	100	95.3	71.5
LSD				
	0.05	insig.	12.95	10.27
	0.01	insig.	17.74	14.32

produced normal seedlings almost in 100%. Water stress reduced seed germinability in all studied genotypes. At water potential -0.3 MPa the germination energy decreased by 10% to 20% in most genotypes, but the observed differences in

Fig. 2. Polypeptide spectra of hordein of the parental genotypes (cv. Aramir and line R567) and selected DH lines of barley.
a – photographic presentation,
b – diagrammatic presentation.

seed germination under these conditions between the studied genotypes were statistically insignificant (Table 2). When the level of stress was increased to -0.6 MPa, the germination energy was 11-95%, depending on the genotype. The highest germination energy under these conditions was found in the DH line C55 (95%) and in the parental form R567 (72%). The lines C23 and C47/1 germinated normally in 30% and 26.4%, respectively. Seeds of the cv. Aramir and DH line C41 distinguished by the lowest germination energy 12% and 11%, respectively. Under the highest stress of -0.9 MPa, only seeds of the parental form R567 (56%) and line C55 (71%) germinated into normal seedlings. After 4 days of germination the studied barley genotypes significantly differed in the length of normally germinated seedlings, the largest differences concerning plumule length (Fig. 3A, B, C and D). Each time the parental form R567 and DH C55 had the longest plumules.

Seed vigour of the parental genotypes and selected DH lines evaluated in growth tests on glass plates and measured in % of seeds germinated into normal seedlings is illustrated in Table 3. Under control conditions and under conditions of a moderate stress (of -0.3 MPa) all studied genotypes produced normal seedlings to 100%. The stress increase to -0.6 MPa decreased the number of normal seedlings by 2-24%, depending on the genotype. However, differences in the number of

Fig. 3A, B, C, D. Seed germination (after 4 days) of parental genotypes (cv. Aramir and line R567) and selected DH lines of barley as influenced by osmotic stress.

TABLE 3. Seed vigour (8 days after sowing) of the parental genotypes (cv. Aramir and line R567) and selected DH lines of barley as influenced by osmotic stress.

Genotypes	Percent seeds germinated into normal seedlings			
	control	-0.3 MPa	-0.6 MPa	-0.9 MPa
Aramir	100	100	76.9	0
R567	100	100	86.5	73.0
C23	100	100	89.1	0
C41	100	100	76.1	0
C47/1	100	100	79.2	0
C55	100	100	98.7	86.7
LSD				
	0.05	insig.	insig.	10.20
	0.01	insig.	insig.	14.30

normal seedlings observed in these conditions between the studied genotypes were statistically insignificant (Table 3).

Water stress caused reduction of the seedling growth, the plumule being more susceptible to drought than roots (Fig. 4A, B, C and D). At water potential -0.9 MPa only the parental form R567 and line C55 produced very short plumules (about 5 mm). The root length under these conditions was reduced in all genotypes by on average 50%. The lines R567 and C55 in comparison to the remaining genotypes were characterized by the smallest plumule reduction under stress conditions – by on average 10%. Besides, it was observed that under control conditions and under moderate stress, seedlings of the DH line C23 were significantly shorter than seedlings of the remaining barley genotypes (Fig. 4A, B).

DISCUSSION

The basic chemical composition of seeds has no influence on their germination energy and capacity. It was, however, noticed that seeds with a high content of small polypeptides germinated more readily and more rapidly than seeds accumulating complex proteins (Grzesiuk and Kulka 1988). Germination capacity in different environmental conditions largely depends on physiological seed activity, among others, on the activity of enzymes participating in protein changes (Grzesiuk and Górecki 1981).

The studied barley genotypes were found to have no relationship between quantitative and qualitative composition of main protein fractions in seeds and germination energy under control conditions. But it was observed that the paternal form R567 and DH line C55 were characterized by the highest main protein fraction content in seed (Table 1), by a richer spectrum of hordein and albumins+globulins (Figs 1 and 2) and by a significantly longer plumule than the remaining genotypes (Fig. 3A). Activity of enzymes associated with protein metabolism was probably higher in germinating seeds of these genotypes. It was found that there is relationship between germination energy and intensity of nitric metabolism in pea seeds (Grzesiuk and Górecki 1981).

The electrophoretic analysis of salt-soluble proteins showed the presence of characteristic additional bands with R_p 0.86 and 0.91 in the lines R567 and C55. These two proteins were found earlier in barley genotypes with naked seeds (Przybylska and Kapała 1974; Kapała 1979). The paternal form

Fig. 4A, B, C, D. Length of plumules and seminal roots (8 days after sowing) of seedlings of the parental genotypes (cv. Aramir and line R567) and selected DH lines of barley as influenced by osmotic stress.

R567 and DH line C55 also belong to genotypes with naked seeds. Proteins with Rp 0.86 and 0.91 are, therefore, associated with morphological seed characters and may be also with a more intensive metabolism in seeds. As follows from the performed studies, rapid plumule growth, which is (among others) undoubtedly a result of effective nitric metabolism in germinating seeds, in the lines R567 and C55 was related with a presence of intensive bands with Rp 0.86 and 0.91.

The lines R567 and C55 differed from the rest of barley genotypes by seed vigour evaluated in growth tests. In Boyd et al. (1971) the observed differences in barley seed vigour were largely caused by differences in seed size. In our studies, we used only similar-size seeds, so differences in seed vigour were caused by other agents.

A limiting water uptake significantly decreased both seed germination and seedling development. El-Sharkawi and Springuel (1977) found the same for barley. Differences in seed germination of the studied barley genotypes were found between the applied tests, i.e. in Petri dishes (Table 2) and on glass plates (Table 3). Higher results of germination were obtained for the studied barley genotypes in growth tests. In growth tests (on glass plates), oxygen conditions were undoubtedly more favourable. A lower percent of seeds germinating into normal seedlings observed in Petri dishes particularly for genotypes with naked seed (cv. Aramir, C23, C41 and C47/1) could be caused by a limiting oxygen uptake. Similar differences in triticale seed germination between the applied tests occurred in the studies conducted by Gawrońska and Grzelak (1971, 1973). Higher results of seed germination were obtained by these authors in growth tests.

The present studies have showed that seeds of the paternal form R567 and line C55 had the highest germination ability under stress conditions. At the osmotic stress of -0.9 MPa, over 50% seeds of these genotypes germinated into normal seedlings, though the plumule length under these conditions was strongly reduced in these lines. As shown by previous studies, inhibition of germination by water stress was not related with the water uptake decrease, but first of all with inhibition of metabolism in cells (Hadas 1976; Stout et al. 1980). It was observed that water stress decreases the ability to form polysomes and to synthesize protein in barley seed (Armstrong and Jones 1973). It is assumed that the primitive form R567 and DH line C55 are characterized by a higher ability to synthesize proteins under conditions of water stress in comparison to other studied genotypes.

It has been found in the growth tests that in all barley genotypes the plumule was more susceptible to water deficit than roots. A higher plumule sensitivity to drought in comparison to roots was also reported by El-Sharkawi and Springuel (1977) for barley, wheat and sorghum and by Gawrońska and Grzelak (1991, 1993) for triticale. Differences in plumule sensitivity to water deficit were observed between the studied genotypes, whereas no significant differences were found in root response (Fig. 3B, C, D and Fig. 4B, C, D). A differential response of triticale roots was observed by Gawrońska and Grzelak in their studies (1991, 1993).

In summary, it should be concluded that independently of germination conditions, the paternal form R567 and DH line C55 were characterized by a significantly longer plumule in comparison to other studied genotypes. A relationship has been found between percent content of main protein fraction in seed, electrophoretic spectrum of albumins + globulins and hordein, and plumule length in these genotypes. The richer B and C hordein spectrum and presence of proteins with mobility 0.86 and 0.91 were related to a longer plumule in the

line R567 and C55 under optimum conditions for germination and seedling growth and under conditions of water stress.

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LITERATURE CITED

- ADAMSKI T. 1979. The obtaining of autotetraploid barley lines using haploids from the cross *Hordeum vulgare* L. x *Hordeum bulbosum* L. Genet. Pol. 20: 31-42.
- ADAMSKI T., KACZMAREK Z., SURMA M. 1995. Wykrywanie sprzężeń genów kontrolujących cechy ilościowe. XII Zjazd PTG (Streszczenia) Jour. Appl. Genet. 36A: 7.
- AKALEHIYWOT T., BEWLEY I.D. 1977. Promotion and synchronization of cereals grain germination by osmotic pretreatment with polyethylene glycol. Journ. Agricult. Sci. 89: 503-506.
- ARMSTRONG J.E., JONES R.L. 1973. Osmotic regulation of α -amylase synthesis and polyribosome formation in aleurone cells of barley. J. Cell Biol. 59: 444-455.
- BARBACKI S., CALIŃSKI T., SURMA M., KURHAŃSKA G., ADAMSKI T., KACZMAREK Z., DOBEK A., KARCZEWSKA A., JEŻOWSKI S. 1978. Transgression in barley (*Hordeum sativum* Jess.) 7a. Transgressions of F_6 and F_7 hybrids from the cross Burea x Brown. Gen. Pol. 19(4): 403-421.
- BOYD W. J. R., GORDON A.G., LACROIX L.J. 1971. Seed size, germination resistance and seedling vigor in barley. Can.J. Plant Sci. 51: 93-99.
- BLUM A., SINMENA B., ZIV O. 1980. An evaluation of seed and seedling drought tolerance screening tests in wheat. Euphytica 29: 727-736.
- DASGUPTA P.R., AUSTENON H.M. 1973. Relations between estimates of seed vigor and field performance in wheat. Can. J. Plant Sci. 53: 43-46.
- DRZEWIECKI J. 1993. Elektroforeza białek i jej zastosowanie w ocenie nasion i hodowli roślin. Biul. IHAR 188: 211-220.
- DRZEWIECKI J. 1997. Ocena tożsamości roślin rolniczych na podstawie cech nasion i siewek- stan obecny i nowe kierunki. Biul. IHAR 203: 7-22.
- EL-SHARKAWI H.M., SPRINGUEL I. 1977. Germination of some crop plant seeds under reduced water potential. Seed Sci. and Technol. 5: 667-688.
- GAWROŃSKA H., GRZELAK K. 1991. Effect of drought stress by polyethylene glycol (PEG) on seed germination and seedling growth of spring Triticale (*Triticosecale* x *Wittmack*). Biul. IHAR 180: 53-64. (in Polish)
- GAWROŃSKA H., GRZELAK K. 1993. Seed germination and seedling vigour of triticale (*Triticosecale* x *Wittmack*) under drought stress. Plant Var. Seeds 6: 9-19.
- GNIAZDOWSKA-SKOCZEK H., KAPALA A. 1996. Effect of soil drought on quantitative and qualitative composition of kernel protein in barley. Proceed. Intern. Conf. Perspectives in plant genetics, Genet. Pol. 37A: 219-222.
- GRZESIUK S., KULKA K. 1988. Biologia ziarniaków zbóż. PWN, Warszawa.
- GRZESIUK S., GÓRECKI R.J. 1981. Wigor nasion jako nowe kryterium ich wartości siewnej oraz metody jego określania. Post. Nauk Rol. 6/81: 39-56.
- HADAS A. 1976. Water uptake and germination of leguminous seeds under changing external water potential in osmotic solution. J. Exp. Bot. 27: 480-489.
- HEISEL S.E., PETERSON D.M., JONES B.L. 1986. Identification of United States barley cultivars by sodium dodecyl polyacrylamide gel electrophoresis of hordeins. Cereal Chem. 63: 500-505.

- INGVERSEN I., KOIE B. 1973. Lysine rich proteins in highlylysine *Hordeum vulgare* grain. *Phytochemistry* 12: 1107-1111.
- IVANKO S. 1971. Changeability of protein fractions and their amino acid composition during maturation of barley grain. *Biol. Plant.* 13: 155-164.
- JENSEN J., JORGENSEN J.M., JENSEN H.P., GIESE H., DOLL H. 1980. Linkage of the hordein loci Hor 1 and Hor 2 with the powdery mildew resistance loci Ml-k and Ml-a on barley chromosome 5. *Theor. Appl. Genet.* 58: 27-31.
- KAPAŁA A. 1979. Characterization of composition of salt-soluble seed proteins in different barley forms (*Hordeum vulgare* L.) *Genet. Pol.* 20: 49-55.
- KAPAŁA A. 1981. Variability of electrophoretic subunit patterns of hordein proteins in spring barley (*Hordeum vulgare* L.) *Genet. Pol.* 22: 163-177.
- KAPAŁA A., PATYNA H. 1993. Genetic control of hordein polypeptides in kernels of spring barley (*Hordeum vulgare* L.) high-lysine mutant C-67-7.
- KAPAŁA A., PATYNA H. 1986. Characterization of seed protein composition in induced mutants of spring barley (*Hordeum vulgare* L.). *Gen. Pol.* 17: 45-54.
- KAPAŁA A. 1994. Genetic suppression of shrunken endosperm and low hordein content in Riso mutant 18 (*Hordeum vulgare* L.) *Genet. Pol.* 35: 249-254.
- KASHA K.J., KAO K.N. 1970. High frequency haploid production in barley (*Hordeum vulgare* L.) *Nature* 225: 874-875.
- LESZCZYŃSKA E. 1988. Odporność na suszę odmian i rodów jęczmienia na podstawie testów fizjologicznych i anatomicznych. *Hod. Rośl. Aklim. i Nasien.* 32: 40-54.
- PERRY D.A. 1977. A vigour test for seeds of barley (*Hordeum vulgare*) based on measurement of plumule growth. *Seed Sci and Technol.* 5: 709-719.
- PRZYBYLSKA J. 1972. Elektroforetyczna analiza białek jako metoda eksperymentalnej taksonomii roślin. *Post. Nauk Rol.* 3: 23-41.
- PRZYBYLSKA J., KAPAŁA A. 1974. Variability of disc electrophoretic patterns of salt-soluble seed proteins in barley (*Hordeum vulgare* L. s1). *Genet. Pol.* 15: 231-244.
- PREMACHANDRA G., SHIMADA T. 1987. The measurement of cell membrane stability using polyethylene glycol as a drought tolerance test in wheat. *Japan. Jour. Crop. Sci.* 15: 92-98.
- STOUT D.G., SIMPSON G.M., FLOTRE D.M. 1980. Drought resistance of *Sorghum bicolor* L. Moench. 3. Seed germination under osmotic stress. *Can. J. Plant Sci.* 60: 13-24.
- SKOCZEK H., SURMA M., ADAMSKI T. 1990. Inheritance of nitrate reductase activity in seedling leaves and roots of doubled haploid barley lines (*Hordeum vulgare* L.) I. Characteristics of doubled haploid lines with regard to nitrate reductase activity and grain protein yield. *Gen. Pol.* 31: 29-36.
- WAGA J., GRZYWA M. 1995. Powiązanie białek hordeinowych z odpornością na mączniaka prawdziwego (*Erysiphe Graminis* f. sp. hordei) jęczmienia jarego. *Hod. Rośl. Aklim. i Nasien.* 39: 205-218.

SKŁAD BIAŁEK NASION WYBRANYCH GENOTYPÓW JĘCZMIENIA ORAZ OCENA ICH ENERGII KIEŁKOWANIA I WIGORU SIEWEK W KONTROLI I W WARUNKACH STRESU WODNEGO

STRESZCZENIE

Badania wykazały, że genotypy rodzicielskie cv. Aramir i linia R567 oraz wybrane linie DH jęczmienia różniły się zawartością głównych frakcji białek w ziarnie. Forma ojcowska R567 i linia DH C55 charakteryzowały się największą ilością białka, natomiast w ziarnie linii C23 w porównaniu do pozostałych genotypów stwierdzono najmniejszą ilość głównych frakcji białka. Zaobserwowano również ilościowe i jakościowe różnice w elektroforetycznych obrazach albumin i globulin oraz w składzie polipeptydowym podfrakcji B i C hordeiny z ziarna badanych genotypów. Bogatsze spektrum tych białek stwierdzono u formy ojcowskiej R567 i linii DH C55. U linii DH C23 spektrum elektroforetyczne albumin i globulin różniło się od pozostałych genotypów jęczmienia, ponadto u tego genotypu obserwowano rekombinację w odniesieniu do składu polipeptydowego podfrakcji B i C hordeiny.

Stres wodny opóźnił zdolność kiełkowania nasion w normalne siewki u wszystkich badanych genotypów. W warunkach stresu największą energią kiełkowania cechowały się forma ojcowska R567 i linia DH C55. Te dwa genotypy w porównaniu do pozostałych odznaczały się też najdłuższą plumulą (koleoptyl z pierwszym liściem) zarówno w kontroli jak też w warunkach stresu wodnego.

Wpływ stresu na wigor siewek wyrażał się istotną redukcją ich długości, przy czym plumula w porównaniu z korzeniami była bardziej wrażliwa na suszę. U formy ojcowskiej R567 i linii DH C55 obserwowano mniejszą redukcję plumuli spowodowaną stresem, natomiast reakcja korzeni na stres wodny była u wszystkich badanych genotypów podobna.

SŁOWA KLUCZOWE: jęczmień, stres wodny, kiełkowanie, skład białek, nasiona, wigor siewek.