Metabolism of aged seeds. Changes in rye embryo polyribosomes during seed aging

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Abstract

Germination, total dehydrogenase activity, ribosomal proteins and ribonucleic acids of embryos obtained from winter rye harvested in different years and of distinctly differing viability were studied. Diminishing viability was accompanied by declines in the amount of ribosome-bound mRNA and a drop in the intensity of its synthesis during germination. Electrophoretic analysis of control embryo (fully viable) ribosome proteins revealed 55 different bands: 10 acidic and 45 basic. The embryos of aged seeds had 43 different bands of which 8 were acidic, 35 basic and almost all of which had an altered electrophoretic mobility as compared with the control sample. As aging progressed, the percentages of lysine, histidine and arginine increased while those of tyrosine, methionine, proline and serine decreased.

Key words: rye, seeds, aging, ribosomal proteins, RNA

INTRODUCTION

The mechanism of seed aging is still not fully understood. It is known, however, that during this process, many of the basic elements of the protein synthesis mechanism undergo numerous unfavorable modifications. The metabolism of rRNA and tRNA during the first hours of germination of aged seeds has been rather well studied to date (Appel et al. 1972, Roberts and Osborne 1973, Bray and Chow 1976, Bray and Dasgupta 1976, Wiśniewski 1978, Zalewski and Weidner 1982a). The fate of other elements participating in translation, such as initiation factors (Dell'acqua

et al. 1978), enzymes (Kulka 1971, Roberts and Osborne 1973, Zalewski 1986) and ribosome proteins (Appel et al. 1971, Zalewski and Weidner 1982b) has been studied less.

Evidence has also been presented for the presence of preformed RNA in dry, mature seeds (Marcus et al. 1975, Payne 1976), part of which is capable of taking part in translation (Delseney et al. 1975, Sanchez de Jimenez and Aguilar 1984). However, the structural and functional modifications of the particular types of mRNA involved in protein biosynthesis in aged seeds have still not been convincingly described (Roberts and Osborne 1973, Zalewski 1989).

MATERIAL AND METHODS

This study was carried out on winter rye cv. Dańkowskie Żłote. The grain was harvested at full ripeness, dried and stored in linen bags in the laboratory at a temperature of 18-20°C and average relative air humidity of 50-55%. Grain from the 1980, 1982 and 1984 harvests was analyzed. Grain from the same variety harvested in 1988, analyzed directly after postharvest dormancy ended, served as the control.

The viability of the seeds was determined by a germination test conducted according to the international ISTA guidelines (Anonymous 1976).

The conditions of imbibition and germination were described earlier (Zalewski 1991). When mRNA was isolated from 24 or 48 hour-old sprouts, preimbibition (10 h, 2°C) of the seeds was carried out in the presence of ^3H -uridine (0.37 MBq/cm³).

Polyribosomes were isolated from embryos and sprouts according to the slightly modified method of Davies et al. (1972) (Zalewski 1985).

RNA was isolated from rye embryo polyribosomes according to the method of Tanifuji et al. (1970). The polyribosomes were suspended in a small amount of buffer (40 mM Tris-HCl, pH 7.4, 10 mM MgCl₂, 20 mM KCl) and an equal volume of a phenol mixture was added (phenol : chloroform : isoamyl alcohol, 50:49:1 v/v/v). The mixture was agitated for 10 minutes at 2-4°C, after which it was centrifuged for 10 minutes at 10 000 × g. The aqueous phase was collected, an equal volume of the phenol mixture added and the procedure repeated as above. The extracted RNA was purified two more times using a mixture of chloroform + isoamyl alcohol (49:1, v/v). After the last centrifugation, 2.5 volumes of cold ethanol were added to the aqueous phase and the entire mixture was stored at -25°C.

Separation of RNA. A column (0.5 × 3 cm) of oligo (dT) cellulose was prepared as directed by the manufacturer with ready-to-use oligo (dT) no. 2 cellulose from Sigma. Approximately 100 optical units (100 A₂₆₀) RNA were

dissolved in 0.5M NaCl in 0.01 M Tris-HCl, pH 7.5 and applied to the column which had previously been equilibrated with the same buffer. RNA (rRNA) was eluted until the absorbance of the eluate dropped to 0.05, after which the buffer was changed to 0.01 Tris-HCl, pH 7.5. Absorption was measured at 260 nm in 1 cm³ fractions. Tritisol (10 cm³) was then added to the fractions (Frick 1973) and radioactivity measured using a Beckman LS 1801 liquid scintillation counter.

Ribosomes were isolated from rye seeds using the method of Golińska and Legocki (1973). Approximately 70 g of embryos obtained by the Johnston and Stern methods (1957) were homogenized for 60 sec. with 450 cm³ buffer (50 mM Tris-HCl, pH 8.05, 50 mM KCl, 5 mM MgCl₂, 5 mM 2-mercaptoethanol, 0.25 M sucrose) with the pH maintained using 1 M Tris. The homogenate was centrifuged twice at 21,000 × g for 15 minutes. The supernatant was applied to two layers of sucrose (4 cm³ 0.5 M sucrose over 4 cm³ 1 M sucrose) and centrifuged for 5 hours at 135,000 × g. The pellet was suspended in a small amount of the following buffer: 50 mM Tris-HCl, pH 7.8, 100 mM KCl, 5 mM MgCl₂, 5 mM 2-mercaptoethanol, 0.25 M sucrose. The suspension was layered over 4 cm³ 0.5 M sucrose and centrifuged for 3 hours at 135,000 × g. The centrifugation procedure was repeated with the resuspended pellet. Protein from ribosomes obtained in this way was isolated using the method of Hardy et al. (1969).

Two-dimensional electrophoresis of ribosomal proteins was carried out according to the method of Kaltschmidt and Wittmann (1970) adapted to small volumes. The first direction was run on 8% acrylamide in 8 M urea (pH 8.2). The samples (50 µg protein dissolved in 8 M urea containing 0.1 M 2-mercaptoethanol) were applied to 2 × 60 mm tubes. Electrophoresis was conducted for 4 hours at 2 mA/tube. The second direction was run using 16% acrylamide in 8 M urea (pH 4.0). Separation was carried out for 12 hours at 80 V, with an initial (for the first 30 minutes) voltage of 40 V. The gels were stained with 0.5% acid black and stored in 7% acetic acid.

Hydrolysis of ribosomal proteins. Approximately 1.5 mg of protein were dissolved in 2 cm³ 6 M HCl and maintained for 36 hours at 100°C, after which the acid was slowly evaporated off (48°C) and the amino acids dissolved in 2 cm³ redistilled water. The process of evaporation of water and redissolution of the amino acids was carried out four times. The amino acids were finally dissolved in 2 cm³ 0.2 M sodium citrate buffer, pH 2.0 and analyzed in a Beckman model 6300 amino acid analyzer.

Total dehydrogenase activity in the embryos was determined after 24 hours of imbibition of the seeds in redistilled water at 20°C. Embryos with discs were isolated by hand. They were then incubated in 0.7% tetrazolium chloride for 24 hrs (20°C), after which they were homogenized with acetone in a porcelain mortar. After decantation the amount of formazan was determined in the supernatant.

Electrophoresis of ribosome proteins and determination of their composition were done in triplicate, the remaining experiments were carried out in four replicates.

RESULTS

Viability of rye grain. The germination capacity of the rye grain in the year of its harvest varied significantly (Table 1). However, in all of the samples it exceeded 90%. The varied duration of storage caused unequal depression of grain viability and vigor which was manifested by decreasing germination capacity and embryo dehydrogenase activity (Table 1). The control samples produced the highest amounts of formazan. In the remaining samples dehydrogenase activity decreased at a greater rate than did loss of viability.

Table 1
The viability and vigor of rye grains of different age

Year of harvest	Germination capacity %		Total dehydrogenase activity (mg phenylformazan per 100 embryos) after aging
	In year of harvest	After period of aging	
1988	94.0	94.0	3242
1984	90.3	40.0	1340
1982	94.2	25.0	961
1980	95.2	4.5	271
LSD, $P = 0,001$	3.11	4.02	108.2

Chromatography of RNA on oligo (dT) columns. The RNA that was isolated from polysomes and 80 S monosomes of germinating rye grains was separated on oligo (dT) cellulose columns into two major fractions: ribosomal RNA and messenger RNA. After 24 hours of germination, the highest rRNA contents were found in the control grains and those harvested in 1984 (Table 2). The highest increase in rRNA content after the next 24 hour period of germination was also observed in the control seeds. In the seeds with the lowest viability, a decrease in rRNA content was seen between 24 and 48 hours of germination. The content of ribosome-bound mRNA both after 24 and 48 hours depended on the degree of aging and declined along with loss of viability. The amount of ribosome-bound mRNA in grain harvested in 1980 and stored for 9 years was minimal and did not change during germination for 24 or 48 hours. Similar results were obtained by analyzing the incorporation of ^3H -uridine into embryo RNA during ger-

mination. The grain with the highest viability was characterized by the highest incorporation after 24 and 48 hours of germination. Declining radioactivity of RNA accompanied loss of seed vigor and viability.

Table 2

Incorporation of ^3H -uridine and RNA content (mRNA + rRNA) in embryos of germinating (8 h, 2°C ; 24, 48 H, 21°C) rye grains of different age

Year of harvest	Absolute radioactivity (imp $\times$ min. $^{-1}$ per 100 embryos)				RNA (mg per 100 embryos)					
	rRNA		mRNA		rRNA			mRNA		
	24 h	48 h	24 h	48 h	8 h, 2°C	24 h	48 h	8 h, 2°C	24 h	48 h
1988	37533	162044	1061	3654	0.926	1.301	3.214	0.022	0.037	0.107
1984	4003	39773	1028	1430	1.089	1.254	1.941	0.021	0.026	0.044
1982	1552	21800	320	298	0.903	0.903	1.202	0.013	0.015	0.026
1980	1633	9006	79	93	1.001	1.022	0.971	0.006	0.005	0.005
LSD, $P = 0.001$	3300	8251	103	202	0.096	0.121	0.225	0.004	0.003	0.0091

Electrophoresis of ribosome proteins. Two-dimensional polyacrylamide gel electrophoresis of ribosome proteins was carried out only on rye embryos obtained from grain harvested in 1980 and that of the highest viability (control). Fractionation of control ribosome proteins resulted in 55 individual bands being distinguished (Fig. 1), of them, 10 were acidic, 45 basic. The proteins from 80 S ribosomes in grain stored for 9 years separated into 43 individual bands, of which 8 were acidic and 35 basic, migrating in the direction of the cathode (Fig. 2).

Fig. 1. Electrophoretic separation of ribosome (80S) proteins isolated from rye embryos of the 1988 harvest (control)

Fig. 2. Electrophoretic separation of ribosome (80S) proteins isolated from rye embryos of the 1980 harvest and stored for 9 years under laboratory conditions

Amino acid composition of ribosome proteins. Protein was extracted from 80 S monoribosomes and subjected to acid hydrolysis. Upon analysis in an amino acid analyzer this mixture produced 17 fractions corresponding to 16 amino acids and NH_3 (Fig. 3). Analysis disclosed that the protein from the control sample contained large amounts of glutamic acid, proline, glycine, serine and aspartic acid (Table 3). Relatively small amounts of methionine, valine and tyrosine were found in rye ribosomal proteins. This experiment revealed that the percentage of some amino acids in ribosomal proteins depends on the degree of aging of the rye grains. It was observed that as the grain lost viability over the long period of storage, the amount of such amino acids as lysine, histidine and arginine increased, while that of tyrosine, methionine and serine, decreased.

Fig. 3. Analysis of a protein hydrolysate of 80S ribosomal proteins isolated from rye embryos from the 1988 harvest (control), using a Beckman 6300 amino acid analyzer

Table 3

The amino acids composition (M %) of protein from 80 S monoribosomes isolated from embryos of rye grains of different ages

Amino acids	Years of harvest			
	1988	1984	1982	1980
Asp	8.842 ± 0.423	7.158 ± 0.091	8.326 ± 0.146	6.497 ± 0.128
Thr	7.995 ± 0.431	5.339 ± 0.082	4.447 ± 0.237	4.283 ± 0.289
Ser	8.577 ± 0.316	8.206 ± 0.014	7.783 ± 0.332	5.744 ± 0.363
Glu	10.589 ± 0.102	10.940 ± 0.041	10.193 ± 0.117	8.945 ± 0.318
Pro	9.888 ± 0.109	9.362 ± 0.022	8.762 ± 0.063	6.709 ± 0.232
Gly	9.825 ± 0.358	9.691 ± 0.101	9.822 ± 0.174	9.742 ± 0.314
Ala	6.258 ± 0.232	8.554 ± 0.023	7.653 ± 0.285	7.963 ± 0.055
Val	3.010 ± 0.279	4.998 ± 0.286	4.762 ± 0.137	5.201 ± 0.128
Met	2.873 ± 0.374	2.571 ± 0.010	1.500 ± 0.133	1.128 ± 0.139
Ile	4.009 ± 0.120	3.779 ± 0.018	3.469 ± 0.099	3.710 ± 0.188
Leu	4.454 ± 0.211	4.942 ± 0.121	4.528 ± 0.208	7.240 ± 0.291
Tyr	3.253 ± 0.133	1.529 ± 0.227	1.000 ± 0.084	0.713 ± 0.093
Phe	4.017 ± 0.028	2.882 ± 0.085	1.790 ± 0.096	2.337 ± 0.098
His	4.067 ± 0.320	6.600 ± 0.223	6.818 ± 0.132	7.728 ± 0.377
Lys	6.845 ± 0.317	6.278 ± 0.103	12.918 ± 0.281	13.511 ± 0.365
Arg	5.498 ± 0.333	6.171 ± 0.088	6.229 ± 0.334	8.186 ± 0.422

Data in the table are supplemented by standard deviation.

Beckman 6300 analyzers do not determine the contents of cysteine and cystine, tryptophan and threonine, therefore no conclusions have been drawn on the quantitative occurrence of these amino acids in ribosomal proteins.

DISCUSSION

The presented data on the vigor and viability of aging rye seeds (Table 1) are in agreement with earlier studies (Blowers et al. 1980, Preistley 1986, Zalewski 1988 and 1991).

From among the numerous methods of determining seed vigor, good results are obtained by determining total dehydrogenase activity. Dehydrogenase activity and the intensity and topography of color related to it are dependent not only on the viability of the seeds but also on the degree of their damage, aging and vigor (Throneberry and Smith 1955, Ovcharov 1976).

It seems that the fall in rRNA content in embryos of aged seeds, as compared with controls, demonstrated in this study, is caused by the depolymerization of 25 and 18 S rRNA. The process of degradation of rRNA into smaller fragments begins first in embryos (Roberts and Osborne 1973, Wiśniewski 1978) and then spreads to the endosperm cells (Grzesiuk and Kulka 1988).

The reason for the decrease in the rate of RNA synthesis in aged grains, as measured by incorporation of ^3H -uridine may be the blocking of transcriptional activity of DNA (Table 2). Repression of genes by cofactors, breaking of DNA strands or increased numbers of chromosome aberrations often accompany the process of loss of viability by cereal grain (Roberts and Osborne 1973, Osborne 1982).

Formation of polysomes and protein biosynthesis can begin very early during seed germination, preceding the onset of transcription because of the presence of preformed mRNA (Marcus et al. 1975, Payne 1976, Sanchez de Jimenez and Aguilar 1984). Our observations, however, indicate that during germination of aged wheat and rye seeds, translation is limited or completely inhibited due to lack of association of mRNA and ribosomes (Zalewski 1982, 1985, 1989). Upon analyzing the data in Table 2 it can be seen that in comparison with the control grains, the amount of mRNA in the embryos from the 1980 harvest was minimal and did not increase during germination conducted 24 or 48 hours. The radioactivity of this fraction also did not increase. This means that the small amount of mRNA present in these embryos belonged to the class of preformed RNA and that no new mRNA was transcribed at this time. Similar results were obtained using antibiotics — inhibitors of RNA synthesis (Zalewski 1989). It should, however, be added that in some species even during imbibition of dead seeds, a small degree of protein synthesis is observed (Anderson 1977).

Increasing amounts of data are indicating that ribosomal proteins, the other component of the ribosome, are responsible for many more functions during translation than previously thought. The number of ribosomal proteins isolated from eukaryotic cells is not the same in all species. Rat liver 80 S ribosomes contain 69 proteins (Sherton and Wool 1972), the yeast, *Saccharomyces cerevisiae*, 76 proteins (Grankowski 1976) and wheat embryos, 79 proteins (Sikorski et al. 1979).

The total number of 55 80S ribosomal proteins obtained for rye embryos in this study (Fig. 1) cannot be considered final. The proteins obtained from entire 80S ribosomes, not separately from the 40 and 60S subunits, were fractionated, so there is no guarantee that the bands on the gels represent single proteins. The proteins of 80S monosomes isolated from embryos of aged seeds, separated electrophoretically into 43 individual proteins with different electrophoretic mobilities in comparison with the controls. Figures 1 and 2 show that only the proteins labelled 11, 16, 26, 28, 31, 36, 52 and 55 on both gels can be said to be identical in terms of position and size. The remaining proteins, mainly the groups of acidic proteins (1, 3, 4, 5, 12) and remaining basic proteins, do not have their counterparts on the gels from the ribosomes of aged seeds. More specific comparisons of both gels without additional column chromatography of the proteins is difficult. These results indicate that ribosomal proteins are labile and undergo significant modifications during aging. App et al. (1971) was the first

to point to the fact that ribosomes isolated from old seeds dissociate into subunits only to a very small degree, which may limit the formation of the 40S-mRNA complex. Osborne et al. (1971) in turn, proved that ribosomes isolated from old rye embryos are "lighter". These results become clearly understandable if one takes into account the depolymerization of rRNA (Roberts and Osborne 1973) and loss of several ribosomal proteins (Fig. 2) from individual ribosomes.

The data presented in Table 3 are additional proof of significant alterations occurring in old rye embryos. Are, however, such drastic changes in the amino acid composition of ribosomal proteins probable? These results should rather be interpreted in the context of loss of specific ribosomal proteins. For example, the loss of proteins rich in tyrosine, methionine, proline and serine could indirectly result in an increase the percentage of other amino acids in the total ribosomal proteins. Many other possible mechanisms are also known which could lead to the modification of enzymatic and structural proteins. One of the well known and, at the same time, important ones in the process of seed aging is the deamination of glutamine and asparagine residues (Robinson and Rudd 1974). This can lead to changes in the electric charges of proteins thus changing their electrophoretic mobility. Such great changes in mRNA content, quantity and quality of ribosomal proteins which occur in the embryos of old seeds undoubtedly have a negative effect on their viability and vigor. They restrict or completely inhibit translation, which is a process absolutely indispensable in the germination of embryos.

REFERENCES

- Anderson J.D., 1977. Adenylate metabolism of embryonic axes from deteriorated soybean seeds. *Plant Physiol.* 59: 610-614.
- Anonim, 1976. International rules for seeds testing. *Seed Sci. Technol.* 4: 3-180.
- App A.A., Bulis M.G., McCarty W.J., 1971. Dissociation of ribosomes and seed germination. *Plant Physiol.* 47: 81-86.
- Blowers L.E., Stormonth D.A., Bray C.M., 1980. Nucleic acid and protein synthesis and loss of vigour in germinating wheat embryos. *Planta* 150: 19-25.
- Bray C.M., Chow T.Y., 1976. Lesions in the ribosomes of nonviable pea (*Pisum arvense*) embryonic axes tissue. *Biochim. Biophys. Acta* 442: 14-22.
- Bray C.M., Dasgupta J., 1976. Ribonucleic acids synthesis and loss of viability in pea seed. *Planta* 132: 103-108.
- Davies E., Larkins B.A., Knight R.H., 1972. Polyribosomes from peas. *Plant Physiol.* 50: 581-584.
- Dell'quila A., De Leo P., Caldirioli E., Zocchi G., 1978. Damages at translational level in aged wheat embryos. *Plant Sci. Letters* 12: 217-226.
- Delseney M., Peralta M.T., Guitton Y., 1975. Effects of cordycepin on RNA metabolism in germinating seedlings. *Biochim. Biophys. Res. Commun.* 63: 1278-1285.
- Fricke U., 1973. Tritosol: a new scintillation cocktail based on Triton X-100. *Anal. Bioch.* 63: 555-558.
- Golińska B., Legocki A.B., 1973. Purification and properties of elongation factor I from wheat germ. *Biochim. Biophys. Acta* 324: 156-170.

- Grankowski N., 1976. Rola białek rybosomalnych *Pracaryota* w procesie translacji. Post. Biochem. 22: 173-195.
- Grzesiuk St., Kulka K., 1988. Biologia ziarniaków zbóż. PWN, Warszawa.
- Hardy J.S., Kurland G.G., Voynow P., Mora G., 1969. The ribosomal proteins of *Escherichia coli*. I. Purification of the 30S ribosomal proteins. Biochemistry 8: 2897-2905.
- Johnston F.B., Stern H., 1957. Mass isolation of viable wheat embryos. Nature 179: 160-161.
- Kaltschmidt E., Wittmann H.G., 1970. Ribosomal proteins VII. Two-dimensional polyacrylamide gel electrophoresis for fingerprinting of ribosomal proteins. Anal. Biochem. 36: 401-416.
- Kulka K., 1971. Biochemiczne aspekty starzenia się ziarna owsa i jęczmienia. Zesz. nauk. WSR Olsztyn, 6: 1-90.
- Marcus A., Spiegel S., Brooker J.D., 1975. Preformed mRNA and the programming of early development. In: Control mechanism in development. R.H. Meints and E. Davies (eds.), pp. 1-19, Plenum Publishing Corp., New York.
- Osborne D.J. Roberts B.E., Hallam N.D., 1971. Protein synthesis and viability in rye. Biochem. J. 124: 7.
- Osborne D.J., 1982. Deoxyribonucleic acid integrity and repair in seed germination: the importance in viability and survival. In: The physiology and biochemistry of seed, development, dormancy and germination. A.A. Khan (ed.). Elsevier Biomedical Press.
- Ovcharov K.E., 1976. Fizjologia formirovania i prorastanija semjan. Kolos, Moskva.
- Payne P.I., 1976. The long-lived messenger ribonucleic acid of flowering-plant seeds. Biol. Rev. 51: 329-363.
- Priestley D.A., 1986. Seed aging. Implications of seed storage and persistence on the soil. Cornell University Press, Ithaca, USA.
- Roberts E.H., Osborne D.J., 1973. Seed ecology. W. Heydecker (ed.), Butterworths, London.
- Robinson A.B., Rudd C.J., 1974. Current topics in cellular regulation. Vol. 8. Academic Press, New York, pp. 247-294.
- Sanchez de Jimenez E., Aguilar R., 1984. Protein synthesis patterns. Relevance of old and new messenger RNA in germinating maize embryos. Plant Physiol. 75: 231-234.
- Sherton C.C., Wool J.G., 1972. Determination of the number of proteins in liver ribosomes and ribosomal subunits by twodimensional polyacrylamide gel electrophoresis. J. Biol. Chem. 247: 4460-4466.
- Sikorski M.M., Przybył D., Legocki A.B., Kudlicki W., Gąsior E., Zając J., Borowski T., 1979. The ribosomal proteins of wheat germ. Distribution and phosphorylation *in vitro*. Plant Sci. Letters 15: 387-397.
- Tanifuji S., Higo M., Shimada T., Higo S., 1970. High molecular weight RNA synthesized in nucleoli of higher plants. Biochim. Biophys. Acta 217: 418-425.
- Throneberry G.O., Smith F.G., 1955. Relation of respiratory and enzymatic activity to corn seed viability. Plant Physiol. 30: 337-343.
- Wiśniewski K., 1978. Biochemiczne aspekty starzenia się ziarniaków pszenicy i żyta przechowywanych w różnych zakresach wilgotności powietrza. Ph. D. Thesis, AR-T Olsztyn.
- Zalewski K., 1982. Formowanie polirybosomów w zarodkach kielkującego ziarna pszenicy o różnej żywotności. Hod. Rośl. Aklim. 26: 1-9.
- Zalewski K., 1985. The metabolism of aged seeds. The formation of polyribosomes in the embryos of germinating rye grains of different viability. Acta Soc. Bot. Pol., 45: 417-427.
- Zalewski K., 1986. The metabolism of aged seeds. The ribonucleic activity of rye grain embryos of different ages. Acta Soc. Bot. Pol. 55: 45-51.
- Zalewski K., 1988. Metabolism of aged seeds. The free and membrane-bound polyribosomes of germinating rye grains of different ages. Acta Soc. Bot. Pol. 57: 261-270.
- Zalewski K., 1989. The metabolism of aged seeds. The effects of actinomycin D and cordycepin on RNA synthesis in germinating rye grains of different ages. Acta Soc. Bot. Pol. 58: 85-95.

- Zalewski K., 1991. The metabolism of aged seeds. The pentose phosphate pathway contribution on the respiratory system in germinating rye grain of different age. Acta Soc. Bot. Pol. In press.
- Zalewski K., Weidner S., 1982a. RNA synthesis during germination of wheat seeds stored at various air humidities. Bull. Acad. Sci. Pol., Biol. 29: 263-269.
- Zalewski K., Weidner S., 1982b. Changes in ribosomal proteins of wheat embryos during accelerated ageing of the grain. Acta Soc. Bot. Pol. 51: 301-308.

Metabolizm starych nasion. Zmiany w polisomach zarodków żyta podczas procesu starzenia się nasion

Streszczenie

Zbadano kiełkowanie, ogólną aktywność dehydrogenaz oraz wykonano analizę części białkowej i rybonukleinowej polisomów wyizolowanych z zarodków ziarna żyta ozimego pochodzącego z różnych lat zbioru, o wyraźnie zróżnicowanej żywotności. Obniżeniu żywotności ziarna żyta towarzyszyło zmniejszenie ilości mRNA związanego z rybosomami oraz spadek natężenia jego syntezy podczas kiełkowania. W wyniku rozdziału elektroforetycznego białek rybosomowych zarodków próby kontrolnej (o pełnej żywotności) uzyskano 55 indywidualnych białek: 10 kwaśnych i 45 zasadowych. W zarodkach ziarniaków zestarzałych stwierdzono 43 białka indywidualne, przy czym 8 to białka kwaśne i 35 to białka zasadowe, oraz zmienioną ruchliwość elektroforetyczną niemal wszystkich białek w stosunku do próby kontrolnej. Wykazano, że procentowy udział kilku aminokwasów w białkach rybosomowych zależy od stopnia zestarzenia ziarna. W miarę utraty żywotności udział ilościowy lizyny, histydyny i argininy zwiększał się, a tyrozyny, metioniny, proliny i seryny malał.