
Morphological properties of mutants, revertants and genetic lines of spring barley

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Genetic resources of spring barley involve chemically induced morphological, biochemical, and quantitative mutants and revertants obtained from the standard Lithuanian varieties 'Auksiniai II' and 'Auksiniai 3'. A collection of lysine mutants "Riso" and genetic marker lines strongly resistant to fungal diseases was established. A comparative characterisation of growth, yielding and morphological properties of the accessions, as well as evaluation for disease susceptibility, protein content, and resistance to lodging were carried out. The collection of mutants and genetic lines is unique in Lithuania. The most valuable accessions are stored in the long-term seed storage at the Lithuanian PGR Centre.

Key words: spring barley, mutant, revertant, genetic line, accession, morphological properties, disease susceptibility, protein content, characterisation, evaluation

INTRODUCTION

Spring barley is one of the most economically important crops in Lithuania. It provides a significant part of food and forage production of Lithuanian agriculture. Therefore it is urgent to conserve and investigate genetic resources of spring barley. The genetic resources of Lithuanian spring barley involve induced morphological, biochemical, and quantitative mutants and revertants of Lithuanian varieties 'Auksiniai II' and 'Auksiniai 3'. The "Riso" collection of proteinic barley mutants of lysine genes was established. The collection of barley genetic resources was enriched with the genetic marker lines strongly resistant to fungal diseases. A collection of lines and populations has been obtained from the Vavilov Institute of Plant Industry, St. Petersburg, Russia. During the period of 15 years it has adapted to the local conditions and therefore the accessions need to be evaluated for their new properties. Expectantly, allelic variants of resistance genes could evolve, adapted to withstand the local races of parasitic fungi. There are interesting mutants in the collection of introduced barley from the point of view of immunity, productivity, resistance to lodging, grain size, protein content [1–8]. The collection of mutants and genetic lines is unique in Lithuania.

METHODS

Barley accessions are regenerated every year in the plots of 2 m² in size with 3 replicas in the field

collection maintained by the Genetic Department of the Botanical Garden of Vilnius University. All of the induced mutants originated from the standard varieties 'Auksiniai II' and 'Auksiniai 3'. Primary varieties, mutants, their sublines, revertants, and genetic lines are cultivated under the same soil conditions without pesticide application.

The period of 1995–1997 was rather good for spring barley evaluation because of the variation of weather conditions from extremely dry in 1995 to very humid in 1996. That provided an opportunity for a versatile evaluation of barley accessions. The time that takes a kernel to mature and the duration of ear formation (both in days) were estimated. Plant height was estimated on a 9-point scale, where 1 is dwarf (41 cm), and 9 – extremely tall (140 cm). Resistance to lodging was also estimated on a 9-point scale, with 1 standing for very low and 9 for very high resistance. Weight of 1000 kernels was estimated on a 9-point scale as well, where 1 is a very low (34.1 g) and 9 a very high (50.0 g) weight. The relative content of crude protein was estimated in grain. Some morphological properties were described according to the IPGRI descriptors list for barley [9]. The data of three years have been summarised.

RESULTS AND DISCUSSION

There are 12 mutants in the *tw* mutant group. They are induced ones, obtained from the varieties 'Auk-

| Table. Properties of barley mutants, revertants and genetic lines (1995–1997) | | | | | | | | | | | | |
|---|----------------|---------------|---------------------|-------------------|----------------------------|----------------------------|-----------------------------|-----------------------------------|--------------------|-------------------------------|---------------|---|
| Descriptor | 'Auksiniai II' | 'Auksiniai 3' | <i>tw</i> (n = 12)* | <i>be</i> (n = 3) | <i>Sparse ear</i> (n = 11) | <i>Eceriferum</i> (n = 19) | <i>Intermedium</i> (n = 19) | <i>Erectum</i> (n = 39) | Revertant (n = 52) | Quantitative mutants (n = 19) | Riso (n = 10) | Genetic lines (n = 16) |
| Plant height | 4 | 4 | 6 | 3 | 4 | 4 | 3 | 5 | 4 | 4 | 4 | 4 |
| Days to be forming ears | 55 | 54 | 61 | 56 | 53 | 59 | 59 | 53 | 54 | 52 | 59 | 54 |
| Days to maturity | 92 | 94 | 94 | 94 | 93 | 93 | 91 | 93 | 92 | 92 | 93 | 92 |
| Protein content, % | 13.5 | 14.3 | 16.9 | 14.0 | 13.4 | 16.5 | 14.9 | 15.3 | 15.2 | 9.5 | – | – |
| Kernel number per spike | 27.7 | 20.8 | 13.7 | 32.5 | 23.3 | 22.9 | 37.3 | 20.6 | 24.2 | 22.4 | 21.2 | 25.5 |
| Row number | 2 | 2 | 2 | 3 | 2 | 2 | 3 | 2 | 2 | 2 | 2 | 2–5 |
| Glume color | yellow | yellow | yellow | yellow | yellow | yellow | yellow | yellow | yellow | yellow | yellow | yellow, black |
| Kernel covering | covered grain | covered grain | semi-covered grain | covered grain | covered grain | semi-covered grain | semi-covered grain | covered grain, semi-covered grain | semi-covered grain | covered grain | covered grain | covered grain, semicovered grain, naked grain |
| 1000 kernel weight | 4 | 4 | 4 | 2 | 6 | 3 | 1 | 3 | 4 | 3 | 4 | 3 |
| Length of ear | 5 | 5 | 3 | 4 | 5 | 4 | 5 | 4 | 5 | 5 | 5 | 3 |
| Resistance to lodging | 5 | 9 | 7 | 8 | 6 | 5 | 5 | 8 | 4 | 7 | 8 | 7 |
| Relative grain yield | 6 | 6 | 4 | 4 | 7 | 6 | 5 | 6 | 7 | 5 | 6 | 4 |
| Susceptibility to <i>Claviceps</i> , % | 0.3 | 0 | 9.5 | 1.9 | – | – | 1.5 | – | – | – | – | 0.7 |

* n – number of accessions.

siniai II' and 'Auksiniai 3'. These are proteinous, recessive, pleiotropic individuals with the mutated ear and tall stiff stem. The *tw* mutants are homeotic. Their lodicules begin to develop in the florets earlier than in the original variety. Because of the alteration of the shape and function of lodicules these mutants may be assigned to the homeotic ones [11]. The purpose of their investigations is based on the expected splitting of the pleiotropic complex of properties and release of valuable breeding material.

The mutants with *branched ear (be)* were induced from the variety 'Auksiniai 3'. There are three different mutants according to the composition of the ear (branching, number of grain rows, etc.). The *be* mutant is phenotypically steady, while the *be₁* is unsteady. There are 5 groups of *be₁* mutants according to the shape of ear, as well as a revertant. The *be₂* mutants have ears branched and with many rows at the base and with two rows on the top.

The group of sparse-ear mutants consists of 11 mutants induced by means of chemical mutagenesis from the varieties 'Auksiniai II' and 'Auksiniai 3'. Their distinctive property is large grains.

The group of mutants *Eceriferum* (waxless) consists of 19 mutants. An increased content of proteins is characteristic of them.

There are 19 mutants *Intermedium* with many-row ears.

The *Erectum* (compact ear) mutants are resistant

to lodging. There are 39 mutants in this group.

There are 52 revertants released from the *tw* mutants.

A big diversity exists within the group of quantitative mutants. There are 19 of them. A chlorophyllous mutant 14m (*striata*) and a physiologic one No. 9, released by V. Rančelis in 1972, stand out in this group. The “Riso” collection of proteinic barley mutants of lysine gene contains 10 mutants. A unique collection of genetic marker lines and populations, particularly resistant to fungal diseases contains 16 accessions (Table).

Table.

All mutants are characterised [10], and most valuable of them are stored in the long-term seed storage at the PGR Centre of Lithuania.

CONCLUSIONS

1. The accessions of barley collection have been evaluated for the productivity, grain size, resistance to lodging, disease susceptibility, compatibility between high protein content in grains and sustainable yielding.

2. The unique collection of barley genetic lines and mutants has been established, which is to be conserved as gene donors for chromosome markers, disease susceptibility, and lysine genes.

3. The collection of mutants is valuable for barley breeding, particularly for high protein content.

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References

1. Mačkinitė R, Kačergius A, Kasparavičius J, Žilinskaitė S, Balčiūnienė L, Vaitkūnienė V, Rančelis V. *Biologija* 1996; 4: 11–8.
2. Rančelis V, Vaišnienė V, Vaitkūnienė V, Balčiūnienė L. *Biologija* 1996; 1: 9–17.
3. Rančelis V, Žilinskaitė S, Vaitkūnienė V, Kačergius A, Kasparavičius J. *Biologija* 1994; 4: 14–23.
4. Vaitkūnienė V, Čėsniene T, Balčiūnienė L, Barysas D, Vaišnienė V, Rančelis V. *Biologija* 1997; 2: 6–11.
5. Balčiūnienė L, Rančelis V. *Biologija* 1996; 3: 19–23.
6. Rančelis V, Vaitkūnienė V. *Biologija* 1998; 4: 10–4.
7. Balčiūnienė L, Rančelis V. *Eksperimentinė biologija* 1992; 3–4: 56–7.
8. Vaitkūnienė V. *Biologija* 1999; 3: 105–7.
9. IPGRI. Descriptors for barley (*Hordeum vulgare* L.) International Plant Genetic Resources Institute, Rome, Italy 1994: 1–45.
10. Catalogue of Lithuanian plant genetic resources. Comp. by Būdvytytė A, Labokas J, Balčiūnienė L. et al. *Dotnuva-Akademija* 1997: 11–60.
11. Bieliūnienė A, Kazlauskaitė D. *Vilniaus universiteto Botanikos sodas amžių sandūroje* 2001: 25–8.

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VASARINIŲ MIEŽIŲ MUTANTŲ, REVERTANTŲ, GENETINIŲ LINIJŲ MORFOLOGINIAI POŽYMIAI

S a n t r a u k a

Vasarinių miežių genetinius išteklius sudaro iš lietuviškų veislių ‘Auksiniai II’ ir ‘Auksiniai 3’ cheminės mutagenės būdu gauti indukuoti mutantai (*tw*, *be*, *retomis* varpomis, *eceriferum*, *intermedium*, *erectum*, kiekybiniai mutantai, revertantai), lizininiai mutantai „Riso“ ir genetinės markerinės linijos, ypatingai atsparios grybinėms ligoms. Mutantai tirti 1995–1997 metais. Palyginta vegetacijos laikotarpio trukmė, augalų aukštis, atsparumas išgulimui, ligoms, derlius, 1000 grūdų svoris ir t. t. Nustatyti produktyvūs – neproduktyvūs, stambiais grūdais, neišgulantys – linę išgulti, atsparūs – jautrūs ligoms, derinantys didesnę baltymų kiekį grūduose su normaliu, nesumažėjusiu derlingumu pavyzdžiai. Sukaupta originali miežių genetinių linijų ir originalių mutantų kolekcija, saugotina kaip genų – markerių chromosomoms, genų – atsparumo ligoms ir genų – lizino genų donorai. Mutantų kolekcija vertinga kaip selekcijos medžiaga, ypač baltymų kiekio atžvilgiu. Visi mutantai aprašyti ir dalis vertingiausių padėta ilgalaikiam saugojimui į Lietuvos genetinių išteklių saugyklą.