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# Variability, heritability and correlations of genetic resources in meadow fescue

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Economically valuable features such as dry matter yield (DMY) of first cut, DMY of aftermath, plant height, days to heading, leafiness, digestibility, crude protein and crude fibre were studied in two cultivars and 22 wild populations of meadow fescue (*Festuca pratensis* Huds.) in the period 2002–2003 at the Lithuanian Institute of Agriculture (Dotnuva). Applying a covariance analysis, the genotypic and phenotypic coefficients of variation, correlation and broad sense heritability were studied. For all traits, the phenotypic coefficients of variation were higher than the genotypic coefficients. The heretability was lowest for plant height (0.05) and highest for dry matter digestibility (0.56). By annual DMY (9.21–12.54 ha$^{-1}$), the cultivar 'Kaita' and two new meadow fescue wild populations (Nos. 2736 and 1661) reliably ($P < 0.05$) exceeded the standard cultivar 'Dotnuva I' (by 9.6–13.4%). Among the wild populations studied, nine (Nos. 2719, 1703, 1486, 3609, 3544, 3129, 2101, 2066 and 3467) showed a reliably ($P < 0.01$) better dry matter digestibility (66.53–69.65%) as compared to the standard (64.71%). The negative, high genotypic correlations ($p < 0.01$) of DMY first cut were noted for dry matter digestibility (–0.921). Positive high genotypic correlations ($p < 0.01$) were found between first cut DMY and crude protein content (0.721). As a simple index for selecting plants combining productivity and quality, crude protein yield is suggested. The highest yield of crude protein was shown by the wild populations Nos. 2341 (0.77 t ha$^{-1}$), 1661 (0.78 t ha$^{-1}$), 2736 (0.80 t ha$^{-1}$) and 1931 (0.83 t ha$^{-1}$) as compared to the standard (0.63 t ha$^{-1}$).

**Key words**: *Festuca pratensis*, heritability, correlation, genotypic variation

## INTRODUCTION

Intensification of the selection process, transition from analytical to synthetical selection requires the knowledge of heritability regularities of quantitative traits allowing a more rational use of breeding methods. For producing new cultivars of open pollinated grasses, the breeding process consisting of two principal stages is considered optimal. The stages are as follows: selection of clones according to genotype in an individual arrangement of plants and evaluation of their genetic value (combining ability) in thick stands [1, 2]. Alongside assessment of the combining ability of the parental forms according to yield as the main criterion for selecting the initial forms in developing synthetic varieties, of importance is also knowledge of separate economically valuable traits.

The high coefficients of trait heritability imply the prevalence of genetic variation in their general phenotypic variation and thus favour a more effective selection of plants according to the genotype [3, 4].

In perennial forage grasses, additive gene action has been the main determinant of variation for many agronomic traits [5, 6, 7]. Genetic variation has been documented within numerous meadow fescue populations for forage yield, *in vitro* digestibility, relative maturity, and resistance to *Drechslera dictyoides* (Drechs.) Shoemaker [8–11]. Both additive and non-additive sources of genetic variation appear to be important for agronomic traits of meadow fescue [8, 11].

The aim of the current study was to elucidate the variability, heritability and correlations among eight economically valuable traits of meadow fescue genetic resources in order to intensify the process of selection and development of new cultivars.

## MATERIALS AND METHODS

As the objects of the study, two meadow fescue cultivars and 22 wild populations developed and collected over the recent years at the Lithuanian Institute of Agriculture were used. Testing experiments were carried out in 2002–2003 in Dotnuva on a sod gleyic moderately heavy drained loam soil with a pH value in the arable layer varying from 6.4 to 7.2 and humus content from 1.9 to 2.2%.

Seeds of wild populations of meadow fescue were collected in various natural habitats of Raseiniai, Varena, Ignalina and Joniškis districts.

Grasses were sown by the method of dense sowing on 8.37 $m^{-2}$ plots in four replications in the first half of June without a cover crop. In the year of use, the grass was cut three times and 0.5 kg herbage samples were taken for dry matter content analysis. The first cut was taken at the beginning of heading of the varieties or populations. Aftermath (2nd and 3rd cuts) was cut 45–55 days following the previous cut. Each year nitrogenous, phosphorous and potassium fertilizers ($N_{150}P_{60}K_{90}$) were applied. As a standard, the 'Dotnuva I' meadow fescue cultivar was used.

Alongside the DMY of first cut and aftermath, in the varieties and wild populations plant height, the number of days from spring regrowth to paniculation and the leafiness were established. The content of digestible matter, crude protein and crude fibre was determined for the first cut plants at the laboratory of the chemical tests on a NIRS-6500 spectrometer [12]. The experimental data were calculated by the covariation analysis method with the application of the breeding-oriented software from the AGROS ver. 2.06 package. Broad sense heritability ($h_b^2$) was calculated as the ratio of the genetic to the phenotypic variance, $h_b^2 = V_g/V_p$,

where $V_g$ is the genetic variance among populations and $V_p$ is the phenotypic variance.

The genotypic and phenotypic coefficients of variation were calculated according to the formulas:

$$CV_g = \frac{\sqrt{V_g}}{\bar{x}} * 100, \quad CV_p = \frac{\sqrt{V_p}}{\bar{x}} * 100. \qquad [13].$$

The phenotypic and genotypic correlations were estimated in the following manner:

$$r_{ph} = \frac{M_{12}}{\sqrt{(M_{11})(M_{22})}}; \quad r_g = \frac{\mathrm{cov}_{p12}}{\sqrt{\sigma^2{}_{p1}\sigma^2{}_{p2}}}. \qquad [14].$$

## RESULTS AND DISCUSSION

The mean values, the F value, coefficients of variability and heritability are presented in Table 1. The 24 genotypes studied showed reliable differences in all eight traits and thus allowed to determine the phenotypic and genotypic variations and broad sense heritability. For all traits, the phenotypic coefficients of variation were higher than the genotypic coefficients. The heretability was lowest for plant height (0.05) and highest for dry matter digestibility (0.56). Below we shall discuss the expression peculiarities of economically valuable traits in different meadow fescue genotypes.

The first cut DMY is less dependent on meteorological factors, as in spring the soil contains moisture enough for the growth and development of plants. According to first cut DMY, only three experimental populations (Nos. 2736, 1661 and 2341) reliably exceeded the standard (cultivar 'Dotnuva I' 0.62–0.71 t $ha^{-1}$, or 10.66–12.21%) (Table 2).

Aftermath yield formation in meadow fescue usually takes place in droughty summer conditions. By aftermath DMY, not any populations of meadow fescue exceeded the standard (Table 2).

The DMY of first cut and aftermath showed an average genotypic variability (CVg %) (9.33 and 7.95, respectively) and a low broad sense heritability ($h_b^2$) (0.10 and 0.06) (Table 1).

**Plant height** in the first cut is closely related to DMY. The height of plants of the numbers studied essentially did not exceed the standard cultivar 'Dotnuva I' (Table 2). Plant height showed a low genetic variability ($CV_g$ % = 4.82) and a very low broad sense heritability ($h_b^2$ = 0.05) (Table 1).

**The period from the beginning of spring regrowth to paniculation** was only 38–42 days. This period showed a very low genotypic variation (CVg % = 2.54) and coefficient of heritability ($h_b^2$ = 0.08) (Table 1).

**Leafiness**. For the new meadow fescue varieties the major problem remains forage quality improvement. In the stage of plant bushing and earing these grasses are readily consumed by cattle, however, in the case of belated cutting green mass soon stiffens and loses its nutritive qualities. By producing cultivars with an improved leaves/stalk ratio it is possible to improve the quality of forage.

Leafiness is an index easy to determine by structural analysis. According to leafiness, the standard cultivar 'Dotnuva I' reliably ($P < 0.01$) exceeds the populations Nos. 2618, 1931, and 1661 (by 20.31–24.52%), (Table 2). Among the wild populations studied, the genotypic variation of this trait ($CV_g$) was low (only 6.34%), though its coefficient of heritability was low and reached 0.22 (Table 1).

Dry matter **digestibility** (*in vitro*) is the basic index of forage quality and shows a tendency to a decrease, which is related to the process of plant ageing. Among the populations studied, nine (Nos. 2719, 1703, 1486, 3609, 3544, 3129, 2101, 2066 and 3467) showed a reliably ($P < 0.01$) better dry matter digestibility (66.55–70.11%) *versus* the standard (64.71%). The genotypic variation ($CV_g$) of this trait was low and reached only 4.01%, whereas the coefficient of heritability ($h_b^2$) was highest (0.56).

**Crude fibre** content in dry mass is inversely proportional to the content of digestible substance and is also one of the basic indices of fodder quality.

Table 1. **Variability and heritability for eight traits of meadow fescue cultivars and wild populations**

| Traits | F value | $\bar{X} \pm S_e$ | Range | $CV_p$ (%) | $CV_g$ (%) | $h_b^2$ |
|---|---|---|---|---|---|---|
| DMY of 1st cut, t $ha^{-1}$ | 11.15** | 5.63 ± 0.11 | 4.75–6.53 | 29.93 | 9.33 | 0.10 |
| DMY of aftermath, t $ha^{-1}$ | 2.78** | 4.99 ± 0.10 | 4.21–6.01 | 34.85 | 7.95 | 0.06 |
| Height of plant, cm | 4.18** | 55.99 ± 0.63 | 48.40–60.50 | 22.27 | 4.82 | 0.05 |
| Heading, days | 12.16** | 34.83 ± 0.22 | 39.0–41.50 | 8.03 | 2.54 | 0.07 |
| Leafiness, % | 3.05** | 72.27 ± 1.14 | 63.80–84.30 | 13.40 | 6.34 | 0.22 |
| Digestibility, % | 34.8** | 64.98 ± 0.54 | 61.13–70.11 | 5.36 | 4.01 | 0.56 |
| Crude protein, % | 3.28** | 11.54 ± 0.21 | 10.08–13.62 | 15.67 | 7.30 | 0.21 |
| Crude fibre, % | 13.16** | 29.45 ± 0.27 | 26.38–31.48 | 5.97 | 4.26 | 0.51 |

*, ** – $P < 0.05$ and $P < 0.01$, respectively.

Table 2. **Mean values of yield, plant height, heading, leafiness, digestibility, crude protein and crude fibre of meadow fescue cultivars and wild populations**

| Cultivar/ breeding population | DMY of 1st cut, t $ha^{-1}$ | DMY of aftermath, t $ha^{-1}$ | Height of plant, cm | Heading, days | Leafiness, % | Digestibility, % | Crude protein, % | Crude fibre, % |
|---|---|---|---|---|---|---|---|---|
| Dotnuva I st. | 5.82 | 5.24 | 60.50 | 38 | 67.70 | 64.71 | 11.01 | 30.59 |
| Kaita | 6.46 | 5.67 | 60.20 | 38 | 69.70 | 63.16– | 11.30 | 29.96 |
| 2736 | 6.53+ + | 5.59 | 58.30 | 39 | 72.70 | 62.06– – | 12.43 | 31.48 |
| 2287 | 5.54 | 5.05 | 55.70– | 41+ + | 72.85 | 64.58 | 11.52 | 29.28– |
| 2712 | 5.79 | 5.24 | 53.30— | 41+ + | 70.95 | 63.45 | 12.68+ | 28.35– |
| 2259 | 6.00 | 5.13 | 55.35– | 39 | 74.55 | 62.21– – | 12.20 | 29.99 |
| 2735 | 5.81 | 5.69 | 56.20 | 39 | 67.85 | 64.28 | 12.09 | 31.43 |
| 2393 | 6.04 | 5.47 | 54.80– | 39 | 70.60 | 61.86– – | 12.32 | 29.34– |
| 2618 | 5.53 | 5.08 | 54.70– | 39 | 81.45+ + | 65.50 | 12.26 | 28.66— |
| 2719 | 5.60 | 5.11 | 51.85— | 41+ + | 80.20 | 66.65+ + | 13.21+ | 29.40– |
| 1931 | 6.21 | 5.48 | 54.05– | 42+ + | 84.30+ + | 62.60– – | 13.62+ + | 26.38— |
| 1661 | 6.53+ + | 6.01 | 59.95 | 42+ + | 82.35+ + | 61.13– – | 11.96 | 27.87— |
| 2341 | 6.44+ | 5.01 | 57.75 | 41+ + | 74.35 | 61.67 | 12.09 | 30.17 |
| 2606 | 5.62 | 4.85 | 60.30 | 39 | 68.20 | 65.12 | 10.08 | 29.74 |
| 1706 | 5.32– | 4.43 | 56.7 | 41+ + | 69.75 | 65.75 | 10.52 | 28.33— |
| 1703 | 4.85– – | 4.56 | 54.75– | 39 | 66.05 | 69.65+ + | 10.48 | 29.77 |
| 1486 | 5.38 | 4.42 | 51.00— | 42+ + | 70.60 | 67.12+ + | 10.70 | 29.46– |
| 3609 | 5.41 | 4.73 | 53.65— | 42+ + | 75.70 | 67.49+ + | 10.26 | 28.50 |
| 3544 | 4.75– – | 4.68 | 48.40— | 42+ + | 76.20 | 70.11+ + | 11.99 | 29.55– |
| 3129 | 4.85– – | 4.44 | 55.85– | 39 | 74.65 | 66.52+ + | 10.80 | 28.76— |
| 430 | 5.49 | 4.43 | 58.25 | 39 | 63.80 | 61.60– – | 11.08 | 30.73 |
| 2101 | 5.00– – | 4.21– | 59.45 | 39 | 66.20 | 68.63+ + | 10.08 | 30.71 |
| 2066 | 5.20– | 4.91 | 56.60 | 39 | 67.25 | 66.55+ + | 10.26 | 31.36 |
| 3467 | 4.94– – | 4.35 | 55.50– | 39 | 66.55 | 67.25+ + | 11.98 | 27.15— |
| $LSD_{05}$ | 0.483 | 0.868 | 4.428 | 0.889 | 9.363 | 1.313 | 1.633 | 1.034 |
| $LSD_{01}$ | 0.655 | 1.179 | 6.009 | 1.207 | 12.706 | 1.782 | 2.216 | 1.403 |

+, + + indicate the highest and –, – – the lowest differences from check data, significance at $P < 0.05$ and $P < 0.01$ probability levels, respectively.

From the meadow fescue wild populations studied, 12 (Nos. 2287, 2712, 2393, 2618, 2719, 1931, 1661, 1706, 1486, 3544, 3129 and 3467) stood out for a reliably ($P < 0.05$) low crude fibre content (26.38–29.34%) in dry mass *versus* the standard (30.59%) (Table 2). The genotypic variation ($CV_g$) of this trait is lower (4.26%) than of crude protein, the heritability coefficient being like that of digestibility (0.51).

**Crude protein** content reflects the content of total nitrogen (albuminous and non-albuminous), which is evaluated in protein by multiplying it by a corresponding coefficient. The higher the yield and crude protein content, the better is fodder in respect of its nutritive value. Crude protein content in fodder mass strongly depends on environmental conditions, therefore among the samples studied the genotypic va-

Table 3. **Genotypic (G) and phenotypic (P) correlation between seven traits of meadow fescue cultivars and wild populations**

| Traits / No. | | 2 | 3 | 4 | 5 | 6 | 7 |
|---|---|---|---|---|---|---|---|
| 1. DMY of 1st cut, t ha$^{-1}$ | G | 0.425* | 0.089 ns | 0.458* | –0.921** | 0.721** | 0.028 ns |
| | P | 0.942** | –0.873** | –0.647** | –0.817** | –0.652** | 0.621** |
| 2. Height of plant, cm | G | | –0.646** | –0.391 ns | –0.533** | –0.353 ns | 0.317 ns |
| | P | | –0.943** | –0.780** | –0.699** | –0.801** | 0.681** |
| 3. Heading, days | G | | | 0.765** | 0.054 ns | 0.303 ns | –0.562** |
| | P | | | 0.816** | 0.622** | 0.767** | –0.730** |
| 4. Leafiness, % | G | | | | –0.233 ns | 0.878** | –0.700** |
| | P | | | | 0.396 ns | 0.781** | –0.709** |
| 5. Digestibility, % | G | | | | | –0.554** | –0.018 ns |
| | P | | | | | 0.298 ns | –0.423* |
| 6. Crude protein, % | G | | | | | | –0.386 ns |
| | P | | | | | | –0.637** |
| 7. Cellulose, % | G | | | | | | |

riation was low (7.30%). The coefficient of heritability of this trait was low (0.21). According to crude protein content in forage mass the standard reliably ($P < 0.05$) exceeded populations Nos. 2712, 2719 and 1931 (by 1.67–2.61%).

The genotypic and phenotypic correlations are measures of the degree of closeness of the linear relationship between the pairs of variables.

The knowledge of intertrait correlations alleviates the choice of the breeding strategy in developing new cultivars. The value of the genotypic correlation depends on the pleiotropic effect of genes and on the heritability coefficients of both traits [9]. The phenotypic and genotypic correlations among seven traits in meadow fescue plants of first cut are shown in Table 3. In six cases, the correlations were very weak and statistically unreliable (Table 3). The negative high correlations were revealed among first cut DMY and dry matter digestibility (–0.921; $P < 0.01$). The positive high genotypic correlations ($P < 0.01$) of first cut DMY were found with crude protein content (0.721; $P < 0.01$). The positive interrelation is probably due to presence of some later-ripeners among the populations studied. The analysis of genotypic correlation shows that later-ripening populations have a better leafiness ($r = 0.765$; $P < 0.01$). In turn, later-ripening populations contain more crude protein in fodder mass ($r = 0.878$; $P < 0.01$) and less crude fibre ($r = –0.700$; $P < 0.01$). Our conclusion coincides with the opinion of breeders [15] that grasses (meadow bromegrass) could be selected for high forage without reducing crude protein concentration. As a simple index for selecting plants combining productivity and quality, crude protein yield is suggested. The highest yield of crude protein was shown by the populations Nos. 2341 (0.77 t ha$^{-1}$), 1661 (0.78 t ha$^{-1}$), 2736 (0.80 t ha$^{-1}$) and 1931 (0.83 t ha$^{-1}$) as compared to the standard (0.63 t ha$^{-1}$). The mentioned wild populations could be used in the future breeding process. Based on the results of the present study, development of higher yielding cultivars with a higher crude protein, and lower acid and neutral detergent fiber concentration could be possible. By a complex of traits, most interesting for breeding is the later-ripening wild population No. 1661 which combines a high yield of dry matter and good parameters of its quality.

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## TIKROJO ERAIÈINO GENETINIØ IÐTEKLIØ POÞYMIØ KINTAMUMAS, PAVELDIMUMAS IR KORELIACIJA

Santrauka

2002–2003 m. Lietuvos þemdirbystës institute (Dotnuva) buvo atlikti tikrojo eraièino (*Festuca pratensis* Huds.) dviejø lietuviðkø veisliø bei 22 laukiniø populiacijø agronomiðkai svarbiø poþymiø tyrimai. Buvo tiriamas I pjûties sausøjø medþiagø derlius (SMD), atolo SMD, augalø aukðtis, ankstyvumas, lapuotumas, virðkinamumas, þalieji proteinai ir làsteliena. Kovariacijos analize buvo nustatyti fenotipinës ir genotipinës variacijos koeficientai, koreliaciniai ryðiai bei poþymiø paveldimumas (plaèiàja prasme). Nustatyta, kad visø poþymiø fenotipinës variacijos koeficientai buvo didesni uþ genotipinës. Augalø aukðèio paveldimumas buvo maþiausias (0,05), o sausøjø medþiagø derliaus virðkinamumas – didþiausias (0,56). Veislë ‘Kaita’ ir dvi laukinës populiacijos (Nr. 2736 ir 1661) metiniu SMD patikimai (P < 0,05) lenkë standartinæ veislæ ‘Dotnuva I’ 9,6–13,4%. Devynios ið tirtø laukiniø populiacijø (Nr. 2719, 1703, 1486, 3609, 3544, 3129, 2101, 2066 ir 3467) pasiþymëjo (P < 0,01) geresniu SMD virðkinamumu (66,53–69,65%), lyginant su standartine veisle (64,71%). Nustatyta aukðta negatyvi genotipinë koreliacija (P < 0,01) tarp I pjûties SMD ir SMD virðkinamumo (–0.921). Pozityvi aukðta genotipinë koreliacija (P < 0,01) buvo iðaiðkinta tarp I pjûties SMD ir þaliøjø proteinø kiekio (0,721). Tikrøjø eraièinø selekcijoje, atrenkant produktyvius ir geros paðarinës vertës augalus, rodikliu galëtø bûti þaliøjø proteinø derlius. Didþiausias þaliøjø proteinø derlius, lyginant su standartinës veislës (0,63 t ha$^{-1}$), nustatytas ðiose laukinëse populiacijoje: Nr. 2341 (0,77 t ha$^{-1}$), 1661 (0,78 t ha$^{-1}$), 2736 (0,80 t ha$^{-1}$) ir 1931 (0,83 t ha$^{-1}$).