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Genetic and phenotypic diversity for drought tolerance in perennial ryegrass (*Lolium perenne* L.)

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Abstract

Perennial ryegrass (*Lolium perenne* L.) is a widely grown species in temperate regions as forage grass as well as for recreational and bioenergy production purposes. Information on perennial ryegrass genetic background facilitates breeding programs by providing an assessment of genetic diversity in exotic material. Genetic diversity of 104 genotypes of perennial ryegrass was evaluated using phenotypic drought traits and amplified fragment length polymorphism (AFLP) data. A high variation was observed for the drought tolerance traits. Chlorophyll fluorescence (F_v/F_m) explained 88.8% of the whole variation observed in the collection, while re-growth accounted for 9.1% of all variation. A principal component analysis on the basis of phenotypic drought tolerance traits classified perennial ryegrass collection into three clusters. Three AFLP primer pairs produced a total of 210 fragments, 202 of which were polymorphic among all accessions. The genetic diversity of the collection was high with an average similarity coefficient of 0.46 and the average polymorphic information content of 0.29. The principal component analysis based on AFLP data did not cluster genotypes into any major group. A total of six AFLP fragments, identified as being prevalent in drought tolerant genotypes, together with the high degree of genetic homogeneity found, could provide a choice of selecting genotypes from this perennial ryegrass collection for a drought tolerance breeding program.

Key words: drought, *Lolium perenne*, molecular markers, phenotypic traits.

Introduction

Drought is one of the most important environmental stresses in agriculture all over the world, which occurs as a result of climate change (Ahuja et al., 2010). It limits land cultivation and destabilizes crop production affecting both yield and quality. Therefore, the ability of a plant species to adapt well to drought stress has become an important task for plant breeders. Perennial ryegrass is one of the most popular cool-season perennial grass species in temperate regions around the world. It is widely used as a good-quality forage crop, for recreational purposes and as an alternative and renewable bioenergy source. Perennial ryegrass is a self-incompatible diploid (2n = 2x = 14) species showing a high degree of genetic diversity within the population (Kubik et al., 2001; Xing et al., 2007). Perennial ryegrass is known for its large variation in morphological and growth characteristics and rapid drought responses because this species requires a relatively large amount of water to sustain its growth (Yu et al., 2013). Therefore, a better understanding of the genetic basis underlying drought tolerance is essential for genetic improvement of fodder crop plants. Knowledge about genetic diversity in available germplasm can support breeders' decision on the selection of cross combinations from large sets of parental genotypes and can greatly help to widen the genetic basis of a breeding program (Bolaric et al., 2005; Herrmann et al., 2005; Bortolini et al., 2006). Phenotypic trait measurements are commonly used parameters for quantifying genetic variation (Paplauskienė, Dabkevičienė, 2012); however, it is a time and labour intensive method. Molecular markers have a number of perceived advantages over the measurement of phenotypic traits and could be used to monitor breeding material at early stages of plant development and are independent of the growth conditions. One such molecular system is amplified fragment length polymorphism (AFLP) technique, which offers a good reproducibility and a high level of polymorphism in a relatively simple and low-cost procedure (Bachem et al., 1996). AFLP markers are randomly distributed throughout the genome and have been reported to be efficient and reliable in supporting conventional plant breeding programs through marker-assisted selection, which offers great potential in deploying favourable gene combinations (Guthridge et al., 2001). There is a sizable body of literature on molecular marker studies of genetic diversity in perennial

ryegrass (Roldán-Ruiz et al., 2000; Kubik et al., 2001; Bolaric et al., 2005; Posselt et al., 2006; Pivorienė et al., 2008; Kopecký et al., 2009); however, the studies of genetic variation among perennial ryegrass germplasm for drought tolerance are limited. The objective of the present study was to examine the genetic diversity in a world-wide collection of cultivated and wild genotypes of perennial ryegrass for drought tolerance based on AFLP analysis and to interpret the observed relationships in terms of the drought tolerance.

Materials and methods

Plant material. The collection of perennial ryegrass consisted of 104 genotypes, of which 52 were cultivars and 52 wild ecotypes (Table 1). Most of the cultivars originate from Europe, except three genotypes coming from the USA. The majority of wild ecotypes are of Lithuanian and Ukrainian origin, but a few of the ecotypes are from Latvia, Poland, Slovakia and the European part of Russia.

Table 1. Description of 104 perennial ryegrass genotypes used in the study

Cultivar / ecotype No.	Origin	Drought tolerance level	Cultivar / ecotype No.	Origin	Drought tolerance level
Juwel	Germany	tolerant	Pennfine	USA	susceptible
Loretta	Germany	tolerant	Pimpirnel	Denmark	susceptible
2908*	Lithuania	tolerant	Premium	The Netherlands	susceptible
3055	Lithuania	tolerant	Priekulskij-59	Latvia	susceptible
3177	Lithuania	tolerant	Recolta	The Netherlands	susceptible
3180	Lithuania	tolerant	Riika	Finland	susceptible
3774	Ukraine	tolerant	Ronja	Sweden	susceptible
3776	Slovakia	tolerant	Salem	The Netherlands	susceptible
3778	Poland	tolerant	Siverskij-809	Russia	susceptible
3784	Latvia	tolerant	Summit	The Netherlands	susceptible
3818	Ukraine	tolerant	Surprise	The Netherlands	susceptible
Barmona	The Netherlands	medium tolerant	Svea	Sweden	susceptible
Lisuna	Germany	medium tolerant	Sydney	Denmark	susceptible
Sakini	Denmark/Sweden	medium tolerant	Taya	Denmark	susceptible
Vigor	Belgium	medium tolerant	Trani	Denmark/The Netherlands	susceptible
2426	Lithuania	medium tolerant	Trimmer	Germany/Sweden	susceptible
2427	Lithuania	medium tolerant	Troubadour	The Netherlands	susceptible
2591	Lithuania	medium tolerant	Veja	Lithuania	susceptible
3385	Russia	medium tolerant	Veritas	The Netherlands	susceptible
3575	Lithuania	medium tolerant	Wendy	The Netherlands	susceptible
3788	Latvia	medium tolerant	2415	Lithuania	susceptible
3817	Ukraine	medium tolerant	2587	Lithuania	susceptible
3822	Ukraine	medium tolerant	2593	Lithuania	susceptible
3826	Ukraine	medium tolerant	2907	Lithuania	susceptible
3893	Ukraine	medium tolerant	3047	Lithuania	susceptible
3911	Ukraine	medium tolerant	3284	Lithuania	susceptible
Amigo	The Netherlands	susceptible	3388	Russia	susceptible
Barclay	The Netherlands/Sweden	susceptible	3392	Russia	susceptible
Blazer	The Netherlands/USA	susceptible	3394	Russia	susceptible
Belida	Denmark	susceptible	3567	Lithuania	susceptible
Bologna	The Netherlands	susceptible	3572	Lithuania	susceptible
Dacapo	Denmark/Sweden	susceptible	3769	Ukraine	susceptible
Danilo	Denmark	susceptible	3772	Ukraine	susceptible
Darius	The Netherlands	susceptible	3773	Ukraine	susceptible
Eden	Denmark	susceptible	3787	Latvia	susceptible
Gladio	The Netherlands	susceptible	3810	Ukraine	susceptible
Heraut	The Netherlands	susceptible	3815	Ukraine	susceptible
Jubilar	The Netherlands	susceptible	3816	Ukraine	susceptible
Karcagi	Hungary	susceptible	3819	Ukraine	susceptible
Langa	Germany	susceptible	3820	Ukraine	susceptible
Leningradskij-80	Russia	susceptible	3823	Ukraine	susceptible
Livree	Germany	susceptible	3824	Ukraine	susceptible
Lorina	Germany	susceptible	3829	Ukraine	susceptible
Magella	The Netherlands	susceptible	3830	Ukraine	susceptible
Magyar	The Netherlands	susceptible	3831	Ukraine	susceptible
Manhattan	USA	susceptible	3833	Ukraine	susceptible
Marietta	Germany	susceptible	3879	Ukraine	susceptible
Mongita	The Netherlands	susceptible	3883	Ukraine	susceptible
Morenne	The Netherlands	susceptible	3891	Ukraine	susceptible
Morgana	The Netherlands	susceptible	3901	Ukraine	susceptible
Naki	Poland	susceptible	3902	Ukraine	susceptible
Ovation	The Netherlands	susceptible	3903	Ukraine	susceptible

* – the number indicates a wild ecotype

Determination of drought tolerance. The plants of perennial ryegrass collection were cloned vegetatively into four replications per genotype and grown in plastic pots (0.3 dm^3) with peat substrate under regular irrigation and fertilization in a greenhouse for three weeks. Later, at tillering stage, plants were transferred into a growth chamber (CLF PlantClimatics GmbH, Germany) with a 16-h photoperiod, photosynthetically active radiation irradiance of 300 μmol m^{-2} s^{-1}, temperature of 20 ± 1°C and relative air humidity of 60 ± 10%. After 7 days of adaptation plants were deprived of water for 9 days and thereafter re-grown under regular irrigation. The experimental design was a randomized complete block with four replications. The plants were scored on the 7th day of water deprivation according to a scale from 0 (fully wilted) to 9 (without any wilting damage). For chlorophyll fluorescence (F_v/F_m) determinations, three fully expanded leaves were measured on the 8th day of water deprivation after 30 min of dark adaptation with chlorophyll fluorometer OS-30p (Opti-Science, USA). Drought tolerance was scored as a re-growth after 14 days of re-watering, according to a scale from 0 (dead) to 9 (fully re-grown).

Amplified fragment length polymorphism (AFLP) analysis. Genomic deoxyribonucleic acid (DNA) was extracted from 100 mg of leaf material according to a modified protocol of Lassner et al. (1989). Additional steps of purification with chlorophorm and ribonucleic acid (RNA) digestion with ribonuclease A were included. The AFLP procedure was conducted as described earlier by Statkeviciute et al. (2012). DNA primers OLIGO63/T00 (5'-CTCGTAGACTGCGTACCTAAT) and OLIGO63/A00 (5'-GACTGCGTACCTAATACG) were used for pre-amplification. Three primer combinations, each of the primer having three selective nucleotides, were used for the selective amplification in AFLP (Table 3). Polymerase chain reaction (PCR) products from the selective amplification were mixed with solution Blue Stop (Li-Cor Inc., USA) and denatured for 5 min at 95°C. Each sample was loaded on a 6.5% denaturing Gel Matrix (Li-Cor Inc.) and the gel was run in 1X Tris-borate-EDTA (TBE) buffer at 1500 V and 40 W for 3.5 h in a DNA analyzer Li-Cor 4300 (Li-Cor Inc.).

Statistical analysis. Phenotypic data were standardized before using basic statistical analysis and principal component analysis (PCA) was then performed. Pearson correlation coefficient was calculated for drought tolerance traits. Each discernible and reproducible AFLP band was treated as an independent character regardless of its intensity. Sizing standard 50–700 bp IRDye700 (Li-Cor Inc.) was used as a reference to calculate molecular size of each AFLP fragment. Distinction of bands was performed using software *SAGA Generation 2* (Li-Cor Inc.) and also manually. The bands were scored as binary data of 1 (presence) or 0 (absence). Pairwise similarities between individuals were calculated using Jaccard's coefficient for qualitative data (Jaccard, 1908). An Euclidean distance matrix for phenotypic data and a Jaccard's genetic similarity matrix for AFLP data were compared using Mantel (1967) matrix correspondence test. These computations, Pearson correlations and PCA were performed with a software package *NTSYSpc 2.2* (Rohlf, 2005). Percentage of polymorphism was calculated as the proportion of polymorphic AFLP bands over the total number of AFLP bands. Genetic variability at each locus was measured by the polymorphic information content (PIC) index (Anderson et al., 1993).

Results

Drought tolerance. World-wide perennial ryegrass collection expressed large variation for drought tolerance traits studied (Table 2). Re-growth was the most variable trait (CV = 74.8%), ranging from 9.7 for wild ecotype No. 3778 to 0.5 for cv. 'Siverskij-809' of Russian origin. This cultivar had the lowest scores for both wilting and F_v/F_m traits, while the wild ecotype No. 3774 was determined as the most tolerant genotype in terms of F_v/F_m trait and No. 3778 was highly scored for wilting. The re-growth and F_v/F_m were the most variable traits in drought susceptible genotypes (CV = 60.5% and CV = 48.7%, respectively). For the medium tolerant group wilting had the widest range (from 6.8 to 4.2) and the variation of this trait was the highest (CV = 22.1%). The correlation between F_v/F_m and re-growth measurements was higher than the correlation between F_v/F_m and wilting ($r = 0.82$, $p < 0.01$ and $r = 0.75$, $p < 0.01$, respectively), whereas the highest correlation was found between re-growth and wilting measurements ($r = 0.93$, $p < 0.01$). Mantel test revealed very low and not significant correlation ($r = 0.07$, $p < 0.27$) between drought traits and genetic distance.

Table 2. Phenotypic diversity for drought tolerance in perennial ryegrass collection

Drought tolerance	Number of genotypes	Chlorophyll fluorescence (F_v/F_m)			Wilting score			Re-growth score		
		mean ± SE	range	CV %	mean ± SE	range	CV %	mean ± SE	range	CV %
Tolerant	12	0.57 ± 0.08	0.71–0.43	14.7	4.55 ± 0.11	5.0–4.2	8.3	3.25 ± 0.19	4.6–2.5	20.6
Medium tolerant	17	0.44 ± 0.06	0.53–0.33	14.8	2.59 ± 0.14	3.5–2.1	22.1	1.70 ± 0.08	2.3–1.3	11.7
Susceptible	75	0.24 ± 0.11	0.53–0.05	48.7	1.25 ± 0.04	1.7–1.0	2.9	0.35 ± 0.05	1.3–0.03	60.5
Total	104	0.31 ± 0.11	0.71–0.05	51.8	1.85 ± 0.11	5.0–1.0	44.7	1.00 ± 0.12	4.6–0.03	74.8

SE – standard error, CV – coefficient of variation

The phenotypic data for drought tolerance were used for conducting PCA to study the genetic diversity among the 104 perennial ryegrass accessions (Fig. 1). The PCA analysis revealed three groups according to their tolerance to drought. Seventy five perennial ryegrass genotypes were indicated as the least tolerant to drought and this group consisted of 42 cultivars and 33 wild ecotypes. The drought tolerant group consisted of 12 genotypes: two cultivars of German origin cvs. 'Juwel' and 'Loretta' along with wild ecotypes from Latvia, Lithuania, Slovakia, Poland and Ukraine. Four cultivars originated from Western Europe and 13 wild ecotypes from Lithuania and Ukraine were clustered as medium tolerant genotypes. The first PCA component accounted for 88.8% of the total variation and, according to the corresponding eigenvector value, was associated with plant F_v/F_m, therefore the perennial ryegrass accessions were mainly clustered according to this drought tolerance trait. The second component accounted for 9.1% of the total variance and genotypes with different re-growth score were distributed along this axis (Fig. 1).

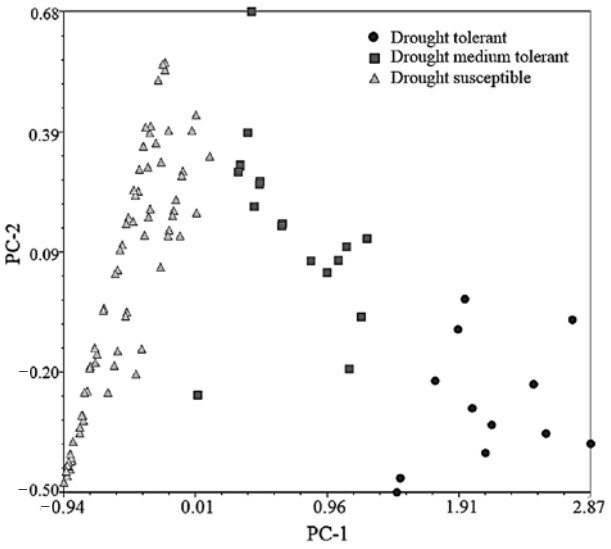

Figure 1. Principal component analysis (PCA) plot of 104 perennial ryegrass genotypes based on drought tolerance traits

Genetic diversity. Three *TaqI* and two *AseI* primers were used to amplify genomic DNA of 104 perennial ryegrass genotypes (Table 3). A total of 210 AFLP bands were identified of which 202 were scored as being polymorphic. Drought tolerant and drought medium tolerant genotypes produced 182 polymorphic bands, while 189 were polymorphic among the drought susceptible genotypes. The number of polymorphic bands per primer combination ranged from 52 to 71 with an average of 59.7 for the drought tolerant and drought medium tolerant genotypes, while for the drought susceptible genotypes, the number of polymorphic bands ranged from 51 to 75 with an average of 58.4 per primer combination (data not shown). Overall PIC ranged from 0.04 to 0.50 with an average value of 0.26 ± 0.15. For the drought tolerant and drought medium tolerant accessions, the average of PIC was 0.27 ± 0.14, while for the drought susceptible genotypes average PIC value reached 0.29 ± 0.16 (Table 3).

Table 3. Genetic diversity in perennial ryegrass collection of 104 genotypes

Primer combination		Amplified fragment length polymorphism (AFLP) bands			Average polymorphic information content (PIC)
TaqI primer	*AseI* primer	total	polymorphic	%	
T-CAC	*A*-ACG	68	56	82.24	0.25 ± 0.14
T-CTA	*A*-ACC	71	52	73.2	0.25 ± 0.15
T-CAA	*A*-ACC	88	71	81.42	0.29 ± 0.16
Mean		75.4	59.7	78.95	0.26 ± 0.15

The number of group-prevalent fragments is presented in Figure 2. A total of six fragments were identified for more than 75% of the genotypes representing drought tolerant group and still were present in 40% drought medium tolerant genotypes and one third of drought susceptible ones. Two fragments were identified only in drought tolerant accessions though percentage of genotypes in the group was only 17%. Drought specific fragments, *A*-ACC/*T*-CTA-181 and *A*-ACC/*T*-CTA-99 were found in genotypes Nos. 3778, 3180 and 3055 of Polish and Lithuanian origin, respectively. The fragment *A*-ACC/*T*-CTA-187 was identified in all drought tolerant genotypes except German cv. 'Juwel' and Lithuanian wild ecotype No. 2587. Eleven fragments were prevalent in drought susceptible genotypes but percentage of genotypes in the group was below 10% (data not shown). Seventy five percent of drought susceptible genotypes amplified the fragment of 333 bp size which was present for only few genotypes of drought medium tolerant and drought tolerant group (Fig. 2).

Jaccard's similarity coefficient was used to estimate the pair-wise genetic diversity among the accessions. Genetic diversity was very high and perennial ryegrass genotypes did not group into any major clusters (Fig. 3). Within 104 genotypes, the highest similarity coefficient (s = 0.66) was detected between cv. 'Troubadour' from the Netherlands and cv. 'Pennfine' originating from the USA. The lowest similarity coefficient (s = 0.32) was recorded between the wild ecotype of Ukrainian origin No. 3823 and the cultivar of Lithuanian origin 'Veja'. The average similarity coefficient for all 104 genotypes was 0.46 ± 0.01. AFLP

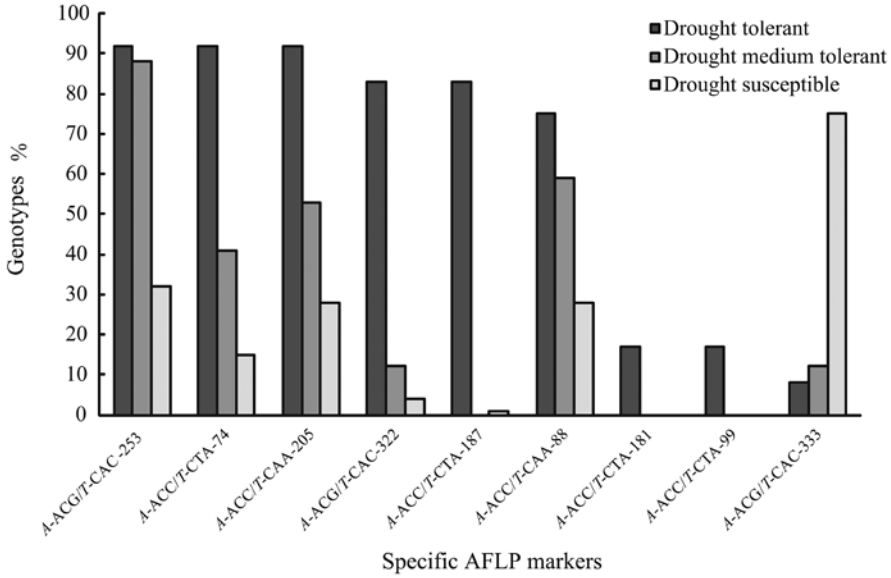

Figure 2. Distribution of specific amplified fragment length polymorphism (AFLP) markers in subgroups of genotypes with differential drought tolerance

data were also used for conducting PCA to further study the genetic diversity among perennial ryegrass accessions. These 104 components of PCA accounted for 100% of the total variation and the whole diversity was explained by all of them. Among them, the first two components accounted for 46.7% of the variance.

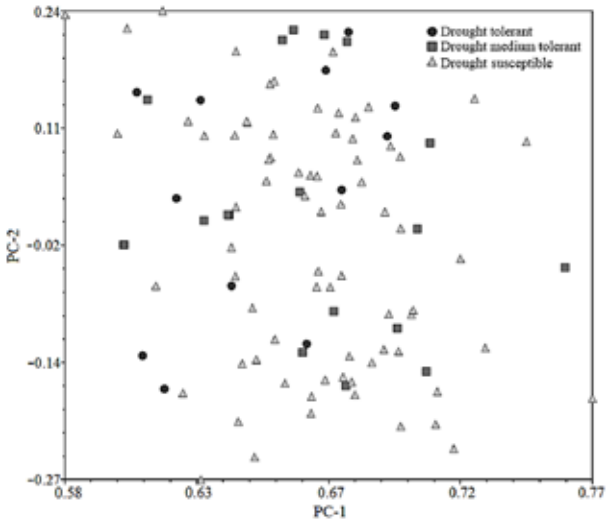

Figure 3. Relationships among 104 perennial ryegrass accessions used for 210 amplified fragment length polymorphism (AFLP) markers based on principal component analysis (PCA)

Discussion

In order to design an optimal plant breeding program it is important to gain knowledge about genetic diversity of parental genotypes used for the development of new cultivars. The use of indigenous materials often representing untapped resources adds value to the breeding programs, even of species for which a sizable body of commercial varieties are already available, since it would expand their genetic basis (Egea-Gilabert et al., 2009). Such programs should start with a precise characterization of existing accessions. The agronomic and molecular analyses described in the present study were made to assess the drought tolerance level and genetic diversity as well as to show the most interesting characteristics of perennial ryegrass germplasm collection for future breeding programs.

Molecular markers are more reliable than phenotypic traits for assessing genetic diversity but phenotyping still is a direct in-the-field/laboratory tool that enables monitoring and gauging the plant performance (Benor et al., 2010). In this study, genotypes of world-wide perennial ryegrass collection were compared under water deficit conditions in the controlled climatic chambers and classified into drought tolerant, drought medium tolerant and drought susceptible groups. Leaf wilting, F_v/F_m and re-growth after the stress provide rapid and easy measurements for the whole-plant responses (Luo et al., 2011; Jonavičienė et al., 2012), thus they were used to screen 104 accessions of perennial ryegrass and characterize drought tolerance at the whole-plant level. Leaf wilting, F_v/F_m and re-growth after the stress were found to be significantly correlated with each other; however, according to Mantel test, no significant correlation was detected between genetic diversity and phenotypic variation. Phenotypic traits tend to be poorly correlated with the molecular markers on the whole-genome scale. This could be due to a few drought traits being measured to reveal plant performance during drought stress and to the fact that many phenotypic characteristics and environmental conditions have an impact on the physiological state of each individual plant. Therefore, it would be useful if a more detailed analysis covering more phenotypic traits were performed.

Molecular markers were used to assess levels of genetic diversity among world-wide accessions of important model plant, perennial ryegrass, in this study. The PIC values for three primer pairs were similar

to those obtained by Roldán-Ruiz et al. (2000), who reported an average PIC value of 0.28 in perennial ryegrass cultivars for AFLP markers. PIC quantifies the number of bands that a marker has and the frequency of each band in the genotypes under study and reflects the genetic diversity among genotypes. The AFLP analysis indicated high genetic diversity within studied perennial ryegrass collection supporting previous findings of Roldán-Ruiz et al. (2000) and Posselt et al. (2006), who studied the genetic diversity in perennial ryegrass forage and turf cultivars as well as wild ecotypes. Although the range of genetic distances among the studied genotypes was high (ranged from 0.32 to 0.66), no clear grouping of genotypes occurred either according to unweighted pair group method with arithmetic mean (UPGMA) method (data not shown) or by PCA. The AFLP markers are suitable for genome wide scanning; however, their use for targeting specific traits can be difficult as only a small percentage of them are expected to be close to particular genes; therefore the low number of markers used in this analysis reduced the chance to hit the sites of particular interest. The need for dense genetic linkage maps was noted in a range of previous studies, characterizing disease resistance traits (Brazauskas et al., 2013), vernalization response (Jensen et al., 2005), evaluating seed yield and fertility traits (Studer et al., 2008) and localizing the genes involved in a water stress response (Jonavičienė et al., 2012). Nevertheless, a number of fragments were prevalent among drought tolerant and drought susceptible genotypes. The number of prevalent fragments in drought susceptible group was much higher, but only one of them was present in 75% of genotypes of drought susceptible group. In addition, six fragments were present in more than 70% of genotypes of drought tolerant group and three fragments occurred solely in drought tolerant genotypes, although two of them represented minor part of the group. The amplified fragments were present in the genotypes of different origin, such as Lithuanian, Ukraine, Slovakia and Latvia, though confirming their linkage more to drought tolerance than origin. Those fragments could be of a particular interest as potential candidates for further development of functional markers for drought tolerance in perennial ryegrass. Candidate gene based association is a powerful tool for the identification of marker-trait associations by testing large numbers of alleles in diverse populations and have been effectively used to establish associations between target genes with known function and complex traits in perennial ryegrass (Skøt et al., 2011; Yu et al., 2013). Another approach for targeting candidate genes is genotyping-by-sequencing technique enabling to rapidly genotype single individuals as well as evaluate allele frequencies within populations. This technique was recently developed in perennial ryegrass and termed genome wide allele frequency fingerprints (GWAFFs) (Byrne et al., 2013). These novel approaches should increase the success in applying molecular markers in breeding programs for drought tolerance in highly heterozygous perennial grasses.

Conclusions

1. World-wide perennial ryegrass collection consisting of 104 genotypes was evaluated for drought tolerance and was grouped into drought tolerant, drought medium tolerant and drought susceptible genotype groups.

2. Amplified fragment length polymorphism (AFLP) markers were a powerful tool to reflect the genetic diversity of perennial ryegrass collection, yet had not distinguished the genotypes into any major group, thus indicating the even distribution of genetic diversity across the collection.

3. A total of six prevalent bands were identified in drought tolerant and medium tolerant genotypes and could be used as the target candidates for further development of functional markers for marker assisted breeding of perennial grasses with improved drought tolerance.

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Daugiametės svidrės (*Lolium perenne* L.) atsparumo sausrai genetinė ir fenotipinė įvairovė

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Santrauka

Vidutinio klimato šalyse daugiametė svidrė (*Lolium perenne* L.) yra plačiai auginama ne tik kaip pašarinė žolė, tačiau naudojama ir rekreacijos reikmėms ar kaip atsinaujinančios energijos šaltinis. Informacija apie jos genetinę kilmę galėtų paspartinti selekcijos procesą. Daugiametės svidrės 104 genotipų fenotipinė įvairovė buvo įvertinta sausros testo sąlygomis, o genetinė įvairovė nustatyta pagausintų fragmentų ilgio polimorfizmo (PFIP) metodu. Atsparumo sausrai požymių įvairovė buvo didelė. Didžiausią dalį (88,8 %) fenotipinės įvairovės atskleidė chlorofilo fluorescencijos (F_v/F_m) požymis, o atžėlimas po sausros paaiškino 9,1 % tirtos daugiametės svidrės kolekcijos fenotipinės variacijos. Fenotipinių požymių principinių komponenčių analizė pagal jų atsparumą sausrai daugiametės svidrės genotipus suskirstė į tris grupes. Trys PFIP pradmenų poros amplifikavo 210 fragmentų, iš kurių 202 buvo polimorfiški ir atskleidė kolekcijos didelę genetinę įvairovę. Genetinės įvairovės panašumo koeficiento vidurkis siekė 0,46, o polimorfiškumo informacijos talpa – 0,29. Tačiau, nepaisant kolekcijos didelės genetinės įvairovės, principinių komponenčių analizė pagal PFIP duomenis genotipų nesuskirstė į didesnes grupes. Šešių PFIP fragmentų, būdingų sausrai atspariems genotipams, identifikavimas ir tirtos kolekcijos homogeniškumas leidžia tikėtis atrinkti vertingus sausrai atsparius daugiametės svidrės genotipus selekcijos programoms.

Reikšminiai žodžiai: daugiametė svidrė, fenotipiniai požymiai, molekuliniai žymekliai, sausra.