

GENETIC AND AGRONOMIC ANALYSIS OF LATVIAN FESCUE (*FESTUCA* SPP.), RYEGRASS (*LOLIUM* SPP.) ACCESSIONS AND THEIR HYBRIDS

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The development of ecologically adaptable fodder crop varieties is of increasing importance, particularly in the context of climate change. New varieties should be phenotypically and ecologically plastic and able to adapt to differing climatic and soil conditions, ensuring high yields and persistence. Combining Festuca and Lolium species and the development of hybrid (Festulolium) cultivars can be a promising method of combining high yield, high feed quality, persistence, as well as cold, frost and drought tolerance. Breeders at the Institute of Agriculture of Latvia University of Life Sciences and Technologies have been utilizing Festulolium germplasm for several decades. Currently, in cooperation with the molecular genetics laboratory and Latvian gene bank at the Latvian State Forest Research Institute "Silava", analysis of Festuca, Lolium and their hybrids with DNA markers has been initiated, in order to gain additional knowledge about the breeding material and to increase the efficiency of the breeding process. Results of the assessment of morphological and agronomic traits in long-term field trials are combined with DNA markers analyses in order to determine the correlation of genetic and phenotypic traits.

Key words: *Festulolium*, fodder crops, hybridization, SSR markers.

INTRODUCTION

The development of ecologically adaptable fodder crop varieties is of increasing importance, particularly in the context of climate change. New varieties should be phenotypically and ecologically plastic and able to adapt to differing climatic and soil conditions, ensuring high yields and persistence. In northern Europe, climate change models predict a decrease of summer precipitation, increased autumn precipitation, and the increased incidence of freezing damages in winter (Becker *et al.*, 2018). This means that breeders must combine high yield, high feed quality, persistence, as well as cold, frost and drought tolerance. Fodder grass productivity and persistence is mainly determined by the genetic potential of species and varieties (Moser *et al.*, 1996). One of the most widely utilised fodder grass species in temperate climates is perennial ryegrass (*Lolium perenne*), which has fast growth, high yields and high nutritive value. *L. perenne* is particularly suited to clay soils and moist, coastal climates. In the Baltic region, *L. perenne* can lack

winter hardiness and persistence (Bērziņš *et al.*, 2018a; Le-mežienē *et al.*, 2004). Therefore, combining *Festuca* and *Lolium* species and the development of hybrid (Festulolium) cultivars can be a promising method of combining these desired agronomic properties. Festulolium hybrids have high combining ability and recombination potential (Thomas and Humphreys, 1991; Casler *et al.*, 2002), which can be utilised for breeding, in order to combine the high yield and fodder quality of *Lolium* species (Wilkins and Humphreys, 2003) with the stress tolerance of *Festuca* species (Thomas *et al.*, 2003; Berzins *et al.*, 2015). Tall fescue (*F. arundinacea*) has high persistence (Berzins *et al.*, 2018b), and is tolerant to both drought and waterlogging (Cougnon *et al.*, 2013). Therefore, in the context of climate change, Festulolium cultivars may be of interest to forage grass breeders due to their high regrowth capacity and nutritive value (Ostrem *et al.*, 2013b). Breeders at the Institute of Agriculture of Latvia University of Life Sciences and Technologies have been utilising Festulolium germplasm for several decades. Currently, in cooperation with the molecu-

lar genetics laboratory and Latvian gene bank at the Latvian State Forest Research Institute “Silava”, analysis of *Festuca*, *Lolium* and their hybrids with DNA markers has been initiated, in order to gain additional knowledge about the breeding material and to increase the efficiency of the breeding process. Results of the assessment of morphological and agronomic traits in long-term field trials are combined with DNA markers analyses in order to determine the correlation of genetic and phenotypic traits. The aim of the study was to assess the agronomic properties of *Lolium*, *Festuca* and hybrid germplasm in the Latvian fodder grass breeding programme, as well as their genetic similarities in order to assess the possibilities for combining their desirable properties.

The use of DNA markers provides the opportunity to determine the genetic diversity and relatedness of individuals, populations and species. One of the fundamental parameters of genetic diversity is allelic diversity (number of alleles). Alleles are differing forms of one genomic location, which can be linked to functional loci and therefore be correlated with phenotypic or other morphological or biochemical variation, or they can be selectively neutral, and reflect the neutral or background genetic variation. The allelic variation within individuals is determined by the genetic composition of the parents, mating type (outcrossing or selfing). In diploid individuals, homozygous loci have two identical alleles, while heterozygous loci have two differing alleles. The overall level of heterozygosity within a population is determined by the genetic diversity of the parents, phenology (the extent of flowering synchronisation) and mating type. The calculation of the extent of allelic similarity between individuals and populations determines their genetic relatedness. In contrast to many field crops, forage grasses are outcrossing, and therefore have genetic diversity within accessions, the extent of which is in part determined by breeding techniques (selection intensity, isolation, choice of parent accessions etc.). This study is an initial survey of a relatively small portion of the germplasm utilised in the Latvian forage grass breeding programme, determining the genetic diversity and relatedness, with the aim of increasing the efficiency of the breeding process.

MATERIALS AND METHODS

Hybrid *Festulolium* cultivars and germplasm can have a wide range of agronomic properties and backgrounds, therefore, within this study, *Festulolium* material refers to *Festuca* and *Lolium* hybrids (mainly *Lolium* spp. × *F. pratensis*) with *Lolium* plant architecture (*Lolium*-type ears). According to morphological traits, the variety ‘Lofa’ can also be included with *Lolium* types, as while it is a hybrid of *L. multiflorum* and *F. arundinacea*, it does not possess any morphological traits of *F. arundinacea*. Three species can be considered as characteristic of *Lolium* — *L. perenne*, *L. multiflorum* and *L. hybridum*. *L. perenne* and *L. multiflorum* can easily hybridise, forming the intermediate form *L. hybridum*. A *Lolium* × *F. pratensis* hybrid cultivar, which has a number of morphological traits characteristic of *L. multi-*

florum, was initially registered in Latvia as a *Festulolium* cultivar ‘Ape’, but subsequently was registered in the European catalogue as the hybrid *Lolium* variety ‘Saikava’. In addition, some germplasm from the gene bank was included in the analysis, including some old varieties that are not currently utilised, e.g. the *F. pratensis* variety ‘Priekuļu 519’. In addition, some varieties were analysed, which have been used to develop new cultivars, e.g. the *L. perenne* cultivar ‘Priekuļu 59’, which was used to develop the new cultivar ‘Gunta’ (not included in the current analysis).

A total of 24 accessions were analysed, including *Festuca*, *Lolium* and hybrid varieties (Table 1). These accessions were selected to represent the range of species and hybrids within the Latvian fodder grass breeding programme. Samples of the analysed accessions were obtained from the gene bank, breeding and cultivar trials, and genetic resource field collections. Accessions were represented by both seed samples as well as plants collected from the field.

To characterise the agro-morphological properties, expert assessment by grass breeders from the Institute of Agriculture in Skrīveri was used based on long-term data and experience. Morphological and agronomic properties were assessed from accessions growing in long-term field trials and collections. In addition, observations were made at other sites where the accessions were growing. Therefore, the morphological assessments were made over several years and from accessions growing in multiple locations.

Seeds were germinated on moistened filter paper in a growth cabinet (22 °C – 20 °C, 16 h light) for approximately two weeks. DNA was extracted from leaf tissue of 8–12 individuals using a CTAB-based method (Porebski *et al.*, 1997). For samples collected from field trials, DNA was extracted from a leaf sample from a single individual, using the previously described method. Genotyping was done using eight simple sequence repeat (SSR) markers — G03_020, G05_033, G07_037, G01_053, G07_065, G05_071, G05_088, and G05_099 (Studer *et al.*, 2008). Each forward primer was labelled with a different fluorophore (6-FAM, HEX or TMR) to facilitate visualisation using capillary electrophoresis. The PCRs were carried out in a 10 µl solution containing 2 µl Hot FirePol Blend MasterMix with 10mM MgCl₂ (Soltis BioDyne, Tartu, Estonia), 0.5 µl each primer (8 µM), and 2 µl DNA solution. The PCR cycling conditions were: 95 °C for 15 minutes, 40 cycles of 95 °C for 20 seconds, 58 °C for 30 seconds, 72 °C for 45 seconds, and 72 °C for 5 minutes. The PCR products were size separated on an ABI 3130xl Genetic Analyzer and genotyped using GeneMapper 4.0 (Applied Biosystems). Genetic diversity parameters were calculated using GenAIE 6.0 (Peakall and Smouse, 2006). Genetic distances and bootstrapping were done using the MSA software package (Dieringer and Schlötterer, 2003). Genetic distances were calculated using the proportion of shared alleles, Nei's chord distance, and Cavalli-Sforza and Edwards chord distance with 1000 bootstrap repetitions. Neighbour-joining trees and consensus trees were constructed using the ‘Neighbour’ and ‘Consense’ programmes in PHYLIP.

Table 1

GENETIC BACKGROUND AND AGRONOMIC PROPERTIES OF *FESTUCA*, *LOLIUM* AND HYBRID ACCESSIONS (WH, FODDER QUALITY AND CULM FORMATION TRAITS SCORED ON SCALE FROM 1–9 ACCORDING TO EXPERT EVALUATIONS)

Cultivar/ Candivar	Origin (morphology)	DMY, t ha ⁻¹	WH (1–9)*	Persistence (years)	Fodder quality (1–9)**	Culms in after- math (1–9)***
Priekuļi 519	<i>F. pratensis</i> (Fp)	7	7	4	7	1
Silva	<i>F. pratensis</i> (Fp)	8	7	5	7	1
Vaira	<i>F. pratensis</i> (Fp)	8	7	5	7	1
Pa SV	<i>F. pratensis</i> (Fp)	6	7	5	7	3
Patra	<i>F. pratensis</i> (Fp)	8	6	4	8	1
Vaive	<i>F. rubra</i> (Fr)	7	9	10	6	1
Baltica	<i>F. arundinacea</i> (Fa)	11	9	10	3	3
Fawn	<i>F. arundinacea</i> (Fa)	10	8	8	3	3
Swai	<i>F. arundinacea</i> (Fa)	10	9	8	4	3
Na SL	<i>F. arundinacea</i> (Fa)	10	9	10	5	3
Felina	<i>L. sp.</i> × <i>F.a</i> (FIF)	10	8	8	5	3
Hikor	<i>L. sp.</i> × <i>F.a</i> (FIF)	11	8	8	5	3
GNK	<i>L. sp.</i> × <i>F.a</i> (FIF)	11	9	10	3	3
Lofa	<i>L. sp.</i> × <i>F.a</i> (FIL)	8	5	2	8	8
Felopa	<i>L. sp.</i> × <i>F. pratensis</i> (FIL)	8	5	5	8	8
Ape	<i>L. sp.</i> × <i>F. pratensis</i> (FIL)	8	7	5	7	5
Saikava	<i>L. sp.</i> × <i>F. pratensis</i> (FIL)	8	7	5	7	5
Vizule	<i>L. sp.</i> × <i>F. pratensis</i> (FIL)	8	7	5	7	6
PSP	<i>F. pratensis</i> × <i>L. sp.</i> (FIL)	8	8	6	7	5
Vetra	<i>L. sp.</i> × <i>F. pratensis</i> (FIL)	9	7	5	7	7
Punia	<i>L. sp.</i> × <i>F. pratensis</i> (FIL)	9	7	5	7	7
Priekuļi 59	<i>L. perenne</i> (Lp)	6	5	3	7	6
Spidola	<i>L. perenne</i> (Lp)	7	6	5	8	5
Uva	<i>L. multiflorum</i> (Lm)	8	1	1	9	9

* winterhardiness scores: 1 – very weak; 9 – excellent

** fodder quality scores: 1 – very poor; 9 – very high

*** tendency to form culms in aftermath: 1 – absent; 9 – very high

Candivar, candidate variety; DMY, dry matter yield; WH, winter hardiness. The designations in brackets after the species or origin of each accession refer to either the species or for hybrid accessions to inflorescence morphology: FIF – *Festuca*-like, FIL – *Lolium*-like.

Phylogenetic trees were visualised using FigTree v1.4.2. A Bayesian clustering approach, implemented using the software STRUCTURE version 2.1 (Pritchard *et al.*, 2000), was used to estimate the most likely number of clusters (K) into which the genotypes were assigned with certain likelihood. The population priors were not used, and a burn-in period of 50 000 iterations followed by 100 000 iterations was used. K was set from 1 to 10, and each run was replicated 25 times. The most likely number of clusters was identified by the delta K criterion with the STRUCTURE HARVESTER Web version 0.6.93 software (Earl and von Holdt, 2012).

RESULTS

Data about dry matter yield, winter hardiness, persistence, fodder quality and culm formation for the analysed accessions was gathered in long-term trials at the Institute of Agriculture in Skrīveri, Latvia (56°37' N and 25°07' E). Tall fescue (*F. arundinacea*) and their hybrid accessions have high yield, winter hardiness, and persistence in normal

moisture conditions. Red fescue (*F. rubra*) also has very high persistence, however yield and fodder quality are lower. Unfortunately, tall fescue cultivars and Festulolium cultivars developed from this species do not have satisfactory fodder quality. The winter hardiness of meadow fescue (*F. pratensis*) is sufficient for Latvian conditions (Berzins *et al.*, 2018a), and is superior to that of perennial ryegrass (*L. perenne*) and *Lolium* type Festulolium accessions, however persistence is comparatively low, and is not significantly different from perennial ryegrass and Festulolium accessions. As current cultivars of these related species combine both positive and negative agronomic traits, the task of breeders is to combine as many positive traits as possible into one cultivar.

Lolium cultivars have a tendency to form culms, while *Festuca* cultivars do not. The culm formation of Festulolium cultivars varies, depending on the genetic contribution from each parental species, and this is one of the morphological indicators of the genetic composition of Festulolium cultivars.

Table 2

GENETIC DIVERSITY PARAMETERS OF THE ANALYSED ACCESSIONS

Cultivar/ Candivar	Inflorescence morphology	N	Genotyping success (%)	Na	Ne	I	Ho	He	F
Priekuļu 519	Fp	8	99	2.500 (0.463)	1.763 (0.285)	0.577 (0.179)	0.221 (0.084)	0.324 (0.101)	0.287 (0.146)
Silva	Fp	12	100	2.625 (0.460)	1.957 (0.293)	0.672 (0.169)	0.365 (0.134)	0.396 (0.093)	-0.024 (0.250)
Vaira	Fp	12	99	3.000 (0.655)	2.024 (0.349)	0.716 (0.181)	0.409 (0.119)	0.411 (0.090)	-0.014 (0.182)
Pa SV	Fp	1	92	1.000 (0.189)	1.000 (0.189)	0.087 (0.087)	0.125 (0.125)	0.063 (0.063)	-1.000 (0.125)
Patra	Fp	8	88	1.625 (0.263)	1.391 (0.167)	0.322 (0.130)	0.203 (0.123)	0.210 (0.085)	0.164 (0.299)
Vaive	Fr	1	87	0.750 (0.313)	0.750 (0.313)	0.173 (0.113)	0.250 (0.164)	0.125 (0.082)	-1.000 (0.000)
Baltica	Fa	1	89	1.750 (0.164)	1.750 (0.164)	0.520 (0.113)	0.750 (0.164)	0.375 (0.082)	-1.000 (0.000)
Fawn	Fa	2	100	2.125 (0.125)	1.933 (0.126)	0.687 (0.055)	0.563 (0.148)	0.469 (0.031)	-0.200 (0.279)
Swai	Fa	1	91	1.750 (0.164)	1.750 (0.164)	0.520 (0.113)	0.750 (0.164)	0.375 (0.082)	-1.000 (0.000)
Na SL	Fa	2	89	1.750 (0.250)	1.658 (0.218)	0.460 (0.143)	0.563 (0.175)	0.313 (0.094)	-0.787 (0.109)
Felina	FIF	2	88	2.000 (0.189)	1.858 (0.169)	0.617 (0.103)	0.500 (0.164)	0.422 (0.067)	-0.181 (0.301)
Hikor	FIF	1	95	1.750 (0.164)	1.750 (0.164)	0.520 (0.113)	0.750 (0.164)	0.375 (0.082)	-1.000 (0.000)
GNK	FIF	2	98	2.125 (0.295)	2.025 (0.308)	0.660 (0.133)	0.750 (0.134)	0.438 (0.075)	-0.714 (0.126)
Lofa	FIL	12	100	4.000 (0.627)	2.578 (0.410)	1.014 (0.177)	0.434 (0.111)	0.525 (0.083)	0.198 (0.136)
Felopa	FIL	12	100	4.875 (0.693)	3.101 (0.535)	1.185 (0.186)	0.580 (0.119)	0.590 (0.085)	0.011 (0.149)
Ape	FIL	12	100	3.500 (0.500)	2.058 (0.351)	0.800 (0.166)	0.484 (0.101)	0.422 (0.085)	-0.150 (0.050)
Saikava	FIL	12	88	3.500 (0.327)	2.101 (0.255)	0.859 (0.118)	0.421 (0.098)	0.474 (0.063)	0.144 (0.158)
Vizule	FIL	12	100	3.375 (0.263)	2.117 (0.250)	0.849 (0.117)	0.469 (0.111)	0.471 (0.070)	0.094 (0.144)
PSP	FIL	2	95	1.500 (0.189)	1.450 (0.176)	0.330 (0.126)	0.313 (0.162)	0.234 (0.090)	-0.333 (0.333)
Vetra	FIL	12	93	4.250 (0.412)	3.039 (0.408)	1.191 (0.105)	0.603 (0.082)	0.638 (0.037)	0.048 (0.122)
Punia	FIL	12	100	3.625 (0.498)	2.293 (0.156)	0.951 (0.090)	0.590 (0.086)	0.549 (0.032)	-0.076 (0.143)
Priekuļu 59	Lp	8	100	3.250 (0.590)	2.567 (0.443)	0.998 (0.168)	0.484 (0.128)	0.560 (0.085)	0.167 (0.173)
Spidola	Lp	8	50	2.500 (0.378)	1.703 (0.235)	0.585 (0.153)	0.353 (0.118)	0.330 (0.089)	-0.065 (0.140)
Uva	Lm	8	100	3.750 (0.675)	2.578 (0.518)	0.976 (0.169)	0.446 (0.083)	0.523 (0.072)	0.170 (0.161)

N, number of individuals analysed per accession; genotyping success, proportion of loci with positive results (8 loci); Na, mean number of different alleles over 8 loci; Ne, number of effective alleles; I, Shannon's Information Index; Ho, observed heterozygosity; He, expected heterozygosity; F, fixation (inbreeding) index.

A total of 75 alleles were identified with the eight SSR markers. The number of alleles identified at each locus ranged from 14 (G07_037) to 4 (G05_099) (mean — 9.375). Mean genetic diversity parameters were calculated for each accession (Table 2). While the fact that only 1–2 individuals were analysed for some of the accessions means that direct comparison of genetic diversity parameters is complicated, some general conclusions can be made, particularly for the accessions where multiple individuals were analysed. The mean number of alleles within each population was higher in the accessions where multiple individuals were analysed, indicating that the accessions were not genetically homogeneous. However, the mean effective number of alleles, which takes into account allele frequencies, was more similar, indicating that the higher allelic diversity was due to low frequency alleles. This type of polymorphism within accessions can be expected due to the outcrossing nature of the analysed species. Shannon's information index, which is a metric of diversity, ranged from 1.191 (Vetra) to 0.087 (Pa SV). The observed heterozygosities were in general higher in the single individual accessions, reflecting the high heterozygosity of individuals. Fixation, or inbreeding indices were only informative for the accessions where multiple individuals were analysed

and for these accessions ranged from 0.287 (Priekuļu 519) to -0.150 (Ape) (mean — 0.068). The differing F indices between the accessions could be an indication of the pedigree and maintenance history of each accession.

Genetic distances between the analysed accessions were calculated using the proportion of shared alleles, and a consensus neighbour-joining tree was constructed, based on 1000 bootstrap analyses. The dendrogram was in good agreement with the origin of the accessions. Three main clades were identified, the first containing the *F. arundinacea* and Festuca-like Festulolium accessions. The second clade consisted of the *Lolium* and *Lolium*-like hybrid accessions, while the third clade contained the *F. pratensis* and one *F. pratensis* × *L. sp.* accession (PSP). The other accession that was not grouped according to pedigree was Lofa, a *L. sp.* × *F. arundinacea* cultivar, but it clustered together with the *Lolium* and *Lolium*-like accessions (Fig. 1). However, the inflorescence morphology of this cultivar is more similar to the *Lolium* cultivars (Table 1), and this is reflected in the genetic analyses as well.

The STRUCTURE software was used to analyse the obtained genotypic results (Pritchard *et al.*, 2000). This approach analyses differences in the distribution of genetic

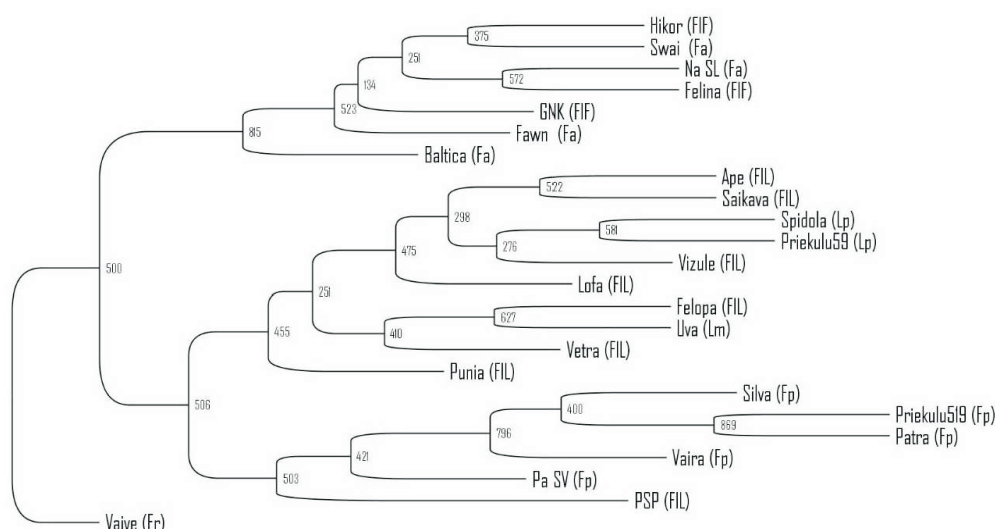


Fig. 1. Consensus neighbour-joining dendrogram based on pairwise genetic distances calculated by the proportion of shared alleles. Bootstrap support (1000 bootstraps) indicated.

variation between populations using a Bayesian iterative algorithm by grouping samples that share similar patterns of variation. STRUCTURE assigns individuals to the group representing the best fit for the variation patterns found (Porrás-Hurtado *et al.*, 2013). According to the delta-K method, the most likely number of groups identified among the analysed accessions was six (Table 3). The grouping was largely consistent with the previous analyses, with the *F. arundinacea* and Festuca-like cultivars grouping together, and the *F. pratensis* accessions clustering, as were the two *L. perenne* accessions. The Lolium-like accessions (FIL) were the most diverse, with two accessions ('Felopa' and 'Vetra') placed in the same group as 'Uva' (*L. multiflorum*) and 'Vaive' (*F. rubra*). One FIL accession was grouped separately ('Punia'), while the other FIL accessions grouped together.

DISCUSSION

The results of the genetic analyses were in agreement with the pedigree, species, morphological and agronomic characteristics of the analysed accessions. For instance, the Festulolium accessions with Lolium-like inflorescence morphology (FIL) tended to cluster with the *Lolium* accessions, while those with Festuca-like inflorescence morphology (FIF) tended to cluster with the *F. arundinacea* accessions. In most cases, the inflorescence morphology was consistent with pedigree; however, one exception was the cultivar 'Lofa', which according to its pedigree was similar to the cultivars 'Felina', 'Hikor' and 'GNK' (*L. sp.* × *F. arundinacea*), but 'Lofa' has *Lolium* type inflorescence morphology. Genetically, it was more similar to the *Lolium* cultivars, and agronomic and morphological traits were also similar to *Lolium* cultivars. In this case, the genetic and morphological results and agronomic properties were in agreement with each other, while the pedigree of the cultivar 'Lofa' did not correspond with its agronomic qualities. The hybrid cultivar 'PSP' was genetically more similar to the *F. pratensis* cultivars, and clustered separately from the other hybrid cultivars with *Lolium* type inflorescence morphology. While 'PSP' has Lolium-like inflorescence morphology,

consistent with its pedigree, it had higher winter hardiness and persistence (traits characteristic of *Festuca*) than the other hybrid cultivars with Lolium-like inflorescence morphology. Interestingly, the hybridisation was in the opposite direction to the other FIL hybrid cultivars, which were *L. sp.* × *F. pratensis*.

Higher levels of heterozygosity were found in the *F. arundinacea* accessions in comparison to the *F. pratensis* and *F. rubra* accessions, which was also noted during breeding, where low levels of morphological diversity were found in *F. pratensis* accessions. The highest levels of diversity were found in the Festulolium accessions, in particular the new Lithuanian variety 'Vetra', as well as 'Felopa' and 'Lofa'. The late accession 'Pa SV' had low genetic diversity indicators, as a result of repeated crossings with earlier varieties. The accession 'Patra' had relatively low genetic diversity parameters, which was a result of the breeding process for this cultivar, which utilised colchicine induced tetraploid *F. pratensis* germplasm. The accession 'Spidola' also had low diversity, and was developed on the base of four selected clones. However, while 'Patra' and 'Spidola' have low genetic diversity, they have good agronomic properties, and are competitive with other European *L. perenne* varieties (Østrem *et al.* 2013a; 2013b). These differences in genetic diversity within the analysed cultivars is a result of the breeding process, reflecting the selection intensity, pedigree and other factors. Higher levels of genetic diversity with a cultivar and variety can have a positive influence on stability and phenotypic plasticity in a range of growing conditions and sites. However, cultivars with relatively lower levels of genetic diversity can also be successfully cultivated in a range of sites and conditions (e.g. 'Patra' and 'Spidola'). Differences in the fixation or inbreeding index can indicate differences in the maintenance and development of varieties. This is illustrated by the contrasting values for 'Ape' (−0.150) and 'Saikava' (0.144). 'Saikava' is a new cultivar developed from 'Ape', and the selection and crossing process has resulted in a relatively outbred accession 'Ape' being transformed into a relatively inbred cultivar 'Saikava'.

Table 3

PROPORTION OF MEMBERSHIP OF EACH PRE-DEFINED POPULATION IN EACH OF 6 CLUSTERS

Accession	Inflorescence morphology	1	2	3	4	5	6
Priekulu519	Fp	0.006	0.008	0.007	0.962	0.011	0.006
Silva	Fp	0.015	0.01	0.006	0.955	0.007	0.008
Vaira	Fp	0.006	0.022	0.005	0.952	0.006	0.008
Pa SV	Fp	0.775	0.018	0.008	0.176	0.017	0.007
Patra	Fp	0.004	0.003	0.003	0.983	0.005	0.003
Vaive	Fr	0.099	0.007	0.832	0.005	0.047	0.01
Baltica	Fa	0.889	0.01	0.082	0.006	0.009	0.004
Fawn	Fa	0.963	0.004	0.011	0.005	0.013	0.004
Swai	Fa	0.977	0.004	0.008	0.004	0.004	0.004
Na SL	Fa	0.932	0.013	0.004	0.034	0.01	0.006
Felina	FIF	0.963	0.005	0.003	0.016	0.004	0.008
Hikor	FIF	0.943	0.004	0.004	0.014	0.004	0.031
GNK	FIF	0.955	0.004	0.005	0.016	0.005	0.015
Lofa	FIL	0.015	0.527	0.214	0.01	0.155	0.079
Felopa	FIL	0.009	0.056	0.887	0.007	0.017	0.024
Ape	FIL	0.006	0.903	0.016	0.032	0.009	0.034
Saikava	FIL	0.01	0.819	0.028	0.012	0.098	0.034
Vizule	FIL	0.009	0.895	0.009	0.031	0.024	0.033
PSP	FIL	0.004	0.274	0.007	0.551	0.006	0.158
Vetra	FIL	0.019	0.186	0.485	0.021	0.054	0.236
Punia	FIL	0.035	0.019	0.014	0.026	0.894	0.012
Priekulu59	Lp	0.045	0.099	0.011	0.005	0.009	0.831
Spidola	Lp	0.005	0.132	0.012	0.006	0.007	0.838
Uva	Lm	0.009	0.024	0.867	0.006	0.064	0.03

Cluster with the highest proportion of membership for each accession is given in bold.

The results from the genetic analysis were in general agreement with the pedigree and the morphological and agronomic properties of the analysed accessions, indicating that the DNA markers utilised were informative for species identification and determination of hybrid composition, as they were potentially indicative of agronomic properties as well. In the cultivars where the genetic data and pedigree did not correspond ('Lofa', 'PSP'), the agronomic properties of this cultivar were in concordance with the genetic results. The germplasm material analysed in this study consisted of cultivars and candidate cultivars, which have been extensively evaluated throughout the breeding process. The further utilisation of these informative DNA markers to evaluate less advanced breeding lines and other germplasm, and genetic analysis will make the breeding process more efficient by providing additional information on genetic diversity and hybrid composition, as well as potential agronomic properties. This can allow for more efficient selection of breeding material for further evaluation of agronomic properties.

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LATVIJĀ IZVEIDOTO AUZEŅU (*FESTUCA* SPP.), AIREŅU (*LOLIUM* SPP.) PERSPEKTĪVO ŠĶIRŅU UN TO HIBRĪDU ĢENĒTISKĀ UN AGRONOMISKĀ ANALĪZĒ

Klimata pārmaiņu kontekstā īpaši aktuāla ir ekoloģiski plastisku zālaugu šķirņu veidošana, kuras spējīgas adaptēties atšķirīgos augsnes un klimatiskajos apstākļos un nodrošināt augstvērtīgus, kvalitatīvus un ilggadīgus zeltēņus. *Festuca* un *Lolium* starpsugu hibrīdu (*Festulolium*) veidošana var būt daudzsoļa metode, kas vienā šķirnē ļauj apvienot augstu ražu, augstu lopbarības kvalitāti, noturību zeltēnī, kā arī aukstuma, sala un sausuma izturību. Latvijas Lauksaimniecības universitātes Zemkopības zinātniskā institūta selekcioniāri jau vairākus gadus desmitus strādā ar auzeņpairoņu starpsugu hibrīdiem. Šobrīd sadarbībā ar Latvijas Valsts mežzinātnes institūta “Silva” molekulārās ģenētikas laboratorijas un Latvijas ģēnu bankas speciālistiem uzsākta *Festuca*, *Lolium* un to hibrīdu analīze ar DNS marķieriem, lai iegūtu papildu zināšanas par selekcijas izejmateriālu un palielinātu selekcijas procesa efektivitāti. Ģenētiskā materiāla morfoloģisko un agronomisko īpašību novērtēšanas rezultāti, kas iegūti ilgtermiņa lauka izmēģinājumos, tiek izvērtēti kopā ar DNS marķieru analīzēm, lai noteiktu sakarības starp ģenotipiskajām un fenotipiskajām pazīmēm.