

INFLUENCE OF INTRASPECIFIC VARIATION OF PERENNIAL RYEGRASS ON QUALITY AND LEVEL OF PRODUCTION

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Abstract. *Lolium perenne* has a global distribution becoming a dominant species in temperate grassland ecosystems and covers a wide range of environmental conditions (length of day, humidity, altitude, soil type and chemistry, etc.). Understanding the patterns and magnitude of the genetic diversity of this allogamous forage species is a first step toward identifying several ecological traits. Intra-population genetic diversity can promote the temporal stability of grassland production, and also large-scale genetic variation can be closely linked to the regional productivity of perennial ryegrass-dominated grasslands. Although total dry matter production remains a key objective in increasing the productive yield of fodder ryegrass, increased emphasis is placed on seasonal dry matter production, seed quality and density. One of the most important productive traits is leaf length as an important feature of forage grasses, and the development of the molecular marker is an opportunity to identify quantitative trait sites (QTLs) and to begin dissecting the genetic regulation of complex traits. Reproduction for long leaves or for a high rate of leaf elongation should contribute to an improvement in the intercepted radiation accumulated during regrowth and would be a way to improve the spring dry matter yield, but the seed yield has not improved. Selection pressures on seed production criteria applied to the breeding process should improve seed yields without a negative impact on feed performance. The continued success of pasture farming depends on supporting programs to grow fodder species that are able to produce improved varieties that meet market needs by manipulating the recombination of the genome of these fodder plants.

Keywords: perennial ryegrass, productive traits, dry matter production

INTRODUCTION

Perennial ryegrass is one of the most important species in sown pastures, lawns and weed populations around the world (Cunliffe et. al., 2004). The species is found predominantly in heavily grazed areas for long periods, but also in various wild habitats, being a native species and the most important component of seeded perennial forage mixtures (Sokolovic et. al., 2007). The control of flowering is crucial for their adaptation and exploitation in an agricultural context (Skøt et. al., 2011), thus, the flowering time has a major influence on the quality of fodder and is an important feature for the production of seeds by fodder plant growers (Byrne et. al., 2009).

Although *Lolium perenne* has a global distribution (Cheplick, 2011), it is a dominant species in temperate grassland ecosystems and covers a wide range of environmental conditions (length of day, humidity, altitude, soil type and chemistry, etc.). Understanding the patterns and magnitude of the genetic diversity is a first step in identifying the site of selection for several ecological traits and also serves as a gateway for gene discovery in other forage species with which it shares considerable synthesis (Blackmore et al., 2015).

Maintaining genetic diversity in grassland forage species is of major importance not only in terms of adaptation potential, but also in terms of productivity and ecosystem services. It has been shown that intra-population genetic diversity can promote the temporal stability of grassland production and also that large-scale genetic variation can be closely linked to the regional productivity of perennial ryegrass-dominated grasslands (Blanco-Pastor et. al., 2018).

It was not until the beginning of the 20th century that varieties of *Lolium perenne* appeared with good agronomic performance, and the growth of this forage species was mainly focused on yield and persistence since the 1970s. Increased emphasis is placed on seasonal dry matter production, seed quality and density.

And another key goal of the perennial ryegrass forage species is to develop more productive and persistent grazing varieties as well as good silo production (McDonagh et. al., 2006). Leaf length is an important feature of forage grasses, and the development of the molecular marker is an opportunity to identify quantitative trait sites (QTLs) and to begin dissecting the genetic regulation of complex traits (Barre et. al., 2009). Reproduction for long leaves or for a high rate of leaf elongation should contribute to an improvement in the intercepted radiation accumulated during regrowth and would be a way to improve the spring dry matter yield, but the seed yield has not improved along with breeding for feed performance.

RESULTS AND DISCUSSION

Selection pressures on seed production criteria applied to the breeding process should improve seed yields without a negative impact on feed performance (Sampoux et. al., 2011). Perennial ryegrass seed yield is low and lacks selection criteria for high seed production, and indirect selection in spaced plants would be effective, but distant plant traits that correlate with seed yield in drilled plots should be identified (Elgersma, 1990).

Genetic improvement of perennial ryegrass is achieved through recurrent intra-population selection and systems based on phenotypic mass selection, complemented by the generation of new populations from interpopulation crosses.

Cultivars are of synthetic populations generated by a random cross-breeding of elite parent plants, and increasing the seasonal and annual level of dry plant yield is an important goal in the reproduction of this species, but nevertheless the rate of genetic gain of dry mass was quite low, between 3 and 4% per decade (Faville et. al., 2018). The continued success of pasture farming depends on supporting programs to grow fodder species that are able to generate improved varieties that respond to climate change and market needs by manipulating the recombination of the genome of these fodder plants. In the last two decades, several studies have been conducted on the behavior of chromosome mating in both diploid and polyploid interspecific hybrids. Taylor & Evans identified in 1977 genotypes of both *Lolium perenne* and *L. temulentum* containing genes that affected the frequency of chiasm in diploid interspecific hybrids ("high" and "low pair" genotypes), both in the presence and absence of B chromosomes. These genes have also been shown to be active in tetraploid hybrids *L. perenne* × *L. temulentum* (Armstead et. al., 1999).

The species has a gametophytic system of self-incompatibility with two sites (S and Z) that were genotyped in a cross between a double haploid plant crossed as a female parent with a normal heterozygous plant. The two locations were mapped to link groups one and two, respectively, according to the *Triticeae* consensus map. There were also associations between the segregation of certain mapping alleles in the S locus region of link group 1 and the mapping alleles in the WG889 / CDO920 loci region of link group 3, which led to significant segregation distortions, but did not found such associations between the Z locus and this region or any other region of the genome (Thorogood et. al., 2002).

In the last 30 years, isoenzyme markers have been widely used to study the genetic structure of plant populations, and population genetic studies have established indirect estimates of gene flow by analyzing differences in allele frequencies at different locations between two or more populations. Genetic flux in forage species can occur through both pollen

and seeds, wind dispersal of pollen is considered to be more important in breeding forage species.

Knowledge of gene flow in forage species is dominated by studies of agricultural situations or experimental fields, but little is known about the genetic flow and genetic structure of forage species in natural populations (Warren et. al., 1998). Global metabotyping, metabolic phenotyping, can provide opportunities to identify all chemical components, followed by modeling their combined effects on digestibility or other complex traits. High-yield metabolism provides the power to analyze the natural metabolic variations of known and new molecules between and within populations, but also the precise detection of associated genes, becoming a powerful platform used to investigate genetic diversity at the metabolic level, to attract associations between phenotypes metabolic and morphological features, to identify genetic loci or to clone genes that govern the accumulation of important biological metabolites (Cao et. al., 2017).

Tetraploid hybrids between perennial fodder species of *Lolium perenne* and *L. multiflorum* have led to stable and successful commercial varieties (Thomas et. al., 2009), being the most ideal forage species used as fodder for animals in the temperate agriculture of the meadows, because they settle and grow quickly, provide very nutritious feed and are easy to digest, which can be transformed into healthy meat but also products of animal origin for human consumption.

However, the use of these feeds is limited because they are not persistent, especially in marginal areas and locations that are subject to summer and winter stress and drought stress (Yamada et. al., 2005), however, survival plant in conditions of easy competition is a quantitative trait that exhibits high variability and high heredity (Auzanneau et. al., 2011). *Lolium perenne* presents has a good ability to recover after strong defoliation by herbivores, however, it is susceptible to a number of foliar diseases, and Crown Rust (*Puccinia coronata f.sp. lolii*) is the most widespread and harmful disease that affects perennial ryegrass, but also infections with stem rust (*P. graminis f.sp. lolii*) affect ryegrass seed producers.

Mandatory reproductive habit of perennial ryegrass leads to high levels of genetic variation and, to a lesser extent, between varieties. Therefore, it is anticipated that conventional breeding for disease resistance will be relatively slow for forage species compared to allogamous species (Dracatos et. al., 2009). To cope with the harmful effects of moisture-deficient stress, plants have developed adaptive mechanisms, including drought tolerance, dehydration evacuation, and improved passive processes, such as hydraulic redistribution.

For perennial forage species to be compatible with their role in agricultural systems, they must often not only tolerate and persist in drought, but also survive the sudden defoliation by animals of their vegetative organs that control the loss. of water by stomatal regulation in dental conditions moderate stress conditions (Hatier et. al., 2014). This species is the best model for studying the association between genes and drought tolerance due to its diploid genetics, available genetic and genomic resources, rapid stress responses and available germplasm collections, and the knowledge gained from studying this species will facilitate the investigation later in other fodder species with more complex genomes, polyploids (Yu et. al., 2013).

Genetic studies for *L. perenne* are needed to understand the extent of intraspecific variation, how diversity is divided in and between populations, and to help deduce phylogeographic patterns. Microsatellite chloroplast markers (cpSSR) have been used successfully to assess the variation and diversity of chloroplast DNA (cpDNA) in a range of other plant species, and cpDNA RFLP restriction fragment length polymorphism markers have

been used to evaluate the phylogeographic structure in wild-*Lolium* populations and to deduce methods and routes of geographical migration of *Lolium* populations (McGrath et. al., 2007).

High quality genetic maps remain a cornerstone of genetics, despite many disadvantages, including a limited representation of the true genetic diversity of a species, and many advances in discovery genetics continue to be made using an almost ten-year time scale, with progress being made in such reference populations by developing genetic maps that are densely populated with genetic markers located in gene regions and sequences characterized in such a way as to allow anchoring to pre-existing or emerging physical maps (Velmurugan et al., 2016). Marker-based genetic mapping has progressed from linkage groups developed largely from restriction fragment length (RFLP) polymorphisms to those developed from combinations of DNA, random amplified polymorphism (RAPD), amplified fragment length polymorphisms (AFLP), and microsatellites / simple, sequence repeats (SSRs).

Although they met their immediate objectives, the lack of a comprehensive set of reference markers limited the number of opportunities to align these maps and therefore the associated feature data produced for various studies (King et. al., 2013). Amplified Fragment Length Polymorphism (AFLP) analysis is an important tool for detecting and quantifying genetic variation in perennial ryegrass, and has been used to measure genetic diversity in *Lolium perenne* and to link intra- and interpopulation variation to breeding history, showing characteristics in consistent with the origins of these varieties. Significant differences in intrapopulation diversity were detected and partial separation of different varieties was observed. Restricted basic varieties, derived from a small number of basic clones, allow almost complete discrimination of closely related varieties (Guthridge et. al., 2001).

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CONCLUSIONS

Perennial ryegrass is one of the most important native species in which significant genetic progress has been made in recent decades. The explanation for this qualitative and productive leap of the new varieties of perennial ryegrass is given by the extremely high intraspecific diversity but also by a great capacity to adapt to very different living conditions.

At present, the aim is to maintain the high intraspecific diversity of this species in order to ensure a good production potential, but especially to ensure the ecosystem functions of the permanent meadows built by the dominant species.

In the future, the selection techniques will allow the obtaining of new varieties that are not necessarily more productive or of a better quality, but the emphasis will be on their capacity.

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