Cytogenetic insights into Festulolium

J. MAJKA1,2*, M. MAJKA1,2, D. KOPECKÝ1, and J. DOLEŽEL1

Czech Academy of Sciences, Institute of Experimental Botany, Centre of the Region Hana for Biotechnological and Agricultural Research, CZ-77900 Olomouc, Czech Republic1
Institute of Plant Genetics, Polish Academy of Sciences, PL-60479 Poznan, Poland2

Abstract

Climate change calls for new methods and plant materials to breed crops adapted to new environmental conditions. Sustainable forage and amenity grass production during periods of severe drought and heat waves during summer, and unequal distribution of precipitation over the year will require drought-tolerant genotypes. However, high-yielding ryegrasses (Lolium spp.), which are the most commonly used grass species, suffer during abiotic stresses. Introgression of drought and heat tolerance from closely related fescues (Festuca spp.) offers an opportunity to develop superior hybrid cultivars to mitigate the negative impact of climate change. Intergeneric cross-hybridization and the development of Festulolium (Festuca × Lolium) hybrids was initiated 100 years ago and resulted in registration of almost one hundred cultivars. For a long time, their genome composition was not known and was debated by breeders and geneticists. In the last three decades, molecular cytogenetic and genomic approaches have enabled their detailed characterization. These studies revealed a gradual replacement of Festuca chromosomes by those of Lolium in consecutive generations leading to an almost complete elimination of Festuca chromatin in the introgression forms. On the other hand, amphiploid cultivars seem to be more stable with the optimal proportions of the Lolium to Festuca genomes at about 2:1. In this mini review, we discuss recent advances in the analysis of the genome composition of Festulolium hybrids with a specific focus on genome (in)stability.

Additional key words: chromosome pairing, Festuca spp., genome balance, genome composition, Lolium spp.

Introduction

Grasslands are one of the largest ecosystems in the world covering about one-third of the Earth’s terrestrial surface and comprising 80% of the agriculturally productive land (Boval and Dixon 2012). Grasses (Poaceae), a family of monocotyledonous plants, encompass cereals, turf, and pasture grasses, and other economical species such as bamboos and energy grass Miscanthus. They are adapted to a full range of environmental conditions, spanning from hot equatorial areas to the coldest regions towards the poles, and from deserts to aquatic habitats. They play an essential role in agriculture, being a major staple for animal diets, and also provide valuable ecosystem services. Grasses reduce water runoff (Macleod et al. 2007), stabilize the soil profile and prevent soil erosion. They also have an aesthetic role and serve as ground cover for cultural and recreational needs such as sport and amenity lawns.

Recently, cultivation of grasses is heavily impacted by the climate change. The last four years were the hottest on record and severe drought periods are more frequent (Trnka et al. 2013, Zahradnicek et al. 2015). Models of future climate predict continuing change in the next few years with a higher frequency of dry and hot periods during summers and more uneven distribution of precipitation over the year (UN Climate Action Summit 2019). Climate change affects humans globally and in response, new market requirements have emerged, especially in agriculture. To mitigate the impact of climate change and to meet new demands, it is necessary to incorporate new strategies into plant breeding to develop new cultivars suitable for future use. The gene pool of each species has its limits of genetic variation, and this variation is regularly narrowed down
even further during cultivar development. Thus, widening of the gene pool and introgression of genes underlying beneficial traits seem a prerequisite for breeding progress and development of cultivars with the ability to withstand future climatic conditions. One of the approaches already applied with considerable success is interspecific (wide) hybridization.

Interspecific hybridization

Interspecific hybridization, frequently accompanied by whole genome duplication (process called allopolyloidization) refers to mating of individuals from different species. Allopolyloidization is widespread in nature and has been an important force in plant evolution and speciation (Soltis and Soltis 2009). Many economically important species are alloploids, including wheat, rapeseed, cotton, and banana (Morgan et al. 2011). Besides these ancient alloploids, which have originated thousands of years ago, recent and ongoing natural interspecific hybridization and allopolyloidization events are known, including Tragopogon and Senecio (Hegarty and Hiscok 2009).

Interspecific hybridization has been used in plant breeding with various aims: 1) merging of entire genomes of parental species to combine their desirable traits (amhiplloid forms), 2) merging of entire genomes of parental species to broaden the gene pools, and 3) introgressions of desirable trait/trait from one (frequently wild) species into elite cultivars of another species (introgression forms). One of the most successful interspecific hybrids synthetically developed is Triticale, a hybrid of wheat (Triticum) and rye (Secale). It combines high yielding property of wheat with the ability to grow in harsher conditions due to abiotic stress tolerance inherited from rye (Arseniuk 2015). Similarly, several agronomically important traits have been transferred from wild relatives into cultivars by wide hybridization such as the soft grain endosperm structure from Aegilops speltoides into wheat (Pshenichnikova et al. 2018), and leaf rust resistance from Brassica carinata into cauliflower (Sharma et al. 2010), black rot resistance from Festulolium glaucescens and and Festulolium arundinacea (introgression forms; Humphreys and Zwierzykowski 2020). However, a recent need for drought tolerance in new cultivars calls for the introduction of different species into the mating schemes. According to Černoch and Kopecký (2020), F. glaucescens and F. mairei are the most promising fescue species for initial hybridization with ryegrasses and the development of resilient Festulolium cultivars.

Mating in such combinations has already been initiated at IBERS (Institute of Biological, Environmental and Rural Sciences, Aberystwyth) and DLF Seeds & Science (Humphreys and Zwierzykowski 2020, V. Černoch, personal communication).

For a long time, the genetic constitution of many Festulolium hybrids remained unknown. Only the availability of molecular methods provided tools for comprehensive investigation of the genome composition of hybrids at either chromosomal, or DNA levels (Thomas et al. 1994, Kopecký et al. 2011). Festulolium hybrids show a unique combination of two features: 1) the similarity between parental Festuca and Lolium chromosomes at the DNA sequence allows for their pairing in meiosis (homoeologous pairing), and, on the other hand, 2) repetitive elements of the two parental species diversified enough for unambiguous identification of the Festuca and Lolium chromosomes in hybrids by the genomic in situ hybridization (GISH) (Fig. 1). Combination of GISH with high-throughput genotyping, e.g., using diversity arrays technology and single nucleotide polymorphism platforms, provides an invaluable tool for tracking genome structure and evolution during the development of new cultivars and for the protection of existing cultivars.

Festulolium cultivars

The wide hybridization approach has also been used in the forage grass breeding. Festulolium hybrids obtained by crossing Festuca ssp. (fescues) with Lolium ssp. (ryegrasses), combine complementary agronomic attributes of the parental species. Ryegrasses are important fodder crops with high seed yield, excel in digestibility and palatability and show highly desirable rapid and intensive spring growth. Fescues, on the other hand, provide traits associated with abiotic and biotic stress tolerance, such as drought tolerance, freezing tolerance, winter hardiness, and resistance to fungal diseases (Thomas and Humphreys 1991, Jauhar 1993, Plažek et al. 2018). To date, 78 Festulolium cultivars have been released worldwide – 33 developed by the amphiploid breeding and 45 resulting from the introgression breeding (Humphreys and Zwierzykowski 2020). Amphiploid cultivars are developed by interventing of F₁ hybrids followed by selection of hybrids with about equal proportions of parental chromatin. On the other hand, introgression cultivars originate from an interspecific F₁ hybrid (frequently created from parents of different ploidy), followed by one or more backcrosses to one of the parents. This results in the forms morphologically close to recurrent parent, but with one or a few improved characteristics introgressed from the other species.

Festulolium cultivars are produced from diverse intergeneric hybrids. The most common cross combinations are L. multiflorum × F. pratensis (amhiplloid forms) and L. multiflorum × F. arundinacea (introgression forms; Humphreys and Zwierzykowski 2020). However, a recent need for drought tolerance in new cultivars calls for the introduction of different species into the mating schemes. According to Černoch and Kopecký (2020), F. glaucescens and F. mairei are the most promising fescue species for initial hybridization with ryegrasses and the development of resilient Festulolium cultivars.

Mating in such combinations has already been initiated at IBERS (Institute of Biological, Environmental and Rural Sciences, Aberystwyth) and DLF Seeds & Science (Humphreys and Zwierzykowski 2020, V. Černoch, personal communication).

For a long time, the genetic constitution of many Festulolium hybrids remained unknown. Only the availability of molecular methods provided tools for comprehensive investigation of the genome composition of hybrids at either chromosomal, or DNA levels (Thomas et al. 1994, Kopecký et al. 2011). Festulolium hybrids show a unique combination of two features: 1) the similarity between parental Festuca and Lolium chromosomes at the DNA sequence allows for their pairing in meiosis (homoeologous pairing), and, on the other hand, 2) repetitive elements of the two parental species diversified enough for unambiguous identification of the Festuca and Lolium chromosomes in hybrids by the genomic in situ hybridization (GISH) (Fig. 1). Combination of GISH with high-throughput genotyping, e.g., using diversity arrays technology and single nucleotide polymorphism platforms, provides an invaluable tool for tracking genome structure and evolution during the development of new cultivars and for the protection of existing cultivars.

Homoeologous chromosome pairing and recombination

It is a general feature of wide hybrids that chromosomes from the parental species (homoeologues) do not pair and recombine in meiosis. The absence of homoeologous chromosome pairing can be a consequence of the DNA sequence dissimilarity or the presence of a genetic system(s) that prevent such pairing. Several meiotic regulators have been identified in alloploids including Ph1 (pairing homoeologous 1) in wheat (Riley and Chapman 1958,
Sears and Okamoto 1958) and PrBn (pairing regulator in Brassica napus) in rapeseed (Jenczewski et al. 2003). There are exceptions to the no-pairing rule in wide hybrids, several such hybrids have been identified where homoeologous chromosome pairing does occur, such as Allium and Lilium hybrids (Van Heusden et al. 2000, Khan et al. 2009). Similarly, promiscuous pairing of the Festuca and Lolium chromosomes has been observed in Festulolium hybrids, indicating high pairing affinity and interchangeability of homoeologous chromosomes from these two genera, and the absence of a meiotic regulator (Humphreys and Pasakinsiene 1996, Zwierzykowski et al. 1998). This feature does lead to extensive meiotic recombination and enormous genetic variability among the progeny, but also to their genomic instability.

Compared to other wide hybrids in plants, the frequency of homoeologous chromosome pairing and recombination in Festulolium is extraordinarily high and in some combinations almost reaches the level of homologous pairing. The actual frequency differs among hybrid combinations. Zwierzykowski et al. (2008) observed 9:1 ratio of homologous vs. homoeologous pairing in tetraploid F. pratensis × L. perenne hybrids. In L. multiflorum (Lm) × F. glaucescens (Fg) hybrids, 8.54 paired Lm-Lm arms, 7.83 Fg-Fg arms and 4.09 associations between homoeologous Lm-Fg arms were observed (Kopecký et al. 2009), similarly to the results of Morgan et al. (2001), who reported the 5:1 ratio. Detailed analysis of tetraploid F1 hybrid of L. multiflorum × F. arundinacea indicated a possible association between the phylogenetic distance separating the parents and the frequency of homoeologous chromosome pairing (Kopecký et al. 2009).

The extent of homoeologous chromosome pairing seems to be affected by the proportion of the total numbers of chromosomes from both parents and by competition for pairing partners. Kopecký et al. (2008) studied the frequency of homoeologous chromosome pairing in monosomic and disomic substitution lines of F. pratensis chromosome(s) in tetraploid L. multiflorum and found that the observed frequency of homoeologous pairing was slightly lower than random in disomic lines (where two F. pratensis and two L. multiflorum chromosomes were present in each orthologous group) suggesting a slight preference for homologous pairing. On the other hand, perfectly normal pairing of homoeologues was observed in monosomic lines (where only a single F. pratensis chromosome was present).

Frequent homoeologous chromosome pairing in Festulolium leads to extensive recombination of the parental genomes via intergeneric chromosome translocations (Thomas et al. 1994, Pasakinsiene et al. 1997, Humphreys et al. 1998). The translocation breakpoints in the recombinad Festuca-Lolium chromosomes are fairly evenly distributed along the chromosome arms, from the centromere to the telomeres, but with infrequent recombination at the most distal and proximal regions (Zwierzykowski et al. 1998, 1999). Accordingly, Kopecký et al. (2010) reported the highest frequency of homoeologous recombination in the interstitial to distal parts of the chromosomes. Recombination cold spots (regions with decreased frequency of recombination) were found in the pericentromeric and centromeric regions, and also in the subtelomeric and telomeric regions (the most distal segments representing 10% of the chromosome length) (Kopecký et al. 2010). It is worth noting that both parental species of the analyzed hybrids, i.e., L. multiflorum, F. arundinacea, and F. pratensis are known to have localized distal chiasmata (Rees and Dale 1974, Karp and Jones 1983) so in hybrids, the patterns of crossing over change quite drastically.

A high level of homoeologous pairing may suggest that a meiotic regulator such as the wheat Phl is not present in Festulolium hybrids. This may not be entirely true. Jauhar (1975) concluded that F. arundinacea possesses a diploid-like pairing regulator. Subsequently, this regulator was identified in all broad-leaved fescues of the Schedonorus subgenus (Jauhar 1975, 1993, Kopecky et al. 2009). The system, however, differs from the Phl, it is hemizygous-ineffective, or haplo-insufficient (Jauhar 1993). As hemizygous-ineffective it is non-functional in the F1 hybrids, such as Lolium × F. arundinacea. This haplo-insufficiency hampers its direct utilization in stabilization of hybrid genomes and one may expect reactivation of its function only after the locus doubling. The origin of this system remains unknown. However, Kopecký et al. (2009) showed that F. arundinacea inherited it from F. glaucescens, one of its progenitor, rather than from F. pratensis, the other progenitor.

**Genome balance and stability of hybrids**

In general, the fertility of allopolyploids relies on regular meiosis, and meiotic irregularities, such as multivalent formation, reduce fertility and may lead to complete sterility. This is not an issue in Festulolium. Despite the...
formation of quadrivalents and meiotic irregularities leading to frequent aneuploidy (up to 80% in cvs. Hostýn and Perseus), fertility is high and seed set is sufficient for commercial production (Ghesquiere et al. 2010, Kopecký et al. 2017).

Another issue affecting the extent of use of Festulolium in the grass business is the stability of hybrid genomes and the potential for the elimination of chromatin of one of the species in consecutive generations of sexual reproduction. It has been observed that the Lolium chromatin prevails in the Festulolium hybrids (Zwierzykowski et al. 1998, 2006, 2011, Kopecký et al. 2006, 2019, Książczyk et al. 2015, Majka et al. 2018a, 2019). Zwierzykowski et al. (2006, 2011) observed slow and gradual replacement of the Festuca chromosomes by those of Lolium in consecutive generations of F. pratensis × L. perenne hybrids (Fig. 2). As this was observed in breeding materials, it was not entirely clear if the gradual elimination of the Festuca was a natural or a selection-induced process. A comparison of unselected and selected F2 - F4 progenies of F. pratensis × L. perenne verified process as natural and independent of selection, suggesting the dominance of the Lolium chromatin over that of Festuca (Zwierzykowski et al. 2012). Similarly, J. Majka et al. (2018) observed a decreasing number of Festuca chromosomes across the F2 - F8 generations of F. pratensis (4x) × L. perenne (4x) together with increasing proportion of rearranged Festuca chromosomes (with translocated Lolium segment). Interestingly, Majka et al. (2019) observed no preference in the transmission of either Festuca or Lolium alleles to the subsequent generations of F. pratensis × L. perenne hybrid using inter-simple sequence repeat (ISSR) markers. However, that results might have been compromised by the dominant character of the ISSR markers. Similarly, all amphiploid Festulolium cultivars analyzed to date show a higher number of chromosomes of Lolium origin compared to those from Festuca (Zwierzykowski et al. 1998, Kopecký et al. 2005, 2006).

Genome composition of Festulolium seems to reflect the phylogenetic relationship of the parental species. Thus, cv. Lueur developed from a L. multiflorum × F. glaucescens hybrid had fewer recombined chromosomes than cultivars developed from L. multiflorum × F. pratensis hybrids (Kopecký et al. 2006). One of the possible explanations is that of a closer relationship of L. multiflorum to F. pratensis than to F. glaucescens. Differences in the genome composition can also mirror different breeding strategies. Closely related cvs. Perun and Perseus (L. multiflorum × F. pratensis) differ in their genome compositions, which is consistent with their breeding history. Perun is the oldest Czech L. multiflorum × F. pratensis cultivar with more equal proportion of the parental genomes. On the contrary, Perseus was developed by selection of plants from Perun, primarily for use in Western Europe and with high seed yield, late heading date, and high dry-matter yield. Thus, its genome composition with a higher proportion of the Lolium chromatin can be expected (Kopecký et al. 2017). Cv. Spring Green has the lowest proportion of the Festuca chromatin among all amphiploid cultivars of L. multiflorum × F. pratensis. It was developed from intercross of cvs. Kemal, Elmet, Prior, and Tandem, and the small amount of Festuca chromatin could be a consequence of the fact that cv. Kemal does not carry any Festuca chromatin detectable by GISH (Kopecký et al. 2006).

Genome stability differs between amphiploid and introgression cultivars of Festulolium (Kopecký et al. 2019). While amphiploids display relatively stable genome composition and no further shifts towards Lolium genome, elimination of introgressed segment(s) has been observed in the introgression forms. Stabilization of the hybrid genome in amphiploid cultivars is observed at about 2:1 proportion of Lolium vs. Festuca chromosomes (Kopecký et al. 2017). This ratio probably creates optimal combinations of parental alleles and the highest heterosis. On the other hand, introgression cultivars appear to be highly unstable and a reversion to the parental (Lolium) forms may be completed even within four generations of multiplication, unless the introgressed segment confers a strong selective advantage (Kopecký et al. 2019). In some cultivars, the Festuca chromatin was not detected in any individual analyzed (Kopecký et al. 2006).

Importantly, the rate of elimination of Festuca chromatin is different for different chromosomes. King et al. (2013) estimated the transmission rates of parental chromosomes in consecutive generations of seven monosomic substitution lines developed from hybrids between Loli perenne and Festuca pratensis. They found a much higher transmission of complete Lolium chromosomes compared to complete Festuca chromosomes in the successive generation after the backcross of diploid monosomic substitution lines of L. perenne × F. pratensis (13L+1F), the proportion was 89:11, instead of expected 1:1) to Lolium parent. Unfortunately, the authors did not indicate the parental origin of the translocated chromosomes and therefore, the overall Festuca chromatin elimination could not be assessed from their study. However, chromosomes 2F, 4F, 5F, and 6F were eliminated more frequently than the remaining three Festuca chromosomes. Similarly, Kopecký et al. (2019) found that chromosome 5F...
was eliminated more frequently than other Festuca chromosomes in tetraploid monosomic L. multiflorum × F. pratensis substitution lines.

From the breeder’s point of view, the mode of operation of the mechanisms causing shift in genome composition is far from a trivial detail, as it determines the ease of transfer of a chromosome segment with the trait of interest to the progeny and its proper transmission to subsequent generations.

Conclusions

Growing number of new Festulolium cultivars as well as the interest among growers demonstrate that Festulolium has become an integral part of the grass industry. Festulolium cultivars are grown throughout the world and their role and diversification of their uses will likely keep expanding along with the global climate change impacts. We envisage three main tasks for the future Festulolium research and breeding: 1) development of a platform for high-throughput and cheap determination of genome composition, cultivar identification, and legal protection to replace the time-consuming and labourious GISH method, and the costly (per plant, not per datapoint) DArTseq method, 2) finding appropriate combinations of parental species and proper genome balance between Festuca and Lolium for different climatic conditions to increase the potential of Festulolium, and 3) identification of the chromosome pairing regulator in polyploid fescues as a prerequisite to develop new and stable Festulolium cultivars with rescue-derived tolerance to abiotic stresses. A close collaboration between the research and breeding should secure a rapid integration of the new knowledge into breeding programs to mitigate the impact of climate change by developing resilient and high-yielding Festulolium cultivars.

References


Humphreys, M.W., Pasakinskiiene, I.: Chromosome painting to locate genes for drought resistance transferred from Festuca arundinacea into Lolium multiflorum. - Heredity 77: 530-534, 1996.


