Biotechnological Approaches of Forage Crop Improvement

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Article history:
Received 29 July 2012
Accepted 09 September 2012
Available online 23 December 2012

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The improvement of forage crops through biotechnological approach has started in late eighties and has made remarkable headway at the global level. The various biotechnological tools include molecular techniques for understanding the genetic structure of the plants, inserting foreign genes directly into the plant genome, in-vitro regeneration of plants from any plant part. A number of techniques such as embryo rescue, micro-propagation, androgenic haploid plant production and creation of novel variations help at one or more steps involved in conventional breeding methods. These techniques save time and energy required for conventional methods. Further, the plants developed through these techniques do not attract attention of those who are against the genetically modified organisms.

Progress in developing interspecific hybrids of berseem at the Indian Grassland and Fodder Research Institute (IGFRI), Jhansi, India has also been made. Regeneration of the plantlets from reproductive parts such as anther results in haploid plant production. Hence, the process is very effective in developing plants with double set of genome in the otherwise tetraploid tropical grasses.

Biotechnological approach offers opportunities for creation of novel variations in forages which as such are not possible through conventional methods. The various means of creating variation in forage grasses and achievement are somaclonal variation, somatic hybridization, genetic transformation, etc. Artificial introduction of some foreign gene in the plant genome is genetic transformation. Insertions of genes may be by chemical, electrical, physical or micro-projectile transfer. In grasses, the success achieved so far has been limited and successful transformation has been reported only in a few perennial grasses, viz. Lolium, Festuca, Agrostis, Dactylis, Paspalum and Dichanthium species. There are several molecular techniques, viz. restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), random amplified polymorphic DNA (RAPD) and isozymes that may be used from time to time for characterization of germplasm, cultivar identification, detection of hybrids and genetic mapping, quality trait loci (QTL) identification and gene tagging. The molecular characterization of agriculturally important plants including forage crops and weeds is equally important because, through the transformation techniques, the genes identified from any plant or living organism can be transferred to the target species on account of similarity in DNA sequence across various species and genera.
Characterization of germplasm is one of the most important aspects, especially in the context of the changing scenario with regard to Plant Biodiversity Act. Presently, forage germplasm characterization is mainly on isozyme basis. There is a need to classify forage germplasm in two objectives—first, for developing DNA fingerprints and second, for identifying the duplicates in the germplasm. It is desirable that the forage crop varieties are also subjected to molecular characterization in order to avoid any dispute regarding use of germplasm in the coming years. The major problem encountered with these molecular markers of the forage species is that most of the cultivars are synthetic populations and variability exists within the population. However, the efforts have been made for characterizing the varieties based on RAPD, RFLP markers and discrimination between the varieties can be based on gene frequencies.

Genetic mapping and gene tagging in forage species have not been attempted much. For single gene control traits, gene tagging is important but in case of forages most of the desirable agronomic traits are multi-genic and hence are difficult to tag. There are also opportunities for improving the amino acid balance of the plants used in intensive feeding production systems. At the Commonwealth Scientific and Industrial Organization (CSIRO), Australia, incorporation of gene normally expressed in sunflower for sulfur amino acid to lupin (deficient in sulfur amino acid) increased sulfur amino acid content of transgenic lupin grain, resulting into higher animal productivity through usage of lupin meal. Another important area needing attention of biotechnologist is the development of stress tolerance, both biotic and abiotic, in fodder crops and range species through gene pyramiding of identified QTLs. Encouraging results have been obtained in different crops in identifying the genes and regulatory elements.

Selection of germplasm for salinity tolerance is very important for efficient utilization of such degraded lands. The germplasm can be screened in vitro at two levels: (i) seedling level and (ii) tissue or cell level. In-vitro studies have shown significant interspecific and intraspecific variation among legume and clover species for salt tolerance. Intracultivar variation had been identified in lucerne (Medicago sativa) and white clover (T. repens). In case of post fertilization incompatibility barriers, embryo rescue is most effective and successful technique.

In grass breeding, identification of genes controlling apomixis is an area that can pay good dividends. Identification and cloning of these genes can well be patented and can also be used in transferring in other cross-pollinated crops for fixing heterosis and thus save on the cost on account of producing hybrid seeds every year. Although this aspect is receiving global attention, success has been very limited till date. Another important aspect is the identification of sexual lines in grasses. There is need to develop reliable molecular techniques for screening of the grass species for the presence of sexuality, as it would accelerate the breeding process in such grasses as many of these plants could be used in crossing. The plants with better agronomic traits and apomixis can be selected and advanced for developing better varieties.