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Micro satellite marker development in genetics

M Jewel*

Department of Genetics, University of Cambridge, London, UK

*Corresponding author. E-mail: jewel@gmail.com

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DESCRIPTION

Microsatellites are made up of straightforward tandemly repeated di- to tetra-nucleotide sequence motifs that are bordered by distinct sequences. They are significant as genetic markers because the Polymerase Chain Reaction (PCR) can be used to quickly and cheaply assess them, they are co-dominant, and they can detect high levels of allelic variation. With the relative frequency of various repeats decreasing with increasing motif size, research from screening a rice genomic library suggests that there are approximately 5700–10000 microsatellites in rice. Microsatellites are evenly distributed among rice's 12 chromosomes, according to a map made up of 120 of them. There are five multiple copy primer sequences that have been found that can be linked to distinct chromosomal regions. As of right now, these Simple Sequence Length Polymorphisms (SSLPs) in rice give enough genome coverage to be helpful for marker-assisted selection in breeding, genotype identification, gene and Quantitative Trait Locus (QTL) analysis, screening of large insert libraries, and genotyping analysis. Up to 25 alleles have been identified at a single locus in studies of allelic diversity, which support the reliability of amplification in wild relatives of *Oryza sativa*. one might anticipate that as more mapped SSLP markers become available, they will supplement already-existing RFLP and AFLP maps, improving the precision and power of genome analysis in rice. In recent years, crop breeding has made considerable use of genomic techniques, particularly molecular markers, to analyse genome dynamics.

In order to comprehend genome variation in crop species at the DNA, RNA, and protein level, a number of modern genomics technologies, including Next Generation Sequencing (NGS), high-throughput marker genotyping have emerged as potent tools. These technologies promise to shed light on the manner in which gene(s) are expressed and regulated in cells and to reveal metabolic pathways involved in trait of interest for breeders, not only in model or major-but even in under-resourced crop species that were traditionally thought of as "orphan" crops. In addition, new genetic techniques like advanced-backcross QTL (AB-QTL) analysis, Introgression Libraries (ILs), Multi-Parent Advanced Generation Intercross (MAGIC) population, and association genetics can be used to capture genetic variation for a species that is present not only in the cultivated genepool but also in landraces and wild species. Through molecular breeding techniques like Marker-Assisted Back Crossing (MABC), Marker Assisted Recurrent Selection (MARS), and genome wide selection, the gene or genomic region responsible for the trait of interest identified either through conventional linkage mapping or can be introgressed or pyramided to develop superior genotypes.

Alfalfa has complicated inheritance, in part because meiosis is an auto-tetraploid process. The fact that alfalfa produces diploid gametes has a significant impact on how it reproduces. The genetics of alfalfa are discussed here in terms of autotetraploid meiosis, and an attempt is made to connect autotetraploid genetics to breeding practises. While neglecting the possibility of twofold reduction, preferential pairing, and nondisjunction, it gives a debate based on the assumption that chromosomal segregation in alfalfa occurs at random. Alfalfa is extremely sensitive to inbreeding, regardless of the cause of inbreeding depression and heterosis. Despite the difficulties of autotetraploidy, alfalfa breeding has been quite successful. When one or a few simply inherited features need to be introduced to an otherwise acceptable variety, backcross breeding has been done.

CONCLUSION

The resequencing of whole plant genomes or the sampling of complete transcriptomes are now more quickly, cheaply, and thoroughly possible thanks to next-generation sequencing methods. Instead of sequencing one genome at a time, we want to sample the genetic diversity within and between germplasm pools by sequencing hundreds or even thousands of related

genomes. Thousands of genetic variants may now be recorded within huge populations thanks to genetic variation tracking methods that are both accurate and efficient. In this paper, we highlight a few key areas, including the extensive development of molecular markers for wide crosses and alien introgression, linkage mapping, association mapping, transcript profiling, population genetics, and organellar genome assembly for which these technologies are expected to advance crop genetics and breeding.