DNA polymorphism

in molecular characterization of horticulture crop

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Introduction

A molecular or DNA marker is a variation in the DNA nucleotide sequence across different species or individuals that is close to or intricately linked to a target gene that manifests a trait. The locus or loci of the molecular marker within the chromosomes may have a known or unknown genomic location. Notably, features connected to the expression or function of the linked gene or genes are unaffected by molecular or DNA markers. If differences known as polymorphisms exist in the marker nucleotide sequences between or among individuals or species, DNA markers may be useful for identifying individual genotypic differences in the same or different species.

DNA polymorphism-based markers are now often used to genotype people, infer details about the genetic makeup of germplasm collections, identify synonymy, and determine kinship. Microsatellites (or SSRs) and SNPs are the DNA markers that are best suited for this scope among the many DNA markers (RFLP, RAPD, AFLP, SSR, ISSR, SAMPL, S-SAP, and others) proposed in the literature of the past two decades, providing the robust data necessary in forensic disputes as well as for intellectual property and patent rights. The opportunities provided by the recent development of sequencing and genotyping platforms, as well as the significance of sport variations in fruit crops, are highlighted in relation to the last component, which deals with essentially derived types. Molecular markers have shown to be effective instruments for evaluating the genetic diversity of populations as well as their genetic divergence from one another. Actually, the area of plant genomics that has demonstrated the most Population genetics has made significant advancements in the utilisation of DNA marker technology. To map Mendelian genes and QTLs, however,

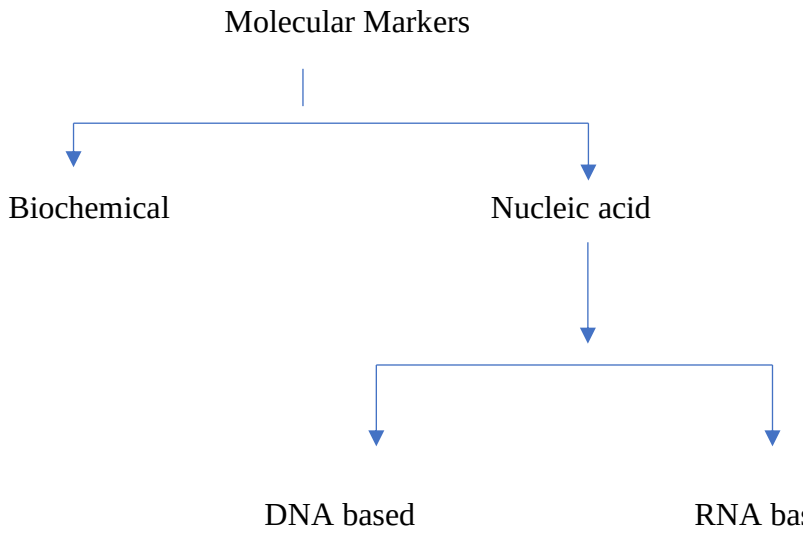
both RFLP and PCR-derived markers have been widely used in plant breeding and genetics.

Landraces are populations with great genetic diversity and adaptability to the anthropological and natural contexts from which they have descended. They serve as both a priceless resource for useful features and an invaluable repository for genotypes with a high degree of co-adaptation the preservation and use of plant germplasm resources, knowledge of genetic variation within local populations and genetic differentiation with breeding stocks is anticipated to have a substantial impact. Natural populations of animals that reproduce vegetatively or by apomixis are polyclonal, consisting of numerous genetically different clones and typically being dominated by a small number of genotypes with favourable adaptations. As a result, genetic variation within populations is spread among clones, and the majority of populations exhibit varying degrees of genotype differentiation.

The genetically related but reproductively independent pure lines that make up landraces of self-pollinated species are mixed together. Due to the presence of fixed genotypes, primarily homozygous for various alleles, in natural populations, genetic as well as phenotypic diversity is primarily apparent among lines.

❖ **Genetic markers can be classified as PCR based and hybridization based.**

- **PCR based genetic markers**: RAPD, ISSR, EST-SSR, microsatellite, CAPS etc.
- **Hybridization based genetic markers**: RFLP, VNTRs, in which targeted gene is digested with restriction enzymes and then hybridized with RFLP probe.



Genetic markers and germplasm characterization

Genetic characterization of the germplasm that is most useful for scientific study and crop development has been done; the basis for this characterization is genetic markers. Determining systematic links, the crucial foundation for organising data on genetic diversity and divergence, is one of the most significant responsibilities for genetic markers.

Additionally, genetic markers aid in accurately classifying germplasm accessions. wild 4x Ipomoea germplasm accessions kept ex situ were not I. *trifida* (Kunth) G. Don f. but rather a 4x race of the

typically 6x sweet potato [*I. batatas* (L.) Lam.] based on morphological indicators (calyx and corolla features). ex situ management per se, genetic marker data may potentially disclose the genetic profiles and populational genetic structure of freshly acquired germplasm. One notable exception to this generality is an integrated isozyme, pigment, morphological, and agronomic marker assessment that yielded recommendations for optimally managing West African okra germplasm [*Abelmoschus esculentus* (L.) Moench].

Genetic markers and genetic enhancement

Last but not least, genetic markers may facilitate genetic improvement, also known as pre-breeding, by allowing alien material to adapt to local conditions while retaining its essential genetic contributions or by allowing yield-enhancing, high-value trait-enhancing, or both genes to be introgressed into already adapted material. Genetic markers' most significant contribution to "base-broadening" campaigns to date has been the a posteriori proof that such initiatives can result in locally adapted germplasm that retains significant amounts of the unadopted germplasm's genome.

DNA markers in PGR characterization

DNA markers are essential tools for assessing plant species diversity. When selecting a technology, affordability of the hardware, throughput, convenience, and ease of assay development are crucial considerations (Rafalski & Tingey, 1993). For PGR characterization, a variety of marker techniques are available, including RAPD, AFLP, SSR, and SNP. Sequence data can be used to infer associations utilising databases based on a large number of potential characters. The benefits of RAPD are its speed, low cost, arbitrary primer use, lack of initial genetic or genomic information requirement, and need for relatively small amounts of target DNA. The absence of prior knowledge of the identity of the amplification products, which in turn causes issues with repeatability and co-migration, are disadvantages of this approach (Lowe et al. 1996). The AFLP technique's main benefit is the high quantity of polymorphisms it produces as compared to other markers. Since AFLP can distinguish between individuals within a population, these analyses, gene-flow experiments, and plant variety registration can all benefit from the technique. In contrast to other markers like RAPD, the AFLP experiment methodology and post-run data analysis takes a lot of time.

Conclusion

The most common and widely applied molecular markers for crop breeding and improvement have been explained in terms of their principles and technique. A total of thirty-four markers have been presented, making this presentation one of the largest and most thorough overviews of molecular markers ever made. The well-known Arbitrarily Amplified DNA (AAD) marker methods, the microsatellite-based marker methods, and the retrotransposon-based molecular marker approaches make up the majority of the molecular marker techniques addressed. Indeed, molecular or DNA marker approaches offer a wealth of molecular genomic research opportunities. However, molecular markers should be used as complementary techniques i. genomics and plant breeding rather than being seen as a replacement for other agro-morphological or biochemical markers.

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