DS Reviews of Research in Life Sciences
Volume 1 Issue 1, 32-37, Apr - Jun 2025
ISSN: XXXX-XXXX

Original Article

Role of Molecular Markers-Based DNA in Providing Information about Genes Association Traits in Plant Germplasms

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Received: 08 April 2025; Revised: 08 May 2025; Accepted: 07 June 2025; Published: 30 June 2025

Abstract - Molecular markers-based DNA is used to screen germplasms by maps to identify, mine and tap important allele's genes due to their dominant and co-dominant nature, reliability, simplicity and high polymorphic information content that are generated by either enriching DNA fragments containing sequences or direct screen size of selected genomic libraries with complementary oligonucleotides. Therefore, they applied in many aspects of plant breeding and plant pathogen control as marker repertoire novel approaches, such as functional genomics and molecular breeding under adverse environmental conditions, to identify genomic regions that determine genetic diversity and population structure for more rapid and precise development of plant improvement strategies.

Keywords - Molecular markers-based DNA, Genetic diversity, Genetic map, Functional genomics, RFLP.

1. Introduction

Molecular markers-based DNA are highly polymorphic, neutral and reliable. They are independent of the environment and plant development stages [1]. There are three groups in which they offer genotype surrounding loci information (group-1) uses Restriction Fragment Length Polymorphism (RFLP), (group-2) based on PCR such as RAPD, SSR, etc., and (group-3) uses amplicon polymorphism and restriction fragments (DArT) or nucleotide Sequence Polymorphism (SNP) [1, 2]. In addition, they are associated with phenotypic traits, allowing for early selection of superior progenies from breeding populations; this significantly expands the scope of plant breeding programs by exhibiting genetic relationships, variability and genetic mapping information through monitoring of alien DNA introgression into progenies [3, 4] providing marker-assisted selection with particular traits and regions of genomic DNA [5-7]. Consequently, they play a significant role in genetic characterization and breeding for many plant species [8], which are inherited in a Mendelian fashion [9-11]. Sum of all, molecular markers-based DNA is

used in genomic prediction for selection because it accelerates genetic gain strategy integrated with precise promising traits to find superior alleles within germplasms.

2. Principal Classes of Molecular Markers-Based DNA

2.1. RFLP

Recorded as first-generation hybridization-based markers with probes, by digestion with various restriction enzymes to produce fragments of different lengths by electrophoresis followed by X-ray.

2.2. AFLP

Use two distinct enzymes to cleave DNA and bind fragments to complementary adaptors by PCR amplification using arbitrarily oriented primers of homologous sequences to adaptors extended in 3′ and visualize results using acrylamide gel. Therefore, only fragments that have different restriction sites at each end are amplified. Hence, this marker has non specific locus on hybridization.

2.3. RAPD

Usually refers to 10-mer oligonucleotides, which can identify polymorphism when information about amplified sequences in complementary sequences hybridization is lacking. So, it must have 60% to 70% (G+C) content without self-complementary ends. In RAPD markers, PCR enables amplification when two sites of hybridization are near each other in the same direction. Therefore, if the DNA of two individuals varies at hybridization sites, polymorphism of presence/absence bands is identified on gel electrophoresis to calculate polymorphic loci.

2.4. SSR

Spread across the genome. Their polymorphism is in a variation of number repetition units developed expressed sequences tags. Therefore, this marker represents a functional molecular marker in highly polymorphic specific loci. Hence, database searches and other in silico analyses used it to determine the putative function.

2.5. DArT

Based on selective amplification of subset amplicons produced by a pair of restriction enzymes for genomic DNA breakdown. So, label, fixed, and hybridization fragments are bound to the DNA chip. Therefore, if it generates a specific amplicon, the chip will recognize it as a complement, leading to a positive signal. While no hybridization signal is obtained if the amplicon is lacking.

2.6. SNP

Denotes nucleotide polymorphism in four nucleotides at specific loci between alleles in the form of biallelic variation. Thus, most variability in quantitative traits is associated with SNP in coding sequences, leading to potential synonymous without changing amino acid sequences. Therefore, significant polymorphisms arising from variations in amino acids can be recognized if they are not synonyms. Hence, SNP serves as a substitute or complementary for map linkage in Genome Wide Association Studies (GWAS), which examine many traits statistically throughout the entire genome to discover gene candidates in the form of association mapping.

3. Genetic Diversity

Refers to differences in gene combinations across and within germplasms [12-14]. Taxonomical level of analysis becomes important when using molecular markers-based DNA to evaluate genetic diversity in the form of construction molecular phylogenies [15] using priming sites that are distributed throughout the genome with a number of polymorphisms approximately 2.5 × 10-9 × G, where G is the size of the haploid genome in base pairs, depending upon primer sequence, genomic sequence and genome size. For instance, the haploid genome of lettuce is about 2 × 109 base pairs in size, and according to the above formula, the reaction should produce five to ten bands

depending upon the degree of genetic heterozygosity. Whereases, as previously mentioned, calculation predicts no bands for most primers for smaller genome sizes such as E. coli (G = 4 × 106 base pairs). Therefore, with the use of molecular marker-based DNA, genetic diversity provides information about gene association with crucial and complex traits (Figure 1) [16] in the results of recombination, genetic drift, migration and selection [17].

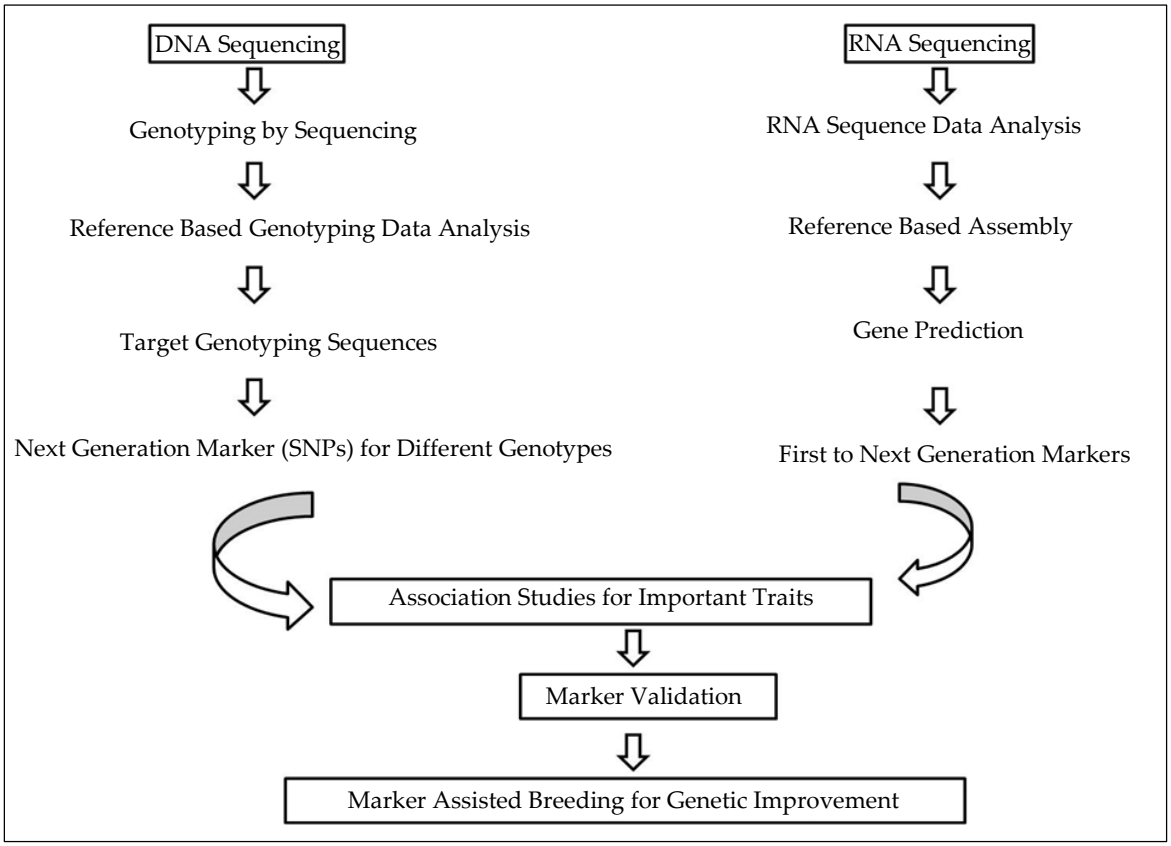

Fig. 1 Finding markers assisted selection by genomic resources

4. DNA Maps Based on Molecular Markers

Complex traits are usually conferred by numerous loci around single regions of genomic DNA, indicating by both association multi-trait single marker and single trait multi-marker offer alternative methods of mining alleles throughout the gene pool. Once a large number of molecular markers-based DNA are available, genomic selection will be an appropriate technique for staking beneficial maps for significant alleles of associated traits [18], leading to the development of millions of novel genes in germplasms [19]. Consequently, it is possible to associate single markers with heritable traits [20, 21]. Therefore, maps based on molecular markers-based DNA become helpful in identifying, analyzing and modifying significant genes that are responsible for both simple and complex traits [22], generating useful data regarding genetic variability [23, 24].

5. Functional Genomics

Conjunction with bioinformatics tools and functional analysis to find gene function through genomics, proteomics and metabolomics approaches (Figure 2). Therefore, it acquires environmental and physiological data into a functional network for gene identification to understand biological systems [25]. Additionally, transposon elements, insertion sequence, DNA repetitions, introns and DNA rearrangement are retaining changes in gene expression response to external factors [26]. As a result, functional genomics is now recognized as the preferred genomics-assisted breeding strategy that can be used in germplasm optimization [27].

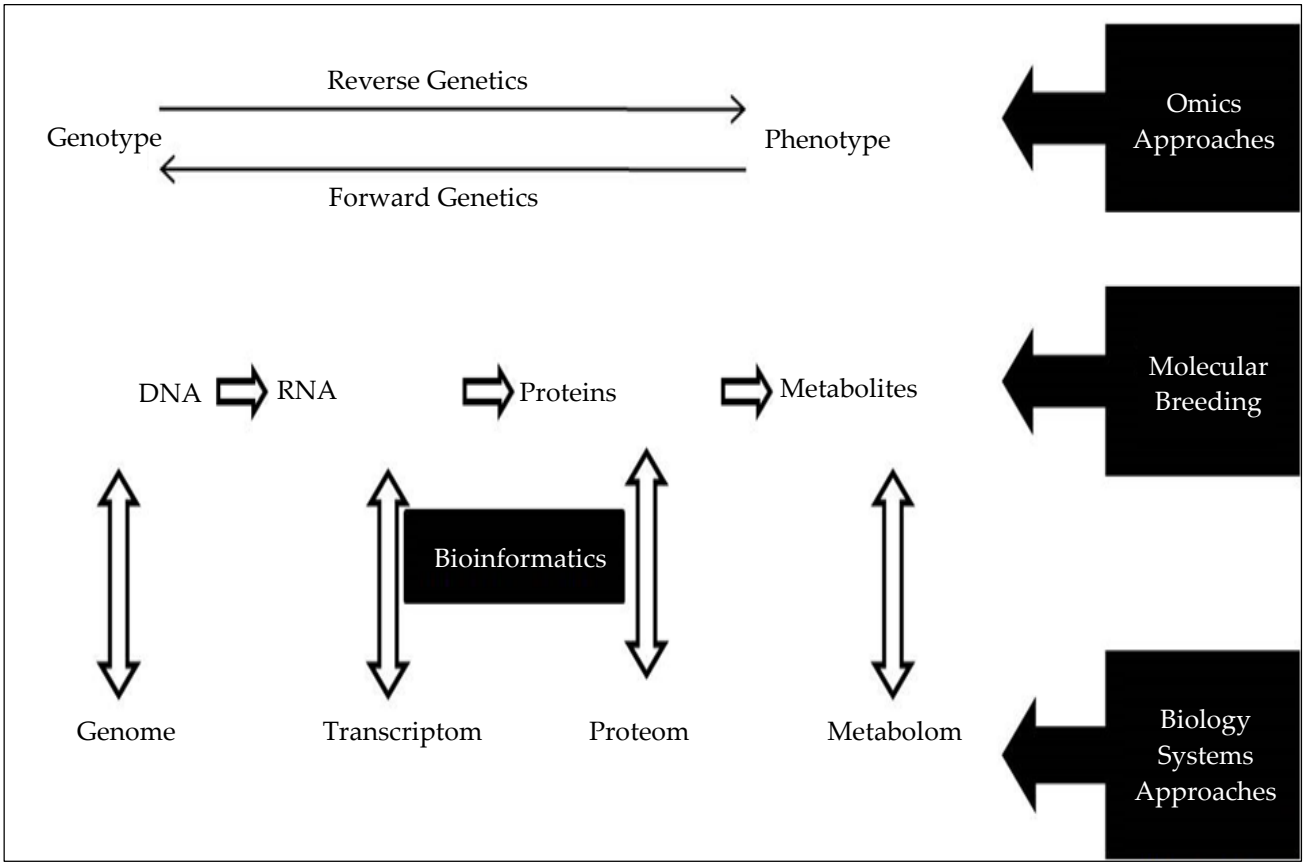

Fig. 2 Moving information from genomic, transcriptome, proteomic and metabolomics toward genetic enhancement

6. Conclusion

Identification of novel genes has become possible through molecular markers-based DNA, which increases selection accuracy and shortens the duration of phenotypic evaluation by facilitating gene introgression into desirable genetic backgrounds, which are useful for mapping rare alleles. Consequently, molecular markers-based DNA is employed reliably for novel genes among and within germplasms, which could be a significant breeding program milestone.

Acknowledgements

This work is supported by the Genetics Department, Faculty of Agriculture, Sohag University, Sohag, Egypt.

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