

Molecular Markers: An Excellent Tool for Genetic Analysis

Faheema Khan*

Department of Botany and Microbiology, College of Science King Saud University, Saudi Arabia

*Corresponding author: Faheema Khan, Department of Botany and Microbiology, College of Science King Saud University, Riyadh 11495, Kingdom of Saudi Arabia, Tel: 9661-46-70-000; E-mail: drfaheemakhan@gmail.com

Rec date: Apr 09, 2015; Acc date: Apr 24, 2015; Pub date: Apr 29, 2015

Copyright: © 2015 Khan F. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Commentary

The exploitation of DNA polymorphisms by an ever-increasing number of molecular marker technologies has begun to have an impact on animal and plant genome research and breeding. A large number of different molecular techniques for genetic diversity analysis are available and each of them differs in its informational content. These techniques not only helped in understanding the different structure and behavior of species genome, but also revolutionized and modernized the ability to characterize genetic variation. Identification of marker linked to useful traits has been based on complete linkage maps and bulked segregation analysis. Markers are therefore used to identify traits, their inheritance and characterize germplasm. Wide range of DNA marker technologies, which require a small amount of DNA has become very useful for screening large population of segregating progenies.

Presently 11 different molecular marker methods: restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), inter-simple sequence repeats (ISSRs), sequence characterized regions (SCARs), sequence tag sites (STSs), cleaved amplified polymorphic sequences (CAPS), microsatellites or simple sequence repeats (SSRs), expressed sequence tags (ESTs), single nucleotide polymorphisms (SNPs), and diversity arrays technology (DArT) as well as use of the molecular marker in the present day agriculture and plant breeding programmes.

Qualitative and quantitative information on diversity is an essential aspect of many fields in biology. The use of so-called molecular markers, however, facilitates all these processes, since it can accelerate the generation of new varieties and allow connection of phenotypic characters with the genomic loci responsible for them.

DNA based markers replaced the enzymes markers in germplasm identification, characterization as well as in gene tagging because of its plasticity, ubiquity and stability. These are phenotypically neutral, and offer great scope for improving the efficiency of conventional research methods by carrying out trait based selection. Besides these markers are not regulated by the environmental conditions and can be detected at any stage of animal/ plant growth.

The idea of using genetic markers appeared very early in literatures [1,2] and its development [3-12] have greatly improved our understanding in biological sciences. They are now widely used to track loci and genome regions in several crop-breeding programmes, as molecular markers tightly linked with a large number of agronomic and disease resistance traits are available in major crop species in Jain et al. and Gupta and Varshney. They can also be utilizing in gene introgression through backcrossing, germplasm characterization, genetic diagnostics, characterization of transformants study of genome organization and phylogenetic analysis in Jain et al. All these

properties make molecular markers indispensable for plant improvement.

Ever since their development, genetic markers are constantly being modified to enhance their utility and to bring about automation in the process of genome analysis. The existence of various molecular techniques and differences in their principles and methodologies require careful consideration in choosing one or more of such marker types [13]. They may differ with respect to important features, such as genomic abundance, level of polymorphism detected, locus specificity, reproducibility, technical requirements and financial investment. The most appropriate genetic marker has depended on the specific application, the presumed level of polymorphism, the presence of sufficient technical facilities. Genetic markers fall into one of the three broad classes: those based on visually assessable traits (morphological and agronomic traits), those based on gene product (biochemical markers), and those relying on a DNA assay (molecular markers).

Molecular markers should not be considered as normal genes, as they usually do not have any biological effect, and instead can be thought of as constant landmarks in the genome. A molecular marker is defined as a particular segment of DNA that is representative of the differences at the genome level. Molecular markers may or may not correlate with phenotypic expression of a trait

Molecular markers offer numerous advantages over conventional phenotype based alternatives as they are stable and detectable in all tissues regardless of growth, differentiation, development, or defense status of the cell are not confounded by the environment, pleiotropic and epistatic effects.

Characteristics of an Ideal Molecular Marker

An ideal molecular marker should have all or at least some of the following characteristics:

- It should be Multiallelic.
- It should be easily available.
- It should be easy to assay.
- It should be non-time consuming.
- It should be highly reproducible.
- It should be phenotypically neutral.
- It can produce exchangeable data.
- It should show polymorphism.
- It should show co dominance inheritance so as to allow discrimination between homozygous and heterozygous.
- It should be non-epistatic.

A series of different molecular markers system, which became available during the last two decades, can be broadly classified into three classes.

- The first generation molecular markers, including RFLPs, RAPDs, and their modification.
- The second-generation molecular marker including SSRs, AFLPs, and their modified forms.
- The third generation molecular markers: ESTs, SNPs and many more.

Several approaches are available for identifying markers linked to trait of interest. Molecular marker maps are now available for most important species. Molecular markers have been looked upon as a tool for a large number of applications ranging from localization of a gene to improvement of species by marker assisted selection. They have also become extremely popular for phylogenetic analysis adding new dimensions to the evolutionary theories in plant and animal research.

References

1. Sax K (1923) The Association of Size Differences with Seed-Coat Pattern and Pigmentation in *PHASEOLUS VULGARIS*. *Genetics* 8: 552-560.
2. Wexelsen H (1933) Linkage between quantitative and qualitative characters in barley. *Hereditas (Lund)* 17: 323-341.
3. Botstein D, White RL, Skolnik M, Davis RW (1980) Construction of a genetic linkage map in man using restriction fragment length polymorphisms. *American Journal of Human Genetics* 32: 314-331.
4. Nakamura Y, Leppert M, O'Connell P, Wolff R, Holm T, et al. (1987) Variable number of tandem repeat (VNTR) markers for human gene mapping. *Science* 235: 1616-1622.
5. Welsh J, McClelland M (1990) Fingerprinting genomes using PCR with arbitrary primers. *Nucleic Acids Res* 18: 7213-7218.
6. Williams JG, Kubelik AR, Livak KJ, Rafalski JA, Tingey SV (1990) DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. *Nucleic Acids Res* 18: 6531-6535.
7. Caetano-Anolles G, Bassam BJ, Gresshoff PM (1991) DNA amplification fingerprinting: a strategy for genome analysis. *Plant Molecular Biology Reporter* 9: 292-305.
8. Akkaya MS, Bhagwat AA, Cregan PB (1992) Length polymorphisms of simple sequence repeat DNA in soybean. *Genetics* 132: 1131-1139.
9. Akopyanz N, Bukanov NO, Westblom TU, Berg DE (1992) PCR-based RFLP analysis of DNA sequence diversity in the gastric pathogen *Helicobacter pylori*. *Nucleic Acids Res* 20: 6221-6225.
10. Zietkiewicz E, Rafalski A, Labuda D (1994) Genome fingerprinting by simple sequence repeat (SSR)-anchored polymerase chain reaction amplification. *Genomics* 20: 176-183.
11. Vos P, Hogers R, Bleeker M, Reijans M, van de Lee T, et al. (1995) AFLP: a new technique for DNA fingerprinting. *Nucleic Acids Res* 23: 4407-4414.
12. Jaccoud D, Peng K, Feinstein D, Kilian A (2001) Diversity arrays: a solid state technology for sequence information independent genotyping. *Nucleic Acids Res* 29: E25.
13. Semagn K, Bjornstad A, Skinnes H, Maroy AG, Tarkegne Y, et al. (2006) Distribution of DArT, AFLP, and SSR markers in a genetic linkage map of a doubled-haploid hexaploid wheat population. *Genome* 49: 545-555.