Potential Applications of Molecular Markers in Plant

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Submission: February 02, 2018; Published: March 14, 2018
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Abstract

Marker may be defined as “Mark of identification”. Molecular markers have several advantages over the traditional phenotypic and biochemical markers in plant. The main uses of DNA markers in agricultural research such as Cultivar identity/assessment of ‘purity’/ Hybrid Testing, Genetic Diversity Analysis, Genetic Linkage Map Construction, Mapping of quantitative trait loci (QTLs), Map based cloning of genes, Mapping of mutations, Marker-assisted selection (MAS), Marker assisted backcross breeding (MAB), Marker-assisted pyramiding, Mapping major genes, Characterization of transformants etc. DNA markers are widely accepted as potentially valuable tools for crop improvement in plant.

Keywords : Molecular marker; Mapping; MAS; Pyramiding; QTLs

Introduction

Molecular marker may be defined as any site (locus) in the genome of an organism at which the DNA base sequence varies among the different individuals of a population. Such markers generally have no apparent effect on the phenotype of the individual. Genetic markers represent genetic differences between individual organisms or species. Generally, they do not represent the target genes themselves but act as ‘signs’or ‘flags’. Genetic markers that are located in close proximity to genes (i.e. tightly linked) may be referred to as gene ‘tags’. DNA (or molecular) markers a type of genetic markers, which reveal sites of variation in DNA [1,2].

Potential Applications in Plant

Cultivar identity/assessment of ‘purity’/Hybrid Testing

Markers can be used to confirm the true identity of individual plants. The maintenance of high levels of genetic purity is essential in cereal hybrid production in order to exploit heterosis. In hybrid rice, SSR and STS markers were used to confirm purity, which was considerably simpler than the standard ‘grow-out tests’ that involve growing the plant to maturity and assessing morphological and floral characteristics [3].

Genetic Diversity Analysis/ Population genetics

DNA markers are useful in the assessment of genetic diversity in germplasm, cultivars and advanced breeding material using several techniques, such as restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP) and microsatellites. In general, type II markers such as RAPDs, microsatellites, and AFLPs are considered to be non-coding. Such markers have found widespread use in population genetic studies [4]. SSR marker based genetic diversity analysis of modern rice varieties and coastal landraces [5]. RAPD-PCR (randomly amplified polymorphic DNA polymerase chain reaction) for a study of the genetic diversity within and among 20 populations of Geum reptans, an outcrossing clonal plant species in the Swiss Alps [6].

Genetic Linkage Map Construction

Genetic linkage maps an important tool in genetic and genomic research. DNA markers can be used for constructing genetic linkage maps [7]. A 2275-marker genetic map of rice (Oryza sativa L) covering 1521.6 cM in the Kosambi function has been constructed [8]. A universal core genetic map developed for rice [9].

Mapping of quantitative trait loci (QTLs)

Quantitative trait locus (QTL) analysis is a statistical method that links two types of information-phenotypic data (trait measurements) and genotypic data (usually molecular markers)-in an attempt to explain the genetic basis of variation in complex traits [10-12]. The first high-density genetic linkage map for P. haitanensis was constructed and fifteen QTLs associated with six economically important traits were identified [13]. Genetic Linkage Map Construction and QTL analysis of Two Inter specific Reproductive Isolation Traits in Sponge Gourd [14].
Mapping of simple traits/ Mapping major genes

Molecular markers are used in molecular biology and biotechnology to identify a particular sequence of DNA in a pool of unknown DNA. Genes conferring resistance to the bacterial blight e.g. xa5 [15], Xa2 [16], Xa25(b) [17] and Rice Blast resistance genes e.g. Pi24 [18].

Mapping of mutations

Genetic mapping of a mutation-defined gene is the first step toward isolating and cloning the corresponding normal gene and ultimately identifying its encoded protein. Genetic mapping using next-generation sequencing that combines single nucleotide polymorphism discovery, mutation localization and potential identification of causal sequence variants [19]. CandISNP is a user-friendly application that will aid in novel discoveries from forward-genetic mutant screens [20].

Map based cloning of genes

Map-based cloning or positional cloning is the process to recognize the genetic basis of a mutant phenotype with the help of linkage to markers whose physical location in the genome is known. Map-Based Cloning of the gene associated with the soybean maturity locus E3 [21]. Map-based cloning of BPH26 revealed that BPH26 encodes a coiled-coil-nucleotide-binding-site-leucine-rich-repeat (CC-NBS-LRR) protein [22]. Isolation of Pto gene in tomato [23] and Xa-1 gene in rice [24]. Positional cloning of several QTL including Brix9-2-5, fw 2.2, Hd1, Hd6, FRI in tomato, Rice and Arabidopsis. MOC-1 is 1st gene isolated for Rice tillering using Map based cloning approach [25].

Marker-assisted selection (MAS)

Once tightly linked markers have been identified to the genes or QTLs, they should be used for MAS. DNA markers are used in the marker assisted or marker aided selection. MAS have several advantages over straight selection. Ribaut & Betran [26] proposed involving MAS at an early generation was called single large-scale MAS (SLS–MAS). MAS for simply inherited traits are gaining increasing importance in breeding programs, allowing an acceleration of the breeding process [27].

Marker-assisted pyramiding

Pyramiding is the simultaneous integration of multiple genes/QTLs into a single genotype. DNA markers may facilitate selection, without phenotyping. The most widely application of pyramiding is the integration of multiple disease resistance genes into a plant to develop “durable” or stable resistance to a disease. For example, Hitralmani et al. [28] combined genes originating from three parents for rice blast resistance using RFLP, STS markers. The combination of quantitative resistance was the pyramiding of a single stripe rust gene and two QTLs using SSR marker [29].

Marker assisted back cross breeding (MAB)

Backcrossing is a plant breeding method most commonly used to incorporate one or a few genes into an adapted or elite variety. The use of DNA markers in backcrossing greatly increases the efficiency of selection. The bacterial blight resistance genes xa5, xa13 and Xa21 foreground selection by STS marker [30], Sub1 QTL select by phenotyping and SSR [31].

Molecular taxonomy and evolution

DNA markers are useful in the study of crop evolution. The development of increasingly informative molecular markers has allowed for detailed investigations of the evolution of a number of crops e.g. identification of crop progenitors [32-36].

Identification of individuals

More recently molecular markers, such as SNPs and simple sequence repeats (SSRs) have been developed for the selection of fragrant rice [37].

Conclusion

Molecular markers are widely used in crop improvement due to its simplicity, reproducibility and precise location. It is not affected to environmental effect reduce breeding cycle. Recently many markers are available, out of this SSR, SNP are mostly used in breeding programme and other study. Application of DNA marker technologies molecular also other areas of plant biology like systematics, population genetics, evolutionary biology and conservation genetics, advances in genomics and identification of the wild progenitors of domestic species, the establishment of geographic patterns of genetic diversity.

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How to cite this article: Lincoln M, Sunil K V, Saugato S, Jawaharlal K. Potential Applications of Molecular Markers in Plant. Curr Trends Biomedical Eng & Biosci. 2018; 12(4): 555844. DOI: 10.19080/CTBEB.2018.12.555844.