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Review Article

Assessment of plant genetic variations using molecular markers: A review

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Abstract

Climatic changes affect various organisms, including plant species, becoming unfavorable for the environment and socioeconomic value, prompting an increase in activities related to plant resources conservation. The successful conservation of plant genetic resources depends on the proper identification and characterization of plant material. One of the notable developments in genetic conservation is the use of molecular markers for assessing the conservation and use of plant genetic resources. This review is devoted to the use of molecular marker techniques for genetic assessment of plant genetic variations. Development in these techniques provides smooth, reliable, and effortless ways for assessing known and unknown taxa, between and within species. These techniques provide a revelation to researchers on taxonomical and evolutionary questions which were not possible earlier. The polymerase chain reaction-based molecular markers give rise to various novel techniques due to the simplicity and high reproducibility of the methods. Examples including a combination of earlier techniques, such as restriction fragment length polymorphism, random amplification of polymorphic DNA, simple sequence repeat, intersimple sequence repeats, single nucleotide polymorphism, and amplified fragment length polymorphism, have been used for plant genetic variations and polymorphism studies. Progress in the advanced high-throughput sequencing techniques or next-generation sequencing technologies has been rapidly utilized to study genetic diversity broadly and to identify suitable genes and alleles rapidly. These techniques offer a practical resolution to the challenges in crop genomics. This review explains the recent advances in the molecular marker techniques, along with the advantages, uses, and limitations. Each technique differs in resolving the genetic variations and polymorphism in plant species.

Keywords: Molecular markers, DNA fingerprinting, assessment of diversity, genetic variation.

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Assessment of plant genetic variations using molecular markers: A review

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ABSTRACT

Climatic changes affect various organisms, including plant species, becoming unfavorable for the environment and socioeconomic value, prompting an increase in activities related to plant resources conservation. The successful conservation of plant genetic resources depends on the proper identification and characterization of plant material. One of the notable developments in genetic conservation is the use of molecular markers for assessing the conservation and use of plant genetic resources. This review is devoted to the use of molecular marker techniques for genetic assessment of plant genetic variations. Development in these techniques provides smooth, reliable, and effortless ways for assessing known and unknown taxa, between and within species. These techniques provide a revelation to researchers on taxonomical and evolutionary questions which were not possible earlier. The polymerase chain reaction-based molecular markers give rise to various novel techniques due to the simplicity and high reproducibility of the methods. Examples including a combination of earlier techniques, such as restriction fragment length polymorphism, random amplification of polymorphic DNA, simple sequence repeat, intersimple sequence repeats, single nucleotide polymorphism, and amplified fragment length polymorphism, have been used for plant genetic variations and polymorphism studies. Progress in the advanced high-throughput sequencing techniques or next-generation sequencing technologies has been rapidly utilized to study genetic diversity broadly and to identify suitable genes and alleles rapidly. These techniques offer a practical resolution to the challenges in crop genomics. This review explains the recent advances in the molecular marker techniques, along with the advantages, uses, and limitations. Each technique differs in resolving the genetic variations and polymorphism in plant species.

1. INTRODUCTION

Climatic change is one of the most considerable challenges in today's world. In the recent decades, the rise in temperature and frequent floods, especially in the midlatitude, decreased global crop productivity [1]. Plant breeders have been provided with an excellent opportunity to develop advanced cultivars with better desirable characteristics by using plant genetic resources [2]. Genetic material can be conserved for years together, by capturing and storing the plant genetic diversity in the plant genetic resources format, such as gene banks, in the repository and DNA library. The exciting advances in molecular genetics in recent years have provided specialists involved in the plant

resources conservation with novel techniques for reputable and straightforward identification of diversity of the plant species [3]. Insufficient knowledge about the present genetic variations in plants and how to use it is one of the crucial motivations for conservation. Proper use of plant genetic resources, as well as the selection of high productivity and resistant variations, requires accurate identification of their accession [4].

Today, the central question for researchers is the translation of natural genetic polymorphism (genotype) into the phenotype and how plants adapt to the environmental changes. The 1,001 Genomes Project has addressed all these and related questions by providing high-resolution insight into global epigenetic and genetic polymorphisms in the model plant *Arabidopsis thaliana* [5] to help in the identification of specific genes with the help of genetic markers. The genetic marker concept is an adage, with Gregor Mendel in the late nineteenth century using a phenotype-based marker in his experiments. The limitations of these

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