

Applications of Mutagenesis processes in Crop Development

Michael Simic*

Department of Veterinary Science, Nihon University, Fujisawa, Japan

DESCRIPTION

Mutant breeding and plant mutations play an important role in enhancing genetic diversity for desired traits in different food crops. Induced mutation is one of the most effective tools used for the identification of key regulatory genes and molecular mechanisms. The development of new varieties with improved agricultural properties such as high stress tolerance (biotic and abiotic stress) and bio-fortification is a promising approach. In addition, various mutation methods have been used to study the evolutionary relationship, as well as for the genetic improvement of many organisms, including microorganisms, animals, and plants. Technological advances in molecular biology have revived mutation breeding, making it more effective than previously thought.

There are several induced mutation methods available for plants. Over the past century, physical mutations such as fast neutron, UV, X-ray and gamma radiation and N-methyl-N-nitrosoria (MNU), sodium azide, Hydrogen Fluoride (HF), Methyl Methanesulfonate (MMS), or Ethyl Methyl (ethyl), were extensively explored. Furthermore, biological mutations include agrobacterium and transposon-dependent chromosomal integration. EMS-induced mutation is the most effective method and, therefore, is commonly used in crop cultivation to develop better crop varieties. The three EMS-induced stay-green mutants and wild-type for drought tolerance in rice. The study reported a novel functional stay-green mutant that exhibits a better yield index under irrigation and drought conditions that can be further used to develop higher yielding pathways. In addition, induced mutagenesis is applied to improve the medicinal plants due to their high demands. For example, Nigella sativa mutation lines were produced by induced mutagenesis and further classified by proteomic analysis to identify proteins associated with plant height, seed yield, and thymouquinone content in the mutation lines. Identified proteins are mostly involved in carbon metabolism, signaling mechanisms, cell differentiation, carbohydrate catabolism, and secondary metabolism; therefore, the identified proteins can be further utilized for the improvement of medicinal plants.

Recently, the use of rapid neutron bombardment has become popular due to the large amount of removal (sometimes >1 Mb) and the large number of irreversible double wounds as well as the mutation of a chromosome in a gene. The benefits of fast neutron mutagenesis to develop a resource for gene removal lines. Such resources help to maintain functional genomics and reverse genomics in plants. Fast neutron mutagenesis has been used successfully in arabidopsis, soybeans, rice and peanuts. However, it is more difficult to develop a faster neutron mutagenesis facility than traditional gamma radiation mutagenesis. Significant efforts are needed to identify the different sources that can be used effectively to obtain highintensity rapid neutron radiation.

Furthermore, genetic inactivation has been used successfully in determining the function of unknown genes in many plant species. In this process, sensible and antisense copies of the target gene were introduced to inactivate the endogenous genes. In other words, the DNA sequence (T-DNA, transposition or retro transposon) was introduced to modify and tag the gene. The role of embedding mutations in rice improvement is an available T-DNA and transposition mutant resources in rice, accelerating the study of functional genomics in rice.

With the advancement of next generation sequencing (NGS) technologies, it has become convenient and costly to detect millions of mutations in a short period of time. Recently, for example, high-output next-generation sequencing-based methods such as MutMap, MutMap-Gap, MutChromSeq, Mut-Ren-Seq, and full-genome sequencing-based mutation mapping have been developed. These methods involve high application and costly tools to identify the desired genes in less time. The next-generation sequence-based mutation mapping approaches to the most crucial novel to accelerate mutation breeding in Tomato. Although physical and chemical-induced mutations accelerate crop improvement, these methods are still under-emphasized due to the random transformation, cost, and time effect. However, genetic modification procedures are more tedious and require the regulation of costly regulations as well.

Correspondence to: Michael Simic, Department of Veterinary Science, Nihon University, Fujisawa, Japan, E-mail: Michael@simic.jp

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