

Molecular TILLING and Eco-TILLING: A Review of Effective Tools for Mutant Gene Detection and Mutant Profiling in Plants Genomics

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Abstract

The discovery of single nucleotide polymorphisms (SNPs) in the gene of interest, whether due to induced mutation or natural nucleotide variation, is a valuable method for improving features in in-plant functional genomics. TILLING stands for Targeting Induced Local Lesions In Genomes, and it is a reverse-genetics method that uses the ability of induced mutation caused by an efficient mutagen to target and recover lesions in certain genes. TILLING detects point mutations in regions of interest by combining chemical mutagenesis with PCR-based screening. It has a high throughput, is low in cost, and may be utilized on a variety of organisms. The method detects induced or natural DNA polymorphisms in a gene of interest using a mismatch-specific endonuclease. TILLING's key principles involve creating an EMS-mutagenized population, using PCR primers to target a gene of interest, and looking for rare mutants among numerous individuals. TILLING has progressed from proof-of-concept to production in the last six years, with the launch of publically available services for Arabidopsis, maize, lotus, and barley. Several other plant species, including wheat, have had pilot-scale initiatives completed [13]. The TILLING methods have been altered for the identification of natural nucleotide diversity; a process known as Eco-TILLING. Eco-TILLING, like TILLING, is a broad technique that has been used on a wide range of plants, including Arabidopsis and poplar. Mapping, association analysis, mutation profiling, and biodiversity are some of the core uses of ECO-TILLING. The capacity to determine the spectrum of variation and genetic mapping based on linkage association analysis is TILLING's key benefit. However, the procedure is also cost-effective. TILLING has several drawbacks, including a poor rate of mutation induction and the need for skilled labor.

Keywords: TILLING, Eco-TILLING, Endonuclease, Mutation profiling, Mapping Association Analysis.