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MutTILL: Development of induced mutant resources for genome-wide mutations screening by using next generation sequencing technologies

Reddaiah Bodanapu, Krishna Lalam, Durga Khandekar, Navitha Kokkonda, Sivarama Prasad Lekkala and Vijay Bhaskar Reddy Lachagari

AgriGenome Labs Pvt. Ltd, Hyderabad, INDIA

Presenting author: reddaiah.b@aggenome.com

Abstract

Mutagenesis based TILLING (MutTILL) is a reverse genetic approach that can be applied in plant research and breeding programs to broaden the genetic variability and for the identification of novel mutant alleles in specific genes of interest with improved varieties. MutTILL method is non-transgenic approach, further removing the barriers in marketing new varieties. It has been widely adapted to different species across genera to study the gene function. Traditionally, TILLING work flow comprises of mutagenesis, followed by scanning of amplicon region of interest and cleavage by mismatch specific endonucleases at the site of mismatch, and detection either by using gel electrophoresis or by high resolution melt analysis. However, with the advent of improving sequencing technologies and the decrease in cost, TILLING can be made less laborious and faster using next-generation sequencing-based approaches. Nevertheless, sequencing the whole genome of thousands of mutagenized individuals remains expensive. But the NGS-based technologies can be applied to TILLING, either in the form of whole exome sequencing or by using target re-sequencing. We at AgriGenome Labs are working on development of NGS-based TILLING platforms in various crop species like Chilli, Cotton, Rice, and Tomato, among others with the plan to further expand to other important crops. Currently, a large mutagenized population of the above crops is at different stages of development. The developed mutant populations will help in the identification of novel mutations for various biotic and abiotic stresses. We are aiming to provide complete and customized solutions to research institutes, companies and individuals for developing and providing genetic variations for their crops of interest with improved trait quality.

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