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Delimit Fungal Virulence via TILLING for the Conservation of Medicinal Plants

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Abstract

To facilitate the identification of mutation, a high-throughput reverse genetic approach i.e. TILLING (Targeting Induced Local Lesions in Genomes) has been successfully used in different plants and animal species in the past decade. This technique requires *a priori* gene information and determines allelic variations by forming heteroduplexes in an artificial mutant library construction. Regardless of species ploidy level and genome size, this can be an effective approach for functional genomic studies not only in crop plants (proven by research) but also in another eukaryotic system such as fungi. Application of TILLING in fungal partners will help researchers to focus on pathogenicity genes; consequently it will help plant breeders to develop effective strategies for the control of pathogen and will help in the enhancement of secondary metabolite concentration in medicinal plants.

Key Words: Fungi; Genome; Genetic variations; Mutagenesis; Polymorphism

1. Introduction

Crop breeding can be performed for enhancing nutrient content, secondary metabolites concentration and for other economically important products. A pre-requisite to elucidate the role of genes, metabolic pathways and governing development phenomenon is organism's genome information which provides access to the relatively complete gene directory for a species. With the advancement in functional genomics via high-throughput sequencing approaches in the past decade, it is now possible to design transgenic crops of desired traits that can tolerate various biotic and abiotic stresses. Alternatively, scientists have simultaneously progressed in the genomics of microorganisms too (particularly bacteria and fungi) to decode the mechanisms responsible for pathogenesis and disease. Host-pathogen interactions have been studied tremendously to understand the mechanisms that can be utilized or the amelioration of the pathogen pressure and elevate the resistance in crop plants (Agrios, 2004). Thus, DNA information of either plants or fungal pathogen is highly crucial to enhance knowledge on the functions of individual genes and their networks, for defining evolutionary relationship, and for identification of potential candidate genes that can be targeted for crop improvement (Bevan and Uauy, 2013; Barkley and Wang, 2008). Advanced approaches such as next-generation sequencing, pyrosequencing, bioinformatics analysis and single nucleotide polymorphism (SNP) discovery have a profound influence on improvement of crops for food and fuel production (Edwards and Batley, 2010). Simultaneously, availability of fungal genome databases and the information provided by gene expression studies is significantly increasing the number and quality of candidates for TILLING, thus useful for breeding programmes.

Mutagenesis provides a direct link for the identification of genes, their function and phenotypic and biochemical responses of the organisms. Many genetic based strategies such as *Agrobacterium*

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