



Molecular Characterization and Mapping of Stress Resistance Genes Using SNP Platform in Legumes

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Kandiah Pakeerathan

Abstract

Legumes play a vital role in agriculture and food security. Biotic and abiotic stresses are major hurdles for legume production and lower the current productivity per unit area. There is an obligation to accelerate genetic improvement of most food legumes by introducing alleles conferring resistance to pests and pathogens, adaptation to abiotic stresses, and high yield potential. The tapping of potential resistance alleles present in the landraces and wild relatives and its exploitation in legume resistance breeding programs with the aid of next-generation molecular breeding approaches are the quickest ways to develop high-yielding elite legume varieties with long-lasting resistance. This chapter attempts to explore the advanced molecular approaches in germplasm characterization, marker-assisted genomic selection, molecular mapping of biotic stress resistance gene(s)/QTLs using single nucleotide polymorphism (SNP) markers, mining of SNPs using various next-generation sequencing (NGS) platforms, marker-assisted selection, and marker-assisted pyramiding of resistance genes in elite germplasm. This chapter also highlights major qualitative/quantitative resistant trait/loci and linked SNP markers, and recently published highly saturated SNP(s) linkage/consensus map information of 13 important food legumes. Genetic, genomic, and marker information elucidated in this chapter will be a guide to the researchers and students who are interested in advanced molecular plant breeding and to address the global challenge of ensuring food security in the face of scarce natural resources and unpredicted climate change-induced stress.

K. Pakeerathan (✉)

Department of Agricultural Biology, Faculty of Agriculture, University of Jaffna, Kilinochchi, Sri Lanka

e-mail: pakeerathank@univ.jfn.ac.lk

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