

IDENTIFICATION AND FUNCTIONAL CHARACTERIZATION OF STRIGA RESISTANCE GENES IN RICE (*Oryza sativa* L.)

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ABSTRACT

Rice, the second most important cereal crop globally, is mainly grown for food and is a staple food for more than half of the world's population. In sub-Saharan Africa, biotic stresses and lack of resources are major production constraints to farmers. An estimated yield loss of 16% attributed to weed infestation is recorded in the region with *Striga* spp. being the most prominent cause. Striga are members of the Orobanchaceae family with 89 genera containing 2061 species. However, *Striga hermonthica* (Del.) Benth. and *Striga asiatica* (L.) Kuntze are of the greatest economic importance in the region. Cultural control methods such as crop rotation, intercropping, different planting techniques, management of soil fertility and seed based technologies, have been tried against Striga with only modest gains. Striga resistance in crops has been attributed to differences in a few genetic regions within the genomes. Resistance or susceptibility to Striga in crops is influenced by genes. The growth regulating factors have been suspected to play a role during striga infection. This study attempts to identify and characterize Striga resistance genes in rice. Cloning of these genes, screening their function in transformed rice roots under laboratory conditions, stable rice transformations with putative resistance genes and assessment of the transgenic rice will be done. *Agrobacterium rhizogenes* will be used for induction of transformed hairy roots in composite plants carrying identified putative Striga resistance genes for analysis of Striga resistance in rice. Real time quantitative polymerase chain reaction will be used for analysis of expression of Striga resistance genes during infection with *Striga hermonthica*. *Agrobacterium tumefaciens* will be used for stable transformation of rice with putative Striga resistance genes and the resistance screened under laboratory conditions. For effective management of striga it is important to understand how it overcomes host defense mechanisms. This will be done through identification of effector genes whose products neutralize host defenses. Rice is an excellent model for genetic studies. Thus identification of Striga resistance genes will help in breeding and development of resistant rice as well as other crops such as maize and sorghum that are seriously affected by Striga in the sub Saharan Africa.