专论与综述

稻瘟病菌致病性的分子遗传学研究进展

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由稻瘟病菌引起的稻瘟病是水稻生产上危害最为严重的真菌病害,对世界粮食生产造成巨大损失。稻瘟 病菌成功侵染寄主包括分生孢子萌发、附着胞形成、侵染钉分化和侵染性菌丝扩展等一系列错综复杂的过程,其 中每一环节都是由特定基因控制的。稻瘟病菌与水稻的互作符合经典的基因对基因学说,二者的不亲和互作是无 毒基因与抗病基因相互作用的结果。近几十年来,世界各国的科学家对稻瘟病菌致病性的生物学及其遗传的分子 机制进行了深入的研究。文章就稻瘟病菌致病性的分子遗传学及其遗传变异机制的研究进行了综述,同时对功能 基因的研究方法进行了总结。

稻瘟病菌 致病性 分子遗传学 关键词

分类号 S435.111.41

The Research Progress on Molecular Genetics of Pathogenicity of Rice Blast 相关信息 **Fungus**

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Abstract

Rice blast disease, caused by heterothallic ascomycete Magnaporthe grisea, is one of the most serious fungal diseases of rice throughout the world. The disease attacks rice plants throughout the season and causes severe yield losses. The pathogenesis of M. grisea is due to a complex process that spans the entire life cycle of the pathogen. The process including germination of conidia, formation of appressoria, differentiation of penetration pegs and proliferation of infectious hyphae is controlled by many genes. The interaction between M. grisea and rice is based on the gene-for-gene hypothesis and the defense responses are often activated by the action of the pathogen avirulence (Avr) gene and the host resistance (R) gene. The studies on molecular biology and genetic mechanism of pathogenicity of M. grisea has occupied pathologists and mycologists for several decades. This paper reviews the research progress related to molecular genetics of pathogenicity of the fungus and its genetic diversity and variation, and summarize research methods of the functional genes.

Key words Magnaporthe grisea pathogenicity molecular genetics

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