中国农学通报 2011, 27(第21期8月) 239-245 DOI: ISSN: 1000-6850 CN: 11-1984/S

植物保护—研究报告

稻瘟病菌几丁质结合蛋白的生物信息学分析

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摘要： 为了弄清稻瘟病菌数据库中可能的几丁质结合蛋白的分布及其结构特点，从而为进一步进行编码基因的功能研究打下良好基础。通过生物信息学技术对稻瘟病菌基因组中假定的几丁质结合蛋白的结构域、亚细胞定位及EST等进行分析，同时构建了系统发育树并预测了这些蛋白在不同发育时期和不同组织中的表达特点。结果共得到了23个可能的几丁质结合蛋白，它们在7条染色体上的分布并不均匀；绝大多数的几丁质结合蛋白都定位在胞外。稻瘟病菌几丁质结合蛋白在不同发育时期和不同组织中的表达也各不相同；不同真菌间的几丁质结合蛋白相互交错，它们之间的进化关系十分复杂。

关键词： 生物信息学 稻瘟病菌 几丁质结合蛋白 EST

Bioinformatics Analysis of Chitin Binding Protein Family in Magnaporthe oryzae

Abstract: In order to know the distribution and structural features of hypothetical chitin-binding protein in Magnaporthe grisea database, which would may a good foundation on further research in the encode genes function. In this paper, bioinformatics approaches were used to analysis the domains, subcellular localization EST and phylogenetic tree construction of putative chitin binding proteins (CBP) in the genome of Magnaporthe oryzae, and predicted the gene expression characteristics in different developmental stages and different tissue. In total, 23 putative CBP family proteins were retrieved from the genome, which distributed inequable in seven chromosomes, the majority of CBP were localized in the extracellular. The expression of CBP in different developmental stages and different tissues were different in Magnaporthe oryzae. The chitin binding proteins interlaced between different species fungi, the evolutionary relationship was complicated between them.

Keywords: bioinformatics Magnaporthe oryzae chitin binding protein EST

收稿日期 2011-04-07 **修回日期** 2011-06-16 **网络版发布日期** 2011-09-06

DOI:

基金项目:

国家自然科学基金

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