

## 基于Solexa高通量测序的黄曲条跳甲转录组学研究

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Transcriptome characteristics of *Phyllotreta striolata* (Fabricius) (Coleoptera: Chrysomelidae) analyzed by u  
Illumina' s Solexa sequencing technology

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**摘要** 黄曲条跳甲 *Phyllotreta striolata* (Fabricius) 是十字花科蔬菜的重要害虫, 为深入了解其遗传信息, 本研究应用新一代高通量测序技术 Illumina' s Solexa 平台对黄曲条跳甲成虫的转录组进行测序, 并结合 SOAPdenovo 拼接聚类分析软件, 获取大量的 EST 和挖掘功能基因。本文最终获得了 4 924 条序列重叠群 (contig), 其中包含 2 209 种与黑腹果蝇 *Drosophila melanogaster* 蛋白基因直系同源的独立基因 (unigene) 和 610 种黄曲条跳甲物种特有的 unigene。结合 Gene Ontology (GO) 数据库进行分析, 发现大部分的 unigene 具结合能力 (binding capability) 和催化活性 (catalytic activity); 上百种 unigene 可聚类于生物学过程分类中的配子发生、生殖腺发育和交配行为等重要功能。另外, 结合 KEGG Pathway 数据库分析发现, 共有 363 种 unigene 参与或涉及了 40 种代谢途径, 其中生物钟调控途径和植物次生代谢物途径等相关基因的发现, 有助于深入研究黄曲条跳甲行为发生的内在机理。Solexa 高通量测序技术作为昆虫功能基因组研究的重要手段, 为发掘黄曲条跳甲功能基因发挥了重要作用, 也为在分子水平上研发黄曲条跳甲的防治新策略提供了更翔实的基因信息。

**关键词:** 黄曲条跳甲 Solexa 测序 序列重叠群 独立基因 转录组

**Abstract:** The striped flea beetle, *Phyllotreta striolata* (Fabricius), is an important pest damaging cruciferous vegetables. In order to investigate the profile of gene expression and elucidate the functional genes, we sequenced the transcriptome of the adult of *P. striolata* by Illumina' s Solexa sequencing technology, and analyzed the data of expressed sequence tags (ESTs) by using SOAPdenovo system. A total of 4 924 contigs were obtained including 2 209 unigenes of orthologous genes relating to *Drosophila melanogaster* and 610 species-specific unigenes of *P. striolata* based on Gene Ontology and KEGG databases. We found that most of unigenes contain function domains with binding capacity and catalytic activity. More than 100 unigenes are involved in gamete generation, ovarian follicle cell development and mating behavior. Three hundred sixty-three unigenes may be involved in 40 different metabolic pathways based on KEGG database. The finding that 363 unigenes are involved in regulation pathway of biological rhythm and plant secondary metabolites will be useful to clarify the mechanism of behaviors of this insect such as oviposition rhythm, etc. Moreover, the sequence resources presented in this study provide useful information to develop new strategies to manage this pest.

**Key words:** *Phyllotreta striolata* Illumina' s Solexa sequencing technology contig unigene transcriptome

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