

Diamondback moth genome provides new clues for sustainable pest management

January 13 2013

An international research consortium, led by Fujian Agriculture, Forestry University (FAFU) and BGI, has completed the first genome sequence of the diamondback moth (DBM), the most destructive pest of *brassica* crops. This work provides wider insights into insect adaptation to host plant and opens new ways for more sustainable pest management. The latest study was published online today in *Nature Genetics*.

The diamondback moth (*Plutella xylostella*) preferentially feeds on economically important [food crops](#) such as rapeseed, cauliflower and cabbage. It has developed resistance to against more than 50 insecticides, including DDT, Bt toxins, among others, making the use of chemicals as a control measurement become ineffective. It is estimated that the total cost associated with the damage and management is US\$4-5 billion per year worldwide.

"The completed genome sequencing of DBM will lay a solid foundation for tracking the [evolutionary mechanisms](#) of how an insect evolves to become a successful herbivore that can defense many insecticides." said Professor Minsheng You, Vice President of FAFU and leader of the research team. "The work here also provides an invaluable resource for scientists to better understand the reasons why DBM is such a serious pest and how new strategies can be developed to control [insect pests](#)."

In this study, researchers sequenced the genome of DBM by whole genome shotgun (WGS) and fosmid clones technologies, yielding ~343 Mb draft genome with 18,071 predicted protein-coding genes.

Compared with other sequenced [insect species](#), they found that the diamondback moth possesses a relatively larger set of genes and a moderate number of [gene families](#), suggesting the expansion of certain gene families. Additionally, the genome-based phylogeny demonstrated that DBM was a basal lepidopteran species, which is well supported by its modal karyotype.

Based on the [genomic data](#) generated from ~1,000 male pupae, researchers identified the genome-wide level of polymorphism within the sequenced DBM strain (Fuzhou-S), which may lay the genetic bases for DBM in adapting to various environmental challenges. They investigated a set of genes preferentially expressed at the larval stage that contribute to odorant chemoreception, food digestion and metabolic detoxification. Interestingly, they found that the co-expression of sulfatase modifying factor 1 (SUMF1) and glucosinolate sulfatase (GSS) genes may be crucial for DBM to become a successful cruciferous herbivore.

Insecticide tolerance or resistance may have contribution to the option of detoxification pathway in insect herbivores. In this study, researchers found DBM has a larger set of insecticide resistance-related genes than silkworm (*B. mori*) that had little exposure to insecticide over 5,000 years of domestication. They identified in DBM obvious gene duplications of four gene families that participated in xenobiotic detoxification in insects, including ATP-binding cassette (ABC) transporter families, the P450 monooxygenases (P450s), glutathione S-transferases (GSTs) and carboxylesterase (COEs). Notably, the further analysis highlighted the potential role of ABC transporters in detoxification.

The clever evolutionary trick has allowed DBM to become such a serious pest, and it may play an important role in the development of its ability to detoxify a wide range of chemicals. "Remarkably, it appears that the

very genetic adaptations that allow DBM to detoxify the chemicals in its food plants, and also allow it to develop immunity to the insecticides used against it." commented by Professor Geoff Gurr of Charles Sturt University, Australia, one of the international collaborators.

Professor Jun Wang, Executive Director of BGI, said, "The availability of a reference genome for a species is extremely important in the deeper understanding of its biology and evolution. We are pleased to be part of this consortium and have the first publicly accessible database of diamondback moth genome. I expect we could translate our achievements into real actions for sustainable [pest management](#) in the near future."

More information: The complete genome sequence of diamondback moth is publicly available via visit: www.iae.fafu.edu.cn/DBM

Provided by BGI Shenzhen

Citation: Diamondback moth genome provides new clues for sustainable pest management (2013, January 13) retrieved 21 May 2024 from <https://phys.org/news/2013-01-diamondback-moth-genome-clues-sustainable.html>

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