

A moth genome provides insights into herbivory and detoxification

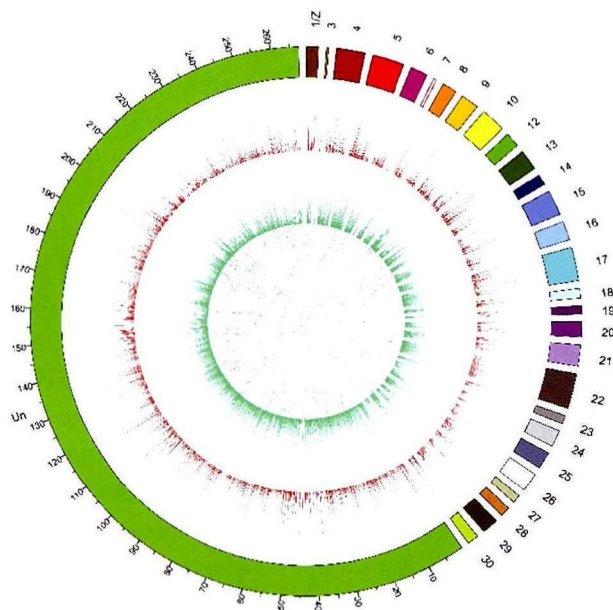
Supported by the National Natural Science Foundation of China, Prof. You Minsheng at Fujian Agriculture and Forestry University and his colleagues published their scientific findings in an article entitled “A heterozygous moth genome provides insights into herbivory and detoxification” in *Nature Genetics* (2013, 45(2): 220—5).

The diamondback moth (DBM, *Plutella xylostella*) tends to be the most destructive pest of economically important food crops such as rapeseed, cauliflower and cabbage. This pest insect has developed resistance to all classes of insecticides, including DDT, and Bt toxins, making it increasingly difficult to control. It is estimated that the total cost associated with the damage and management is US\$ 4—5 billion per year worldwide. Due to the lack of genomic information, however, studies on the genetics and molecular biology of DBM are fairly backward compared with other model insects.

To overcome the difficulty of high-level heterozygosity, the researchers successfully developed and used a novel strategy of incorporating fosmid-to-fosmid and whole genome shotgun for sequencing and assembling, yielding a ~343 Mb draft DBM genome with 18071 predicted protein-coding genes. 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 ~1000 male pupae, the genome-wide level of polymorphism within the sequenced DBM strain (Fuzhou-S) was explored to reveal the genetic bases of DBM in adapting to various environmental stresses. Transcriptome sequencing helped identify the genes preferentially expressed in the midgut of larvae, especially a set of genes that contribute to odorant chemoreception, food digestion and metabolic detoxification. The co-expression of sulfatase modifying factor 1 (*SUMF1*) and glucosinolate sulfatase (*GSS*) genes might be crucial for DBM to become a successful cruciferous herbivore. The analysis of four gene families that are involved in xenobiotic detoxification in insects highlighted the potential role of ABC transporters in detoxification.

The completion of DBM genome will lay a solid foundation for clarifying the mechanisms of how an insect evolves to become a successful herbivore with crucifer specificity and insecticide resistance, and provide invaluable resources for better developing pest management strategies and programs.



Genomic variations of DBM. The outermost circle shows the DBM genome assembly. Scaffolds that could be assigned to linkage groups are joined to generate the partial sequences of 28 chromosomes. The green segment represents the scaffolds that were unable to be assigned (Un). The innermost circle denotes segmental duplications, with connections shown between segment origins and duplication locations. Histograms indicate the number of SNPs (red), and indels (light green).