A Mini-Review: Molecular Profiles of Diamondback Moth (*Plutella xylostella*)

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Abstract *Plutella xylostella* (L.), also known as diamondback moth (DBM), is deemed to be a basal and primitive as well as highly heterozygous insect in the Plutellidae Family of Lepidoptera Order. Diamondback moth diverged about 124 million years ago from two other lepidopterans species, *B. mori* and *D. plexippus*. Diamondback moth has 31 chromosomes (n = 31) with a genome size of roughly 343Mb. Its genome consists of 18 071 protein-coding genes 781 non-coding RNAs, and repetitive sequences that represent 33.97% of the genome. In its genome, 1 412 genes are found to be unique to Diamondback moth. There are abundant DNA variations present in *P. xylostella*’s genome in the forms of SNPs, InDels, structural variations and complex segmental duplication patterns. DMB is able to adapt to a variety of environmental challenges as a result of preferential expression of a set of genes at the larval stage that contributes to odorant chemoreception, food digestion, metabolic detoxification, and in particular, a biological detoxification pathway in long-term evolution that is able to detoxify many chemicals including Bt toxins, thus making it a notorious lepidopteran pests.

Keywords Diamondback moth (DBM); *Plutella xylostella* (L.); Genome; Molecular variation; Molecular evolution; Molecular adaptation

*Plutella xylostella* (L.) belongs to the family of Plutellidae in Lepidoptera Order, commonly known Diamondback moth (DBM), because the adult male back forms three yellow diamonds at rest when the wings are folded (Ankersmit et al., 1953). Diamondback moth feeds on cruciferous plant, and it’s becoming one of the most intensively studied Lepidopteran agricultural pests due to its devastating harm to the important cruciferous crops, as well as its resistance to many chemical pesticides and biological pesticides (Talekar and Shelton, 1993; Furlong et al., 2012). With the rapid development of modern biotechnology, a lot of studies have focused on the biological characteristics of diamondback moth at the molecular level, and significant progress is achieved regarding genomics and genetics, as well as molecular evolution and adaptation (Xie, 2013).

1 The genome of Diamondback moth
Diamondback moth has a genome size of about 343Mb, containing approximately about 18 071 protein encoding genes and 781 non-coding RNAs, and repetitive sequence (You et al., 2013). The diamondback moth has 1 412 genes unique to itself, most of which is involved in basic biological pathways of environmental information processing, chromosome replication or repair, transcriptional regulation, as well as carbohydrates, and protein metabolism (You et al., 2013).

2 Molecular genetics of diamondback moth
Diamondback moth is a highly heterozygous insect with 31 chromosomes (n=31). There are abundant DNA variations in genome such as SNPs, InDels and structural variation, as well as composite fragment repeats (Figure 1) (You et al., 2013). Baxter et al. built a linkage map of the diamondback moth by using next generation RAD sequencing technology (Baxter et al., 2011B). 3 177 maternally inherited RAD alleles were mapped on 31 chromosomes, making it possible to identify pesticide resistance genes and W/Z sex chromosome. The genome-wide linkage map spans 1 292 cM in length with 2 878 segregating RAD alleles inherited from the backcross father (Figure 2) (Baxter et al 2011). In the same year, Baxter also genetically mapped membrane transporter (ABCC2) to a locus contributing to Bt Cry1Ac toxin resistance in two lepidopteran insects, implying that this protein...
plays a crucial role in the Bt function (Baxter et al. 2011).

3 Molecular evolution of Diamondback moth

*Plutella xylostella* (Linnaeus, 1758) belongs to the family Plutellidae of Lepidoptera order in the Insecta class, Arthropoda phylum and Animalia kingdom. Diamondback moth diverged from two other lepidopterans *Bombyx mori* and black monarch butterflies (*D. plexippus*) about 124 million years ago. Based on the existing insect genomic phylogeny, diamondback moth was confirmed as a basal and primitive lepidopteran insect (You et al., 2013). Phylogenetic analysis further confirmed that the estimated divergence time of insecta orders was about 265–332 million years ago, which is consistent with the divergence of monocotyledonous and dicotyledonous plants 304 million years ago, indicating the co-evolution of insect behavior and host plant existence. When the cruciferous plants diverged from the Caricaceae about 54–90 million years ago, the diamondback moth also evolved to become a cruciferous plant-eating insects (You et al., 2013).

4 Molecular adaptation of diamondback moth

The diamondback moth originated in Europe. It was first found in North America in Illinois in 1854, and it spread to Florida and the Rocky Mountains in 1883. It was reported in British Columbia in 1905. Nowadays diamondback moth can be found in every corner of the planet where cabbage is planted (Furlong et al., 2012). Clearly, DMB has evolved to adapt to a variety of environmental challenges as a result of the complex network of genes preferentially expressed in the larval stage that contributes to odorant chemoreception, food digestion and metabolic detoxification.

DMB has become particularly resistant to chemical and biological pesticides in recent years. In the 1950s, Diamond moth was reported to have evolved resistance to DDT(Ankersmit et al., 1953), followed by a decline in the effectiveness of pyrethroid insecticides in the 1980s and reports of Diamond moth’s resistance to Bt toxins in the 1990s (Heckel et al., 1999; Tabashnik et al., 1999). Thereafter, virtually all kinds of pesticides have become ineffective. This adaption to insecticides contributes to the formation of biological detoxification pathways in long-term evolutionary process (You et al., 2013), and the ability to detoxify many chemical pesticides makes diamond moth a notorious lepidopteran pest.

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Figure 2 Linkage map of the *Plutella xylostella* (n = 31) genome (adapted from Baxter et al., 2011B)

This was inferred from 2,878 RAD alleles collapsed into 285 discrete RAD markers. Each linkage group contains between 10 to 158 RAD alleles (labelled RADs) and the total map length is 1,292 cM. Each RAD marker is labelled with three numbers (i ii iii) corresponding to (i) the RAD marker (1~285), (ii) the chromosome number (1~31) and (iii) the number of RAD alleles at that marker. Linkage groups 1~28 are homologous to the *B. mori* (n=28) chromosome numbering system, and LG29, LG30 and LG31 represent...
fusions to chromosomes 11, 23 and 24 respectively in *B. mori*. Dashed lines represent manual linkages inferred from 3, 4 or 5 genotype differences that were otherwise left ungrouped due to small sample sizes. As 20 progenies were used to construct the map, distances were approximated as 5 cM (1/20) per 1 crossing-over (c/o) event. On chromosomes 14, 16 and 22, markers formed two distinct groups and may be separated by regions of high recombination rates or chromosomal assignment error. In total, 11 of the 285 RAD markers could not be confidently assigned to their predicted chromosome. Linkage group 28 contained only four RAD markers at a single locus. Six additional markers were identified for this chromosome using JoinMap 3.0, from the remaining paternal markers not assigned to linkage groups. 

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