

Genetic Variation of the Diamondback Moth, *Plutella xylostella* (Lepidoptera: Yponomeutidae) in China Inferred from Mitochondrial COI Gene Sequence

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The diamondback moth, *Plutella xylostella*, is a worldwide notorious insect pest damaging to cruciferous plants. To know the pattern and magnitude of genetic variation of the species in China we sequenced a portion of mitochondrial (mt) COI gene of the *P. xylostella* collected over six Chinese and two Korean localities, which cover ~2,151,600 km². Sequence analysis of the 681-bp mt COI gene from 80 individuals resulted in 16 haplotypes, ranging in sequence divergence from 0.1% (one nucleotide) to 0.9% (six nucleotides), indicating moderate to low sequence divergence of the species. All, but one nucleotide position among 16 variable sites were transitional substitutions and no position resulted in amino acid substitutions. Phylogenetic analysis showed that all haplotypes were highly interrelated to each other. In geographic perspective, most haplotypes were found singly in one or two localities, but three haplotypes were widely distributed. Absence of statistically significant genetic distance between several pairs of populations suggests that gene flow is a significant demographic factor governing this species.