

2-14. Mitochondrial DNA Sequence Variation of the Diamondback Moth, *Plutella xylostella*, in Korea

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The diamondback moth, *Plutella xylostella*, known as a serious cosmopolitan pest for cruciferous plant has been subjected to the issue of study for the control of the pest. Therefore, researches on the genetic variation and population genetic structure also were of great interest, because the knowledge on these aspects were expected to provide with better understanding on the aspects of field ecology. We, thus, sequenced a portion of mitochondrial COI gene (438 bp) of 86 *P. xylostella* collected over 11 localities in Korea to investigate the magnitude and nature of genetic variation of the species in Korea. Although the maximum sequence divergence of the species was moderate to high compared with other insect species in Korea, numerical numbers of mtDNA haplotypes were exceptionally high (52 haplotype). Phylogenetic analysis by maximum likelihood method revealed very close relationships among most haplotypes, whereas presence of a few distinct haplotypes was noteworthy. Within-locality distribution pattern of haplotypes suggests that each Korean population is characterized as co-existence of several unique haplotypes and a few co-occurring haplotypes in most populations. Analyses of population genetic structure showed that most of the Korean populations were not genetically differentiated and high gene flow ratio among populations was characteristic. Taken these findings together, the nature of genetic divergence of the Korean diamondback moth populations was characterized as one that possessing high haplotype diversity, high gene flow, and a few immigrants from outside study area.