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Mitochondrial DNA Polymorphism and Population Genetic Structure of Diamondback Moths, *Plutella xylostella* (Lepidoptera: Yponomeutidae), in Korea

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We used a portion of mitochondrial COI gene sequences (438 bp) to investigate the phylogenetic and population genetic characteristics of the diamondback moth, *Plutella xylostella*, in Korea. A total of 27 mtDNA haplotypes were obtained from the samples collected from eight localities mostly in southern part of Korea. One haplotype, DB24, obtained from Muju in Chunrabuk Province formed an independent phylogenetic group in the PAUP and PHYLIP analyses, separated by 1.8%-2.7% of sequence divergence from others. This distinct haplotype appears to be one that carried by immigrants from outside study areas, but further study is required. Even excluding DB24, sequence divergence was moderate to substantial (0.2%-1.4%) and haplotype diversity within populations was substantially higher (mean H=0.95), compared with other relevant studies. Although most haplotypes were confined within one locality, female gene flow was substantial or high (Nm=10.6-infinite). The same pattern was observed in the hierarchical genetic analysis, showing that local populations were composed of heterogeneous haplotypes, and the genetic distance between localities were not statistically significant. These findings allowed us to conclude that the local diamondback moth populations were formed with randomly dispersed individuals, survived from the diversified use of insecticides over geographic areas.