

Haplotype Diversity and Gene Flow of the Diamondback
Moth, *Plutella xylostella* (L.) (Lepidoptera:
Yponomeutidae), in Korea

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A portion of mitochondrial COI gene (438 bp) was sequenced from the samples of *plutella xylostella* from four localities in Korea to investigate the population genetic structure and characteristics by measuring the magnitude of genetic diversity and the degree of gene flow among populations. Thirteen haplotypes ranging in nucleotide divergence 0.3% to 1.4%, were obtained from 21 individuals. The nucleotide divergence was similar to the other related studies, but haplotype diversity was substantially higher (mean $h=0.81$). The genetic distance among geographically remote Cheju Island population and the two Kimhae populations, distant 11km to each other, was not statistically significant ($p<0.05$). Instead, a substantial or high female gene flow was detected ($Nm=2-30$). One Hawaiian haplotype of the diamondback moth obtained through GenBank search also was genetically similar to the ones obtained from this study. Collectively, the genetic population structure of the diamondback moth in Korea can be characterized into two aspects. First, the diamondback moths in Korea possesses overall moderate genetic divergence based on a high number of haplotypes. Second, a high haplotype diversity within each population due to the long distance dispersal with a substantial dispersal power and the resultant genetic similarity among geographic populations is characteristic.