Molecular Characterization of Pheromone Biosynthesis Activating Neuropeptide from the Diamondback Moth, *Plutella xylostella* (L.)

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Pheromone biosynthesis activating neuropeptide (PBAN) produced in the subesophageal ganglion of insects stimulates pheromone production in the pheromone gland. A cDNA isolated from female adult heads of the diamondback moth (DBM, *Plutella xylostella*(L.)) encodes 193 amino acids including PBAN, designated as Plx-PBAN, and four other neuropeptides (NPs): diapause hormone (DH) homologue, α-NP, β-NP and γ-NP. All of the peptides are amidated in their C-termini and shared a conserved motif, FXPR/KL structure, as reported from other PBAN cDNAs. Plx-PBAN consists of 30 amino acids, the shortest PBAN so far reported. Plx-PBAN exhibited below 50% homology, compared with other known PBANs.The Plx-DH homologue is structurally different from DH of *B. mori.* The length of Plx-β-NP (16 amino acids) was the shortest and showed relatively low similarity, whereas γ-NP (10 amino acids in length) was the longest among γ-NPs examined. When female adults were injected with synthetic Plx-PBAN, pheromone production showed a peak 1 hr post-injection. RT-PCR screening revealed that Plx-PBAN cDNA was expressed in all examined body parts, with the highest expression level in the head of female adults. Analysis of RT-PCR products indicated the Plx-PBAN sequence was identical in all examined body parts of both sexes. Phylogenetic analysis revealed that the Plx-PBAN gene is distantly related to other PBANs, demonstrated by the relatively low homology.