

# Proteomic Analysis of Parasitism by *Cotesia plutellae*

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A braconid wasp, *Cotesia plutellae*, parasitized diamondback moth, *Plutella xylostella* and alters diverse host physiology. Based on key roles of two major parasitic components, polydnavirus and teratocyte, of *C. plutellae*, the expressed proteins of the parasitized host were resolved by two dimensional (2D) electrophoresis and analyzed by 2D clustering program. More or less 2,000 proteins expressed in parasitized or non-parasitized hosts were grouped according to their temporal pattern and specificity in parasitized host. Most conspicuous expression in parasitized host was found in five spots, where three spots was expressed at 1 and 2 days after parasitization and the one two spots at 4 and 5 days after parasitization. A specific protein in parasitized host was found in SDS-PAGE at 15 KDa region (PSP15). N-terminal sequence was conducted by Edman degradation method and subsequently used for cloning the gene using degenerate primer-based RT-PCR. The cloned PSP15 gene contains 133 amino acid residues and shares high homology (36%) with cap-binding protein of *Homo sapiens*.