

cDNA sequences of two biliproteins, BP1 and BP2, from the  
cabbage white butterfly, *Pieris rapae* and their tissue- and  
stage-specific accumulation

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Two similar full-length cDNAs of biliprotein were isolated and shown to encode the two isoelectric forms, BP1 and BP2 in *Pieris rapae*. Sequence analysis of two cDNA clones shows that both BPs contain a 567-bp open reading frame which predicts a 189-amino acid protein and a 15-amino acid signal peptide. The calculated isoelectric points are pI = 7.25 (BP1) and 6.74 (BP2), respectively. Comparison of two sequences of BP1 and BP2 reveals 12 base differences in the open reading frame, of which three nucleotide changes lead to two amino acid substitutions. The 5'-UTR from the two clones shows no difference, but an additional 45-bp fragment is inserted in the 3'-UTR of BP2 making its message a little longer than that of BP1. Northern blot analysis confirmed that the BP mRNAs are expressed from the late 4th instar to the adult stage with exception of prepupae and newly ecdysed pupae. While the BP1 transcript was prevalent in the larval stage, the BP2 transcript was abundant in the whole body only after the pupal stage in *Pieris rapae*. Both BPs were detected in a stage-specific pattern in the epidermis, testis, hindgut, wing, brain, and egg, with a lesser amount in the fat body. Two-dimensional gel electrophoresis and Western blot analyses revealed that BP1 was dominant in tissues from larvae, BP2 was dominant in tissues from pupal stages, and both

BPs appeared in tissues from the adult stage, though BP2 was predominant.