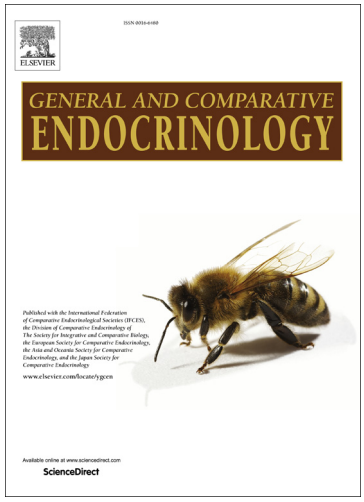

Genes and associated peptides involved with aestivation in a land snail

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Genes and associated peptides involved with aestivation in a land snail

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Abstract

Some animals can undergo a remarkable transition from active normal life to a dormant state called aestivation; entry into this hypometabolic state ensures that life continues even during long periods of environmental hardship. In this study, we aimed to identify those central nervous system (CNS) peptides that may regulate metabolic suppression leading to aestivation in land snails. Mass spectral-based neuropeptidome analysis of the CNS comparing active and aestivating states, revealed 19 differentially produced peptides; 2 were upregulated in active animals and 17 were upregulated in aestivated animals. Of those, the buccalin neuropeptide was further investigated since there is existing evidence in molluscs that buccalin modulates physiology by muscle contraction. The *T. pisana* CNS contains two buccalin transcripts that encode precursor proteins that are capable of releasing numerous buccalin peptides. Of these, *Tpi-buccalin-2* is most highly expressed within our CNS transcriptome derived from multiple metabolic states. No significant difference was observed at the level of gene expression levels for *Tpi-buccalin-2* between active and aestivated animals, suggesting that regulation may reside at the level of post-translational control of peptide abundance. Spatial gene and peptide expression analysis of aestivated snail CNS demonstrated that buccalin-2 has widespread distribution within regions that control several physiological roles. In conclusion, we provide the first detailed molecular analysis of the peptides and associated genes that are related to hypometabolism in a gastropod snail known to undergo extended periods of aestivation.

Key words: Snail; *Theba pisana*; peptides; neuropeptides; aestivation; central nervous system