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Expression profiles of venom components in some social hymenopteran species over different post-capture periods

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Abstract

To explore and compare the expression patterns of venom components depending on post-capture periods, venom gland-specific transcriptome and proteome analyses were conducted for five model hymenopteran species at a series of time points after capture. Venom gland-specific genes with signal sequences were considered as putative venom component genes. Expression patterns of venom gland-specific genes in all the social wasps and bees examined varied considerably depending on the post-capture period. Higher numbers of venom genes exhibited a decreasing expression pattern than an increasing pattern as the capture period increased. For example, genes encoding most of the allergens (dipeptidyl peptidase 4, endocuticle structural glycoprotein, odorant-binding protein, phospholipase A1, A2, B1, serine protease, serine protease inhibitor and venom allergen 5), pain-producing factor (mast cell degranulating peptide), and paralyzing factor (neprilysin) commonly exhibited decreasing expression patterns in all of the hymenopteran species tested, except for some of the major venom genes in *Apis mellifera* and *Bombus ignitus*, which showed an increasing pattern. These findings indicate species- or group-specific variations in the expression patterns of major venom genes. Taken together, flash freezing in liquid nitrogen immediately after capture was determined to be the best way to obtain the most natural expression profiles of venom components in social wasp species, thus, enabling a better understanding of the toxic potential of venom in wasp sting accidents. This study provides guidance for establishing optimal protocols for venom gland isolation and venom extraction from wasps and bees that can ensure the most naturally represented venom composition.

Keywords : Stress-dependent toxicity, Transcriptome analysis, Proteome analysis, Social wasp, Honeybee, Bumblebee

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