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FROM BUTTERFLY DIVERSITY TO PEPTIDE DRUG DISCOVERY

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INTRODUCTION:
Biodiversity is a valuable resource for discovering new drugs that can save millions of lives from diseases, such as cancers, stroke, diabetes, and cardiovascular disease. Bioactive peptides in animal venoms, particularly from 5s animals (snake, scorpion spider, cone snail, and sea anemone), have long been a subject of interest. Some toxins have been intensively investigated and developed into approved drugs. Toxins from caterpillars have been overlooked until recently. At least 70 species of caterpillars from 15 family taxa are venomous, which cause varying effects from mild iteration to death due to hemorrhagic syndrome. In 2021, three new papers used next-generation sequencing and proteomic approach to identify toxin peptide components from three caterpillar species (*Parasa lepida*, *Doratifera vulnerans,* and *Premolis semirufa*). The growing knowledge can help elucidate the hidden diversity of peptides with pharmacologic properties from the caterpillar venoms.

OBJECTIVES:
This study aims to identify toxin peptides from the stinging nettle caterpillar, *Parasa consocia*, and compare its toxin component with other caterpillar species from the same family taxa (Limacodidae) to identify their common characteristics.

METHOD / DESIGN:
The RNA-seq data from stinging hairs of *Parasa consocia* was downloaded from the NCBI database and assembled into a transcriptome using tools in the UseGalaxy cloud platform. Its toxin genes were identified following a previously published annotation pipeline. Orthologous relationships of toxin genes from different caterpillar species were analyzed using OrthoVenn2. Phylogenetic relationships of genes were analyzed using the maximum likelihood method.

RESULTS:
A total of 142 candidate toxin genes from *P. consocia* were identified. This includes proteolytic enzymes (serine protease; peptidase; metalloproteinase), peptidase inhibitors (serpin, kazal-type inhibitor, trypsin inhibitor-like), and allergens (carboxylesterase, CAP superfamily, acid phosphatase, antimicrobial peptide, and phospholipase A2). Comparing these results with *P. lepida* and *Doratifera vulnerans* (Family Limacodidae) and *Premolis semirufa* (Family Erebidae) suggest that the common components in Limacodids venoms are antimicrobial peptides (cecropin-like), knottin-like peptides (predicted structure similar to spider neurotoxins), and allergens commonly found in bee venoms (carboxylesterase-6 and venom acid phosphatase).

CONCLUSIONS:
Caterpillar venoms contain diverse peptides with potential pharmaceutical properties. Some interesting candidate drugs from Limacodids include cecropin-like antimicrobial peptides and knottin-like neurotoxins, which could inhibit pain receptors. Future functional analyses are essential to validate their antimicrobial properties or their use for treating chronic pain.

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