

Integrative peptidomics and bioinformatic analysis of four wasp venoms reveals diverse peptides and novel cryptides

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INTRODUCTION

Bee venom therapy has been officially integrated into traditional Chinese medicine and is widely used as an adjunct treatment for various diseases. In contrast, wasp venom, with its complex composition and potent biological activities, remains a valuable yet underexplored source of bioactive molecules.



VS



Bee venom therapy widely used

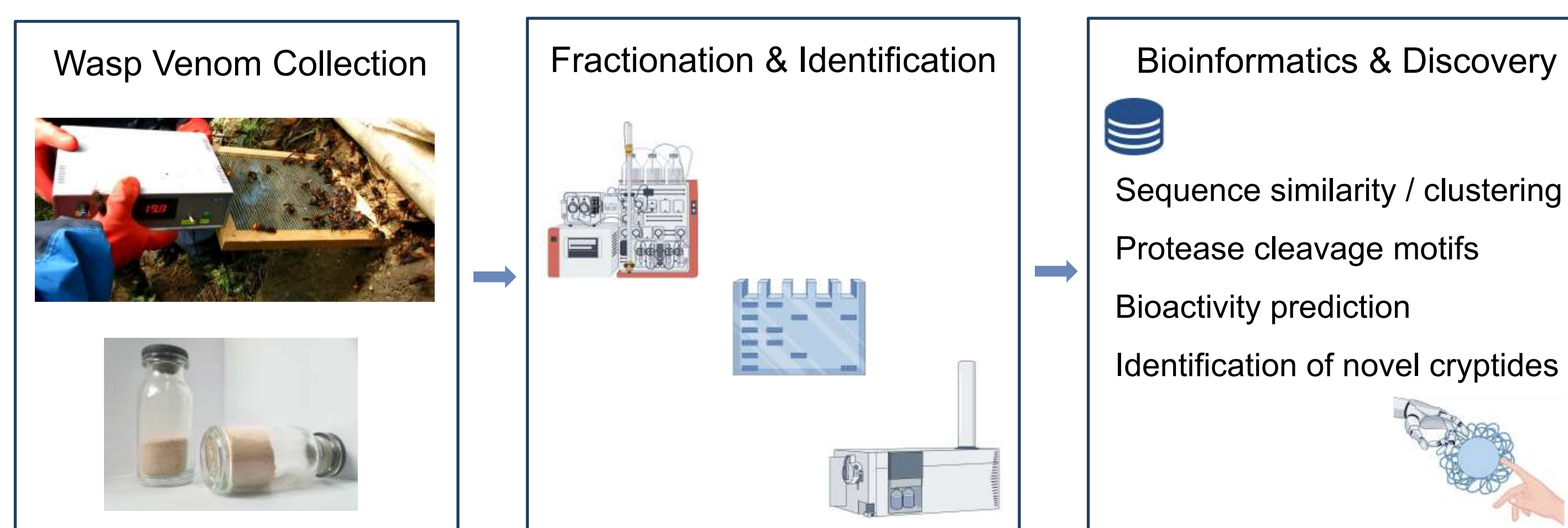
Wasp venom largely unexplored

OBJECTIVES

To systematically investigate the peptidome of wasp venoms and evaluate their potential pharmacological activities for drug discovery and rational utilization of venom-derived resources.

METHODS

Venoms from four wasp species (*Vespa mandarinia*, *V. velutina*, *V. basalis*, and *Provespa barthelemyi*) were collected by electrical stimulation and analyzed using liquid chromatography–tandem mass spectrometry (LC–MS/MS).



RESULTS

All four wasp venoms were successfully fractionated.

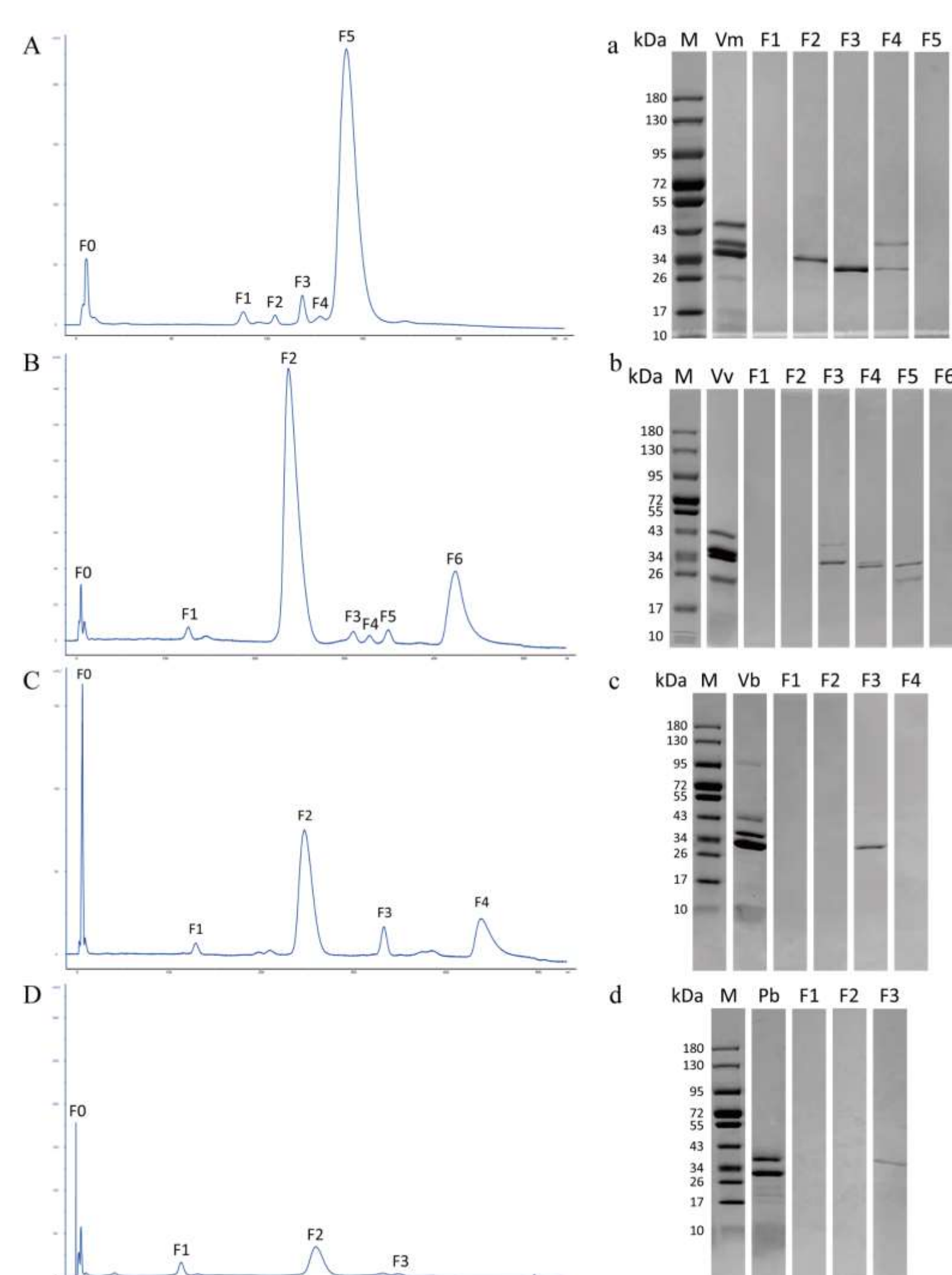


Fig. 1. Cation exchange chromatography elution profiles (A–D) and SDS-PAGE analyses (a–d) of four wasp venom samples. Venom samples A–D (a–d) represent: A, a – *Vespa mandarinia*; B, b – *V. velutina*; C, c – *V. basalis*; D, d – *Provespa barthelemyi*.

Peptide-rich fractions were obtained for peptidome analysis.

RESULTS (continued)

A total of 681 peptides were identified, nearly 90% of which represent novel sequences.

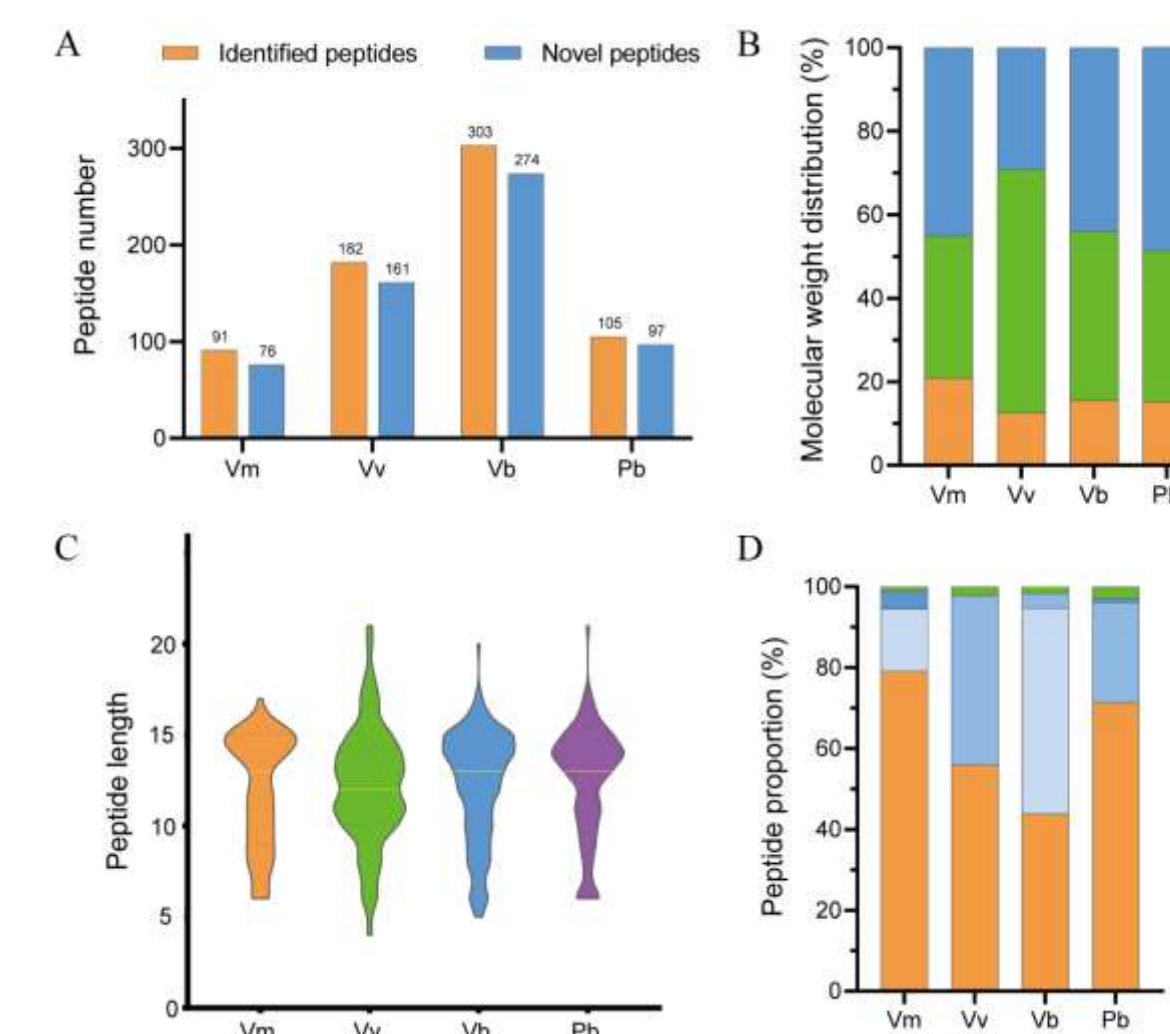


Fig. 2. Peptidomic characterization of venom extracts from four wasp species.

Comparative analysis revealed that most peptides were species-specific, while only a few were shared among species, indicating marked species-dependent patterns in wasp venom peptidomes.

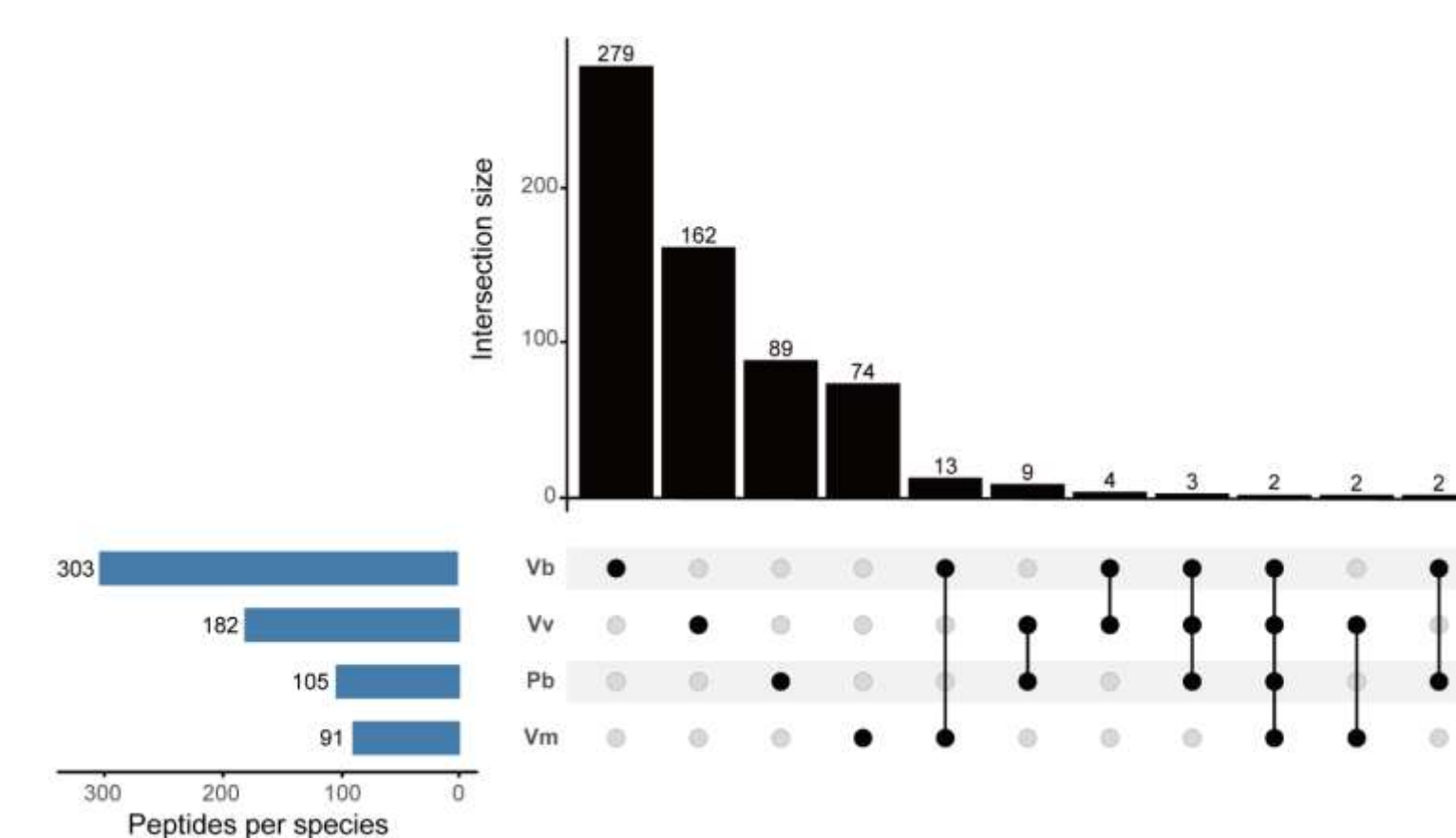


Fig. 3. Comparative analysis of unique and shared peptides in the venoms of four wasp species.

Peptide release may be regulated by specific proteolytic cleavage mechanisms.

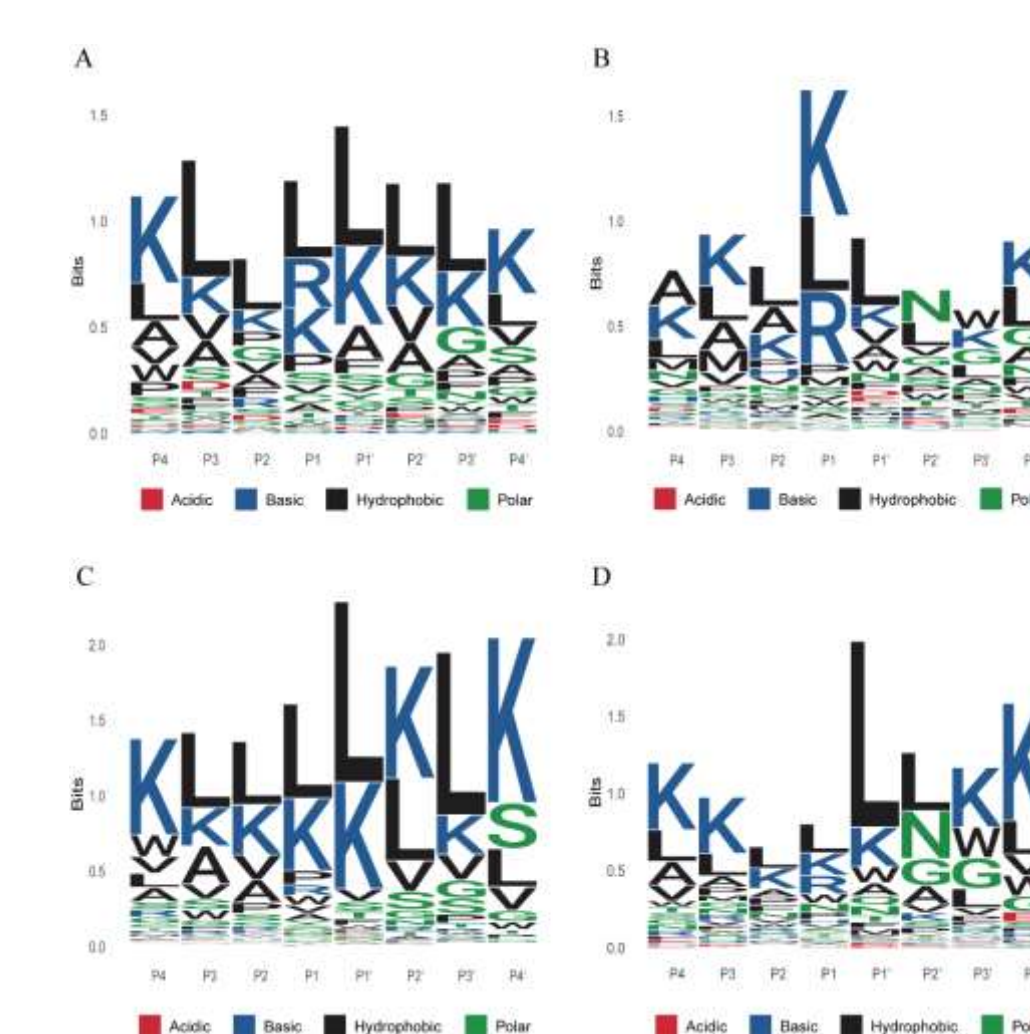


Fig. 4. Sequence logos showing amino acid frequency motifs from positions P4 to P4' in venom-derived peptides of *Vespa mandarinia* (A), *V. velutina* (B), *V. basalis* (C), and *Provespa barthelemyi* (D).

Bioinformatic predictions indicated that 291 peptides exhibit potential activities, including ACE and DPP4 inhibition, suggesting therapeutic potential in hypertension and diabetes.

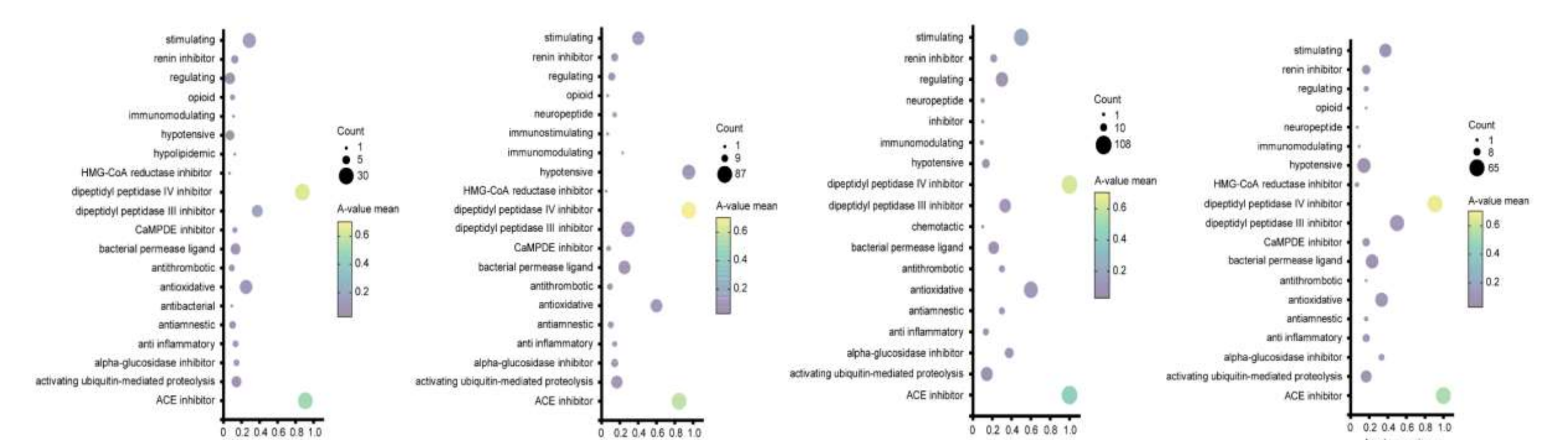


Fig. 5. Predicted bioactivity landscape of wasp venom peptides.

Ten novel cryptides were identified.

CONCLUSIONS

This study provides the first comprehensive comparative analysis of the peptidomes of four wasp venoms, revealing their diversity, generation mechanisms, and bioactivity potential.

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