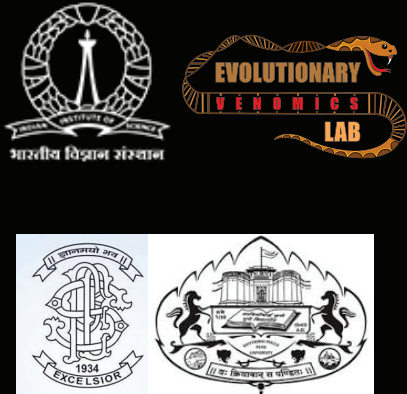


Unveiling the venom complexity of *Hypnale hypnale*: Regional variation, transcriptomics and clinical implications from the Western Ghats, India

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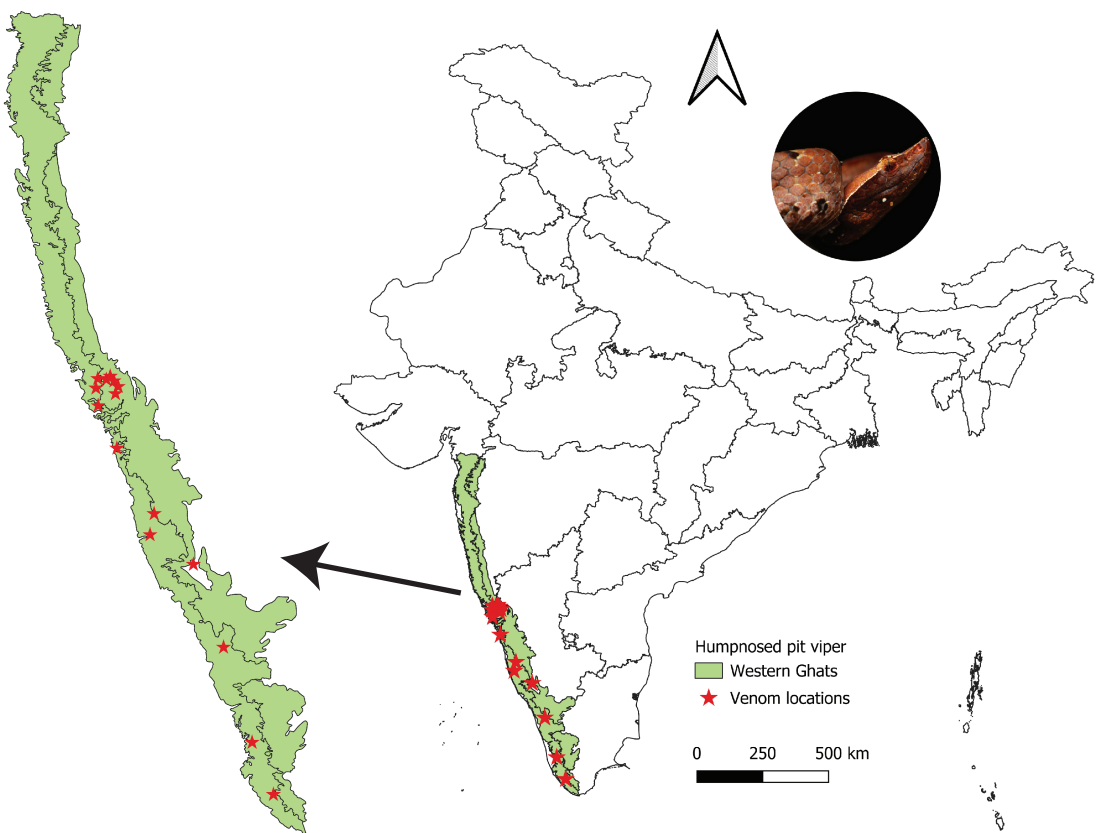
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Introduction

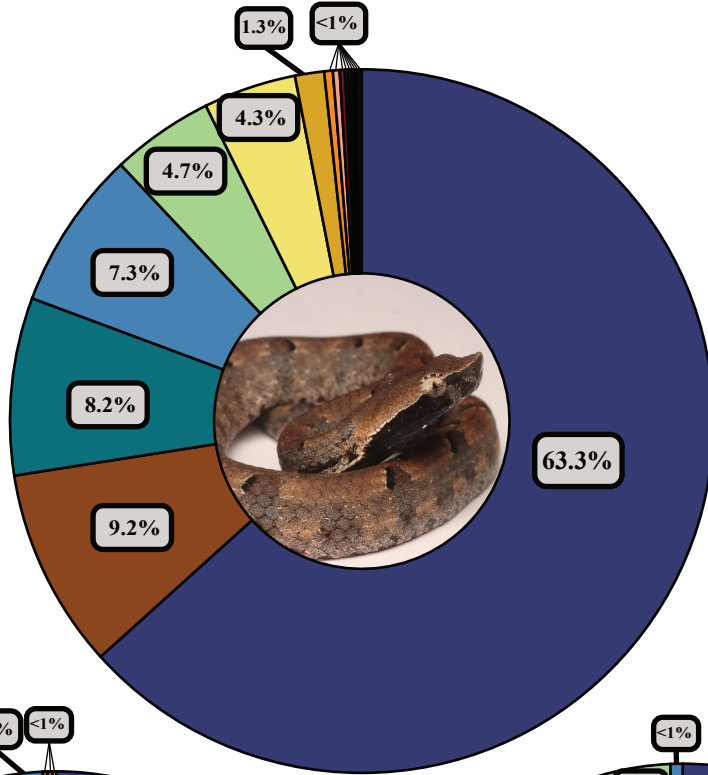
Hypnale is a medically relevant pit viper genus endemic to the Western Ghats of India and Sri Lanka, with three species: *H. hypnale*, *H. nepa*, and *H. zara*. Only *H. hypnale* occurs in India, forming a monophyletic lineage across the Western Ghats and Sri Lanka. Despite the clinical significance, *H. hypnale* venoms are poorly studied. Envenomation can lead to coagulopathy, local tissue necrosis, acute kidney injury, and even multi-organ failure; however, no antivenom is available for treatment. Misidentification and inadequate clinical recognition worsens its impact. The complex topography of the Western Ghats could harbour cryptic *Hypnale* lineages. We collected *H. hypnale* samples from the Western Ghats to proteo-transcriptomically and biochemically characterise their venom. The findings underscore the urgency for *Hypnale*-specific antivenom to improve the clinical outcomes and address this neglected health threat.

Sampling

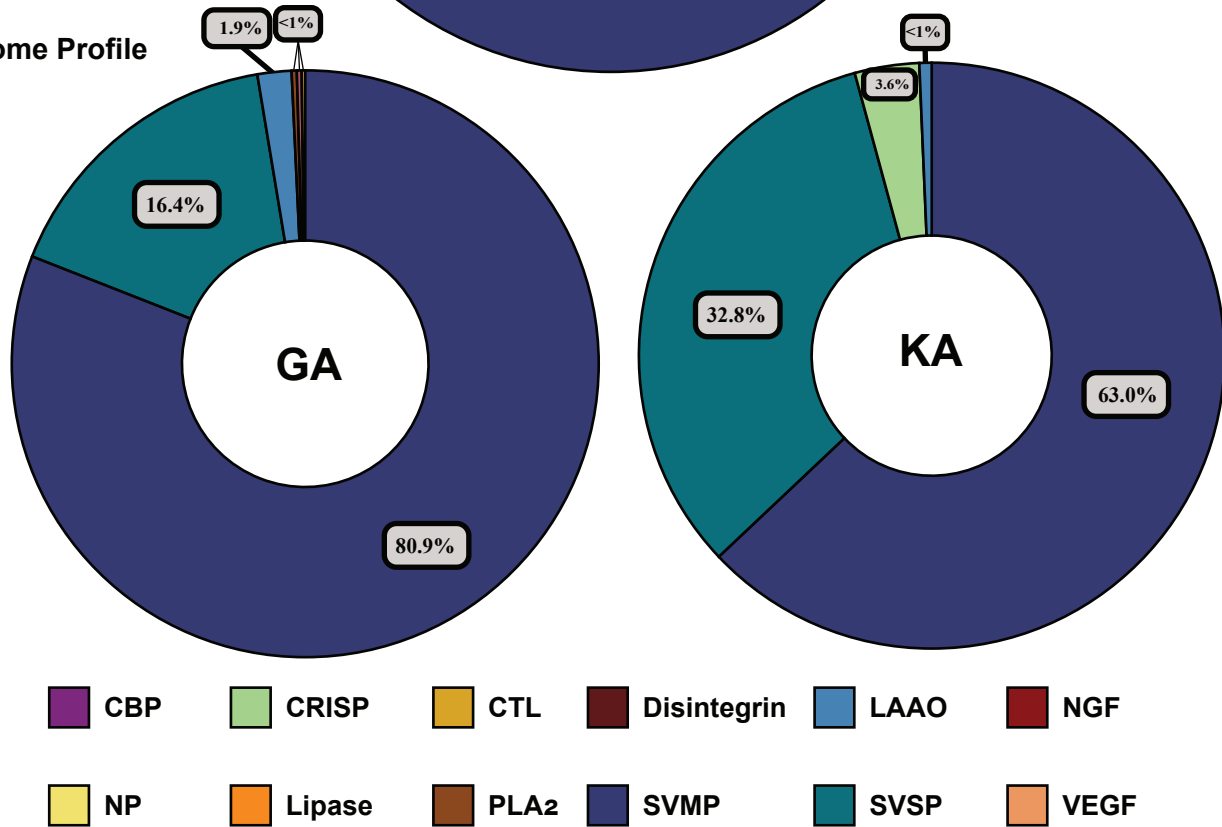


Proteotranscriptomic characterisation

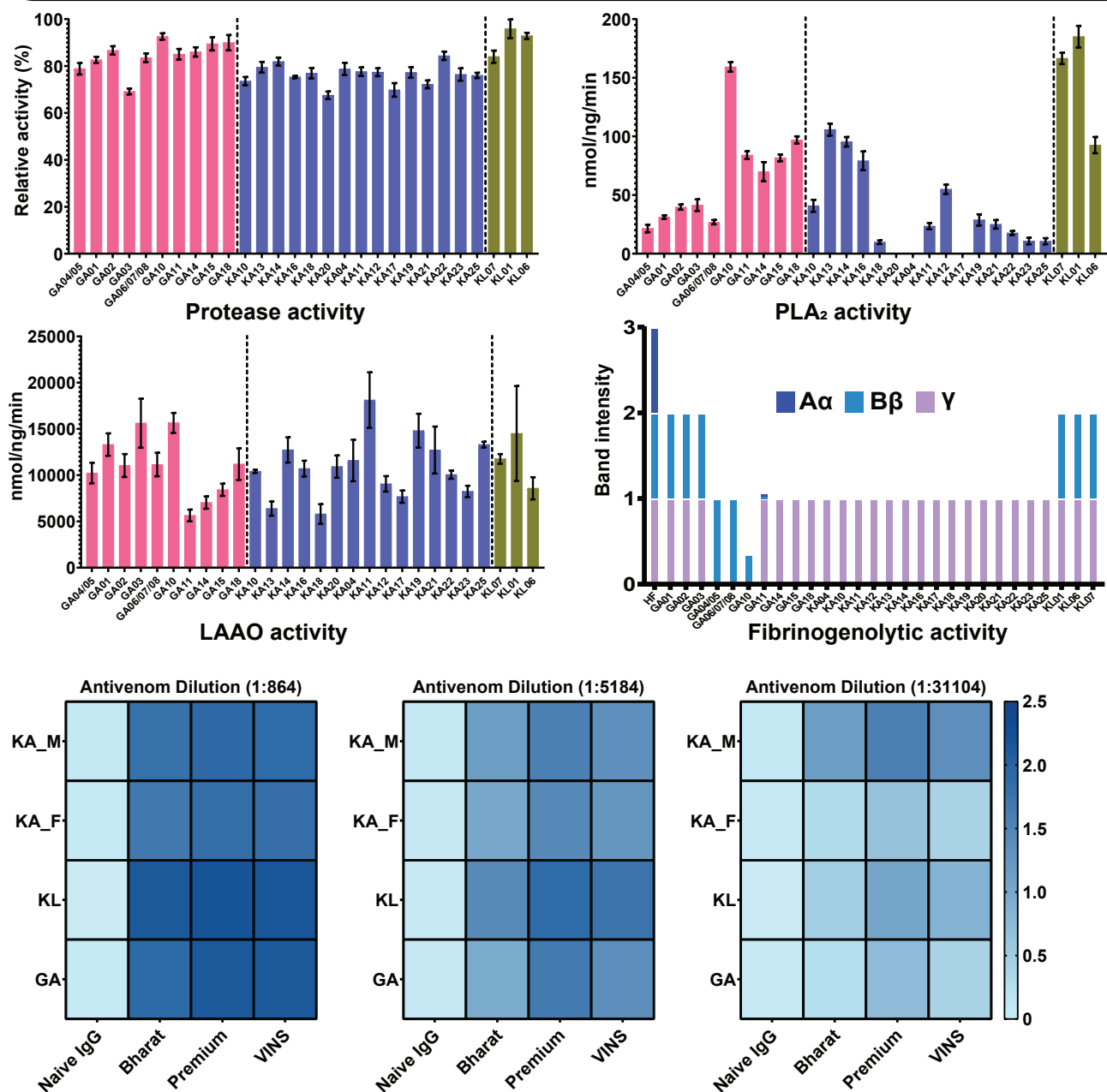
A Transcriptome Profile



B Proteome Profile



Biochemical and *in vitro* asessment



Conclusions and Future Directions

H. hypnale venom is rich in snake venom metalloproteinases, as revealed by biochemical and proteo-transcriptomic analyses.

Interpopulation venom variation causes differences in recognition by Indian ‘big four’ polyvalent antivenoms, highlighting the need for improved therapeutics.

In vivo studies are underway to assess venom lethality and antivenom neutralization efficacy.

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