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NEWS AND COMMENTARY

Scorpion venom gland transcriptome revealed

What's your poison?

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In the animal kingdom, venoms (defined as toxic substances that are administered by injection, as opposed to substances that are toxic after ingestion) are widespread chemical weapon systems found in virtually all major phyla. Well-known venomous animals include groups such as Cnidaria (jellyfish, sea anemones, corals), some molluscs (cone shells, blue-ringed octopus), many arthropods (wasps and bees, spiders, scorpions, centipedes) and a number of major vertebrate lineages, including several fish clades, many reptiles, and even a few birds and mammals. The primary biological function of venoms is most commonly prey acquisition, although defence against predation is an important secondary function in many groups (for example, spiders, scorpions, snakes) and the principal function in many fish. In most of these organisms, the venoms consist primarily of complex cocktails of bioactive peptides, enzymes and proteins encoded by the animal's own genome, unlike the toxins of many poisonous animals that are obtained through the food chain and accumulated in the animal's tissues. The origins of these toxins can be found in ordinary 'housekeeping' protein families that have been recruited into a venom role, are expressed in the venom gland, and undergo extensive neofunctionalization while evolving as multi-locus gene families through the birth-and-death model of gene family evolution (Nei *et al*., 1997; Fry, 2005).

The characterization and sequencing of individual venom peptides through conventional cloning or protein techniques has generated considerable information on the diversity of toxins present in many animals. However, the advent of transcriptomic approaches, which seek to characterize the entire set of genes being transcribed in the gland rather than focusing on a restricted group of toxins, has allowed major leaps in our understanding of the nature and origin of venoms, particularly in reptiles (Fry *et al*., 2006). On the other hand, transcriptomic studies of scorpions have lagged behind those of many other venomous taxa. As a result, the paper of Ma *et al*. (2009), in which they investigated the venom gland transcriptome of the scorpion *Scorpiops jendeki*, yielding a new database of 871 expressed sequence tags, is particularly welcome. Whereas the majority of scorpion toxin sequences previously lodged with public databases were from species of the medically important family Buthidae, Ma *et al*. (2009) chose a harmless species of the family Euscorpiidae. By providing toxin data across a greater part of the span of the evolutionary tree of scorpions, this paper will contribute enormously to our ability to investigate the origins and mode of evolution of scorpion venoms.

The new database was able to reveal not only the absence of some toxin families from the venom of *S. jendeki*, in particular the sodium channel-specific neurotoxins, which are an important part of buthid venoms, but also the likely presence of a number of hitherto uncharacterized toxin families. As many animal venom toxins have highly specific modes of action that are targeted at particular receptors, sometimes in a very restricted range of target taxa, the new data provide a first glimpse of a vast cornucopia of hitherto unknown bioactive compounds of potential interest for drug discovery, pest control or other uses.

The phylogenetic breadth of coverage is also pivotal for other purposes. First, owing to the phylogenetic distance between the Euscorpiidae and the Buthidae, this comprehensive transcriptomic database provides a first opportunity to investigate the origin of different toxin families found in scorpion venom glands. The use of toxin gene family phylogenies incorporating toxins from distantly related taxa has proved particularly useful in reconstructing the timing and recruitment of different toxin families into the arsenals of reptiles and other venomous organisms (Fry and Wüster, 2004; Fry *et al*., 2006), and has provided clear examples of parallels in the mode of recruitment and evolution of toxin families across multiple phyla (Binford *et al*., 2009). Until now, there has been little opportunity for this line of work in scorpions because of the lack of comprehensive inventories of their venoms and sequences. Additional important lines of work facilitated by transcriptomic studies include the detection of evolutionary phenomena such as accelerated evolution (Nakashima *et al*., 1993), which is a common phenomenon in animal toxin evolution that is likely to be linked to adaptive evolution in response to natural selection for prey-specific venom activity, across a wider range of toxins.

Through the publication of this Expressed Sequence Tags database, Ma *et al*. (2009) have started the process of entering scorpion venoms into the transcriptomic age. As in the case of other venomous organisms, the future will undoubtedly bring a plethora of new discoveries.

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Editor's suggested reading:

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