

Lack of Signal for the Impact of Conotoxin Gene Diversity on Speciation Rates in Cone Snails

Publons ID	34511485
Wos ID	WOS:000489700900008
Doi	10.1093/sysbio/syz016
Title	Lack of Signal for the Impact of Conotoxin Gene Diversity on Speciation Rates in Cone Snails
First Author	Phuong, Mark A.; Alfaro, Michael E.; Mahardika, Gusti N.;
Last Author	Puillandre, Nicolas
Authors	Phuong, MA; Alfaro, ME; Mahardika, GN; Marwoto, RM; Prabowo, RE; von Rintelen, T; Vogt, PWH; Hendricks, JR; Puillandre, N;
Publish Date	SEP 2019
Journal Name	SYSTEMATIC BIOLOGY
Citation	10
Abstract	<p>Understanding why some groups of organisms are more diverse than others is a central goal in macroevolution. Evolvability, or the intrinsic capacity of lineages for evolutionary change, is thought to influence disparities in species diversity across taxa. Over macroevolutionary time scales, clades that exhibit high evolvability are expected to have higher speciation rates. Cone snails (family: Conidae, 900 spp.) provide a unique opportunity to test this prediction because their toxin genes can be used to characterize differences in evolvability between clades. Cone snails are carnivorous, use prey-specific venom (conotoxins) to capture prey, and the genes that encode venom are known and diversify through gene duplication. Theory predicts that higher gene diversity confers a greater potential to generate novel phenotypes for specialization and adaptation. Therefore, if conotoxin gene diversity gives rise to varying levels of evolvability, conotoxin gene diversity should be coupled with macroevolutionary speciation rates. We applied exon capture techniques to recover phylogenetic markers and conotoxin loci across 314 species, the largest venom discovery effort in a single study. We paired a reconstructed timetree using 12 fossil calibrations with species-specific estimates of conotoxin gene diversity and used trait-dependent diversification methods to test the impact of evolvability on diversification patterns. Surprisingly, we did not detect any signal for the relationship between conotoxin gene diversity and speciation rates, suggesting that venom evolution may not be the rate-limiting factor controlling diversification dynamics in Conidae. Comparative analyses showed some signal for the impact of diet and larval dispersal strategy on diversification patterns, though detection of a signal depended on the dataset and the method. If our results remain true with increased taxonomic sampling in future studies, they suggest that the rapid evolution of conid venom may cause other factors to become more critical to diversification, such as ecological opportunity or traits that promote isolation among lineages.</p>
Publish Type	Journal
Publish Year	2019
Page Begin	781
Page End	796
Issn	1063-5157
Eissn	1076-836X
Url	https://www.webofscience.com/wos/woscc/full-record/WOS:000489700900008
Author	ROMANUS EDY PRABOWO, S.Si, Ph.D