Table S1. Results of maximum-likelihood estimates of ω values for A-superfamily genes of *Conus* species. Gene sets with and without type III pseudogenes were both used for *C. lividus* and *C. sanguinolentus*; a short sequence (livi_51) was also excluded for analyses of sequences of *C. lividus*. The null model included one ω rate across the whole phylogeny while the alternative model used one ω for expressed genes and another one for non-expressed genes. *P*-values were determined by Likelihood Ratio Tests of log-likelihoods of null and alternative models with one degree of freedom.

Gene Set	**Model**	**ω**	**Ln(L)**	***P*-value**
C. diadema	Null: One rate	ω= 0.679	-572.480	0.073
	Alternative: Two rates	ω_1=0.624, ω_2= 999	-570.874	
C. lividus	Null: One rate	ω= 1.429	-730.687	0.008
	Alternative: Two rates	ω_1= 1.181, ω_2= 999	-727.245	
C. lividus, no pseudogenes	Null: One rate	ω= 1.285	-682.324	0.008
	Alternative: Two rates	ω_1= 1.069, ω_2= 999	-678.802	
C. quercinus, no pseudogenes	Null: One rate	ω= 1.379	-300.619	0.428
	Alternative: Two rates	ω_1= 1.790, ω_2= 0.939	-300.305	
C. sanguinolentus	Null: One rate	ω= 1.082	-685.390	0.041
	Alternative: Two rates	ω_1= 0.981, ω_2= 999	-683.310	
C. sanguinolentus, no pseudogenes	Null: One rate	ω= 0.970	-642.142	0.032
	Alternative: Two rates	ω_1= 0.862, ω_2= 999	-639.839	

Figure S1. Relative expression levels of coexpressed orthologs between species and inparalogs within species. Names of loci recovered from *C. lividus* begin with the letter L, *C. diadema* with D, *C. quercinus* with Q and *C. sanguinolentus* with S; numbers after the first letter correspond to numbers in the sequence labels given in Figure 1.

(A) Relative expression levels of orthologous conotoxin loci coexpressed by two *Conus* species. Dark and light grey bars represent orthologous loci expressed by each species.

(B) Relative expression levels of coexpressed inparalogs (those apparently generated by lineage-specific gene duplications). Dark and light grey bars represent the paralogous genes expressed within individuals of each species.

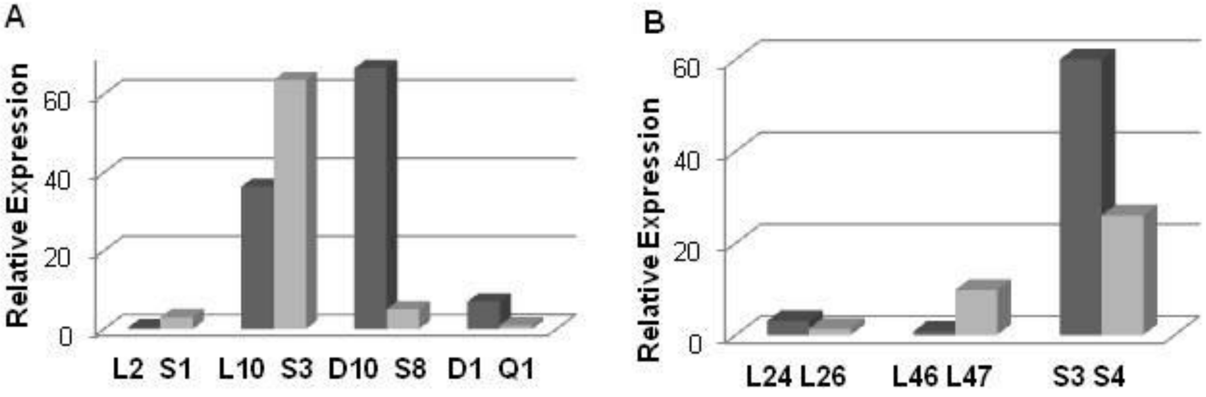

Figure S2. Boxplots of numbers of synonymous substitutions per synonymous site (*d*s, y-axis) against categories of expression (1: neither of the gene pair is expressed; 2: one gene is expressed; 3: both genes are expressed) of four *Conus* species. Sample sizes are labeled next to each category. (A) *C. lividus*, (B) *C. sanguinolentus*, (C) *C. diadema*, and (D) *C. quercinus*.