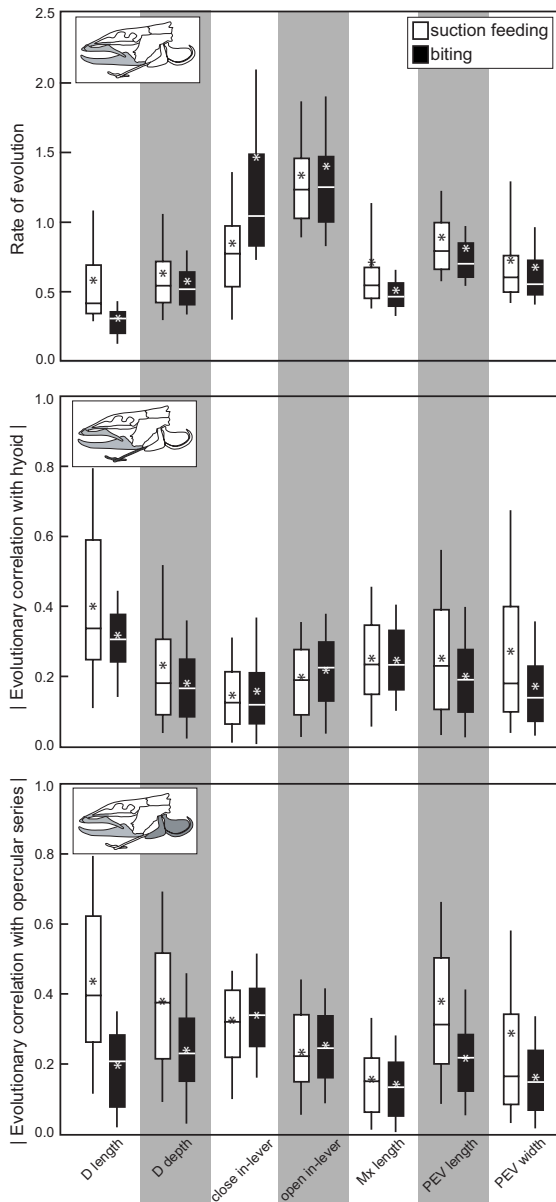
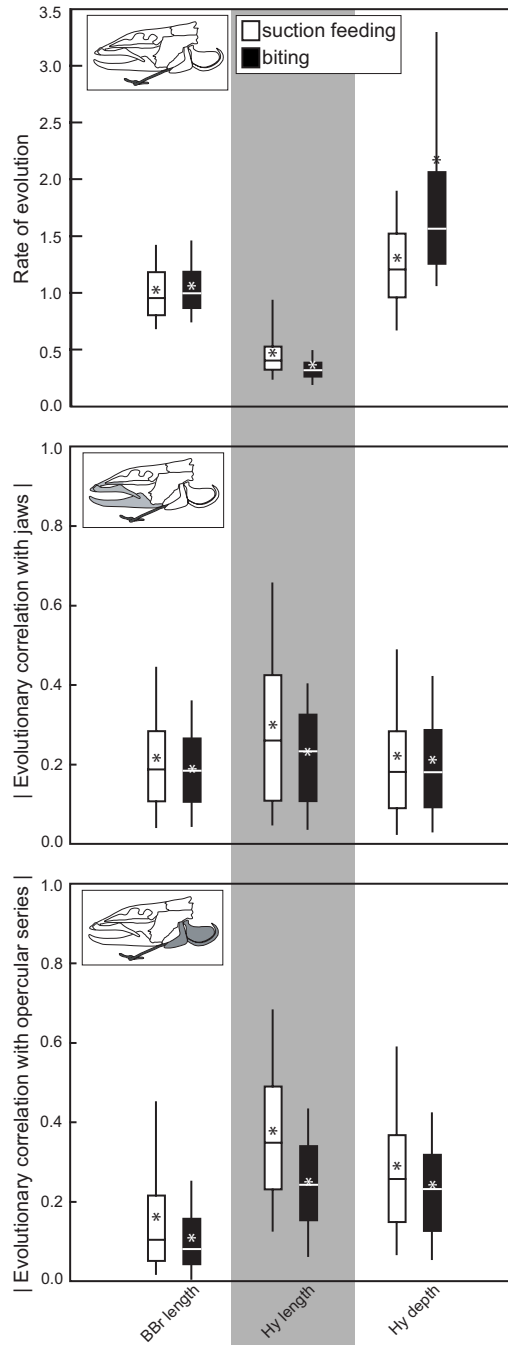




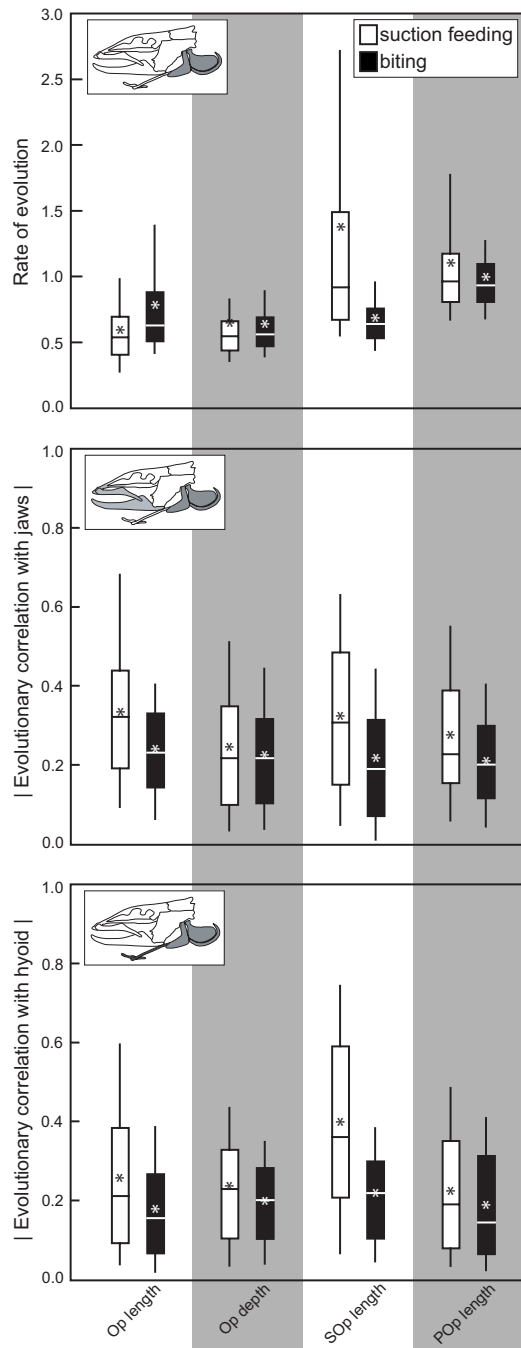
**Supplementary Figure 1 Sampled history of suction feeding and biting in elopomorph fishes.** The phylogenetic reconstruction is the maximum clade credibility tree resulting from Bayesian phylogenetic analysis. Asterisks indicate nodes supported by at least 0.90 Bayesian posterior probabilities, and branch lengths are in relative time (tree depth equals 1.0). Branch colors show inferred feeding modes for lineages (black is suction feeding, red is biting) based on stochastic character mapping.



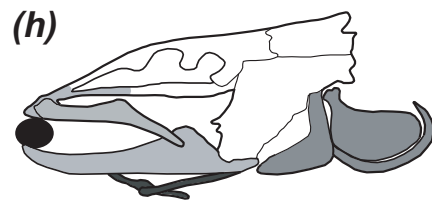
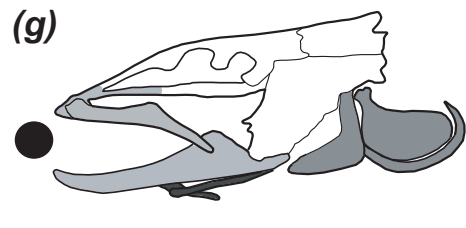
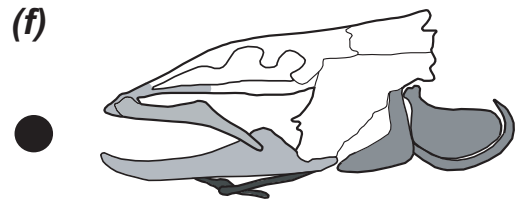
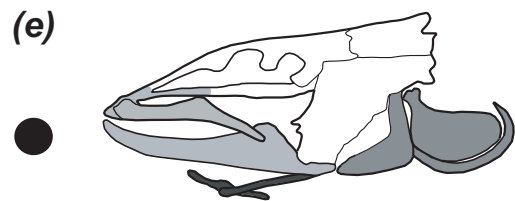
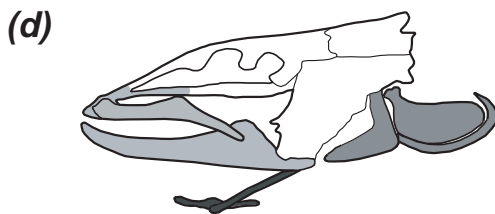
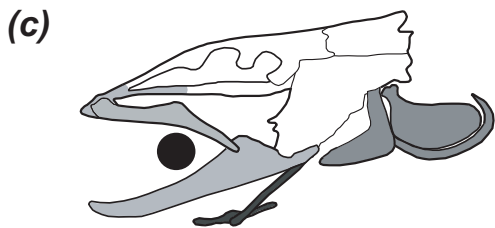
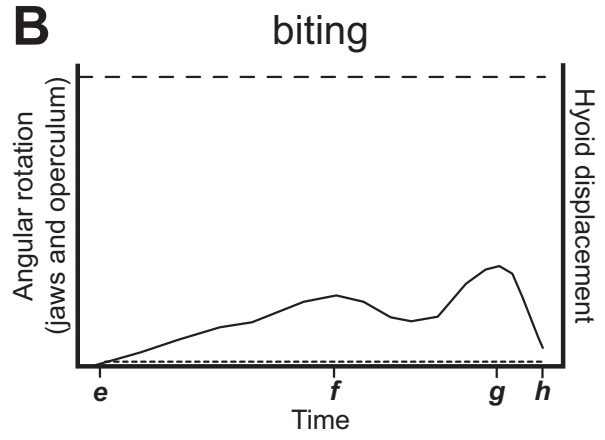
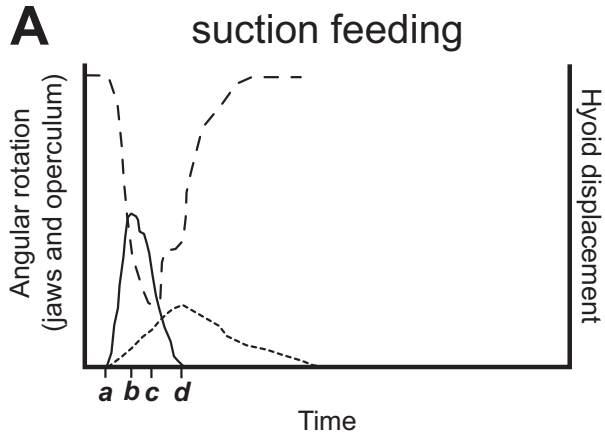
**Supplementary Figure 2 Rates and correlations for individual jaw traits.** Graphs show rates of evolution for morphological traits that make up the jaws (top) and absolute values of evolutionary correlations between jaw and hyoid traits (center) and between jaw and opercular series traits (bottom). D is dentary bone, Mx is maxilla, PEV is premaxillo-ethmo-vomerine bone. White boxes show distributions of estimates for suction feeders and black boxes are the distributions for biters. Boxplots show 9<sup>th</sup> and 91<sup>st</sup> percentiles (whiskers), first and third quartiles (boxes), medians (bands within boxes), and means (asterisks) of the distributions.



**Supplementary Figure 3 Rates and correlations for individual hyoid traits.** Graphs show rates of evolution for morphological traits that make up the hyoid (top) and absolute values of evolutionary correlations between hyoid and jaw traits (center) and between hyoid and opercular series traits (bottom). BBr is basibranchial, Hy is hyoid. See Fig. S5 for description of boxplots.

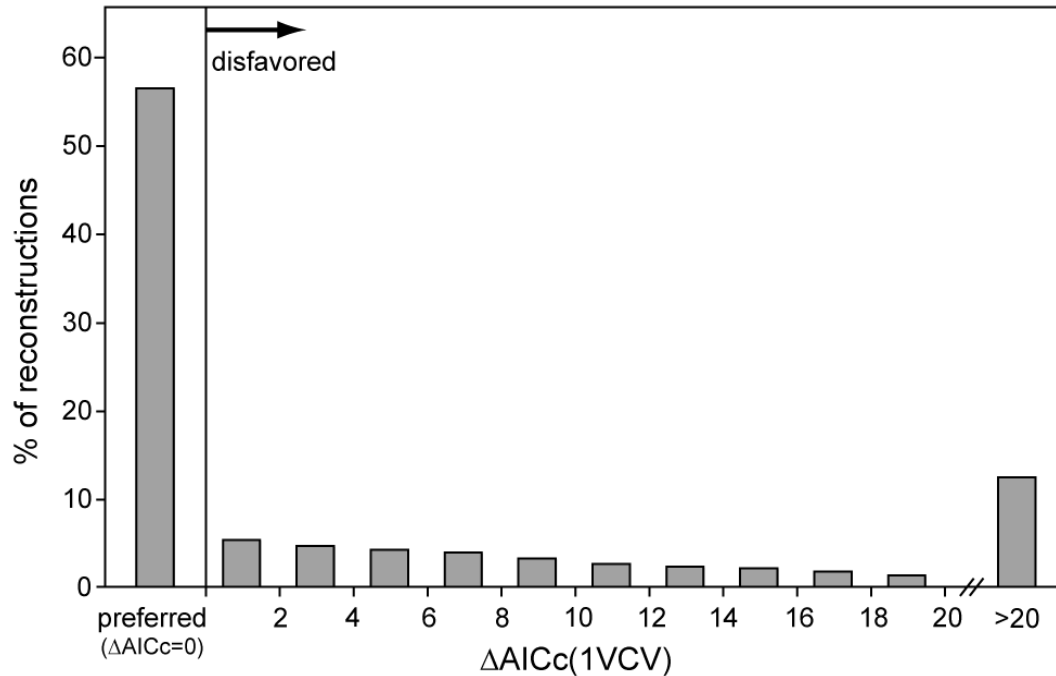


**Supplementary Figure 4 Rates and correlations for individual opercular traits.** Graphs show rates of evolution for morphological traits that make up the opercular series (top) and evolutionary correlations between opercular series and jaw traits (center) and between opercular series and hyoid traits (bottom). Op is opercle, SOp is subopercle, POp is preopercle. See Fig. S5 for description of boxplots.



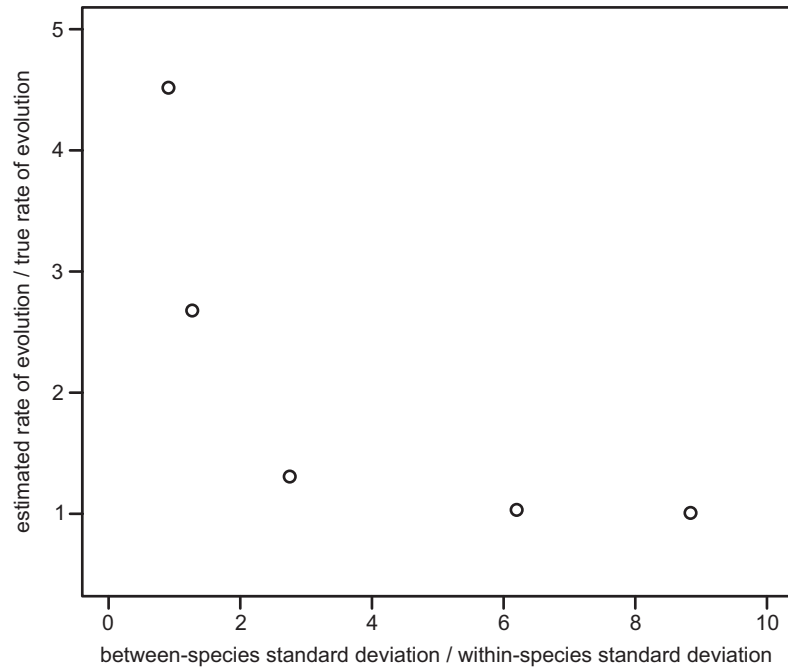
### **Supplementary Figure 5 Schematic illustration of functional integration during suction**

**feeding and biting.** (A) Suction feeding requires tight coordination between the jaws, hyoid, and operculum to rapidly expand the oral cavity and generate water flow that carries prey into the mouth. The graph shows representative kinematic traces for the jaws (solid line), hyoid (dashed line), and operculum (dotted line), which sequentially reach their peak excursions to generate an anterior-to-posterior moving wave of cranial expansion. Skull diagrams show displacements of mechanical units (light gray is the jaws, dark gray is the hyoid, and intermediate gray is the operculum) and position of the prey (black dot) at four points during the strike: (*a*) just before expansion, (*b*) peak gape, (*c*) peak hyoid displacement, and (*d*) mouth closure. Note that operculum movement is not obvious in the drawings because it rotates laterally—out of the plane of the image. (B) Biting entails flexible jaw movements to make contact with prey and requires little coordination among the jaws, hyoid, and operculum. The plot shows an example kinematic trace for biting (solid and dashed lines correspond to the same mechanical units as in A). This strike features two phases of jaw opening and closing, which is common during biting as jaws adjust position to contact the prey<sup>1</sup>. These jaw movements occur independently of hyoid displacement and opercular rotation. Also note the time axes for the graphs in A and B are the same, and biting tends to be considerably slower than suction feeding strikes. Skull diagrams show mechanical unit movements and prey position at four points during the strike: (*e*) immediately prior to strike initiation, (*f*) the first peak gape, (*g*) the second peak gape, and (*h*) mouth closure and prey capture. Kinematic traces in (A) and (B) are based on data presented in Mehta and Wainwright<sup>1</sup>.



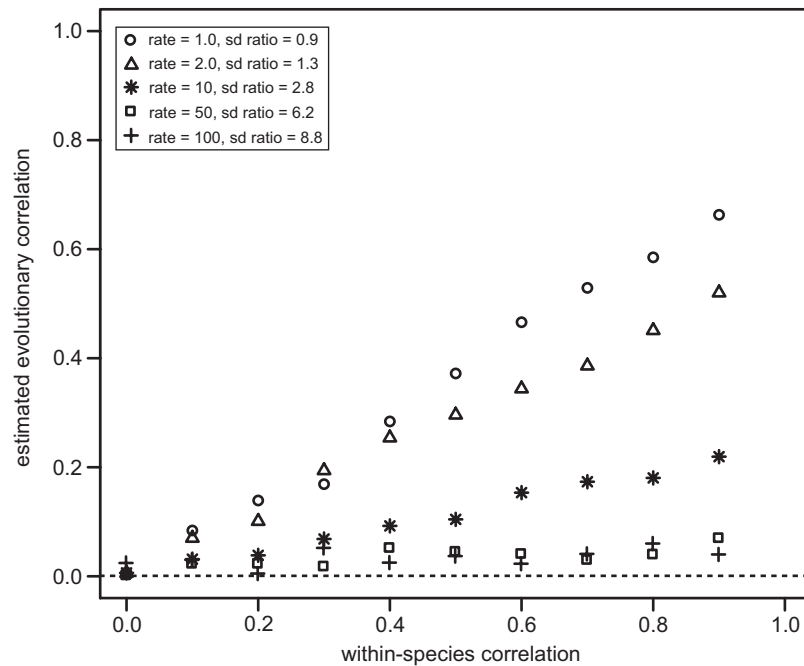
**Supplementary Figure 6 Histogram of  $\Delta AICc$  for the one evolutionary rate matrix model.**

The one-matrix (abbreviated 1VCV) model specifies equal evolutionary rates within and covariances between mechanical units in suction feeding and biting elopomorph lineages.  $\Delta AICc$  is the difference between a model's  $AICc$  and the minimum  $AICc$  among fitted models and equals zero when the model is preferred. When  $\Delta AICc$  for the 1VCV model is greater than zero, the two-matrix model, which allows rates and covariances to differ between feeding modes, is preferred. Variation in  $\Delta AICc$  is a result of fitting models to a sample of 1000 phylogeny and feeding mode reconstructions.



**Supplementary Figure 7 Bias in evolutionary rate estimation resulting from within-species variation.** Plot shows bias, which is represented as the ratio of estimated rate of evolution to the true rate of evolution, as a function of the ratio of between- to within-species standard deviation. The ratios of between- to within-species standard deviation for all mechanical unit PC 1s are 6.5 or greater (see Supplementary Table 3), at which point bias in rate estimation is negligible.





**Supplementary Figure 8 Bias in evolutionary correlation estimates resulting from within-species variation and covariation.** Plot shows the estimated evolutionary correlation as a function of within-species correlation for five levels of evolutionary rate, which correspond to varying ratios of between- to within-species standard deviations (sd ratio). The true evolutionary correlation for all simulations was equal to 0.0. Standard deviation ratios for mechanical unit PC 1s were greater than 6.2 (see Supplementary Table 3). These simulations indicate that at this level of between-species variation (i.e., when between-species variation is considerably greater than within-species variation), within-species correlation creates little bias in estimates of evolutionary correlations.

**Supplementary Table 1** Species' feeding mode assignments based on states of four morphological traits that differentiate suction feeders and biters.

Species	Oral jaw teeth	PMxEtV teeth	Mouth shape	Hyom orient	Bite score	Feeding mode
<i>Albula vulpes</i>	0	1	0	0	1	suction
<i>Conger verreaxi</i> (s)	0	0	1	0	1	suction
<i>Conger wilsoni</i>	0	0	1	0	1	suction
<i>Elops saurus</i>	0	1	0	0	1	suction
<i>Gorgasia taiwanensis</i>	0	0	1	0	1	suction
<i>Heteroconger hassi</i>	0	1	0	0	1	suction
<i>Megalops cyprinoides</i>	0	1	0	0	1	suction
<i>Paraconger notialis</i> (s)	0	0	1	0	1	suction
<i>Anguilla anguilla</i>	0	1	1	0	2	suction
<i>Anguilla bicolor</i>	0	1	1	0	2	suction
<i>Anguilla japonica</i>	0	1	1	0	2	suction
<i>Anguilla rostrata</i>	0	1	1	0	2	suction
<i>Ariosoma anago</i>	0	1	1	0	2	suction
<i>Ariosoma balearicum</i>	0	1	1	0	2	suction
<i>Ariosoma shiroanago</i>	0	1	1	0	2	suction
<i>Conger japonicus</i>	0	0	2	0	2	suction
<i>Conger myriaster</i>	0	1	1	0	2	suction
<i>Congresox talabonoides</i>	0	1	1	0	2	suction
<i>Gnathophis longicauda</i> (s)	0	1	1	0	2	suction
<i>Myrichthys breviceps</i>	0	1	1	0	2	suction
<i>Ophichthus zophochir</i>	0	1	1	0	2	suction
<i>Parabathymyrus macrophthalmus</i> (s)	0	1	1	0	2	suction
<i>Poeciloconger kapala</i>	0	1	1	0	2	suction
<i>Rhynchoconger flavus</i> (s)	0	1	1	0	2	suction
<i>Myrichthys maculosus</i>	0	1	1	1	3	suction

Species	Oral jaw teeth	PMxEtV teeth	Mouth shape	Hyom orient	Bite score	Feeding mode
<i>Myrichthys magnificus</i>	0	1	1	1	3	suction
<i>Ophichthus serpentinus</i> (s)	0	1	1	1	3	suction
<i>Scolecenchelys breviceps</i>	0	1	2	0	3	suction
<i>Simenchelys parasitica</i>	0	1	2	0	3	suction
<i>Uroconger lepturus</i>	0	1	1	1	3	suction
<i>Facciolella gilbertii</i> (b)	0	1	3	0	4	bite
<i>Gavialiceps taeniola</i> (b)	0	1	3	0	4	bite
<i>Kaupichthys hyoprroides</i>	0	1	2	1	4	bite
<i>Moringua edwardsi</i>	0	1	2	1	4	bite
<i>Moringua javanica</i>	0	1	2	1	4	bite
<i>Nemichthys scolopaceus</i> (b)	0	1	3	0	4	bite
<i>Nettastoma melanurum</i> (b)	0	1	3	0	4	bite
<i>Oxyconger leptognathus</i> (b)	1	0	3	0	4	bite
<i>Saurenychelys fierasfer</i>	0	1	3	0	4	bite
<i>Venefica proboscidea</i> (b)	0	1	3	0	4	bite
<i>Bathyroconger vicinus</i>	1	2	2	0	5	bite
<i>Ichthyapus ophioneus</i>	0	1	2	2	5	bite
<i>Muraenesox bagio</i>	0	1	2	2	5	bite
<i>Muraenesox cinereus</i>	0	1	2	2	5	bite
<i>Serrivomer beanii</i> (b)	0	2	3	0	5	bite
<i>Serrivomer sector</i>	0	2	3	0	5	bite
<i>Synaphobranchus kaupii</i>	0	1	2	2	5	bite
<i>Kaupichthys nuchalis</i>	1	2	2	1	6	bite
<i>Myrophis vafer</i>	1	2	2	1	6	bite
<i>Pisodonophis cancrivorus</i>	1	2	2	1	6	bite
<i>Brachysomophis crocodilinus</i>	1	2	3	1	7	bite
<i>Cynoponticus ferox</i>	1	2	2	2	7	bite
<i>Dysomma anguillare</i>	1	2	2	2	7	bite

Species	Oral jaw teeth	PMxEtV teeth	Mouth shape	Hyom orient	Bite score	Feeding mode
<i>Scuticaria tigrina</i>	1	2	3	1	7	bite
<i>Gymnothorax castaneus</i>	1	2	3	2	8	bite
<i>Gymnothorax flavimarginatus</i>	1	2	3	2	8	bite
<i>Gymnothorax kidako</i>	1	2	3	2	8	bite
<i>Gymnothorax moringa</i>	1	2	3	2	8	bite
<i>Gymnothorax pseudothyrsoides</i>	1	2	3	2	8	bite
<i>Gymnothorax reticularis</i>	1	2	3	2	8	bite
<i>Rhinomuraena quaesita</i>	1	2	3	2	8	bite
<i>Uropterygius micropterus</i>	1	2	3	2	8	bite

(s), (b) indicate species has been observed to capture prey by suction feeding or biting, respectively.

Oral Jaw Teeth: 0 = short, 1 = long

PMxEtV Teeth (Premaxillo-ethmovomerine Teeth): 0 = absent, 1 = present and short, 2 = present and long

Hyom Orient (Hyomandibular Orientation): 0 = anteriorly directed, 1 = vertical, 2 = posteriorly directed

Mouth Shape: 0 = rounded, 1 = semi-rounded, 2 = notched, 3 = highly notched

**Supplementary Table 2** Summary of principal component (PC) 1 for each mechanical unit.

<b>Mechanical unit</b>	<b>Trait</b>	<b>Jaws PC 1</b>	<b>Hyoid PC 1</b>	<b>Opercular PC 1</b>
<b>Jaws</b>	dentary length	0.68 ± 0.12	---	---
	dentary depth	-0.24 ± 0.36	---	---
	close in-lever	-0.24 ± 0.31	---	---
	open in-lever	-0.55 ± 0.22	---	---
	maxilla length	0.76 ± 0.12	---	---
	PMx-Et-V length	0.78 ± 0.08	---	---
	PMx-Et-V width	-0.18 ± 0.26	---	---
<b>Hyoid</b>	basibr length	---	-0.55 ± 0.05	---
	hyoid length	---	0.78 ± 0.02	---
	hyoid depth	---	-0.65 ± 0.04	---
<b>Opercle</b>	operc length	---	---	0.85 ± 0.01
	operc depth	---	---	0.74 ± 0.03
	suboperc length	---	---	0.77 ± 0.01
	preoperc length	---	---	0.42 ± 0.02
<b>Eigenvalue</b>		2.49 ± 0.03	1.33 ± 0.05	2.05 ± 0.04
<b>% variance</b>		35.5 ± 0.4	44.3 ± 0.2	51.3 ± 0.9

Values are means ± standard error, where standard error is based on phylogenetic PCA performed on a sample of 1000 phylogenetic trees (see Methods for details).

**Supplementary Table 3** Summary of pooled within-species standard deviations for each mechanical unit PC 1 and pooled within-species correlations in suction feeders ( $n = 70$ ) and biters ( $n = 67$ ).

STANDARD DEVIATIONS						
	Within-species			Between-species : Within-species		
	Jaws	Hyoid	Opercle	Jaws	Hyoid	Opercle
<b>Suction</b>	0.117 [0.101, 0.141]	0.064 [0.055, 0.077]	0.100 [0.086, 0.120]	6.56	7.16	8.11
<b>Biting</b>	0.125 [0.107, 0.151]	0.096 [0.082, 0.116]	0.118 [0.101, 0.142]	12.56	10.38	11.36

CORRELATIONS			
	Jaws, Hyoid	Jaws, Opercle	Hyoid, Opercle
	<b>Suction</b>	0.02 [-0.22, 0.25]	0.04 [-0.20, 0.27]
<b>Biting</b>	0.00 [-0.24, 0.24]	-0.04 [-0.28, 0.20]	-0.02 [-0.25, 0.23]

## Supplementary Methods

**Effects of within-species variation on evolutionary rates and correlations.** To determine the effects of within-species variation on our results, we first quantified pooled within-species standard deviations and correlations separately in suction feeders and biters. We determined mechanical unit PC 1 scores for individual specimens following size-correction using the allometric equation obtained from phylogenetic regression of species means and transformation by the eigenvectors for mechanical unit PC 1s obtained by phylogenetic PCA involving species means (see Methods section, *Quantifying mechanical unit morphology*). We subtracted species means from individuals' PC 1 scores to remove the effect of species differences, and we culled individuals that were the sole sample for their species. We then calculated pooled within-species standard deviations for each mechanical unit PC 1, evaluated the correlations between each pair of mechanical units, and determined their 95% confidence intervals. Because the bias in evolutionary rate and correlation estimates will be less when between-species differences are large relative to within-species variation<sup>1,2</sup>, we also calculated the ratio of among-species to within-species standard deviations for each mechanical unit and each feeding mode.

We used numerical simulations to quantify bias in our estimates of evolutionary rates and correlations generated by differing levels of within-species variation in suction feeders and biters. In two instances, comparisons of within-species variation between suction feeders and biters indicated the potential for parameter estimation bias to lead us to commit Type I errors (see below), and we sought to determine the effects of these differences on our results. We simulated species values for two continuous traits given a subsample of 100 elopomorph trees from the Bayesian posterior probability distribution (see Methods section *Reconstructing Phylogenetic and Feeding Mode History*) and a Brownian motion model with a two-by-two

evolutionary rate matrix which contains the evolutionary rates for the two traits on the diagonal and evolutionary covariance on the off-diagonal<sup>3,4</sup>. We performed four sets of simulations, which differed in the specified evolutionary rate matrix. To examine the effects of different amounts of between-species variation, we examined four levels of evolutionary rates ( $\sigma^2_{\text{trait1}} = \sigma^2_{\text{trait2}} = 0.1, 0.5, 1.0, 2.0$ ). We set the evolutionary correlation for all simulations equal to zero in order to determine whether within-species variation and covariation can lead to inference of evolutionary correlation when none exists. We performed one evolutionary simulation per phylogenetic tree using the `sim.char` function of the `geiger`<sup>5</sup> package for R<sup>6</sup>.

For each simulated set of species values, we introduced within-species variation and covariation according to the following procedure. For each species, we sampled between one and four individuals (following our sampling effort) from a bivariate normal distribution with mean vector containing that species' simulated (i.e., true) trait values and covariance matrix containing unit variance for each trait and a specified covariance (see below). We then estimated species values as the means from this sample of individuals. To examine the effect of within-species covariance on estimation of the evolutionary correlation, we generated multiple samples within species for each simulation corresponding to different levels of within-species covariance, which varied between 0.0 and 0.9 by 0.1 increments. Each evolutionary simulation therefore contained 10 sets of species values based on sampling from distributions that differed in the strength of within-species covariance. For each set of species values, we then estimated evolutionary rates and correlations given the tree used in evolutionary simulations (i.e., the true tree) and compared these estimates to their known values.

In general, we found no evidence that within-species variation had a significant effect on our results. Suction feeders and biters exhibit similar within-species standard deviations for the



jaws and opercular series. Although the standard deviation of the hyoid is greater in biters—a difference that could upwardly bias estimates of evolutionary rate in biters and cause a Type I error—our results indicated no difference in the rate of hyoid evolution between feeding modes (Fig. 3). In addition, across all mechanical units and both feeding modes, between-species differences were large relative to within-species standard deviations (see Supplementary Table 3), and numerical simulations under a Brownian motion model of evolution indicate that this level of within-species variation generates little bias in evolutionary rate estimation (Supplementary Fig. 7). Correlations between the jaws and hyoid and between the jaws and opercular series were similar within suction feeding and biting species. The correlation between the hyoid and opercular series was greater in suction feeders than biters (Supplementary Table 3)—another difference that could potentially lead to Type I error—but simulations indicate that this level of within-species correlation only minimally biases evolutionary correlation estimates (Supplementary Fig. 8).

### **Supplementary References**

1. Mehta, R. S. & Wainwright, P. C. Biting releases constraints on moray eel feeding kinematics. *J. Exp. Biol.* **210**, 495-504 (2007).
2. Harmon, L. J. & Losos, J. B. The effect of intraspecific sample size on type I and type II error rates in comparative studies. *Evolution* **59**, 2705-2710 (2005).
3. Felsenstein, J. Comparative methods with sampling error and within-species variation: contrasts revisited and revised. *Am. Nat.* **171**, 713-725 (2008).

4. Revell, L. J. & Harmon, L. J. Testing quantitative genetic hypotheses about the evolutionary rate matrix for continuous characters. *Evol. Ecol. Res.* **10**, 311-331 (2008).
5. Revell, L. J. & Collar, D. C. Phylogenetic analysis of the evolutionary correlation using likelihood. *Evolution* **63**, 1090-1100 (2009).
6. Harmon, L. J., Weir, J. T., Brock, C. D., Glor, R. E. & Challenger, W. GEIGER: investigating evolutionary radiations. *Bioinformatics* **24**, 129-131 (2008).
7. R Development Core Team. R: a language and environment for statistical computing. R Foundation for Statistical Computing, Vienna (2013).