Supporting Information

Rubinoff and Schmitz 10.1073/pnas.0912501107

Fig. S1. *Hyposmocoma* cone case-bearing larvae (arrows) resting communally, hiding in small holes on dry rocks downstream above and under the water line.
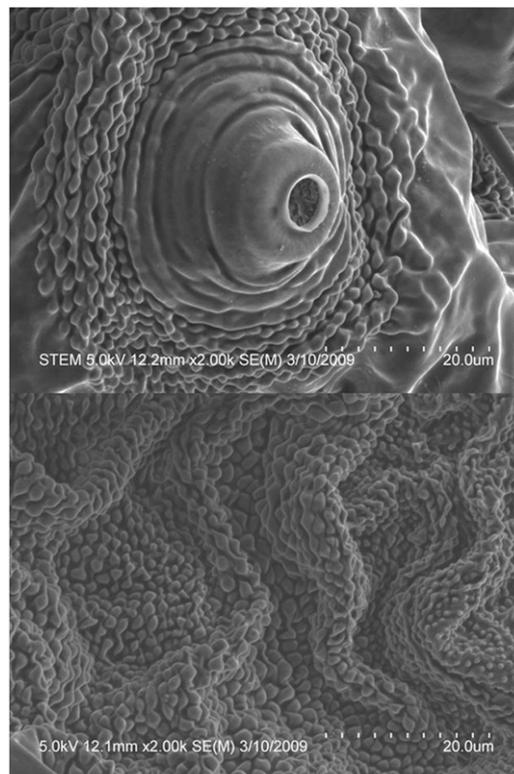
Fig. S2. Scanning electron microscope images taken from an amphibious *Hyposmocoma* larva, showing details of an unmodified spiracle and of the hydrophilic abdominal surface of the cuticle.
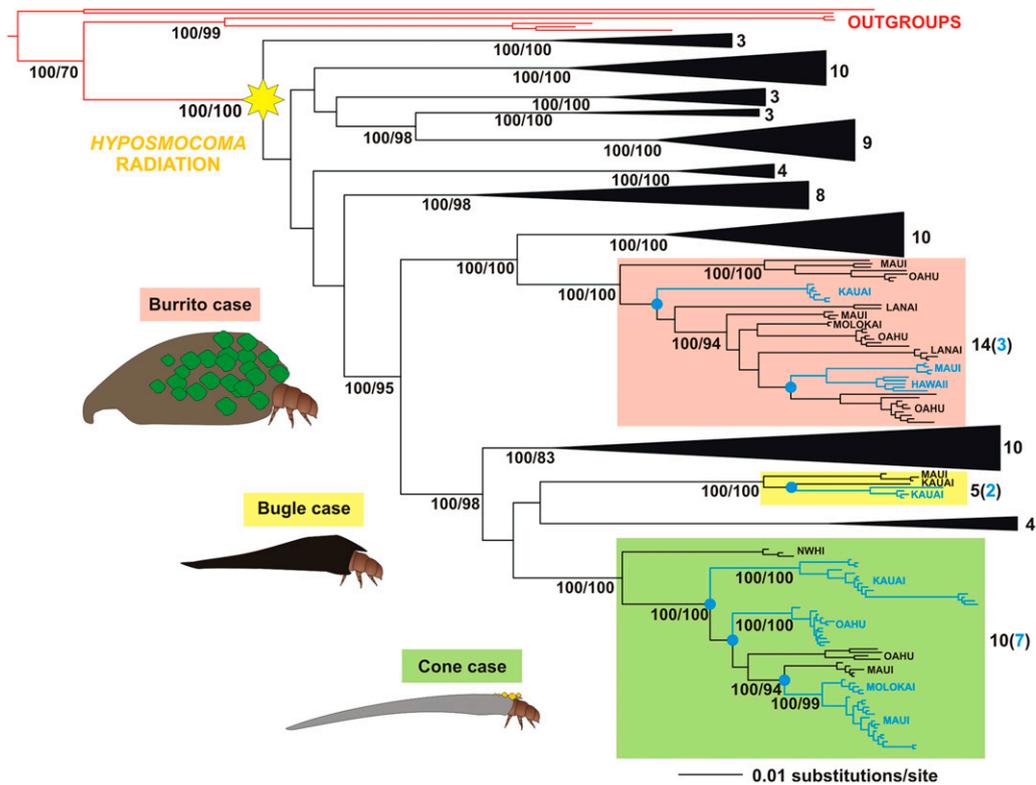
Fig. S3. Phylogeny of *Hyposmocoma* moths based on molecular data with the three lineages including amphibious species highlighted. Shown is the Bayesian tree based on combined analysis of three genes of interest. Bayesian posterior probabilities ≥95 and nonparametric bootstrap supports ≥70 are given under each corresponding node and clade. This topology is congruent with the maximum likelihood topology. Numbers on the right of the different terrestrial clades represent species per clade, with blue numbers in brackets representing total of aquatic species. Blue dots show multiple derivations of the aquatic life history.

Fig. S4. Phylogeny of *Hyposmocoma* moths based on molecular data with the three lineages including amphibious species highlighted. Shown is the maximum likelihood tree based on partitioned analysis of three genes of interest. Bootstrap support values >70 are given under each corresponding node and clade (RAxML/Garli). This topology is congruent with the maximum likelihood (Fig. 3 in main text) and Bayesian topology (Fig. S3). Numbers on the right of the different terrestrial clades represent species per clade, with blue numbers in brackets representing total of aquatic species. Blue dots show multiple derivations of the aquatic life history.

Fig. S5. Phylogeny of *Hyposmocoma* moths based on molecular data with the three lineages including amphibious species highlighted. Shown is the maximum likelihood tree based on separated analyses of three genes of interest. Bootstrap support values >70 are given under each corresponding node and clade (RAxML). Numbers on the right of the different terrestrial clades represent species per clade, with blue numbers in brackets representing total of aquatic species. Yellow star indicates the *Hyposmocoma* radiation.

Fig. S6. Phylogeny of *Hyposmocoma* moths based on molecular data with the three lineages including amphibious species highlighted. Shown is the maximum likelihood tree based on combined analysis of three genes of interest (Fig. 3). Proportional likelihood values of ancestral states are mapped onto each node of interest (red = terrestrial; blue = aquatic). Numbers on the right of the different terrestrial clades represent species per clade, with blue numbers in brackets representing total of aquatic species.

Table S1. Appropriate substitution models and estimated model parameters for data partitions using the Akaike information criterion (AIC)

Ingroup/dataset	Partition	Base pairs	Informative sites	Nucleotide bias (A/T)	Model selected (AIC)	-lnL	I	Γ
Ingroup (209 taxa)	COI	761	274	72	TVM+I+Γ	12,303.69	0.53	0.48
	CAD	708	232	62	TIM+I+Γ	5,549.55	0.50	1.99
	EF1α	773	187	49	GTR+I+Γ	5,427.60	0.58	0.99
	Combined data	2,243	693	61	GTR+I+Γ	24,781.31	0.52	0.58
Dataset (216 taxa)	COI	761	282	72	GTR+I+Γ	13,108.11	0.52	0.42
	CAD	708	260	62	TIM+I+Γ	6,451.04	0.46	1.47
	EF1α	773	210	49	SYM+I+Γ	6,235.21	0.59	1.19
	Combined data	2,243	752	61	GTR+I+Γ	27,499.45	0.50	0.57

Values are presented for the ingroup and the whole dataset. COI, cytochrome oxidase I; CAD, carbomoylphosphate synthase; EF1α, elongation factor 1α; TIM, Transitional Model; TVM, Transversional Model; SYM, Symmetrical Model; GTR, General Time Reversible Model.

Movie S1.   Aquatic burrito case-bearing *Hyposmocoma* larva in stream returning to the substrate with the aid of its silk drag line after being dislodged.

Movie S1.

Movie S2.   Aquatic bugle case-bearing *Hyposmocoma* larva crawling on dry rock, meters from stream.

Movie S2.