

Supplementary tables

Table A1. List of the primers used.

Gene	Name	Sense	Sequence	Reference
<i>cox1</i>	Jerry (M202)	F	CAACATTTATTTTGATTTTTTGG	1
	Pat (M70)	R	TCCA(A)TGCACTAATCTGCCATATTA	1
	Chy	F	T(A/T)GTAGCCCA(T/C)TTTCATTA(T/C)GT	2
	Tom	R	AC(A/G)TAATGAAA(A/G)TGGGCTAC(T/A)A	2
	Tom-2	R	A(A/G)GGGAATCATTGAATAAA(A/T)CC	2
<i>cyb</i>	CB3	F	GAGGAGCAACTGTAATTACTAA	3
	CB4	R	AAAAGAAA(AG)TATCATTGAGTTGAAT	3
<i>rrnL-nad1</i>	16saR (M14)	F	CGCCTGTTTA(A/T)CAAAAACAT	1
	16Sa	R	ATGTTTTTGTAAACAGGCG	1
	16Sb	R	CCGGTCTGAACTCAGATCATGT	1
	16SAIf1	R	GCATCACAAAAAGGCTGAGG	4
	ND1A (M223)	R	GGTCCCTTACGAATTTGAATATATCCT	1
	16Sbi	F	ACATGATCTGAGTTCAAACCGG	1
	FawND1	R	TAGAATTAGAAGATCAACCAGC	1
<i>rrnS</i>	12S ai	F	AAACTAGGATTAGATACCCTATTAT	1
	12S bi	R	AAGAGCGACGGGCGATGTGT	1
<i>SSU</i>	5'	F	GACAACCTGGTTGATCCTGCCAGT	5
	b5.0	R	TAACCGCAACAACCTTAAAT	5
<i>LSU</i>	Ka	F	ACACGGACCAAGGAGTCTAGCATG	2
	Kb	R	CGTCCTGCTGCTTAAGTTAC	2

¹ Simon C., Frati F., Beckenbach A., Crespi B., Liu H. & Flook P. 1994: Evolution, weighting, and phylogenetic utility of mitochondrial gene-sequences and a compilation of conserved polymerase chain-reaction primers. *Ann. ent. Soc. Am.* 87: 651-701.

² Ribera I., Fresneda J., Bucur R., Izquierdo A., Vogler A.P., Salgado J.M. & Cieslak A. 2010: Ancient origin of a Western Mediterranean radiation of subterranean beetles. *BMC Evolutionary Biology* 10: 29.

³ Barraclough T.G., Hogan J.E. & Vogler A.P. 1999: Testing whether ecological factors promote cladogenesis in a group of tiger beetles (Coleoptera : Cicindelidae). *Proc R Soc Lond B* 266(1423):1061-1067.

⁴ Vogler A.P., Desalle R., Assmann T., Knisley C.B. & Schultz T.D. 1993: Molecular population genetics of the endangered tiger beetle *Cicindela dorsalis* (Coleoptera, Cicindelidae). *Ann ent Soc Am* 86: 142-152.

⁵ Shull V.L., Vogler A.P., Baker M.D., Maddison D.R., Hammond P.M. 2001: Sequence alignment of 18S ribosomal RNA and the basal relationships of Adephagan beetles: evidence for monophyly of aquatic families and the placement of Trachypachidae. *Syst. Biol.*, 50: 945-969.

Table A2. Results of age versus range-size regressions.

Lineage	R²	slope	slope different 0?	linear vs. quadratic
<i>Ilybius</i>	0.007	0.011	$F_{1,25} = 0.18, p = 0.676$	$F_{1,24} = 1.12, p = 0.302$
<i>Deronectes</i>	0.006	-0.022	$F_{1,22} = 0.14, p = 0.710$	$F_{1,21} = 0.89, p = 0.355$
<i>Enicocerus</i>	0.047	0.034	$F_{1,7} = 0.35, p = 0.573$	$F_{1,6} = 0.11, p = 0.756$
<i>Limnebius</i>	0.1	3.545	$F_{1,8} = 0.89, p = 0.373$	$F_{1,7} = 0.43, p = 0.532$
<i>H. gracilis</i>	0.072	0.528	$F_{1,12} = 0.93, p = 0.353$	$F_{1,11} = 0.70, p = 0.421$
<i>H. dentipes</i>	0.258	0.303	$F_{1,18} = 6.27, p = 0.022$	$F_{1,17} = 0.34, p = 0.570$
<i>Phothydraena</i>	0.000	0.003	$F_{1,7} = 0.00, p = 0.986$	$F_{1,6} = 0.81, p = 0.404$
<i>Graptodytes</i>	0.000	0.013	$F_{1,16} = 0.01, p = 0.942$	$F_{1,15} = 2.47, p = 0.137$
<i>Hydroporus</i>	0.129	0.125	$F_{1,28} = 4.18, p = 0.050$	$F_{1,27} = 0.26, p = 0.613$
<i>Hydrochus</i>	0.014	0.039	$F_{1,11} = 0.16, p = 0.701$	$F_{1,10} = 0.00, p = 0.989$

Table A3. Results of phylogenetic comparative tests for associations between the northern latitudinal limit of geographic species' range and biogeographical and ecological variables using Phylogenetic Generalized Least Squares.

		maxLon	minLon	minLat	LonC	LatC	aveB	nB	Hab
<i>Ilybius</i>	α	15.5	15.5	15.5	15.5	15.5	15.5	15.5	
	r	0.20	-0.35	0.26	-0.14	0.91	0.14	0.44	--
	P	0.254	0.101	0.068	0.589	0.000*	0.520	0.076	
<i>Deronectes</i>	α	15.5	15.5	15.5	15.5	15.5	15.5	15.5	
	r	0.31	-0.09	0.27	0.15	0.8	0.54	0.57	--
	P	0.094	0.957	0.153	0.341	0.000*	0.004*	0.004*	
<i>Enicocerus</i>	α	15.5	15.5	15.5	15.5	2.69	15.5	15.5	
	r	0.58	0.22	0.19	0.47	0.96	0.64	0.72	--
	P	0.105	0.571	0.631	0.207	0.000*	0.063	0.028	
<i>Limnebius</i>	α	0.98	0.81	0.70	0.56	5.97	0.64	15.5	
	r	0.812	-0.171	0.26	0.59	0.96	-0.04	0.79	--
	P	0.005	0.680	0.467	0.072	0.000*	0.870	0.008	
<i>H. gracilis</i>	α	15.5	2.81	11.17	15.5	1.20	15.5	15.5	
	r	0.57	-0.53	0.18	0.3	0.97	0.33	0.43	--
	P	0.031	0.192	0.584	0.280	0.000*	0.232	0.108	
<i>H. dentipes</i>	α	2.25	0.99	0.80	1.50	15.50	1.44	2.37	
	r	0.76	0.06	0.37	0.53	0.96	0.48	0.77	--
	P	0.000*	0.469	0.081	0.004*	0.000*	0.008	0.000*	
Phothydraena	α	15.5	15.5	15.5	15.5	15.5	15.5	15.5	5.03
	r	0.1	-0.3	0.37	-0.11	0.93	0.14	0.59	0.83
	P	0.860	0.411	0.276	0.730	0.000*	0.796	0.100	0.014
<i>Graptodytes</i>	α	6.89	2.07	6.70	5.79	15.50	3.34	6.06	2.90
	r	0.70	-0.42	0.34	0.4	0.87	0.58	0.720	0.05
	P	0.000*	0.212	0.054	0.041	0.000*	0.009	0.000*	0.871
<i>Hydroporus</i>	α	15.50	2.13	9.66	15.50	15.50	6.67	15.50	6.10
	r	0.82	-0.38	0.36	0.6	0.95	0.59	0.79	0.59
	P	0.000*	0.138	0.038	0.001	0.000*	0.000*	0.000*	0.000*
<i>Hydrochus</i>	α	4.24	2.58	2.88	3.42	6.00	15.50	4.50	2.36
	r	0.61	-0.27	-0.34	0.23	0.86	0.55	0.51	0.51
	P	0.024	0.422	0.229	0.421	0.000*	0.050	0.069	0.102

The maximum likelihood estimate of evolutionary constraint (α) is provided, and parameter estimates given that maximum likelihood. Significant correlations are indicated with boldface type. Asterisk indicates significant p-values after Bonferroni correction for multiple tests ($p < 0.005$). Codes as in Table 2; Hab, habitat preference (lotic, lentic or both).