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Supplemental Information

Diversity in Morphology and Locomotory Behavior

Is Associated with Niche Expansion

in the Semi-aquatic Bugs

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Figure S1: Phylogeny and ancestral character state reconstruction. Related to Figure 1, Figure 2 and Figure S4, Table S1, Table S2.

(A) Phylogenetic relationships between species sampled for this study. Phylogenetic construction of our sample using both Maximum Likelihood (bootstrap in black) and Bayesian methods (posterior probability in blue). (B) Phylogenetic reconstruction of ancestral state of speed of locomotion in the Gerromorpha and terrestrial outgroups. Increased speed is a derived state and correlates with preference for water surface habitat. (C) Phylogenetic reconstruction of ancestral state of stroke frequencies. Increased stroke frequency is a derived state and correlates with preference for water surface habitat for species using the tripod gait but not for species using the rowing gait. Phylogenetic reconstruction of ancestral state of the ratio leg length by body length for the foreleg (D), the midleg (E) and the hindleg (F). The elongated midleg is a derived state and correlates with preference for water surface habitat. Phylogenetic signals λ and associated significance are indicated for each ancestral reconstruction.

Figure S2: Ratio of leg length to body length across heteroptera including fossil record. Related to Figure 2, Table S2.

Phylogenetic relationships and ratios of leg length by body length across a sample of extant and extinct Heteropteran species. Extant Gerromorpha have generally longer legs than terrestrial relatives. *O.fas*, *Oncopeltus fasciatus*; *Y.mag*, *Yuripopovina magnifica* [S1]; *H.vas*, *Hypsipteryx vasarhelyii* [S2]; *L.pop*, *Libanohypselosoma popovi* [S3, S4]; *M.dom, Mesovelia dominicana* [S5]; *M.and*, *Miohebrus anderseni* [S5]; *C.bra*, *Cretaceometra brasiliensis* [S6]; *P.bor*, *Perittopus borneensis* [S7]; *P.asi*, *Perittopus asiaticus* [S7]; *R.obe, Rhagovelia obesa*; *V.cap*, *Velia caprai*; *H.ele, Halovelia electrodominica* [S8]; *M.ele, Microvelia electra* [S9]; *M.gri*, *Microvelia grimaldii* [S9]; *M.pol*, *Microvelia polhemi* [S10]; *C.alb, Cretogerris albianus* [S11]; *E.spi*, *Electrobates spinipes* [S12]; *M.hes, Metrobates hesperius*. Red asterisks indicate extinct species. Error bars represent the standard deviation.

Figure S3: Stroke frequency and leg motion pattern across the Gerromorpha and terrestrial outgroups. Related to Figure 3, Figure 4 and Figure S4, Table S1, Table S3.

(A) Quantification of stroke frequencies during locomotion on ground (green bars) and on water (blue bars). Low stroke frequencies for species using the tripod gait are associated with life on ground. High stroke frequencies are associated with life on water surface for species using the tripod gait. Low stroke frequencies are associated with life on water surface only for species using the derived rowing gait. (B) Analysis of leg motion pattern on ground showing that the stance phase is longer than the swing phase for species using the tripod gait. (C) The same analysis on water showing that species with preference for water and using the tripod gait have similar stance and swing phases whereas species with preference for ground still have a longer stance phase than swing phase. Derived species using the rowing gait have a shorter stance phase compared to swing phase. This pattern is associated with life on water surface. Error bars represent standard deviation.

 0.8

 0.6

 04

 0.2

 $\overline{0}$

 -0.2

 -0.4

 -0.6 -0.8

*** P-value < 0.01 **** P-value < 0.001 * P-value < 0.1 ** P-value < 0.05 FDR adjustment of P-values for multiple comparisons

Figure S4: Matrix of correlation for the different correlation tests performed. R**elated to Figure 1, Figure 2, Figure 3, Figure 4 and Figure S1, Figure S3 and Table S1.**

(A) Matrix of correlation for the whole dataset (tripod gait and rowing gait) and for (B) the dataset of species using only the tripod gait. Squares and number indicates the rho of the Sperman correlation test conducted with phylogenetic correction (PIC). FDR adjustment of P-values for multiple comparisons is applied. Stars indicate the P-values.

Table S1: Data of locomotion characteristics across the sample of species tested. Related to Figure 1, Figure 2, Figure 4, Figure S1, Figure S3. Mean values for speed in centimeters per second (cm/s) and body length per second (bl/s) and stroke frequency in number of strokes per second (st/s), on ground and water for species analyzed with sample size (N) . \pm Indicates the standard deviation. NA: not available. Energy expenditure per stroke and per second for each species with the associated mean weight. Highlighted in clear grey are species using the tripod gait and in dark grey are species using the rowing gait. Student t-tests are performed to compare the mean energy expenditure per stroke and per second between the two ways of locomotion.

Table S2: Mean values for leg length and body length with corresponding ratios. Related to Figure 1, Figure 2, Figure 4, Figure S1, Figure S2. Habitat preference, number of individuals and collecting locations or references for each extant or fossil (*) species used in this study are provided. ± indicates the standard deviation. These data are plotted in Figure S2.

Table S3: Comparison of leg deployment and amplitude of movements during ground locomotion and locomotion on water surface. Related to Figure 3.

The locomotion of *Hebrus sp.*, *Mesovelia furcata*, *Microvelia americana* and *Gerris buenoi* are analysed. There is no important differences between ground and water locomotion for *Hebrus sp.*. The hindleg and mostly the midleg become more important during water surface locomotion in *Mesovelia* and *Microvelia*. Midleg is the most important leg for locomotion in *Gerris*. Each number is a mean of 18 measurements for *Hebrus sp.*, *Mesovelia furcata* and *Microvelia americana* and a mean of 6 values for *Gerris buenoi.* (±) indicates standard deviation. Student t- tests were performed.

Movie S1: Comparison between tripod gait and rowing gait during water surface locomotion. *Mesovelia furcata* using the tripod gait (top) and *Gerris buenoi* using the rowing gait (bottom) during water surface locomotion. Videos were taken on a grid for size reference.

Supplemental experimental procedures

Insect sampling and culture

Extant specimens were collected during fieldwork in the locations indicated in Table S2. All species were kept in water tanks at 25°C, 55% humidity, 14 hours of day light and fed on live crickets.

Phylogenetic reconstruction

Sequences were retrieved from in house transcriptome and genomic sequence databases for the following markers: *12S RNA*; *16S RNA*; *18S RNA*; *28S RNA*; *Cytochrome Oxydase subunit I* (*COI*); *Cytochrome Oxydase subunit II* (*COII*); *Cytochorme Oxydase subunit III* (*COIII*); *Cytochrome b* (*cyt b*); *NADH-ubiquinone oxidoreductase chain 1* (*ND1*); *Ultrabithorax* (*Ubx*); *Sex combs reduced* (*Scr*); *Gamma interferon inducible thiol reductase* (*gilt*); *Antennapedia* (*Antp*); *Distal-less* (*dll*). All these markers were submitted to GenBank and their accession numbers can be found in the Dryad Digital Repository: http://dx.doi.org/10.5061/dryad.134c4. Sequences were aligned with MAFFT version 7.017 [S13] using default parameters. The alignments were visualized, corrected and concatenated in Geneious Version 7.1.9. Phylogenetic analysis was performed with MRBAYES version 3.2.6 [S14] (1 million generations; 25% burnin) and PhyML version 3.0 [S15], using GTR model with 100 bootstraps. Concatenation of sequence alignments and phylogenetic tree in Newick format are also available in the Dryad Digital Repository: http://dx.doi.org/10.5061/dryad.134c4.

Habitat classification

Andersen [S16, S17] classified the various habitats of the Gerromorpha into eight classes: (1) terrestrial habitat far from water, (2) humid terrestrial habitat such as litter or humid gravel not necessary close to water, (3) marginal aquatic comprising moss, plants or rocks close to water, (4) plant-covered water surface, (5) water surface (with some plants), (6) streaming water with hood debris and foam, (7) stagnant water (such as ponds), (8) flowing water (such as streams). For simplicity, we consolidated these classes into the following four: terrestrial (Andersen's 1 and 2); marginal aquatic with preference for solid substrates (Andersen's 3); marginal aquatic with preference for water surface (Andersen's 4 and 5); and open water surface (Andersen's 6, 7 and 8). Each species was assigned to one of these four classes based on previous descriptions [S16-S20] and on the environment where we caught them.

Video acquisition, quantification of speed and stroke frequency

A set of adult individuals for each species were filmed at 2000 frames per second, both on water surface and on a solid substrate with a grid paper in the background as a calibration scale. Video acquisition was performed using the Phantom *Miro M310* Digital High Speed *Camera* and PCC Software (Vision research, Ametek). Videos were analyzed using TEMA 3.7 software (Images system) to extract speed values. To calculate speed, a mean value was extracted from a defined interval plateau phase from velocity curve along each video. This interval represents the max speed during the run of the individual. For speed, sample sizes were (on land/on water): *P. apt* (n=14/Not Applicable (NA)); *C. ali* (n=14/NA); *H.* sp*.* (n=10/10); *H. sta* (n=10/10); *M. fur* (n=10/12); *P. bul* (n=10/10); *M. ame* (n=9/8); *O. cun* (n=10/8); *S. str* (n=10/10); *S. ter* (n=10/11); *P. bra* (n=NA/18); *P. con* (n=10/3); *H. tur* (n=9/10); *G. bue* (n=8/8); *L. dis* (n=NA/8); *A. pal* (n=NA/8). Stroke frequency was determined as the number of strokes performed by the individuals during a given locomotion duration and converted into number of strokes per second. For stroke frequency, sample sizes were (on land/on water): *P. apt* (n=14/NA); *C. ali* (n=14/NA); *H.* sp*.* (n=10/10); *H. sta* (n=10/10); *M. fur* (n=10/12); *P. bul* (n=10/10); *M. ame* (n=10/9); *O. cun* (n=10/10); *S. str* (n=10/10); *S. ter* (n=10/22); *P. bra* (n=NA/35); *P. con* (n=10/6); *H. tur* (n=9/10); *G. bue* (n=8/8); *L. dis* (n=NA/8); *A. pal* (n=NA/8).

Measurements of leg length and body length

Measurements of the legs and body were performed using a SteREO Discovery V12 (Zeiss) with ZEN 2011 software (Zeiss). Body and leg length of the fossil species in (Figure S3) were extracted from the references in Table S1 and in the supplementary online information. Sample sizes used to perform these measurements were: *P. apt:* (n=10); *O. fas:* (n=10)*; Y. mag:* (n=1); *C. ali:* (n=6)*; H. vas:* (n=1); *L. pop:* (n=1); *S. meg:* (n=1); *M. dom:* (n=1); *M. fur:* (n=10)*; M. and:* (n=1); *H. sp:* (n=9)*; C. bra:* (n=1); *H. sta:* (n=10)*; P. bor:* (n=1); *P. asi:* (n=1); *R. obe:* (n=10)*; S. str:* (n=8)*; S. ter:* (n=10); *P. bra:* (n=3); *V. cap:* (n=6)*; O. cun:* (n=10); *P. bul:* (n=5)*; P. bip:* (n=1); *P. con:* (n=1); *H. ele:* (n=1); *H. tur:* (n=6)*; M. ele:* (n=1); *M. gri:* (n=1); *M. pol:* (n=1); *M. ame:* (n=10)*; C. alb:* (n=1); *E. spi:* (n=1); *M. hes:* (n=10)*; L. dis:* (n=10)*; G. bue:* (n=6); *A. pal:* (n=8)*.*

Analysis of leg pattern during locomotion

The deployment of the leg (distance from the body to the tip of the leg) and the amplitude of leg movement (distance between the point where the leg starts to push on substrate and the point where it loses contact with substrate) were extracted from the high-speed videos. To measure these parameters we took 3 videos on ground and 3 videos on water for *Hebrus sp., Mesovelia furcata* and *Microvelia americana*. In each video we extracted 6 strokes (n=18) to obtain an average of leg deployment and the amplitude of leg movements for the three legs. For *Gerris buenoi* we used 6 videos with 1 stroke per video (n=6). Measurements were performed using Image J software [S21]. To measure the duration of stance phases and swing phases we extracted 6 gait cycles for each species from our high-speed videos during both locomotion on ground and locomotion on water. Then we recorded the duration of each phases using the PCC Software (Vision research, Ametek).

Reconstruction of ancestral trait

Ancestral reconstruction for habitat was performed in Rstudio version 0.99.486 using a maximum likelihood method adapted to discrete characters (ace, package ape, [S22]) and represented using phytools [S23]. The simplest model "ER", with equal transition rates across all 4 habitat categories, was the best both with AIC and likelihood comparisons (p value = 0.28 for comparison ER and SYM; failure of convergence of ARD model). The pies for ancestral nodes represent marginal ancestral states. We reconstructed the ancestral value of the quantitative characters on the internal nodes of the phylogenetic tree using contMap (ML reconstructions, package Phytools, [S23]). The resulting figures are maps of the observed and ancestral reconstructed phenotypic trait values onto the tree using a color gradient. This was done for the different variables (T1-leg/Body, T2 leg/Body, T3-leg/Body, speed, stroke frequency). The R script used and the data are available in the Dryad Digital Repository: http://dx.doi.org/10.5061/dryad.134c4.

Inference of energy consumption

We inferred the amount of energy spent per stroke based on the procedure from [S24]. Kinetic energy (E_k in Joules) used during a stroke is determined using the following expression:

 $E_k = 0.5$ mv²

where m is the mass of the insect in grams and v the velocity generated during one stroke in meters per second. The analyses were performed using speed data extracted from the high-speed movies. We first extracted, using PCC software (Vision research, Ametek), the time of takeoff that corresponds to the interval of time when the leg starts to apply pressure on the substrate until the leg loses contact with the substrate. The distance travelled during this interval of time is recorded using ImageJ [S21] and a takeoff velocity is calculated. Pools of live insects were weighted to determine a mean weight for one individual for each species. Then the energy per stroke is calculated using the mass and the takeoff velocity. Because individuals from *Paravelia bullialata, Stridulivelia strigosa, Platyvelia brachialis,* and *Husseyella turmalis* died during the interval of time between video acquisition and weight recording, the samples were conserved in absolute ethanol and rehydrated using the procedure from [S25] to obtain body mass. Control of rehydration was performed on dead insects compare to live specimens from a control species to evaluate the accuracy of the protocol (data not shown). The numbers of individuals per species weighted are the following: *M. fur:* (n=10)*; M. ame:* (n=10)*; O. cun:* (n=10); *P. bul:* (n=4)*; S. str:* (n=6)*; S. ter:* (n=10); *P. bra:* (n=3); *H. tur:* (n=5)*; L. dis:* (n=6)*; G. bue:* (n=5); *A. pal:* (n=6)*.* The numbers of videos used to measure the take-off velocity are the following: *M. fur:* (n=12)*; M. ame:* (n=10)*; O. cun:* (n=10); *P. bul:* (n=10)*; S. str:* (n=10)*; S. ter:* (n=22); *P. bra:* (n=12); *H. tur:* (n=10)*; L. dis:* (n=8)*; G. bue:* (n=8); *A. pal:* (n=8)*.*

Statistical analyses

The quantitative variables (T1-leg/Body, T2-leg/Body, T3-leg/Body, speed, stroke frequency) did not follow a normal distribution (Shapiro tests), and hence were log-transformed and a mean value is calculated for each species and for each variable. The "habitat" variable is semi-quantitative and was not log transformed. Because habitat and speed did not follow a normal distribution we performed a classical non-parametric Spearman correlation test and non-parametric Spearman correlation test with Phylogenetic Independent Contrast (PIC) in order to take into account for the non independence of data points resulting from a phylogeny ([S26]; implemented in ape version 3.5 and Picante version 1.6-2 packages [S22, S27]). FDR P-value correction for multiple tests was applied (rho and P-value are indicated on figures). Parametric Pearson correlation test with and without PIC correction were also performed. These results are available in supplementary online information available in the Dryad Digital Repository: http://dx.doi.org/10.5061/dryad.134c4. For the quantification of leg deployment and leg movement, statistical significance between ground and water locomotion was determined by performing a Student t-tests. P-values are indicated in Table S3. Comparison of energy expenditure between species using the tripod gait and species using the rowing gait is performed using a non-parametric Wilcoxon test and graphically represented using the scatterplot3d version 0.3-37 package. Results are indicated in Table

S1. Statistical analyses were performed using RStudio Version 0.99.486 [S28]. Graphs were made using both RStudio and GraphPad Prism (version 6.01). Correlation matrixes were made using Picante version 1.6-2 package for the calculation and Corrplot version 0.77 package for the graphs [S29]. The R script used and the data are available in the Dryad Digital Repository: http://dx.doi.org/10.5061/dryad.134c4.

Online ressources

Genbank accession numbers as well as sequence alignments for phylogenetic and tree reconstruction, the R script and dataset table used for phylogenetic and statistical analyses can be found in Dryad. Data available from the Dryad Digital Repository: http://dx.doi.org/10.5061/dryad.134c4.

Supplemental references

- S1. D. Azar, A. Nel, M. S. Engel, R. Garrouste, and Matocq, A. (2011). A new family of Coreoidea from the Lower Cretaceous Lebanese amber (Hemiptera: Pentatomomorpha). . Polish Journal of Entomology, 627-644.
- S2. Redei, D. (2007). A new species of the family Hypsipterygidae from Vietnam, with notes on the hypsipterygid fore wing venation (Heteroptera, Dipsocoromorpha). Deut Entomol Z *54*, 43-50.
- S3. Azar, D., and Nel, A. (2010). The earliest fossil schizopterid bug (Insecta: Heteroptera) in the Lower Cretaceous amber of Lebanon. Ann Soc Entomol Fr *46*, 193-197.
- S4. Yao, Y.Z., Zhang, W.T., and Ren, D. (2012). The first report of Mesoveliidae (Heteroptera: Gerromorpha) from the Yixian Formation of China and its taxonomic significance. Alcheringa *36*, 107- 116.
- S5. Garrouste, R., and Nel, A. (2010). First semi-aquatic bugs Mesoveliidae and Hebridae (Hemiptera: Heteroptera: Gerromorpha) in Miocene Dominican amber. Insect Syst Evol *41*, 93-102.
- S6. Nel, A., and Popov, Y.A. (2000). The oldest known fossil Hydrometridae from the Lower Cretaceous of Brazil (Heteroptera : Gerromorpha). J Nat Hist *34*, 2315-2322.
- S7. Zettel, H. (2001). Five new species of Perittopus Fieber, 1861 (Hemiptera : Veliidae) from Southeast Asia. Raffles B Zool *49*, 109-119.
- S8. Andersen, N.M., and Poinar, G.O. (1998). A marine water strider (Hemiptera : Veliidae) from Dominican amber. Entomol Scand *29*, 1-9.
- S9. Andersen, N.M. (2000). Fossil water striders in the Oligocene/Miocene Dominican amber (Hemiptera : Gerromorpha). Insect Syst Evol *31*, 411-431.
- S10. Andersen, N.M. (1999). Microvelia polhemi, n. sp (Heteroptera : Veliidae) from Dominican amber: The first fossil record of a phytotelmic water strider. J New York Entomol S *107*, 135-144.
- S11. Perrichot, V., Nel, A., and Neraudeau, D. (2005). Gerromorphan bugs in Early Cretaceous French amber (Insecta : Heteroptera): first representatives of Gerridae and their phylogenetic and palaeoecological implications. Cretaceous Res *26*, 793-800.
- S12. Andersen, N.M., and Poinar, G.O. (1992). Phylogeny and Classification of an Extinct Water Strider Genus (Hemiptera, Gerridae) from Dominican Amber, with Evidence of Mate Guarding in a Fossil Insect. Z Zool Syst Evol *30*, 256-267.
- S13. Katoh, K., Misawa, K., Kuma, K., and Miyata, T. (2002). MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Res *30*, 3059-3066.
- S14. Huelsenbeck, J.P., and Ronquist, F. (2001). MRBAYES: Bayesian inference of phylogenetic trees. Bioinformatics *17*, 754-755.
- S15. Guindon, S., and Gascuel, O. (2003). A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. Syst Biol *52*, 696-704.
- S16. Andersen, N.M. (1979). Phylogenetic Inference as Applied to the Study of Evolutionary Diversification of Semiaquatic Bugs (Hemiptera, Gerromorpha). Syst Zool *28*, 554-578.
- S17. Andersen, N.M. (1982). The semiaquatic bugs (Hemiptera: Gerromorpha). Volume Entomonograph Vol. 3. , (Klampenborg, Denmark.: Scandinavian Science Press LTD.).
- S18. Dias-Silva, K., Moreira, F.F.F., Giehl, N.F.D., Nobrega, C.C., and Cabette, H.S.R. (2013). Gerromorpha (Hemiptera: Heteroptera) of eastern Mato Grosso State, Brazil: checklist, new records, and species distribution modeling. Zootaxa *3736*, 201-235.
- S19. Heiss, E., and Pericart, J. (2007). Faune n° 91 Hémiptères Aradidae, Piesmatidae et Dipsocoromorphes, (Fédération Française des Sociétés de Sciences naturelles).
- S20. Schuh, R.T., and Slater, J.A. (1995). True bugs of the world (Hemiptera: Heteroptera) : classification and natural history, (Ithaca ; London: Comstock Publishing Associates, a division of Cornell University Press).
- S21. Schneider, C.A., Rasband, W.S., and Eliceiri, K.W. (2012). NIH Image to ImageJ: 25 years of image analysis. Nat Methods *9*, 671-675.
- S22. Paradis, E., Claude, J., and Strimmer, K. (2004). APE: Analyses of Phylogenetics and Evolution in R language. Bioinformatics *20*, 289-290.
- S23. Revell, L.J. (2012). phytools: an R package for phylogenetic comparative biology (and other things). Methods Ecol Evol *3*, 217-223.
- S24. Burrows, M., and Dorosenko, M. (2014). Jumping mechanisms in lacewings (Neuroptera, Chrysopidae and Hemerobiidae). J Exp Biol *217*, 4252-4261.
- S25. Ungureanu, E.M. (1972). Methods for dissecting dry insects and insects preserved in fixative solutions or by refrigeration. Bull. Wld Hlth Org. *47*, 239-244.
- S26. Felsenstein, J. (1985). Phylogenies and the Comparative Method. Am Nat *125*, 1-15.
- S27. Kembel, S.W., Cowan, P.D., Helmus, M.R., Cornwell, W.K., Morlon, H., Ackerly, D.D., Blomberg, S.P., and Webb, C.O. (2010). Picante: R tools for integrating phylogenies and ecology. Bioinformatics *26*, 1463-1464.
- S28. Team, R. (2015). RStudio: Integrated Development for R. .
- S29. Garland, T., Harvey, P.H., and Ives, A.R. (1992). Procedures for the Analysis of Comparative Data Using Phylogenetically Independent Contrasts. Syst Biol *41*, 18-32.