

Table 2. Allometric scaling of tracheal and exoskeletal structures (volume and cross-sectional areas) with body mass (mg) in four species of tenebrionid beetles ($\log_{10} Y = \text{intercept} + \text{slope} \times \log_{10} \text{body mass}$)

A	Standard major axis (1) line-fit on phylogenetically independent contrasts; phylogenetic correction based on tree with all branch lengths set to one (2)							
	Slope	SE	<i>r</i>	<i>t</i> _{Comp}	<i>p</i> _{Comp}	SI _{Hyp}	<i>t</i> _{Hyp}	<i>p</i> _{Hyp}
Log tracheal volume, ml	1.294	0.061	0.998	4.824	0.040	1	5.861	0.028
Log head orifice, mm ²	0.622	0.024	0.999	1.842	0.207	0.67	2.381	0.140
Log head trachea, mm ²	0.783	0.040	0.997	2.909	0.101	0.67	2.972	0.097
Log leg orifice, mm ²	0.770	0.062	0.993	1.670	0.237	0.67	1.651	0.240
Log leg trachea, mm ²	1.024	0.024	0.999	15.140	0.004	0.67	20.20	0.002

B	Standard major axis line-fit on phylogenetically independent contrasts; phylogenetic correction based on tree of figure 51 ref. 3							
	Slope	SE	<i>r</i>	<i>t</i> _{Comp}	<i>p</i> _{Comp}	SI _{Hyp}	<i>t</i> _{Hyp}	<i>p</i> _{Hyp}
Log tracheal volume, ml	1.284	0.060	0.998	0.120	0.908	1	4.745	0.042
Log head orifice, mm ²	0.617	0.024	0.998	0.153	0.883	0.67	2.029	0.180
Log head trachea, mm ²	0.772	0.042	0.997	0.182	0.862	0.67	2.504	0.129
Log leg orifice, mm ²	0.754	0.064	0.993	0.168	0.872	0.67	1.373	0.303
Log leg trachea, mm ²)	1.026	0.023	0.9995	0.088	0.933	0.67	15.91	0.004

C	Ordinary least-square regression on phylogenetically independent contrasts; phylogenetic correction based on tree in Fig. 3 (see Table 1)							
	Slope	SE	<i>r</i>	<i>t</i> _{Comp}	<i>p</i> _{Comp}	SI _{Hyp}	<i>t</i> _{Hyp}	<i>p</i> _{Hyp}
Log tracheal volume, ml	1.291	0.061	0.998	0.033	0.974	1	4.776	0.041
Log head orifice, mm ²	0.621	0.024	0.999	0.027	0.979	0.67	1.881	0.201
Log head trachea, mm ²	0.781	0.040	0.997	0.036	0.972	0.67	2.858	0.104
Log leg orifice, mm ²	0.765	0.062	0.993	0.057	0.956	0.67	1.589	0.253
Log leg trachea, mm ²	1.023	0.024	0.999	0.016	0.988	0.67	15.12	0.004

D	Standard major axis line-fit on species mean values without phylogenetic correction							
	Slope	SE	<i>r</i>	<i>t</i> _{Comp}	<i>p</i> _{Comp}	SI _{Hyp}	<i>t</i> _{Hyp}	<i>p</i> _{Hyp}
Log tracheal volume, ml	1.264	0.041	0.999	0.408	0.697	1	6.439	0.023
Log head orifice, mm ²	0.607	0.018	0.999	0.532	0.614	0.67	3.356	0.078
Log head trachea, mm ²	0.750	0.033	0.998	0.641	0.545	0.67	2.518	0.128
Log leg orifice, mm ²	0.721	0.049	0.995	0.610	0.564	0.67	1.117	0.380
Log leg trachea, mm ²	1.016	0.037	0.998	0.173	0.868	0.67	9.459	0.011

E	Ordinary least-square regression analysis on species mean values without phylogenetic correction							
	Slope	SE	<i>r</i>	<i>t</i> _{Comp}	<i>p</i> _{Comp}	SI _{Hyp}	<i>t</i> _{Hyp}	<i>p</i> _{Hyp}
Log tracheal volume, ml	1.264	0.040	0.999	0.416	0.692	1	6.664	0.022
Log head orifice, mm ²	0.606	0.018	0.999	0.549	0.603	0.67	3.377	0.078
Log head trachea, mm ²	0.748	0.033	0.998	0.672	0.526	0.67	2.455	0.134
Log leg orifice, mm ²	0.718	0.049	0.995	0.652	0.539	0.67	1.050	0.404
Log leg trachea, mm ²	1.034	0.014	0.9998	0.374	0.721	0.67	25.63	0.002

F	Standard major axis line-fit on all individual data points without phylogenetic correction							
	Slope	SE	<i>r</i>	<i>t</i> _{Comp}	<i>p</i> _{Comp}	SI _{Hyp}	<i>t</i> _{Hyp}	<i>p</i> _{Hyp}
Log tracheal volume, ml	1.272	0.017	0.997	0.414	0.681	1	15.90	0.004
Log head orifice, mm ²	0.611	0.011	0.993	0.546	0.588	0.67	5.519	0.031
Log head trachea, mm ²	0.755	0.013	0.995	0.761	0.451	0.67	6.596	0.022
Log leg orifice, mm ²	0.731	0.015	0.992	0.689	0.495	0.67	3.908	0.060
Log leg trachea, mm ²	1.042	0.013	0.997	0.566	0.575	0.67	28.70	0.001

Comparison of slopes from two different line-fit analyses with or without phylogenetic correction on species means and individual values. Standard major axis (1) line-fit on phylogenetically independent contrasts (2). Phylogenetic correction to minimize variance of independent contrasts is based on the combination of two phylogenetic trees with branch lengths normalized by tree length (figure 49 in ref. 3; ref. 4). SE, standard error of slope; *r*, Pearson's correlation coefficient; SI_{Hyp}, hypothetical slope for the null hypothesis of isometry); *t*_{Hyp}, *t* value for comparison of actual and hypothetical slope (5); *p*_{Hyp}, probability of equal slopes (significance level is 0.05); *t*_{Comp}, *t* value of slopes compared between this line-fit analysis and analysis from Table 1; *p*_{Comp}, error probability for equal slopes.

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