

Hypothesis	Response	Predictor	<i>p</i>	CI-l	CI-h
<i>Polar pressuris hypothesis</i>	CTmax	Polar	0.008	0.007	0.009
	CTmin	Polar	< 0.001	0.000	0.000
<i>Eurythermality hypothesis</i>	CTrange	Invasive	0.263	0.224	0.301

**Table S2:** Means of the *p* values from the 100 trees derived for the Bayesian analyses. CI correspond to 95% confidence interval, CI-l correspond to low value and CI-h correspond to high value.

Phylogenetic signal	<i>k</i> -statistic	<i>p</i>	CI-l	CI-h
<b>CTmax</b>	0.058	0.314	0.155	0.473
<b>CTmin</b>	0.229	0.032	0.003	0.061
<b>CTrange</b>	0.046	0.36	0.19	0.52

**Table S3:** Means of the *k*-statistic and *p* values from the 100 trees derived for the Bayesian analyses. CI correspond to 95% confidence interval, CI-l correspond to low value and CI-h correspond to high value.

Hypothesis	Response	Predictor 1	Predictor 2	Predictor 3	<i>p</i> 1	<i>p</i> 2	<i>p</i> 3	AIC
<i>Polar pressure hypothesis</i>	CTmax	Polar	Acclimation time	Duration trial	0.006	< 0.001	< 0.001	335.8
	CTmin	Polar	Acclimation time	Duration trial	< 0.001	< 0.001	0.45	296.2

**Table S4:** Results of the PGLS with additive effect of acclimation time and duration trial. *p* 1 correspond to the significance of Predictor 1, *p* 2 correspond to the significance of Predictor 2 and *p* 3 correspond to the significance of Predictor 3. We selected the best model according to the AIC criteria with  $\Delta$  AIC < 2. All values of this table come from the average of the values of the 100 best trees.