

Supplementary Material

We were interested in whether different Defence Types produced different relationships between Defense score and EQ. Unfortunately, the fact that all species with Defence Type = 0 had a Defence score = 0, we could not run a phylogenetic ANCOVA with the interaction term between Defence Type and Defence score. We therefore approached the analysis in two ways. First we ran the model without the interaction term to test for the overall effect of Defence score on EQ. The full results are below:

```
Generalized least squares fit by REML
Model: log10(EQ) ~ DefType + Defense + PrimInsect + Open
Data: EQdata6
      AIC      BIC    logLik
-642.8718 -602.7186 330.4359
```

```
Correlation Structure: corPagel
Formula: ~1
Parameter estimate(s):
  lambda
0.8515244
```

```
Coefficients:
              Value  Std.Error  t-value p-value
(Intercept) -0.04913420 0.11256308 -0.4365037 0.6626
DefType1     0.14415381 0.06111960  2.3585527 0.0186
DefType2     0.11969665 0.06348903  1.8853123 0.0598
DefType3    -0.04919038 0.13034659 -0.3773814 0.7060
Defense      -0.00427511 0.00145461 -2.9390108 0.0034
PrimInsect1  0.03044011 0.02131898  1.4278407 0.1538
Open        -0.02226866 0.02973175 -0.7489856 0.4541
```

```
Correlation:
      (Intr)  DfTy1  DfTy2  DfTy3  Defens  PrmIn1
DefType1    -0.048
DefType2     0.023  0.289
DefType3     0.004  0.278  0.315
Defense     -0.042 -0.509 -0.558 -0.523
PrimInsect1 -0.066  0.011 -0.005 -0.005 -0.087
Open        -0.105  0.035 -0.005 -0.023 -0.015 -0.038
```

```
Standardized residuals:
      Min      Q1      Med      Q3      Max
-2.3493172 -0.2827564  0.1735680  0.6323864  3.2979809
```

```
Residual standard error: 0.2522192
Degrees of freedom: 647 total; 640 residual
```

In order to test whether the relationship between Defence and EQ differed among the three different Defence Types (i.e., do the three slopes differ significantly from each other), we needed to run the model with interaction term but generated random variation in Defence score for species with Defence Type = 0. We generated random Defence scores (DefenseX) between -2 and 2 (so they remained centered on 0) for species with Defence Type 0, and then ran the full phylogenetic ANOVA, with interaction effect:

Generalized least squares fit by REML

Model: log10(EQ) ~ DefType * DefenseX + PrimInsect + Open

Data: EQdata6

AIC	BIC	logLik
-615.1043	-561.6231	319.5522

Correlation Structure: corPagel

Formula: ~1

Parameter estimate(s):

lambda

0.8528339

Coefficients:

	Value	Std.Error	t-value	p-value
(Intercept)	-0.0412598	0.1131263	-0.3647232	0.7154
DefType1	0.1836026	0.0699553	2.6245722	0.0089
DefType2	0.0780844	0.0716211	1.0902423	0.2760
DefType3	1.1132887	1.2049480	0.9239309	0.3559
DefenseX	0.0017139	0.0045822	0.3740313	0.7085
PrimInsect1	0.0274358	0.0214978	1.2762184	0.2023
Open	-0.0221952	0.0297607	-0.7457861	0.4561
DefType1:DefenseX	-0.0077865	0.0050589	-1.5391594	0.1243
DefType2:DefenseX	-0.0042886	0.0050048	-0.8568855	0.3918
DefType3:DefenseX	-0.0304964	0.0257104	-1.1861522	0.2360

Correlation:

	(Intr)	DfTy1	DfTy2	DfTy3	DefnsX	PrmIn1	Open	DT1:D	DT2:D
DefType1	-0.013								
DefType2	-0.007	0.003							
DefType3	0.003	0.002	-0.002						
DefenseX	-0.010	0.008	-0.001	-0.002					
PrimInsect1	-0.068	-0.006	0.017	-0.110	0.037				
Open	-0.106	0.020	0.005	0.013	0.027	-0.037			
DefType1:DefenseX	-0.022	-0.285	0.001	0.003	-0.906	-0.048	-0.021		
DefType2:DefenseX	0.013	-0.007	-0.267	0.006	-0.918	-0.072	-0.034	0.832	
DefType3:DefenseX	-0.003	-0.002	0.004	-0.980	-0.176	0.097	-0.021	0.158	0.158

Standardized residuals:

Min	Q1	Med	Q3	Max
-2.4761207	-0.3097824	0.1403727	0.5892626	3.2593139

Residual standard error: 0.2528642

Degrees of freedom: 647 total; 637 residual

We then calculated the coefficients (i.e., slopes) of each Defence Type line and the error variance of each using this information:

Defence Type 1	slope = -0.0060726	variance = 2.32107×10^{-6}
Defence Type 2	slope = -0.0025747	variance = 1.66997×10^{-6}
Defence Type 3	slope = -0.0287825	variance = 6.38317×10^{-4}

We calculated a pooled weighted variance across the three Defence Types and then used a Tukey's test to determine if the two most different slopes (types 2 and 3) different at a statistically significant level: $q=2.8466$, $p=0.1166$. Therefore the two most different slopes did not differ significantly at the $\alpha=0.05$ level, and we stopped the analysis there.

The full model results for the phylogenetic ANOVA using Log Brain Mass and Log Body Mass are below:

Generalized least squares fit by REML

Model: LogBrainMass ~ LogMass + DefType + Defense + PrimInsect + Open

Data: EQdata6

	AIC	BIC	logLik
	-793.9941	-749.395	406.997

Correlation Structure: corPagel

Formula: ~1

Parameter estimate(s):

lambda
0.9265906

Coefficients:

	Value	Std.Error	t-value	p-value
(Intercept)	-0.8975085	0.12311993	-7.28971	0.0000
LogMass	0.6069434	0.00999317	60.73585	0.0000
DefType1	0.1340435	0.05835688	2.29696	0.0219
DefType2	0.0612484	0.05899772	1.03815	0.2996
DefType3	-0.0388774	0.13065551	-0.29756	0.7661
Defense	-0.0032129	0.00131518	-2.44298	0.0148
PrimInsect1	-0.0101406	0.01948778	-0.52036	0.6030
Open	-0.0284967	0.02586975	-1.10155	0.2711

Correlation:

	(Intr)	LgMss	DfTy1	DfTy2	DfTy3	Defens	PrmIn1
LogMass	-0.244						
DefType1	-0.059	0.051					
DefType2	-0.001	0.081	0.250				
DefType3	-0.002	0.003	0.227	0.270			
Defense	-0.017	-0.082	-0.462	-0.532	-0.469		
PrimInsect1	-0.091	0.150	0.013	0.001	-0.009	-0.092	
Open	-0.092	0.039	0.032	-0.002	-0.023	-0.011	-0.035

Standardized residuals:

	Min	Q1	Med	Q3	Max
	-2.7378901	-0.6400488	-0.1776734	0.5723134	4.2159133

Residual standard error: 0.2589479

Degrees of freedom: 647 total; 639 residual