Electronic Supplementary Material

Supporting information to the following paper in Biodiversity and Conservation:

Bumble bees show trait-dependent vulnerability to landscape simplification

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Introduction

To further evaluate the confidence with which community responses can be assigned to single traits or to different life history strategies composed of several traits, and to dismiss the possibility that such traits combinations co-occur simply by descent, we investigated the evidence for phylogenetic signals in traits.

Methods

We tested for phylogenetic signals in the individual continuous or discrete ordered traits using the K-statistic (Blomberg, Garland and Ives 2003), which compares the distribution of independent contrasts to that expected under a Brownian motion (BM) model of trait evolution. Values of K close to zero indicate phylogenetic independence, a value of one that species’ traits are distributed as expected under BM and a value above one that traits are more similar between related species than under BM. Phylogenetic distance data was based on analyses by Cameron, Hines and Williams (2007). For the discrete unordered trait “nesting habitat”, we use a comparison of observed evolutionary transitions, or state changes, and those expected under a randomization of characters, keeping the tree fixed (Maddison and Slatkin 1991). For those traits for which we detected pairwise correlations, we conducted
phylogenetic generalised models to explore to what extent the relationship among traits are
due to actual functional trait correlations or correlations mediated by descent. We used the R
package *picante* version 1.3-0 (function *phylosignal*) for the K-statistic and associated P-
values, and the R-code communicated by Enrico Rezende to the *R-sig-phylo* mailing list (2-
Mar-2011) for the implementation of the test presented in Maddison and Slatkin (1991).

Results using the K-statistic did not qualitatively differ from test using Pagel’s λ (not shown).

**Results**

There were fewer estimated state changes than expected along the phylogenetic tree, resulting
in a significant phylogenetic signal for nesting habitat (randomization-based $P = 0.019$) and
for colony size ($Z_{13} = -2.22, P = 0.0030$). The phylogenetic signal was not found to be
significantly stronger than expected under a Brownian motion model of trait evolution for any
of the continuous traits or their CV, nor for queen emergence time or colony cycle length
(Table A). We built a phylogenetic generalised least squares model for colony size, with
nesting habitat and emergence time as fixed explanatory variables and a phylogenetic
correlation structure (Pagel's λ). Both fixed variables were highly significant ($P < 0.0010$).

The phylogenetic correlation was not significant when either both nesting site and emergence
time, or only nesting habitat were included as explanatory variables, as suggested by a
likelihood-test comparing the model with and without the phylogenetic correlation (both
variables included: Likelihood-Ratio $< 0.0010$, $P = 0.98$, $\lambda = -0.0090$; only nesting habitat
included: Likelihood-Ratio $= 0.80$, $P = 0.37$, $\lambda = 0.75$). When including just emergence time
among the explanatory terms, the model comparison suggested that a phylogenetic correlation
structure contributed significantly to the model (Likelihood-Ratio $= 6.86$, $P = 0.0090$, $\lambda =
1.60$).
**Table A.** Tests for phylogenetic signal (a) for continuous or discrete ordered traits and (b) for a discrete unordered trait. Values in (a) are K-statistic, mean observed PIC variance, \( P \)-value of observed vs. random variance of PICs and Z-score of observed vs. random variance of PICs. Values in (b) are the evolutionary transitions observed and the median number expected under randomization, CV: coefficient of variation. Significant results are typed in bold.

### a)

<table>
<thead>
<tr>
<th>Trait</th>
<th>K</th>
<th>PIC variance</th>
<th>PIC variance</th>
<th>( P )-value</th>
<th>Z-value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>( K )</td>
<td>Observed</td>
<td>Random</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Thorax width</td>
<td>0.458</td>
<td>0.485</td>
<td>0.453</td>
<td>0.63</td>
<td>0.217</td>
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<tr>
<td>CV thorax width</td>
<td>0.615</td>
<td>11.033</td>
<td>13.759</td>
<td>0.32</td>
<td>-0.597</td>
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<tr>
<td>Proboscis length</td>
<td>0.909</td>
<td>4.809</td>
<td>8.585</td>
<td>0.068</td>
<td>-1.116</td>
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<tr>
<td>CV proboscis length</td>
<td>0.674</td>
<td>48.536</td>
<td>64.784</td>
<td>0.24</td>
<td>-0.797</td>
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<tr>
<td>Colony size</td>
<td>1.174</td>
<td>1.145</td>
<td>3.017</td>
<td>\textbf{0.0030}</td>
<td>-2.220</td>
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<td>Queen emergence</td>
<td>0.489</td>
<td>1.093</td>
<td>1.283</td>
<td>0.22</td>
<td>-0.551</td>
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<tr>
<td>Colony cycle length</td>
<td>0.350</td>
<td>4.477</td>
<td>3.836</td>
<td>0.70</td>
<td>0.622</td>
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### b)

<table>
<thead>
<tr>
<th>Trait</th>
<th>Evolutionary transitions</th>
<th>( P )-value</th>
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</thead>
<tbody>
<tr>
<td>Observed</td>
<td>Random</td>
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<td>Nesting habitat</td>
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### References

