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Hiding among holes: Host plants have partially driven masquerade evolution in flea beetles (Chrysomelidae)

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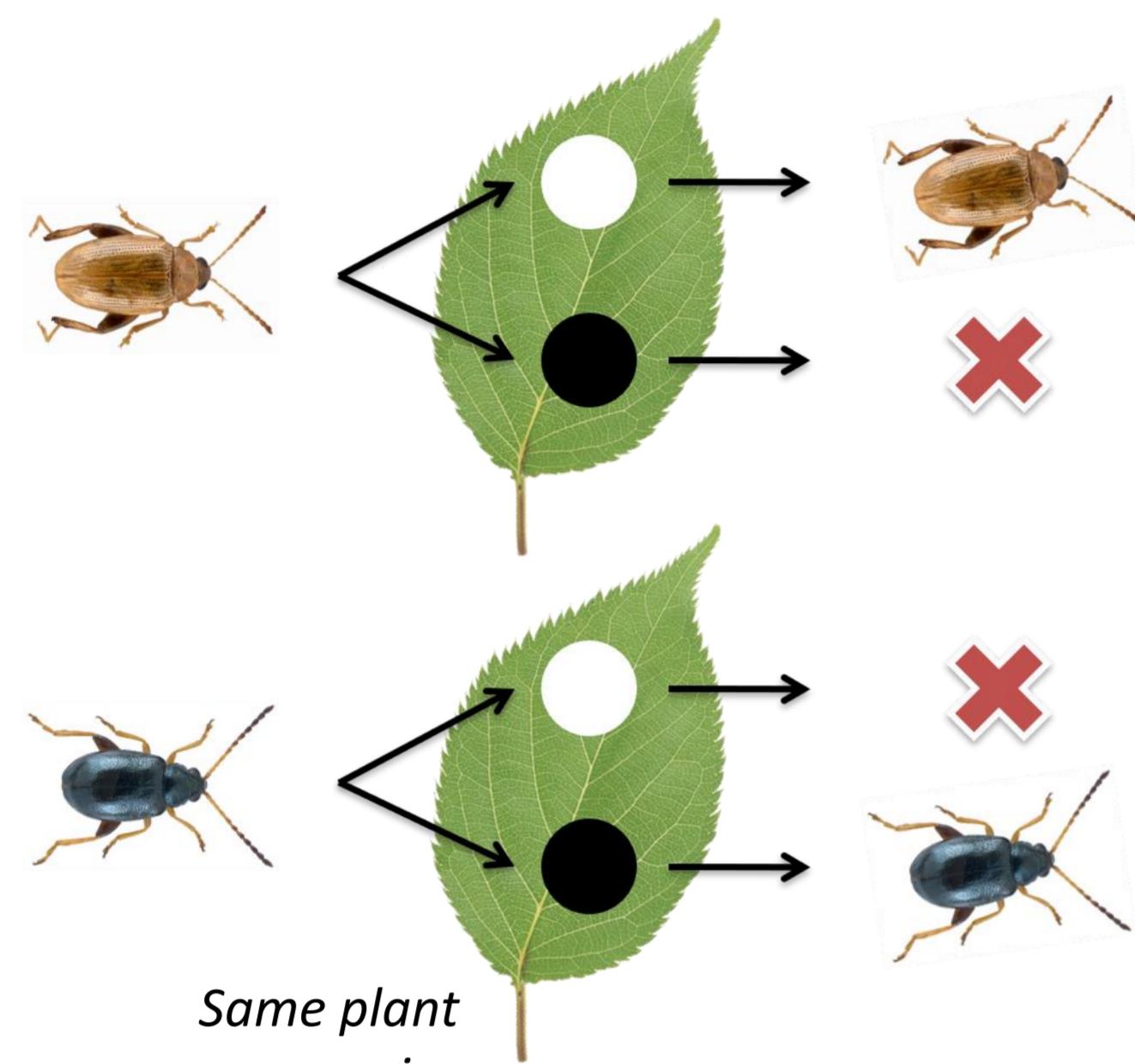


Background¹

The small herbivorous flea beetles (Chrysomelidae: Alticinae) evolved a masquerading strategy by concealing themselves as their feeding damage. Colour and size similarities between beetle body and its leaf feeding damage may act as a defence that reduces the risk of prey being recognised by visually oriented predators. Two hypotheses have been proposed for the evolutionary origin of this type of mimicry:

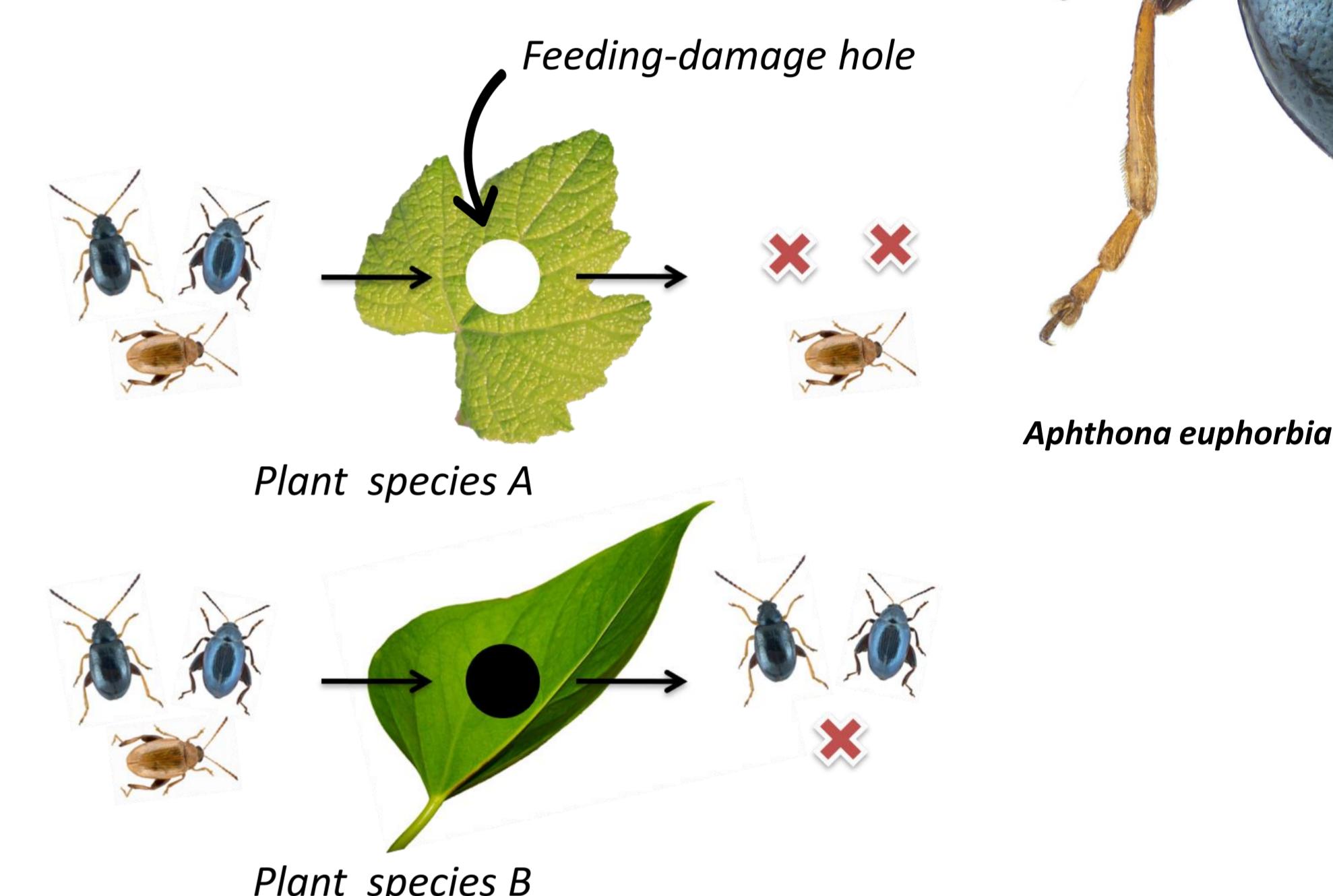
- (H1) beetle colour and size could drive, through natural selection, the feeding behaviour of flea beetles → depending on its colour and size each species would evolve a specific way of damaging its host plant;
- (H2) leaf tissues of host plants are prone to being damaged in a particular way (i.e. superficial damages [light holes] or deep damages [dark holes]) → plants would drive beetle colour and size through natural selection.

HYPOTHESIS 1 Beetle "decides" damage type



Altica brevicollis and feeding-damage holes over Corylus avellana.

HYPOTHESIS 2 Plant tissues condition damage type



Aim

To study the evolutionary processes underlying this form of masquerade. Under H2 (plant leaves characteristics drive beetle colour and size through natural selection) we expect an association between host plant families and beetles traits; on the contrary, no association should be expected under H1 (beetle feeding behaviour depends on beetle colour and size).

Material & Methods

Data: a total of 292 beetle species from the French fauna² characterized by body traits (colour as dark/light and size as small/medium/large), and 59 host plant families.

Statistical methods: to assess whether the frequency of an association between a given plant family and a beetle trait (colour or size) is non-random, we applied a χ^2 test. We built a bipartite network of feeding interactions between beetle species and their host plant families. Then, we estimated network modules and evaluated if the beetles within each module shared a common body characteristic. For this purpose, we compared colour (as the % of dark beetles) and size (as the standard deviation) distributions within modules with null expectations.

Results

Colour test

The proportion of dark vs. light-coloured species was significantly different ($P < 0.05$) from null expectations in 4 out of 11 modules (36%) → Association between beetle colour and plant families is consistent with H2.

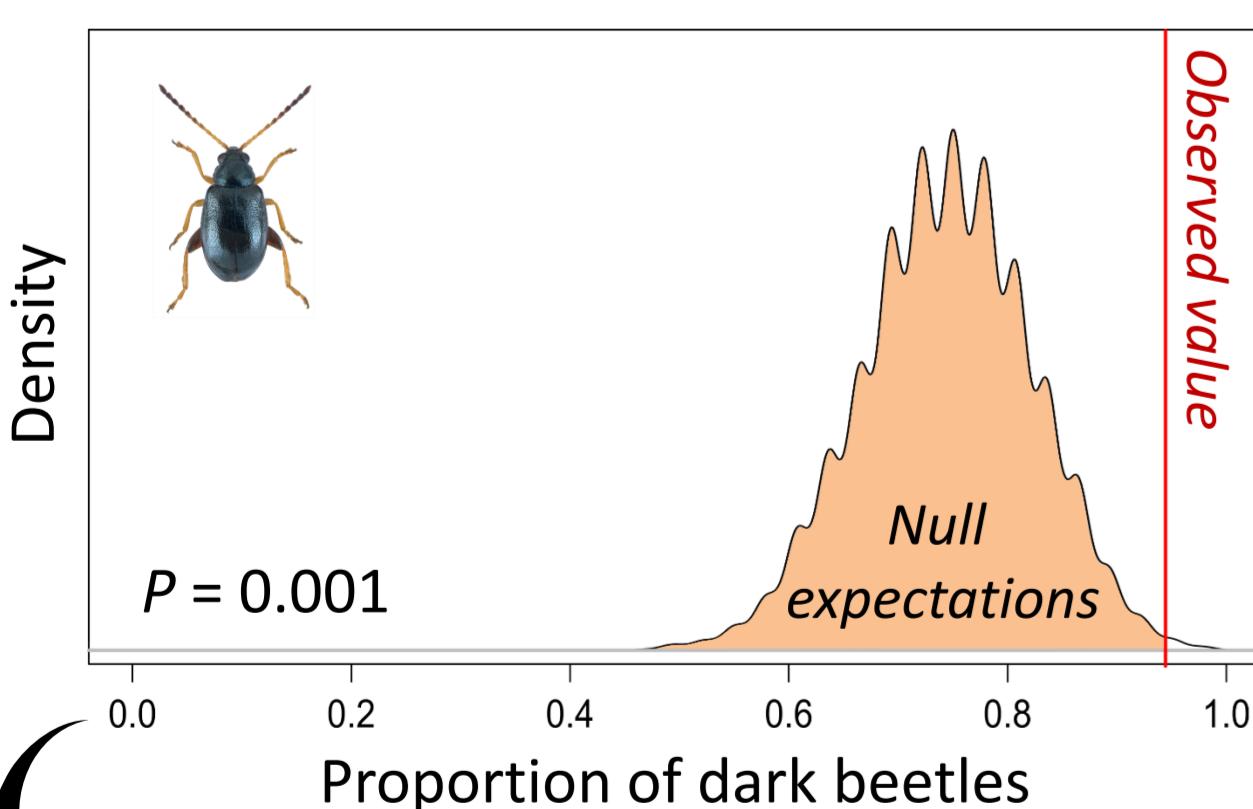
H2 supported in 36% of cases

Size test

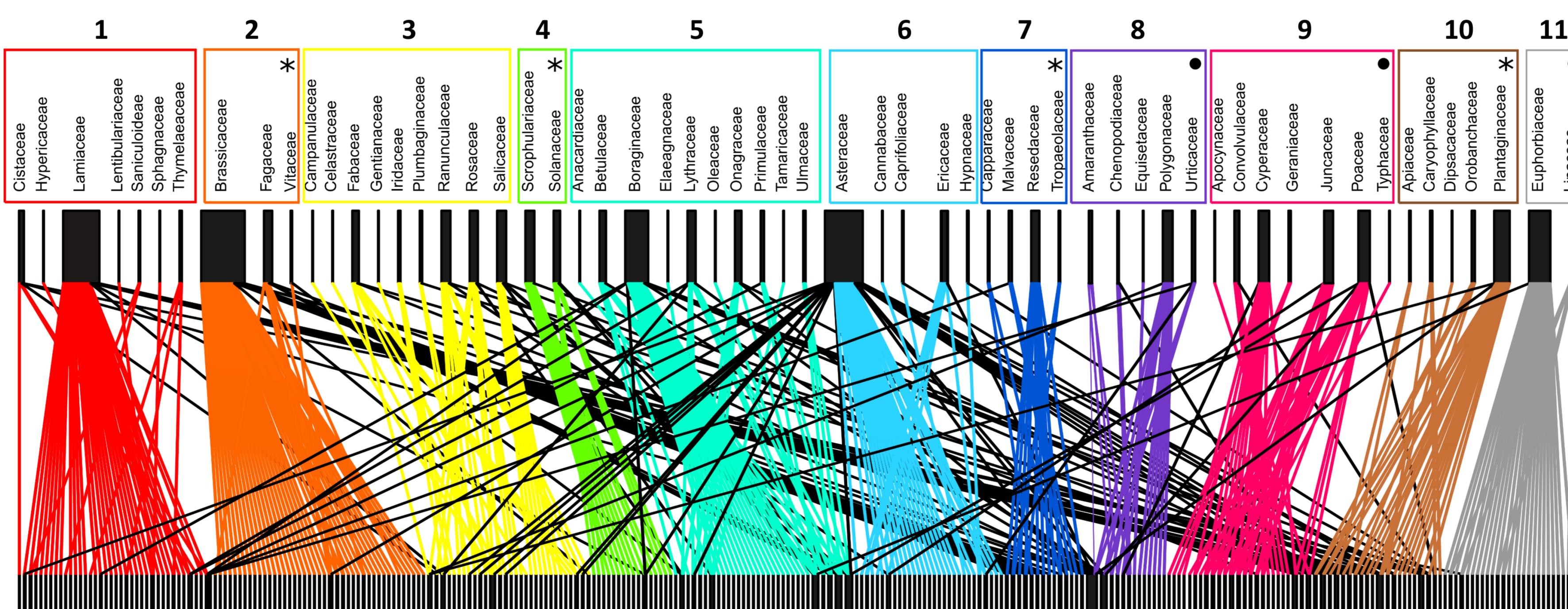
The variation (SD) in body size across beetle species belonging to a given module was significantly smaller ($P < 0.05$) than null expectations in 3 out of 11 modules (27%) → Association between beetle size and plant families is consistent with H2.

H2 supported in 27% of cases

Module 2: proportion of dark beetles

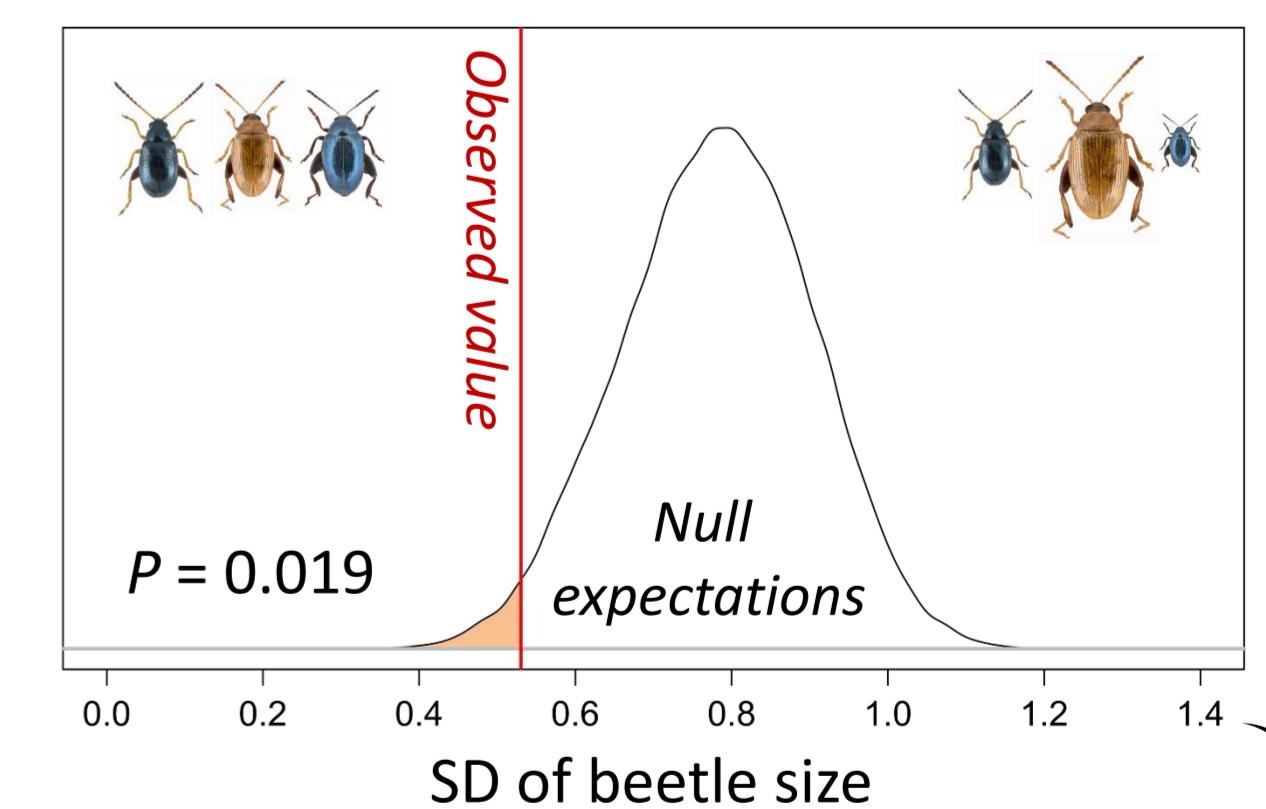


The proportion of dark beetles is significantly higher than expected in a random association between beetles and plant families → Support for H2



Feeding interactions among host plants were non-randomly distributed and highly modular (modularity test: $Q = 0.686, P < 0.0001$). Modules marked by * or • presented colour or size distributions significantly different from null expectations, respectively.

Module 11: standard deviation of size



The standard deviation of size is significantly smaller than expected in a random association between beetles and plant families → Support for H2

Conclusions

- (1) Two masquerading mechanisms may exist. In some network modules, colour and size of flea beetles seem to be constrained by non-random processes, as expected under Hypothesis 2. However, most network modules do not show any significant deviation from random distributions of beetle colour and size, as expected under Hypothesis 1.
- (2) To conclude if the high proportion of modules with no significant results is related to the presence of non-masquerading beetle species or to evolutionary H1 mechanisms, it would be interesting to have information about masquerading occurrence in natural communities.