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IN FOCUS

- Natural history matters: how biological constraints shape diversified interactions in pollination networks
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Species-specific traits and life-history characteristics constrain 21 the ways organisms interact in nature. For example, gape-limited predators are constrained in the sizes of prey they can handle and 23 efficiently consume. When we consider the ubiquity of such constrains it is evident how hard it can be to be a generalist partner 25 in ecological interactions: a free living animal or plant can't simply interact with every available partner it encounters. Some pairwise interactions among coexisting species simply do not occur; they are impossible to observe despite the fact that partners coexist in the same place. Sazatornil et al. (1) explore the nature of such constraints in the mutualisms among hawkmoths and the plants they pollinate. In this iconic interaction, used by Darwin and Wallace to vividly illustrate the power of natural selection in shaping evolutionary change, both pollinators and plants are sharply constrained in their interaction modes and outcomes.

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Size-limited foragers show clear restrictions on the size of prey items they 39 can efficiently handle. In the case of plant-pollinator interactions, size uncoupling between pollinator bodies and flower sizes (i.e., length of spur or 41 corolla tubes) or structure are specially relevant in filtering out a range of potential partners (2). As a general trend, also observed in frugivorus anim-43 als dispersing seeds, larger (long-tongued) species can exploit longer-tubed flowers and a wider range of flower sizes. The size of the feeding apparatus 45 (e.g., tongue length, gape width) limits the maximum size of flower or fruit an animal mutualist can efficiently use. Phenotypic trait matching is thus a key influence in the effectiveness of plant-animal interactions shaped by 48 these size effects, where the interaction outcomes depend on close matching. 49 The idea, when applied to the bizarre flowers of some plants pollinated by sphingid moths (Lepidoptera: Sphingidae) (Fig. 1), was seminal in Darwinian evolutionary theory to support the potential of natural selection in shaping adaptations (3). Wallace (4) in his book, Creation by law, vividly uses the famous example of the Malagasy orchid and its sphingid pollinator to refute the arguments of the Duke of Argyll against natural selection and Darwinism:

"There is a Madagascar Orchis—the Angræcum sesquipedale—with an immensely long and deep nectary. How did such an extraordinary organ come to be developed? Mr. Darwin's [[p. 475]] explanation is this. The pollen of this flower can only be removed by the proboscis of some very large moths trying to get at the nectar at the bottom of the vessel. The moths with the longest proboscis would do this most effectually; they would be rewarded for their long noses by getting the most nectar; whilst on the other hand, the flowers with the deepest nectaries would be the best fertilized by the largest moths preferring them. Consequently, the deepest nectaried Orchids and the longest nosed

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moths would each confer on the other a great advantage in the 'battle of life.' This would tend to their respective perpetuation and to the constant lengthening of nectar and noses."

Phenotypic fitting of corolla length and shape and the pollinators' feeding 71 apparatus and body sizes are important because the better the fit, the better 72 the consequences in terms of fitness outcomes for the interaction partners 73 (5). Yet the expectation of perfect trait matching across populations or com-74 munities is too simplistic (6): "arms races" as initially suggested by Darwin and Wallace are frequently asymmetric, originating pollinator shifts rather 76 than tight phenotypic trait matching (Fig. 2)(7). Therefore, extensive local variation in phenotypic mismatch exists in different plant-pollinator systems (e.g., 2; 6; 8), with pollinator-mediated selection geographic mosaics of locally coevolved partners where tight phenotypic matching is not necessarily the rule.

Recent work by Sazatornil et al. (1) provides evidences that the types
of trait mismatching outlined in Fig. 2 limit the ranges of host plants for
sphingid pollinators, and ultimately shape their complex plant-pollinator networks. By using a comparative analysis of five different hawkmoth/flower
assemblages across four South American biotas (Atlantic rainforest and Cerrado in Brazil, Chaco montane dry woodland, and the ecotone between western Chaco woodland and Yungas montane rain forest in Argentina) they
tested the contributions of phenotypic matching to explain observed patterns
of moth-flower interactions.

How are these moth-flower interactions assembled? Pairwise patterns of trait matching scale-up to conform complex webs of interaction where in some cases interaction topology is linked to phenotypic fit between partners

while in others the interaction pattern appears more determined by neutral processes (i.e., probability of interspecific encounter). Sazatornil et al. (1) use a comparative analysis of hawkmoth proboscis length (HPL) and 96 the effective length of the flower (EFL) for every pairwise interaction recorded. EFL is just the corolla tube length (as in Fig. 2 for long-tubed 98 and salverform corollas) or the stamen protrusion length in brush-type and funnel-shape flowers (as in Fig. 1). The authors first tested a neutral model, 100 where interactions are independent of trait-matching and driven solely by 101 variation in local abundance. Under this hypothesis distribution paramet-102 ers (mean and standard deviation) must be the same for both the simulated 103 and empirical distributions. They further tested a Forbidden links hypo-104 thesis, where interactions occurred only if $HPL \geq EFL$. Sazatornil et al. 105 further tested the morphological match hypothesis, where the probability of 106 occurrence of an interaction depends on the frequency of possible pairwise 107 differences between HPL and EFL, i.e., all possible pairwise HPL - EFL108 differences were weighted by their respective interaction frequency. 109

The trait matching between HPL and EFL is crucial in this type of 110 interaction and determines its outcome in terms of fitness for both partners. 111 Nilsson (5) demonstrated experimentally that shortening the nectary tube 112 of long-spurred corollas decreased both seed set and pollinia removal for 113 Platanthera orchids. Further experimental evidence has been provided for 114 long-tongued nemestrinid flies pollinating long-tubed irises in South Africa, 115 where increased mismatch decreases both plant fitness and the nectar extraction efficiency of the pollinators (9) (also see 6, and references therein). 117 Sazatornil et al. extend those results to the scale of the whole moth-plant 118

assemblage and demonstrate that trait matching successfully predicts the 119 diversity of interactions recorded. Interestingly enough, the interaction pat-120 terns in two local assemblages from ecotone areas of the argentinian Chaco 121 woodland-Yungas montane rain forest transition are better fitted by a neutral 122 model where pairwise interactions are driven by probability of interspecific 123 encounter. Yet Sazatornil et al. did not include the morphological difference for parameter estimation when interactions were not recorded. Thus the test 125 of the mismatch hypothesis implicitly includes forbidden links effects: a full 126 mismatch of corolla tube/proboscis lengths actually means a forbidden link. 127 Furthermore, a fraction of unobserved interactions was likely caused by phen-128 ological uncoupling between flowering and hawkmoth activity phenophases 129 (14; 1). In any case the mismatch hypothesis somehow captures the fact 130 that a fraction of the unobserved interactions in these hawkmoth/flower as-131 semblages is due to extreme phenotypic mismatch, i.e., size-related forbidden 132 links (1); also see (10) for evidences with humming bird-flower interactions. 133 Forbidden links represent a family of causes for not observing specific in-134 teractions when sampling diversified plant-animal interaction networks, and 135 stem on biological causes deeply linked to the fascinating natural history de-136 tails of these interactions (14). The raw material for phenotypic mismatches 137 in the specific case of hawkmoth-flower interactions is the extreme variability 138 of the two pivotal traits determining their outcomes: proboscis length and 139 corolla/spur or nectary depth (Fig. 2) (2; 3; 5; 11). This variation is extens-140

Sazatornil et al. approach would be most useful for proper tests of coe-

ive for both the plant and pollinator partners and observable at individual,

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population and species levels.

volutionary hypotheses in hawkmoth/flower assemblages (and plant-animal 144 mutualisms in general): assessing match/mismatch patterns for every possible pairwise interaction among partners within complex webs of interac-146 tion where multiple life-history attributes may contribute biological reasons for forbidden links. The morphological match hypothesis is not the only 148 mechanism to explain patterns of hawkmoth-plant interactions, where other life-history limitations may operate generating forbidden links, e.g., pheno-150 logical mismatches (for example in the case of long-distance or elevational 151 migratory hawkmoths), constraints from foraging for oviposition sites (12), 152 energetic constraints due to balances of nectar availability/foraging costs 153 (13), etc. Most importantly, this paper nicely illustrates how the fascinating 154 natural history details of these interactions can be use to build meaningful 155 testable models to assess the mechanisms beyond structure and function of 156 megadiversified webs of interactions among free-living species. 157

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Figures

Figure 1. Morphological mismatches set important biological constraints 213 for size-limited foragers, including e.g., predators, pollinators, and frugi-214 In plant-animal mutualisms (e.g., plant-pollinator interactions), a 215 morphological mismatch between partners sets size limits that filter out a 216 range of phenotypes that otherwise could eventually interact. Two main coe-217 volutionary trends in hawkmoth-flower interactions involve arms-race trends 218 (with progressively longer spurs and proboscides) and pollinator shifts (where 219 short-tongued moths are replaced as legitimate pollinators by long-tongued 220 species when corolla tubes increase in length). In many cases, pollination is 221 impossible when the proboscis is longer than the spurs because the pollen 222 or pollinaria are attached further from the base of the proboscis. When this 223 happens the pollen or pollinaria may be be scratched away by the forelegs when the proboscis is rolled to a loose spiral; yet in other cases, actual pollen 225 transfer may occur when long-tongued moths visit short-tubed flowers. If 226 the proboscis is shorter than the spur, transfer of the pollen or pollinaria is 227 possible as long as the proboscis can get in contact with the sexual organs of the flowers. Other reasons for forbidden links include, e.g., phenological 229 differences (14). Thus, a number of the potential interactions that could take 230 place in a given mutualistic assemblage simply cannot occur because of bio-231 logical reasons: these are forbidden interactions. Photo: courtesy of Andrea Cocucci. A sphingid moth, Agrius cinqulata, visiting a flower of Bauhinia 233 mollis (Fabaceae), Las Yungas, Argentina. 234

Figure 2. The mechanistic basis of morphological mismatches in hawkmoth-236 flower interactions. For example, nectar accessibility in Angraecum sesqui-237 pedale long-tubed flowers. A, only small volumes of nectar can be exploited 238 if the spur is 27 cm long. B, moths with an average tongue length of 22 cm 239 can obtain about 50 μL nectar from a spur of 33.3 cm average length and 240 an average nectar volume of 165 μL . C, a spur 43 cm long could offer nectar to a moth with a 22-cm-long proboscis only if it contains more than 240 μL 242 nectar. Lack of fit prevents interactions, but also marginal fitting renders 243 interactions unlikely because of energetic constraints. Modified and redrawn 244 from (3). 245

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