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Photic niche invasions: phylogenetic history of the dim-light foraging augochlorine bees (Halictidae)

Simon M. Tierney1,*, Oris Sanjur1, Grethel G. Grajales1, Leandro M. Santos2, Eldredge Bermingham1 and William T. Wcislo1,*

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Most bees rely on flowering plants and hence are diurnal foragers. From this ancestral state, dim-light foraging in bees requires significant adaptations to a new photic environment. We used DNA sequences to evaluate the phylogenetic history of the most diverse clade of Apoidea that is adapted to dim-light environments (Augochlorini: Megalopta, Megaloptidia and Megommation). The most speciose lineage, Megalopta, is distal to the remaining dim-light genera, and its closest diurnal relative (Xenochlora) is recovered as a lineage that has secondarily reverted to diurnal foraging. Tests for adaptive protein evolution indicate that long-wavelength opsin shows strong evidence of stabilizing selection, with no more than five codons (2%) under positive selection, depending on analytical procedure. In the branch leading to Megalopta, the amino acid of the single positively selected codon is conserved among ancestral Halictidae examined, and is homologous to codons known to influence molecular structure at the chromophore-binding pocket. Theoretically, such mutations can shift photopigment \( \lambda_{\text{max}} \) sensitivity and enable visual transduction in alternate photic environments. Results are discussed in light of the available evidence on photopigment structure, morphological specialization and biogeographic distributions over geological time.

Keywords: opsin; dim-light; Augochlorini; adaptive radiation; relictual taxa

1. INTRODUCTION

The invasion of a novel sensory environment represents a significant niche shift [1,2]. For photic niche shifts, photosensitivity of the eye is a target of selection, which may be associated with evolutionary diversification in many animal taxa [1,3]. Despite the independent origins of eyes, many elements of the visual system are conserved, such as the photopigment proteins (the opsins) that originate from a common metazoan ancestor [4–6]. Opsin genes are routinely used for reconstructing phylogenetic history (e.g. [7] for bees), but they also provide a potentially powerful signal for understanding the molecular basis of behavioural transitions to novel light environments, especially when viewed from a comparative phylogenetic perspective [8].

Visual pigments consist of a photon-absorbing chromophore (11-cis-retinal) which is surrounded by an apo-protein (opsin), embedded in the transmembrane of photoreceptor cells, and the expression of variant opsins (short/medium/long \( \lambda \)) permits chromatic vision [4,9]. Changes in either a small set, or single point mutations, of amino acids relative to the chromophore-binding pocket can shift spectral sensitivity [10–13]. The same result also can be achieved via gene duplication within opsin classes and differential expression of alternate copies [14,15], or the use of rhabdomeric filters to modify photopigment activation [16].

Here we explore the phylogenetic history of the obligate dim-light foraging augochlorine sweat bees (Megalopta, Megaloptidia and Megommation), the most diverse radiation of dim-light bees within the Apoidea (reviewed by Wcislo & Tierney [17]). These bees forage under light conditions that are orders of magnitude dimmer than related diurnal taxa [18–20] (reviewed by Wcislo & Tierney [17] and Warrant [21]), so there are reasons to expect that augochlorine opsin proteins may be under strong selection that led to adaptive radiations, as in other taxa such as cichlid fishes [8,22]. If so, opsin may be unsuitable for our phylogenetic purposes, which we test by comparison with two non-photic nuclear protein-coding genes. We estimate relative rates of non-synonymous to synonymous mutations using distance and phylogenetically informed likelihood procedures, comparing dim-light foraging taxa with their close diurnal relatives. We also use dating estimates to place the evolutionary ecology of the dim-light foraging Augochlorini within a historical context.

2. MATERIAL AND METHODS
(a) Specimen collection and study taxa

Bees were collected at light traps or from nests (see [23–26]) at localities given in the electronic supplementary material, table S1. The most abundant genus is Megalopta (approx. 30 species, including five parasites), which are distributed...
from Mexico to northern Argentina and southern Brazil, predominantly in lowlands, with one Central American montane species [24,27–31]. Megaloptidia (three species) occur in the Amazon basin and Guiana Shield [28,32], and Megomnattion s. str. (two species) occur in eastern Brazil, and northern Argentina and Paraguay [28,33]. Multiple specimens of the same morphospecies from different locations were used to assess potential problems associated with prior taxonomy (see electronic supplementary material, M1). Voucher specimens are located in the dry reference collection of the Smithsonian Tropical Research Institute.

(b) DNA sequence compilation
Bi-directional fragments of three protein-coding nuclear gene regions, long-wavelength green opsin (LwOp), the F2 copy of elongation factor-1 alpha (EF-1a) and wingless (Wg) were obtained (for gene maps see [34,35]). Primer oligos and polymerase chain reaction conditions are detailed in the electronic supplementary material, M2. Sequences were edited (Sequencher 4.6) and aligned (Se-Al v. 2.0a11 Carbon) to the coding sequence region of pre-existing halictid bees accessed from GenBank, and accession numbers JN106067 to JN106163 represent new sequences obtained for this study (see electronic supplementary material, table S1). Introns were excluded from analyses, identified in accordance with the coding regions of exemplars: LwOp—U26026 Aps mellifera; EF-1a—AF015267 A. mellifera; Wg—J03650 Drosophila melanogaster.

(c) Phylogenetic inference
Phylogenetic inference was performed using MrBayes 3.1.2. Data were partitioned by codon position within each gene. We took an objective approach ([36], see electronic supplementary material, M3), and used the most parameter rich, yet least restrictive model (GTR + I + G), for each partition and used default priors for other all parameters, which were unlinked across partitions. Default heating procedures were performed on two independent parallel runs, sampling likelihoods every 1000th generation. We ran analyses for 100 M generations so that the modelling procedure reached stationarity, and to obtain a large sample size from which to assess confidence in estimates of node divergence times. We used 10 per cent burn-in points (n = 90 K trees) and ran three analyses: (i) a combined three gene dataset, (ii) non-photic: EF-1a + Wg, and (iii) photic: LwOp only.

(d) Tests for adaptive evolution: relative rates of dN/dS—ω
We followed standard methods to test for signals of adaptive evolution from nucleotide sequences by assessing the relative rates (ω) of non-synonymous (dN) to synonymous (dS) substitutions. We first used distance measures (Δ-tests, MEGA v. 4.0) to test for positive selection (H1: dN > dS) within all gene fragments that were used to construct the phylogeny. Then we compared LwOp by foraging mode across our dataset, as well as independent pairwise analyses among 11 pairs of bee taxa with nocturnal versus diurnal foraging behaviour, for which comparable sequences are available (listed in the electronic supplementary material, table S1); behavioural categorizations were taken from Wcislo & Tierney [17].

Distance measures may suggest selection is operating, but do not indicate which sequenced regions are undergoing selection, and hence how selection is operating. Maximum-likelihood procedures were undertaken within a phylogenetic context (HyPhy v. 1.0) with consensus LwOp trees derived from Bayesian analyses. We assessed Global versus Local (specific branch) models, and a priori we selected clades and branches that may be expected to be under differential selection (i.e. dim-light versus diurnal foragers), and used modified data matrices (a, all specimens; b, single specimen/species; c, ancestral halictids added to matrix b) to account for the potential effect that altering outgroups may have on ingroup comparisons of ω. Finally, we used site-specific modelling procedures, employing both single likelihood ancestor counting as well as a more thorough branch-site fixed effect likelihood methodology (further details in electronic supplementary material, M4).

(e) Divergence time estimation
We use two relaxed clock analytical methods to estimate divergence dates for internal nodes of the Bayesian consensus tree, a simplistic path-length analysis with fine-scale optimization for smoothing substitutional rate variation (PATHd8 v. 1.0), and a more rigorous penalized likelihood approach that optimizes smoothing rates across the tree, which then controls for extreme rate variation among branches, and importantly permits estimation of confidence measures on node age (r8s v. 1.71).

Justification of fossil usage, and analytical details are provided in electronic supplementary material, M5. Synthesizing the fossil (amber, pollen, compression and trace) and biogeographic evidence, the existence of ancestral halictid lineages in Maastrichtian (70.6–65.5 Myr ago) South America is plausible and conforms to molecular-derived age estimates of supra-family level for the Aculeata [37]. The most probable match of any ichnofossil to extant bee lineages is that of Uruguay (Maastrichtian ichnogenus) to Augochlorini (e.g. Pseudoaugochlora), but see arguments by Michener [28, p. 101] and Genise & Bown [38]. Thus, we use the root age of 65 Ma, for the node representing the most recent common ancestor (MRCA) of Augochlorini + Caenohalictini (Halictinidae), which agrees with prior phylogenetic studies of Halictidae [34,39].

We used Dominican amber inclusion fossils of halictine bees (reviewed by Engel & Peñalver [40]) as an internal minimum age constraint between 15 and 20 Ma [41]. Bees in our phylogenetic analyses that contain ancestral lineages represented in Dominican amber include: Augochloris, Augochloropsis (but see [40]), Caenohalictis and Neocorynura. To create credible boundaries for the upper and lower ages for amber calibrates, we identified two nodes: the earliest possible crown node, Amber Early (MRCA of Augochloropsis and Augochloris); and the most distal stem node, Amber Late (MRCA of Augochloris).

The most conservative use of age calibrates was a fixed Root of 65 Ma and a minimum age constraint of 15 Ma at Amber Late. We then shifted the minimum age constraint to the node Amber Early. Next, we removed the internal constraint, so that analyses rely solely on the Halictinae Root age. Finally, we modified the phylogeny into sub-trees so that the upper (Amber Early) and lower (Amber Late) internal constraint nodes are transformed to become independent fixed ages, with all ancestral taxa leading to those nodes pruned from the tree and analysis. We then explored the robustness of age estimates by adjusting age constraints at 5 Ma intervals. Thus, five broad variations on node-age calibration were performed: (i) Root fixed at 65 Ma, Amber Late constrained to 15/20/25/30/35/40/45 Ma, (ii) Root fixed at 65 Ma, Amber Early constrained to 15/20/25/30/35/40/
The combined phylogenetic data recovered 2049 aligned
Megalopta byroni
Megalopta ecuadoria
Proc. R. Soc. B
(2012)
796 S. M. Tierney at 5/10/15/20/25/30/35 Ma; and (v) ancestral taxa
pruned; Amber Early fixed at 15/20/25/30/35/40/45 Ma.
Standard confidence interval measures are not appropri-
ate because placing constraints on node age necessarily
leads to skewed distributions, thus violating assumptions of
normality. Confidence limits for node-age variability were
assessed using the Bayesian analysis consensus tree as a
filter constraint (PAUP* v. 4.0 b10), to yield a pool of topo-
logically alike trees with variable branch lengths, that we then
imported into r8s to assess variation in node age. Central dis-
tribution 95% confidence limits (CLs) were determined by
the upper and lower 2.5 per cent quantile of node ages.

3. RESULTS
(a) Phylogeny
The combined phylogenetic data recovered 2049 aligned
coding region nucleotides (LwOp 702 bp, EF-1a 754 bp,
Wg 593 bp), with introns excluded. The consensus tree
(figure 1a; corresponding phylogram—electronic supple-
mental material, figure S1a) gives posterior probability (PP)
node support for nodes with less than 100 PP. Relationships among the diurnal augochlorine taxa are well supported. All dim-light taxa form a mono-
phyletic clade, but with only moderate support (80 PP).
The monophyletic grouping of (Megaloptidia +
(Megalopta + Xenochlora)) is maximally supported, as is
the monophyly of Megaloptidia. Megalopta is not mono-
phyletic, as the diurnal Xenochlora forms a fully
supported monophyly with Megalopta atra (the only mont-
tane Megalopta species), which renders Megalopta
paraphyletic. The group (Xenochlora + M. atra) forms a
sister clade to the remaining lowland Megalopta, which
is a fully supported monophyletic group. These lowland
lineages can be broadly divided by sculpturing on the
basal area of the propodeum [42], into two well sup-
ported main clades: (i) one clade is comprised species
with a smooth basal area of the propodeum (84 PP),
which contains all specimens of Megalopta centralis (i.e.
Megalopta ecuadoria in earlier publications); and (ii)
one clade is comprised the parasitic Megalopta byroni and
the remaining Megalopta with striate basal area of the
propodeum (100 PP). Resolution among terminal branches
within both of these lowland clades, however, is weak.
In order to assess the effects of including multiple
specimens per morphospecies, we ran a second analysis with just one representative per taxa. This analysis gener-
ated the identical topological relationships among genera
and subgenera (electronic supplementary material, figure
S1b). Node support was also broadly equivalent, apart from
the MRCA of the augochlorines that dropped from 99 to 89 PP support and the relationship between the parasite (M. byroni) and known host (Megommation gene-
alis) was resolved (90 PP); the remaining members of the
clad with striate basal area of the propodeum collapsed into a three-way polytomy.
When the opsin fragment was removed from the
matrix, very few of the above relationships hold (elec-
tronic supplementary material, figure S2). The MRCA
of the augochlorines collapsed into a polytomy. The
dim-light taxa no longer form a monophyletic clade;
Megommation and Megaloptidia are grouped with other
diurnal taxa with poor support (less than 67 PP). The
only fully supported monophyletic grouping is that of
Megalopta and Xenochlora, whereby (M. atra + Xenochlora nigrofemorata) form a clade (87 PP) that is sister group to a
polytomous grouping of all the remaining lowland
Megalopta.
When only opsin is used to reconstruct the phylogeny
(electronic supplementary material, figure S3a), some
resolution is lost among the diurnal outgroups but again
the dim-light taxa are recovered within a common clade
with strong support (94 PP). Within this clade, the
grouping of Megommation with Megaloptidia is fully sup-
ported, as is Xenochlora with Megalopta. In the latter,
Xenochlora is recovered as a distinct sister group to M.
atra; in this analysis monophyly of the genus Megalopta
is very poorly supported (60 PP). Within Megalopta, the
highland M. atra is again isolated from the lowland Me-
galopta wherein dichotomous resolution is lost. These
analyses suggest that opsin provides good resolution
among the augochlorine genera included in this study,
but not at the species level for Megalopta. However,
when only a single representative per species is used,
and incomplete sequences are removed, resolution some-
what improves (electronic supplementary material, figure
S3b). If the gene is undergoing positive selection, how-
ever, then the apparent resolution it provides may be
spurious.

(b) Tests for adaptive evolution
(i) Distance measures of \( \omega \) averaged across the matrix
Results from the z-tests (electronic supplementary
material, table S2), for all three gene fragments, showed
evidence of stabilizing selection (all \( p < 0.001 \)), but no
evidence of positive selection (all \( p = 1.0 \)). The same
trends and significance values were found when the speci-
mens were split into groups based on foraging mode
(diurnal versus dim-light) for LwOp.
(ii) Pairwise measures of \( \omega \)
Using 15 GenBank sequences of LwOp and five derived
from the current study (electronic supplementary
material, table S3), we found 11 suitable pairs of dim-
light/diurnal foraging bees for pairwise measures. In two
of these analyses (Megalopta versus Xenochlora, and
L. (Sphecodogastra) versus L. (Evylaeus)), neutrality was
not rejected. The other nine comparisons rejected neu-
trality and found very high support for stabilizing
selection (all \( p < 0.001 \)), and no support for positive
selection.
(iii) Maximum-likelihood measures of \( \omega \)
Likelihood measures on the LwOp coding sequence were
performed on three dataset perturbations with in-
complete sequences removed: (i) the original taxon matrix
(\( n = 38 \)) + electronic supplementary material, figure S3a;
(ii) a single specimen/species matrix (\( n = 16 \)) + electronic
supplementary material, figure S3b; and (iii) all available
ancestral halictids added to matrix \( b (n = 33) \) + electronic
supplementary material, figure S3c (sequences sourced
from GenBank; see electronic supplementary material,
table S1). Akaike Information Criterion tests for LwOp
rate procedures selected the HKY85 model. For all
analyses, we used Muse–Gaut likelihood rate matrices

in combination with either a HKY85 or a more parameter-rich GTR codon model, depending on whether graphical user interface or batch files were used. Consensus trees (electronic supplementary material, figure S3) were derived from the corresponding Bayesian analysis and results discussed below are presented in the electronic supplementary material, table S4. We found no evidence of recombination events in our data.

*Global* (shared) estimates of ω across the entire tree corroborate distance-based z-tests in rejecting neutral evolution, as confidence intervals do not overlap 1. Analyses (i) and (ii) yielded equivalent values (ω = 0.2), while inclusion of ancestral taxa (analysis (iii)) generated a slightly weaker indication of directional selection (ω = 0.1). Likelihood ratio tests comparing Global (H₂) versus Local (H₀) rates provided highly significant evidence for local branch-by-branch variation in ω for all trees. We also found evidence for *interclade* variation in ω when the tree was split by photic niche for foraging. All three matrices supported a nested model (dim-light clade + branch leading to it, in comparison with the diurnal clade), in preference to global estimates, with evidence of slightly stronger rates of stabilizing selection in the diurnal clade (ω range: 0.1–0.13), when compared with the dim-light clade (ω range: 0.34–0.36). Likelihood ratio tests comparing ω between terminal and internal branches supported H₀, indicating that terminal branches experience significantly different rates of ω compared with the rest of the tree.

The general *site and branch* Single Likelihood Ancestor Count procedure tested for both positive and stabilizing selection at each codon (n = 234) in the sequence. The procedure first counted across the entire tree and then counted the terminal (T) and internal (I) branches independently. Again, there is evidence of stabilizing selection, but no indications of sites under positive selection. Full counts suggested 12–41% of the sequence is undergoing positive selection. Among-branch analyses of site Augochlorini suggest a noticeable phylogenetic path-length differences are less pronounced when ancestral halictids are incorporated (matrix range: 0.34–0.36). Likelihood ratio tests comparing Global (H₂) versus Local (H₀) rates provided highly significant evidence for local branch-by-branch variation in ω for all trees.

Figure 1. Total evidence and opsin-only phylogenies. (a) Consensus chronogram for all three genes, posterior probability node support indicated when less than 100. Foraging environment denoted by branch colour (diurnal, grey; dim-light, black), and node colour (diurnal MRCA, white circle; dim-light MRCA, black circle). Open circle with black dot denotes age-calibration node. Branch lengths derived from *rbs* analysis: *Root* fixed 65 Ma; *Amber Late* constrained 15 Ma. Horizontal bars represent 95% CL’s for a 65 Ma fixed *Root* and a constraint age of 15 Ma (light grey bars) or 20 Ma (dark grey bars). Mean node age indicated by a vertical black line within these bars. (b) Ancestral halictid *LeOp* summary cladogram, modified from electronic supplementary material, figure S3c. Indicates two positions that were positively selected (all datasets) in branches leading to the MRCA of dim-light foraging clades (see electronic supplementary material, table S5). Codon Gly11Cys is homologous to the chrophore-binding pocket sites of *Papilio*-142 and bovine-123. *Megalota* is summarized by lineage: diurnal (*Xenochlora*), montane (*Megalota atra*) and two main lowland clades possessing either smooth (*M. centralis*) or striate basal area of propodeum (remaining morphotypes). Asterisk, *Dufourea* sequence may be questionable (see electronic supplementary material, R2).
dim-light augochlorines and all derived nodes of each
dim-light genus, and finally on the ancestral branches
leading to all of the aforementioned nodes. Electronic
supplementary material, table S4 details the sum count
deriving from orthogonally selected codons, followed by the
position of positively selected codons. Each dataset gave rise to no
more than five sites undergoing positive selection in each
dataset and yielded no supplementary material, table S4 details the sum count
dim-light genus, and finally on the ancestral branches
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pocket.

The functionality of our positively selected amino acid
mutations of long-wavelength opsins at positions homolo-
gous to bovine tuning sites alter sensitivity of
Drosophila chromophores [13]. Our codon 11 (Apis 138, Papilio
142, bovine 123 [43]) is the only positively selected
codon on the ancestral branch leading to MRCA of the most diverse dim-light foraging augochlorine clade (Megalopta); the amino acid is conserved in ancestral
lineages and then switches Gly11Cys (figure 1b, electronic
supplementary material, table S5). Homology modelling
of the crystal structure and ultimately mutagenic exper-
iments are required to assess the functionality of this
mutation. Comparisons to previous studies on Lepidop-
tera and bees [43], however, suggest that this codon may
be associated with structural changes that influence the
chromophore-binding pocket, and potentially shift the absorption \( \lambda_{\text{max}} \) of the visual pigment.

(c) Divergence estimates
We used the total data consensus tree for all PATHIt
analyses, and as the constraint topology to filter trees (n =
5144) to gain 95% CLs for r8s analyses. Figure 1a pre-
2012)
Table 1. Divergence age estimates. (Subset of penalized likelihood (r8s) results for alternate age-calibration procedures, indicating the time calibrate for each analysis, the mean node-age estimate in millions of years and 95% CL.)

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<th>caenohalictine</th>
<th>Amber Late</th>
<th>dim light</th>
<th>Megaloptidia</th>
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<sup>a</sup>Fixed age.

<sup>b</sup>Minimum constraint age.
Reversion to diurnal foraging

Xenochlora, the closest diurnal relative of Megalopeta, was elevated to generic status [56] based on a suite of morphological characters (e.g. coloration and ocellar size), but otherwise appears to resemble Megalopeta in form, social behaviour and nesting biology [25]. Owing to a lack of ethological data, we cannot rule out facultative crepuscular activity, but we do know they are diurnal foragers (D. W. Roubik 1991, unpublished observation, cited in Engel et al. [56]). Our data support the incorporation of Xenochlora within Megalopeta, forming a fully supported sister clade with M. atra. Males of Xenochlora are unknown; Michener [28, p. 412] considered that the phylogenetic position of Xenochlora was uncertain, but based on available evidence he would have treated it as a basal subgenus within Megalopeta. Our data show that Megalopeta is paraphyletic, and imply that the common ancestor for this genus foraged in dim light. If substantiated, Megalopeta (Xenochlora) represents a reversion to diurnal foraging. There are various examples in vertebrate evolution where both dim-light vision and colour vision have reversed (reviewed by Yokoyama [8]). A morphological study retains X. nigrofemorata as the sister taxon to Megalopeta [55], as per our LwOp results, but we recovered poor support for M. atra as sister clade to the remaining lowland Megalopeta (electronic supplementary material, figure S3a). Our total evidence tree recovers the arrangement of ((M. (Xenochlora) + M. atra), (lowland Megalopeta)) with maximal support (figure 1a).

Single tribal origin of dim-light foraging

Our results place Megommation, Megalopitidia and Megalopeta within a monophyletic clade, suggesting a single origin of obligate dim-light foraging, with a reversion to diurnal foraging from a dim-light common ancestor. Our conclusions should be considered tentative given the limited generic sampling in the tribe (9 of 25 (36%) augochlorine genera recognized by Michener [28]), and inconsistent support for the node leading to Megommation (moderate or high support in the total evidence tree, but poor support in the LwOp tree, respectively). A précis of previous augochlorine systematics is provided in the electronic supplementary material, D1. Our tree differs from these analyses [42,57,58], in that Megalopeta is distal to Megommation and the sister clade of Megalopitidia. This finding is probably not a sampling artefact, as the arrangement is robust to data matrix modifications.

Our recovery of Megommation as basal sister group to the remaining dim-light augochlorines is consistent with nesting behaviour. The primitive state for Augochlorini is ground nesting [59], and Megommation is a ground nester [60]. Nesting behaviour in Megalopitidia is unknown. Anatomical features of mandibles, and scale-like setae surrounding the median pseudopygidial slit, are convergent for wood nesting augochlorines [61]; Megalopitidia possess a broad mandible with a subapical tooth [32], but differ from Megalopeta in lacking: (i) teeth on the inner surface of the mandible [28, p. 408]; and (ii) tergal scale-setae. Both Megalopeta and Xenochlora are stem nesters [23–26], which may be ecologically advantageous in the humid tropics.

Antiquity of dim-light augochlorines: ecological association with night-flowering plants and biogeography

Our temporal estimates were robust to perturbations of fossil-derived calibrates and our root age of 65 Ma for the origin of Halictinae is consistent with independent studies of bee phylogenetics [34,39]. Palaeopalynological evidence suggests that the structure of low latitude South American forest communities have remained relatively stable since the Early Eocene [62], which roughly equates with our estimates for the origin of the Augochlorini. Our results also suggest that dim-light augochlorines predate the origin of phyllostomid bats [63]. Megalopeta bees use more than 60 angiosperm species at one site in central Panama (I. Lopez, A. R. Smith & W. Wcislo 2007, unpublished data), but little is known of their role as potential pollinators. Hopkins et al. [64] noted that Megalopeta was the most abundant visitor to Parkia velutina in Brazil, and hypothesized that nocturnal bees may have played a role in opening a new niche (night-blooming flowers), which was subsequently exploited by bats (for a more detailed discussion, see [17]).

Our arrangement places (M. atra + M. (Xenochlora)) as the basal sister clade to all other Megalopeta. Megalopeta atra is unique in its montane distribution, found only at mid-elevations (approx. 1000–1500 m) in Costa Rica and Panama [24,27]. Mountain peaks as species isolation mechanisms have been empirically demonstrated [65], and should be more extreme in the tropics [66], owing to a decreased range in temperature tolerance relative to temperate species. Our results suggest a Late Miocene origin for Megalopeta (approx. 11.2 Ma) and the MRCA of (M. atra + M. (Xenochlora)) (approx. 7.6 Ma). Current estimates indicate that the final closure of the Panamanian isthmus occurred in the Pliocene [67], and it is feasible [68] that ancestral Megalopeta lineages traversed the Panamanian Seaway before final closure. Colonization of cloud forests during cooler climes (more broadly distributed at lower elevations) and subsequent isolation from younger lineages may be accounted for by more recent (Quaternary) climatic events, or by competitive exclusion [69,70]. The contemporary lowland lineages radiated less than 5 Ma. It seems unlikely that the common ancestor of Megalopeta was a Central American cloud forest bee, and we hypothesize that M. atra represents a relictual highland species (for other examples, see [48,71,72]).

5. SUMMARY

This study provides a phylogenetic platform from which evolutionary inferences on vision and behaviour in dim-light augochlorine bees can proceed. Results suggest a tribal origin of dim-light foraging in the Late Miocene, with a secondary reversion to diurnal foraging (Xenochlora) within the distal and most diverse lineage Megalopeta. Adaptive selection tests suggest that LwOp is broadly under stabilizing selection, with a handful of sites under positive selection. Further investigation is...
required to fully determine the modes of visual transduction among these bees, and to relate the molecular evolution of all opsins proteins with rates of expression.

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REFERENCES


