

insights into the patterns of social evolution in halictid bees. First, eusociality has arisen three times within the halictid bees with multiple reversals to solitary nesting within each of the eusocial clades. Second, by combining our DNA sequence data set with fossil information and Bayesian relaxed clock methods, we have been able to reconstruct the historical timeframe of social evolution in halictid bees. Our results indicate that the three origins of eusociality in halictid bees arose within a narrow window of time approximately 20-22 million years ago, during a period of global warming. The hypothesis that global warming could have favored the origin of eusociality in halictid bees is consistent with latitudinal and altitudinal trends within socially polymorphic species. This is the first study to link the origins of eusociality in insects with global climate trends.

40 - A REVIEW OF THE BEE FAMILY ANDRENIDAE

J. S. Ascher

American Museum of Natural History, USA

Andrenidae is a large family of generally host specific (oligolectic) bees that has recently been revised at the generic level based on a phylogenetic analysis of adult morphological, larval, and molecular characters. The goal of this contribution is to summarize novel and controversial aspects of andrenid phylogeny, biogeography, and evolution, with emphasis on patterns relevant to bees as a whole. Patterns of andrenid diversity and their failure to evolve eusocial behavior are explained with reference to historical and ecological factors such as their varied and highly specialized floral host associations. Support is marshalled for a revised classification for the group.

41 - THE EVOLUTION OF OIL COLLECTION AND OIL-COLLECTING STRUCTURES IN THE MELITTIDAE

K. E. Steiner, B. Cruz

California Academy of Sciences, USA

We have used data from two nuclear genes (EF1-alpha and RNA polymerase II) and two mitochondrial genes (COI and CytB) to explore the phylogeny of the Melittidae, with a special emphasis on the Melittinae. Our data suggest that oil-collection in *Macropis* and *Rediviva* had a single origin in a common ancestor of the Melittinae with subsequent loss of this behavior in *Melitta* and *Redivivoides*. Our data also suggest that *Rediviva* is paraphyletic with *Redivivoides* embedded within *Rediviva*. The loss of oil-collecting behavior in *Melitta* and *Redivivoides* is assumed to be the result of host plant switching during the course of evolution. *Rediviva* is unique among the bees in the extreme variation in foreleg length that is tied to the morphology of its oil-secreting host plants. Although support for a single well-resolved phylogeny for *Rediviva* is weak, small well-supported clades within the genus show that changes in leg length have not progressed in a simple linear fashion. Instead, both increases and decreases in leg length have occurred during the course of evolution.

42 - PHYLOGENY AND FLORAL CHOICES INHERITANCE IN BEES

D. Michez¹, S. Patiny², P. Rasmont³, N. Vereecken⁴

¹University of Mons-Hainaut, Belgium; ²Faculté universitaire des Sciences agronomiques de Gembloux, Belgium; ³University of Mons-Hainaut, Belgium; ⁴Free University of Brussels, Belgium

Animal pollinators have long been pointed out as major drivers of phenotypic diversity in angiosperms. Bees represent one of the prevalent groups of animal pollinators in most ecosystems, and their exclusive reliance upon pollen, nectar and other floral rewards makes bee-flower interactions a textbook case of animal-plant mutualisms. Bees constitute a monophyletic group of >16,000 described species ranging worldwide except in polar areas. Whereas many bee species exhibit floral specificity, visiting only a restricted number of plant taxa throughout their geographical range (i.e., monolecty or oligolecty), others display a wider spectrum of pollen hosts (i.e., mesolecty or polylecty). In this study, we investigated whether speciation in selected groups of oligolectic bees is associated with shifts in pollen hosts (floral choices inheritance). Specifically, we combined (1) species-level phylogenetic data representing 7 genera in the basal bee families Andrenidae (genus *Panurgus*), Halictidae (*Systropha*), Megachilidae (*Lithurgus*) and Melittidae (*Dasygaster*, *Melitta* and *Macropis*) and (2) data on bee pollen host specificity to examine whether sister bee taxa forage on closely-related pollen hosts and whether shifts

from specialization (monolecty or oligolecty) to generalization (mesolecty or polylecty) are perceptible. Our results show that most speciation events at the specific/subgeneric level are not associated with shifts in pollen hosts (i.e., floral choice inheritance is strong), and that there is no evidence for shifts from specialization to generalization). For example, all species of *Macropis* (Melittidae) and *Systropha* (Halictidae) are pollen specialists associated to *Lysimachia* sp. (Primulaceae) and *Convolvulus* sp. (Convolvulaceae), respectively. Where speciation is associated with shifts in pollen hosts, the latter are usually closely-related and belong to the same section within angiosperms (e.g. Rosidae, Asteridae). We therefore hypothesize that pollen specialization is a plesiomorphic condition in bees and that speciation in most cases is unlikely to be driven by pollen host shifts.

43 - BIOGEOGRAPHY AND EVOLUTION OF AUSTRALIAN BEES

R. Leijs¹, K. Hogendoorn²

¹*South Australian Museum and The University of Adelaide, Australia;* ²*The University of Adelaide, Australia*

With recent advances in phylogenetic methods, particularly using molecular data and molecular clock analyses, bee phylogenies are accumulating. We review the available information for different bee families with the specific focus on the historical biogeography of the families occurring in Australia. Since the break-up of Gondwanaland (80-120 Mya) until contacting the New Guinean shelf (15 Mya) the Australian continent has been in an isolated position for a long time. This long-term isolation reduces the number of plausible historical biogeographic hypotheses for the arrival of the bee taxa: (1) bee taxa occurring in Australia are derived from ancestral taxa by vicariance resulting from break-up of Gondwana land. Deep divergences (> 80 Mya) between genera in Australia and the mainland would be indicative of such early splits; (2) Australian bee taxa are derived from ancestors that dispersed into Australia from SE-Asia in more recent times (< 20 Mya) when Australia's close proximity to SE-Asia increased the chance of intercontinental dispersal. By reviewing bee phylogenies we show that most bee families/tribes have arrived relatively recently (<35 Mya) in Australia. Other evidence supporting the recent arrival of bees in Australia is the rarity of parasitic bee genera in Australia. Major bee radiations in Australia seem to be correlated with a change in climate from tropical to xeric conditions starting 20-15 Mya. The implications of these inferences are important for our understanding of the evolution of flowering plants and their pollinators. The evidence shows that during the major part of the evolution of the flowering plants in Australia there were no bees present. Current flower shapes and abundance of birds and mammals feeding on pollen and nectar indicates the absence of bees as pollinators during the earlier evolutionary stages of Australian angiosperms, and may have substantially contributed to the unique character of the Australian flora.

44 - PHYLOGENETICS OF ALLODAPINE BEES: IMPLICATIONS FOR SOCIAL EVOLUTION

M. P. Schwarz¹, S. M. Tierney²

¹*Flinders University, Australia;* ²*Smithsonian Tropical Research Institute, Panama*

It has been assumed that allodapines, with their small colony sizes and near-total lack of morphological castes, represented early stages in the evolution of social behaviour. Furthermore, early studies of allodapine bees suggested that sociality evolved from non-social forms within extant clades of the tribe, and that the transition from solitary to social living coincided with a transition from mass to progressive provisioning. Recent studies challenge both of these assumptions. Firstly, they show that sociality is plesiomorphic for the entire tribe and that apparently non-social clades initially thought to be basally situated are actually highly derived. Furthermore, recent studies by Chenoweth on the biology of several critical taxa show that there are no strictly solitary species, and therefore no reversions to solitary living. Using penalised likelihood analyses based on Bayesian phylograms we show that extant allodapine lineages have an origin older than 40 mya. The ancient origin of sociality in this tribe helps explain the complexity of social organization in many species in very diverse clades. The lack of reversions to solitary living contrasts strongly with halictine bees and is probably due to major differences in key life-history traits that affect vulnerability of brood to enemies-at-the-nest. Halictines mass provision their brood in sealed cells, which provide some physical protection against enemies even after maternal death, whereas in allodapines brood are highly vulnerable in the absence of adults. Vulnerability of brood could be greatly reduced if alloparents can assume brood rearing and defence roles in the case of orphaning. This latter feature should select for tolerance of younger females by dominant females, and at the same time provide strong incentives for younger females to remain in their natal nest as potential alloparents and future reproductives.