

Reworking Family Trees for Lorries

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Lories and lorikeets (Loriinae: Psittacidae) are brilliantly colored parrots that feed primarily on nectar, fruits, and pollen (Forshaw 1973, Low 1977, 1998) and probably insects (Low 1977). Their digestive tract possesses special adaptations for a life of nectivory (Richardson & Wooller 1990), including a remarkable brush-tipped tongue (Salvadori 1891). Lorries range throughout islands and archipelagos of the southern Pacific Ocean, where they are challenging to study in the field due to difficult terrain and remote locations. However, lorries are accessible because they are widely bred in captivity by zoos and private aviculturists throughout America and many parts of the world.

Even though lorries are easily distinguished from other parrots by their brush-tipped tongue, distinct beak shape, and feeding habits, they are very similar to each other and may have recently evolved into distinct species (Christidis et al. 1991). Initially, lorries were classified into genera (plural for "genus") primarily based upon external features and plumage color patterns (Salvadori 1891). Despite widespread criticism of the original family tree, this arrangement is still used by others (Peters 1937, Forshaw 1973). However, the lack of truly definitive characters has resulted in confusion; some lory species have been placed into 5 or 6 genera during the past 150 years and, surprisingly, into two or three genera since Peters' "checklist" (1937) was published. Thus, lory classification remains a topic of lively debate among ornithologists and aviculturists. This lack of knowledge presents many problems for both conservation and ornithological pursuits. In this article, I will present

a brief overview of some of the taxonomic difficulties that exist for lorries and propose a solution: construction of a molecular (DNA-based) phylogeny of the Loriinae.

Currently, most taxonomists divide lorries into 8, 9, 11 or 12 genera containing 53 or 55 species. Recently, a combination of traditional and new methodologies indicates these classification schemes should be revised. For example, according to Joshua (1994),

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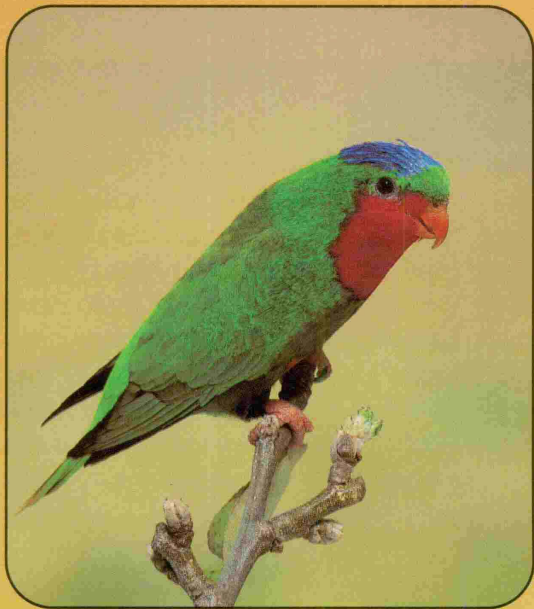
whose recent taxonomic study of lorries was based upon analysis of chromosome structure and number (karyotype data), there are three major lory lineages. One lineage is comprised of the two genera *Charmosyna* and *Vini*, while the second group includes *Glossopsitta*, *Trichoglossus*, *Chalcopsitta*, *Eos*, *Lorius*, and *Neopsittacus* and the third distinct karyotypic form is *Pseudeos*, a monotypic (single species) genus.

Morphological and behavioral similarities suggest that *Charmosyna* and *Vini* could be combined into one genus (Amadon 1942). Additionally, it is interesting to note that *Phigys* and *Vini* share skeletal structures that are unique from other psittacines, suggesting that *Phigys* could be subsumed into *Vini* based on these features (Steadman & Zarriello 1987). Further, karyotype data, which is lacking for *Phigys*, reveals striking similarities between *Vini* and *Charmosyna*, implying early evolution of this lineage away from other lorries (Joshua 1994).

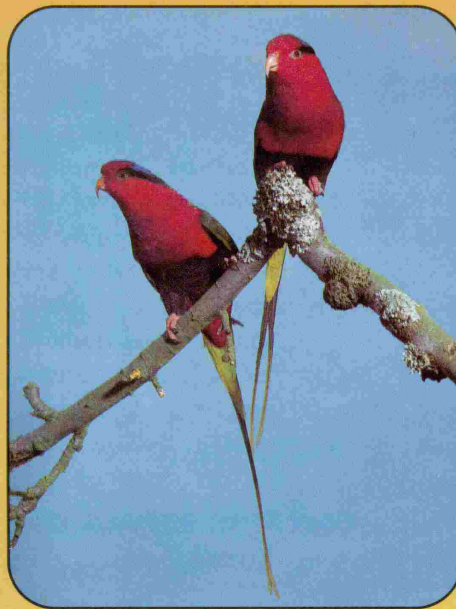
The second lineage comprises the majority of lory genera and therefore, it also is the most confusing. Traditionally, *Glossopsitta* was distinguished from *Trichoglossus* by their

black beaks, elongated first primary and smaller overall size and *Psitteuteles* was separated on the basis of their predominantly green plumage and different color patterns (Mivart 1898). However, many experts argue about the validity of *Glossopsitta* and currently *Psitteuteles* is not generally recognized as a separate genus. Further, biochemical work indicates that *Glossopsitta* and *Psitteuteles* should both be included in *Trichoglossus* (Christidis et al. 1991). Indeed, this taxonomic ambiguity extends throughout many of the other *Trichoglossus* as well. For example, *Trichoglossus haematodus* is comprised of so many distinct geographically isolated varieties that it is the most intricate superspecies complex among the psittacines.

To my knowledge, *Chalcopsitta*, *Eos*, *Lorius* and *Pseudeos* have never been carefully studied, however, they are considered by many to be very close. This confusion also extends to the species level for these genera, particularly for *Chalcopsitta* species. According to Diamond (1972), the three *Chalcopsitta* native to New Guinea comprise a "superspecies ring" of poorly defined taxa ranging throughout the lowlands. The different forms apparently result from regional contact being broken and reestablished a number of times between these semispecies: *C. duivenbodei* on the north coast, *C. atra* in the far west and *C. scintillata* from the south coast and Aru island. In fact, it is likely that the unique type specimen, *C. spectabilis*, is a naturally occurring hybrid between *C. atra insignis* and *C. scintillata scintillata* (Low 1998). The fourth *Chalcopsitta* species, the entirely red *C. cardinalis*, is found on the Solomon Islands instead of New Guinea and is often included in *Eos* due to similarities in karyotype (Joshua 1994) or plumage color and pattern (Forshaw 1973). Similarly, *Eos* and *Lorius* are also poorly defined. These taxa were classified separately based solely on behavior and plumage pattern: *Lorius* are sedentary and lack red on their



Vini australis



Chamosyna papou goliathina

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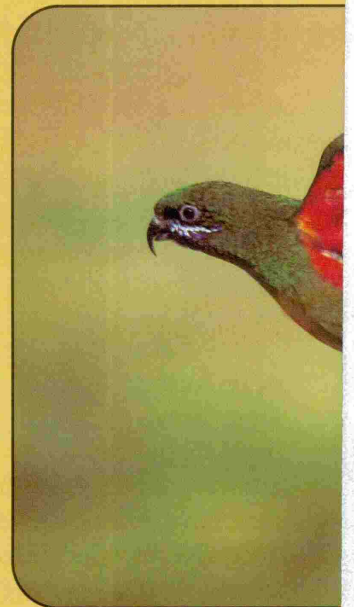
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Glossopsitta porphyrocephala



Chalcopsitta duivenbodei



Oreops



Chalcopsitta scintillata rubrifrons



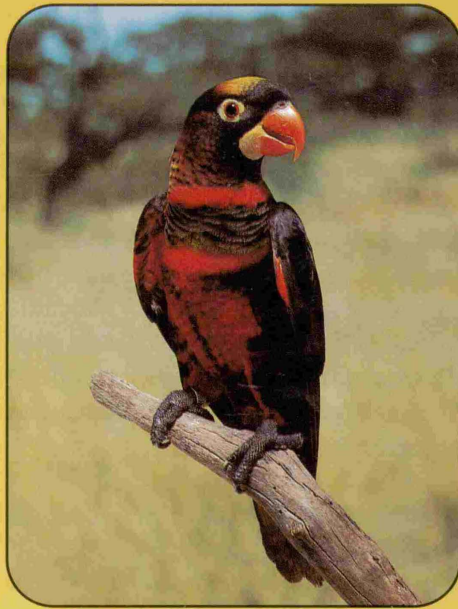
Chalcopsitta cardinalis



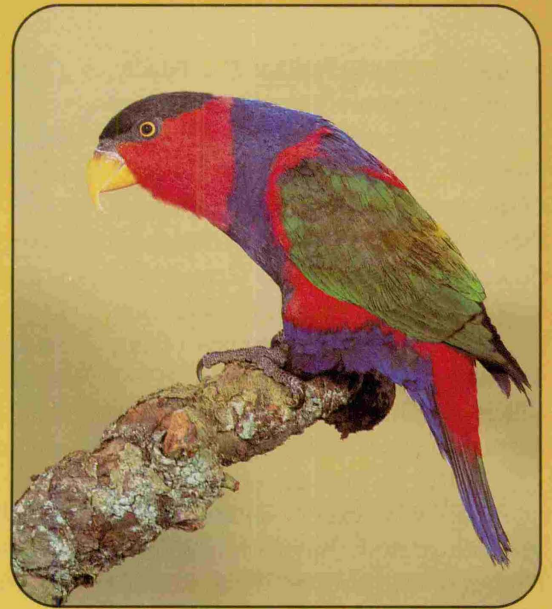
Trichog

GALLERY of most LORY era

by Cyril Laubscher



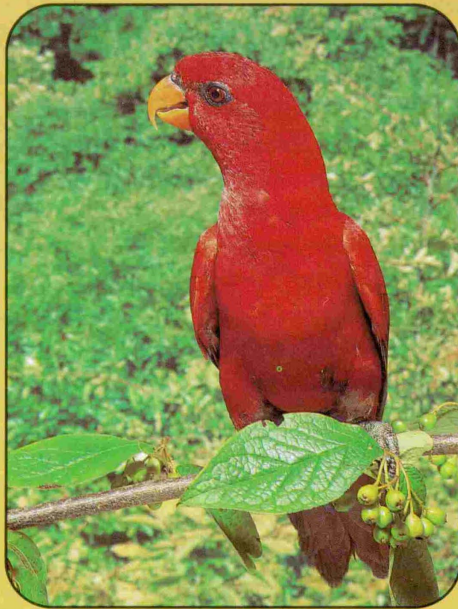
Pseudeos fuscata



Lorius lori



...us arfaki



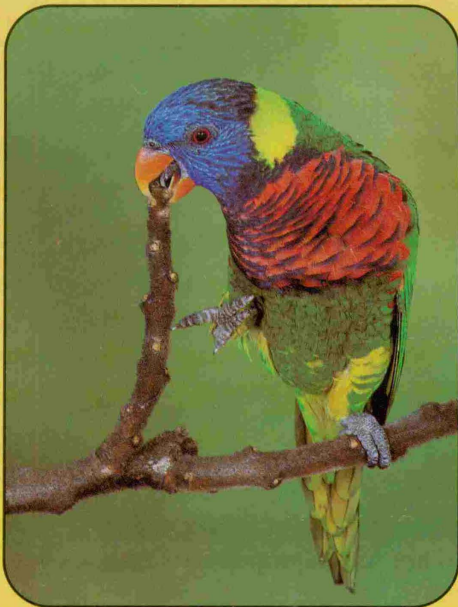
Eos bornea



Neopsittacus musschenbroekii



...us goldiei



Trichoglossus h. haematodus



Trichoglossus h. weberi

wings (Low 1998), unlike *Eos*. Finally, despite the name "*Pseudo-Eos*," chromosome structure indicates that *Pseudeos* may have close links to *Chalcopsitta* (Joshua 1994). However, *Pseudeos* chicks resemble *Eos* more closely than *Chalcopsitta* (Low 1998). In spite of these similarities, *Pseudeos* has the fewest chromosomes of any parrot studied so far (Joshua 1994), which presumably is the reason for its status as a separate lineage.

Perhaps the uncertainty surrounding lory classification can be best illustrated by Goldie's lory, *Trichoglossus goldiei*. This species was originally placed into *Glossopsitta* by Salvadori (1891), but was subsequently reclassified as *Psitteuteles* by Peters (1937). Later, Forshaw (1973) reluctantly moved this species into *Trichoglossus* but stated that further work may remove *T. goldiei* to a monotypic genus. Certainly, its distinctive karyotype and lack of close allies in *Trichoglossus* support reclassification of *T. goldiei*; shared range and similar plumage patterns hint at a possible close relationship with *Oreopsittacus arfaki* (Joshua 1994). However, *Oreopsittacus*, another monotypic genus, is distinguished from other lorries – indeed, from all other parrots – by having 14 rather than 12 tail feathers.

Additional studies of the lorries will probably identify cryptic species – those species that are not formally recognized because they are so similar in appearance to other described species. One example is the Flores Island Lory, *Trichoglossus haematodus weberi*, which was alternately classified into the Rainbow Lory superspecies complex (Peters 1937) after previous elevation to a true species by Mivart (1896) from its original status as a subspecies of Rainbow Lory (Salvadori 1891). According to those who have studied this bird in the field, it is similar to the remotely located and highly variable Olive-headed Lory, *T. b. flavicans* (John Pilgrim, personal communication); however, others claim it is closer to the Perfect Lory, *Psitteuteles*

(*Trichoglossus euteles*) (Smith 1975).

Even though this taxonomic confusion seems almost hopeless, it can be resolved by modern technology. Modern DNA techniques can detect small changes in specific DNA regions contained within birds' chromosomes. By identifying, comparing and statistically analyzing these differences in DNA sequences between lory populations, species and genera, we can construct a new family tree.

This family tree will describe the evolutionary relationships between and among lorries as revealed by their DNA. Recently, these technologies have been used to clarify species relationships within many avian taxa, including the Birds of Paradise (Paradisaeidae) (Nunn & Cracraft 1995), Woodpeckers (Picidae) (Prychitko & Moore 2000), and Goatsuckers and Nighthawks (Caprimulgidae) (Mariaux & Braun 1996). However, these same technologies have not been applied to any of the Psittacines, until now. The author has begun this work with lorries at the American Museum of Natural History in New York City. Preliminary results should be forthcoming within one year.

Understanding the evolutionary history of lorries is very important for many reasons. First, ornithologists would have a better model against which they can measure the validity of various distinguishing characters for lorries, such as color patterns and courtship behaviors, for assigning species and genus status. Further, biologists are particularly interested in evolutionary patterns of island species. Because lorries have successfully colonized many small islands throughout the southern Pacific Ocean, their historic colonization routes may be revealed to biologists who track small but detectable differences in their DNA. These colonization routes will likely provide a clearer picture of this family's evolutionary origins and rate of speciation. The lorries may reveal similar patterns of movement and

differentiation that exist for other parrots and, indeed, other avian taxa in the region.

Additionally, on a practical level, definitive identification of species makes it easier for conservation organizations to prioritize and allocate increasingly scarce funds and will allow zoos and aviculturists to effectively manage limited captive populations of lorries.

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