All in the Family

The Parrot Family Tree

The deep roots of the parrot family tree have long been a mysterious affair. With their stocky bodies, fleshy ceres, strongly curved bills and zygodactyl feet (two toes forward and two back) the parrots (Order Psittaciformes) are easily distinguished from all other orders of birds. However, the physical similarities shared across the parrots has made it difficult for taxonomists to agree on the ordering of relationships among different genera and species. In some cases it has been difficult to decide whether different populations of a species represent distinct species or may simply be the result of the variation within a single species. The identification of such cryptic species is vital for effective conservation. If genetic evidence shows that a small sub-population of a widespread species is actually a distinct species, then saving this rare new species becomes a conservation priority. Such a discovery might also suggest modifications of avicultural practices by zoos and private breeders. In addition to these practical issues, resolving the evolutionary history of a group is valuable for biologists who want to better understand the evolution of the very traits that make the parrots so interesting, such as their long lifespans, colourful plumage, keen intelligence and striking vocal abilities.

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To shed light on the mysterious relationships within parrots, we have worked for the last several years to create an evolutionary family tree of parrots (a phylogeny) using genetic data collected with modern molecular techniques.

In order to obtain a broad sample of parrot species, we collaborated with an international team of scientists and veterinarians (see Special thanks below). The legal complexities of transporting parrot samples (generally preserved blood or frozen tissue) meant that in the end, one of us, (Erin) actually travelled to each of these foreign countries in order to perform the lab work necessary to collect the genetic data.

Our globe-trotting efforts resulted in a large family tree (Figure 1) which includes representative species of 69 of the 82 recognized genera.

Interpreting phylogenetic trees can be confusing to the uninitiated, so here we answer some basic questions about the phylogeny and some of the evolutionary patterns it shows.

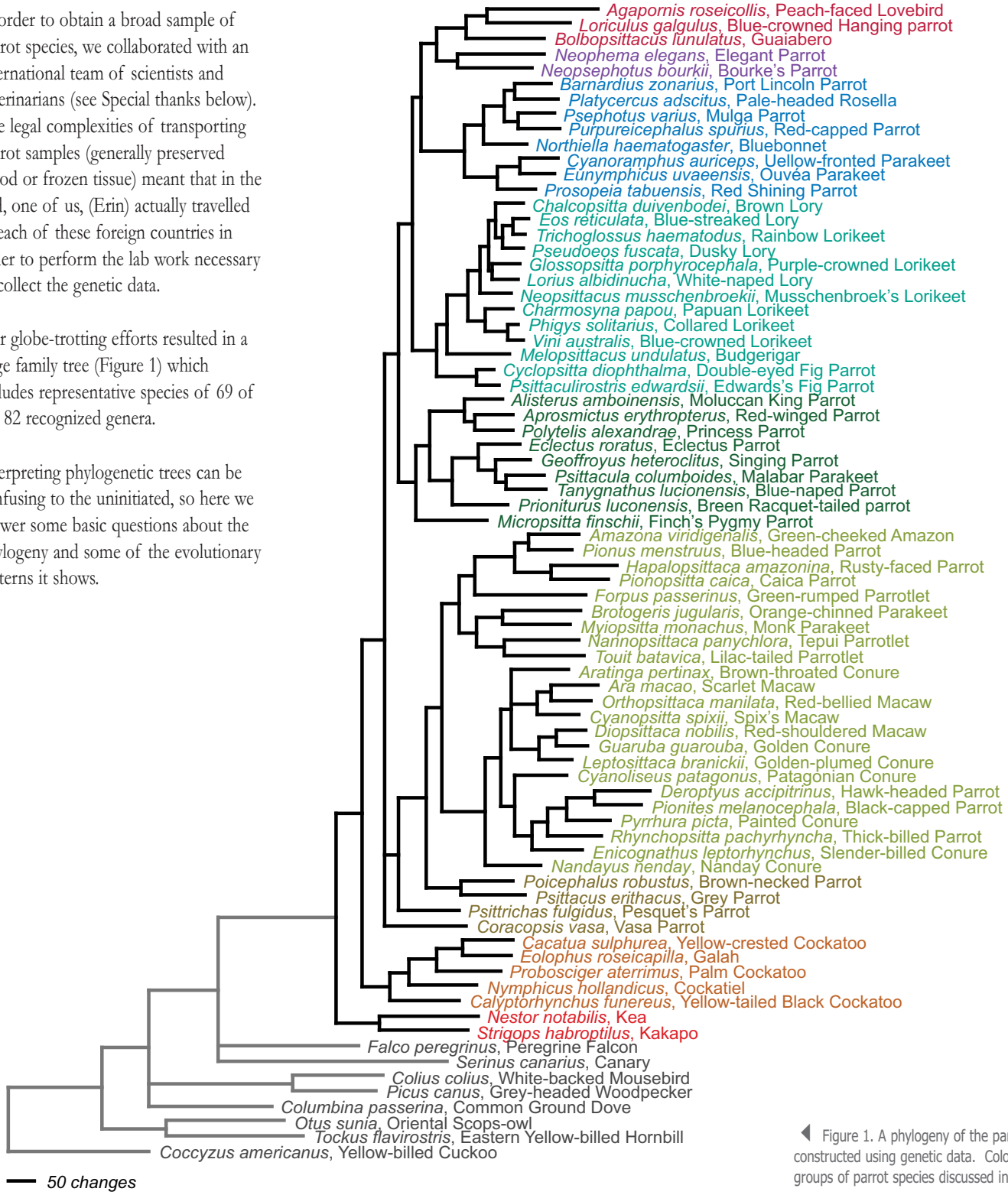

Figure 1. A phylogeny of the parrots constructed using genetic data. Colours denote groups of parrot species discussed in the text

Questions? If you have further questions about the parrot family tree, please send them to Joanna Eckles, *PsittaScene* Editor, at joanna@worldparrottrust.org. We look forward to answering them in a future issue.

For more information consult our more detailed paper published in the journal *Molecular Biology and Evolution* (Wright et al 2008, 25(10) 2141-2156), a version of which is posted at our website http://biology-web.nmsu.edu/twright/.

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1) How do you read a phylogeny?

Phylogenies can be thought of as a family tree with descendants branching outward from a single ancestral species. The tips of the tree (on the right in Figure 1) are the species that are currently in existence. The places where two branches join are called nodes, which represent the last common ancestor of those two living species. For example, at the top of the phylogeny, the place where the branches leading from the Peach-faced Lovebird (*Agapornis roseicollis*) and the Blue-crowned Hanging Parrot, (*Loriculus galgulus*), meet is the node and represents the last common ancestor of those two species. All the branches coming out of a node towards the tips on the right side of the tree are the descendents of that ancestor, and the species at the ends of these branches are thus more closely related to each other than to those coming from a different node. The length of the branches separating a tip from a node, or two nodes from each other, represents the amount of evolution between those nodes. In our case the length of the branches represents the amount of genetic change seen between the sampled DNA sequences.

2) How did you choose the species in your tree?

Our species were chosen to represent as many of the existing parrot genera as possible. In general our choice of which species to use within a genus was guided by availability of samples appropriate for genetic analysis, either a tissue sample in a museum or a live bird in a zoo collection from which we could obtain a blood sample.

3) Who are the closest relatives of the parrots?

The non-parrots in our tree include an owl, a songbird, a hornbill, a woodpecker, a cuckoo, a mousebird, a falcon and a dove. These orders were chosen because at one time or another they had been suggested as the closest relatives to parrots either by morphological or genetic evidence. They are shaded in grey and branch outward from the most basal node, which represents the common ancestor of all these avian orders. In this particular tree the falcon and the songbird species branch from the same node that leads to all of the parrots, suggesting that they are the closest relatives of parrots. This result, however, was not consistently found in other trees we constructed from subsets of the data or with different tree building methods. Furthermore, other recently published phylogenies that have sampled more widely across avian orders have also found contradictory results regarding who the closest relatives of parrots might be. This continuing confusion suggests that parrots are indeed a very ancient order of birds that split from the ancestors of other modern birds a very long time ago, perhaps as long as 80-90 million years ago during the Cretaceous Period. The identity of their closest relative remains a mystery awaiting further investigation.

4) Who are the most ancient parrots?

If you work your way along the tree from the basal node connecting the parrots to the non-parrots, you will see that the first parrot group to split off from the common ancestor of parrots is a group (or 'clade') of New Zealand parrots that includes the Kea and the Kakapo (red clade in Figure 1). This split indicates they are the group that is most-distantly related to the remainder of the parrots and has interesting implications for the geographic origins of parrots, as New Zealand is one of first landforms to split from the ancient supercontinent of Gondwana, around 82 million years ago. It supports a long-standing hypothesis that the ancestors of the modern parrots originated on this continent and that present distribution of parrots in Australia, South America, southeast Asia and Africa can largely be explained by the subsequent breakup of this supercontinent into these modern continents.

5) I thought cockatoos were the most ancestral parrots?

Cockatoos have been thought by many to represent the most ancient lineage of parrots based on some unique anatomical characteristics (including their erectile crests), but this hypothesis was not supported by our genetic data. They were the next group to split off after the New Zealand species and are strongly supported as a distinct group by the genetic data (orange clade).

6) What comes next in the tree?

If you follow the tree up from the node that leads to cockatoos, you will see a large number of nodes separated by short branches, suggesting that there was a rapid diversification of parrots that led to the modern groups such as the lories, the Neotropical parrots, the African parrots, the various groups found in Australia and Asia.

7) Why do some of these groups seem jumbled up?

There are some distinct surprises in the parrot family tree. One is that the Budgerigar is not closely related to the rosellas, bluebonnets and other Platycercine parrots of Australia. Instead it is a member of a clade that includes the lorikeets and Fig Parrots (teal clade). Also, the African parrots do not form a single clade; instead the African Grey and parrots of the genus *Poicephalus* are closely related to each other, while the Vasa Parrot of Madagascar diverged earlier in the tree and the lovebirds of the genus *Agapornis* are in an entirely different clade that also includes the Hanging Parrots of Indonesia (genus *Loriculus*) and the odd Guaiabero found only in the Philippines (top clade in magenta). This pattern suggests that Africa may have been colonized by several different lineages of parrots at different times.

8) Is nothing of the old classifications sacred?

Some historically recognized groups are strongly supported by our tree. In addition to the cockatoos and lories (albeit with a surprising Budgerigar relative) already mentioned, a core group of the Psittaculine parrots of Australasia that includes the Eclectus Parrot, the Singing Parrot, King Parrot and the Princess Parrot received strong support (dark green clade). A second well-supported clade is the Platycercine parrots that include the Australian rosellas, the bluebonnet, Mulga Parrot and Port Lincoln Parrot, and some species found in New Zealand and as far away as Fiji (blue clade). A third strongly supported clade is the Neotropical parrots of Mexico, Central America, South America and the West Indies, which are all more closely related to each other than they are to any other parrots (largest clade in pale green).

9) What's next?

We are continuing our work by filling in missing genera and by starting to amass data for all species in certain clades. Next up, as part of Erin's PhD dissertation, is a species-level phylogeny of the Neotropical parrots. Stay tuned for more exciting revelations about the parrot family tree!