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# Origin of Tepui Avifauna

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## COMPETING HYPOTHESES



### Introduction

Tepuis are ancient, weathered mountain formations found in NE South America in S Venezuela, S Guyana and NW Brazil. They are characterized by isolated flat plateaus at the summit and sheer escarpments at the sides. Due to their isolation and unique habitat, tepuis harbor a lot of unusual and endemic species. Their isolation and high endemism inspired the novel *The Lost World* by Arthur Conan Doyle.

Many bird species found on the tepuis are also unique. Some species have relatives in lowland habitats nearby, but others have relatives only in mountainous areas far away. Due to the remoteness of the tepuis and the difficulty in reaching the tops, the expeditions to collect specimens are challenging. However, there has been much interest in the origin of the endemic biota at this center of biodiversity. Mayr and Phelps (1967) analyzed the tepui avifauna and came up with several hypotheses to explain the distribution of the birds here. The current project aims to support or refute these hypotheses by molecular studies on the relationship of tepui birds.

### Vicariance



A widespread population becomes fragmented by a natural barrier like a river or mountain range. These represent ancient populations.

### Habitat Shift



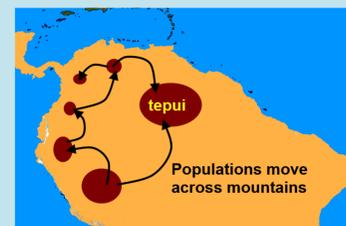
Species gradually tend to adapt to different habitats as time progresses. In this case lowland species adapt to higher elevations in the tepuis.

### Dispersal out of tepuis



Dispersal can occur from tepuis resulting in an endemic older than other related taxa.

### Dispersal to tepuis



Populations disperse from nearby or distant mountains by "island hopping" resulting in new endemic species.



## Results and Future of Project

From the few tepui birds that have been studied so far, a few tentative conclusions can be derived. Based on molecular data, various species of birds fit different patterns of distribution.

Some species from the tepuis such as *Myioborus* redstarts appear to have come from the nearby Paria mountains of N. Venezuela (Lovette et al., 2010). This suggests dispersal to the tepuis in an "island hopping" scenario.

Several other species (e.g. *Thamnophilus atricapillus*, *Heliodoxa xanthogonys*) appear to have their closest relatives in the Andes of Peru (McGuire et al., 2008). This suggests either long-distance dispersal or an ancient habitat connection through the "Acre Arch" that has since disappeared (vicariance). Similarly several species like *Caprimulgus whitelyi* and *Aulacorhynchus whitelianus* appear to be basal members of their species group (Han et al., 2010; Bonaccorso et al., 2011). They may have been ancestors to at least some of their closer relatives.

In several cases, these results contradict prior hypotheses of origin for these same bird species. Resampling of some of these species complex has been done and we are awaiting results. These and subsequent phylogenies that shall be generated will help us better understand the origin of tepui birds.

## Materials and Methods

Tissue samples of several tepui birds and their closest relatives collected from various expeditions and stored in several institutions were used to extract DNA. More than 500 ultra-conserved elements (UCE's) were isolated from genomic DNA (see Faircloth et al.) and sequenced on an Illumina HiSeq machine. The UCE sequences were used to create alignments, which will be used to infer phylogenies of tepui birds. Some previously published phylogenetic trees were also studied. The position in the trees of the tepui endemics with respect to their close relatives provides a test of the prior hypotheses of origin of the tepui endemics.

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