

# Molecular methods are not sufficient in systematics and evolution

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Modern evolutionary systematists often use molecular methods, such like mitochondrial DNA analysis, to differentiate between species and subspecies. These molecular methods are a flashy symbol of modern science cleverly exploited by media to draw interest of public and by laboratory scientists to draw attention of government funding agencies. However, current research indicates that the picture painted by these methods may be false, and only a creative combination of classical field-based ecology, museum-based systematics and DNA-based phylogenetics, can lead to right conclusions.

In the last issue of the internationally acclaimed *Ornithological Monographs* (pages: 90-102), a team of biologists from the Universidad Central de Venezuela, Allegheny College in USA, Seoul National University in South Korea and Centre for Ecological Studies in Poland demonstrate how modern [evolutionary biology](#) needs the "old-style" biology in order to explain evolution and systematics of birds.

The team composed of Jorge Perez-Eman, Ronald Mumme, and Piotr Jablonski studied mitochondrial DNA, plumage coloration and behavior of 10 subspecies of a Central and South American warbler the Slate-throated redstart, an inhabitant of montane forests. Mitochondrial DNA analyses indicated that evolution of these birds started over 70 millions years ago, in the Pleistocene, in northern and central areas of modern Mexico. First, the birds rapidly expanded southwards to South America diversifying into several genetically and morphologically different subspecies. Second, about 40-70 million years ago, when today's

montane forest types existed at lower elevations, a rapid expansion started producing several morphologically distinct subspecies that differ in the coloration of their bellies from yellow, orange, through red, and in the tail pattern from small to large white patches, but do not differ in the mitochondrial DNA. The researchers believe that during this rapid expansion of the populations, the genes responsible for these morphological traits have evolved rapidly due to adaptation to local habitats, while the mitochondrial genes often used in the phylogenetic research, remained unaffected by the evolutionary change.

Why would local conditions lead to rapid changes in the plumage pattern? The answer to this question can be found in the role of tail pattern in foraging of these warblers. The Slate-throated redstarts, as well as their relatives, the Painted Redstarts, use "flush-pursue foraging". The foraging birds look like butterflies when they spread their tails and wings in order to be conspicuously visible by the insects. Insects, such like treehoppers or flies, are scared by the sudden visual displays and are flushed away from their resting sites on leaves and branches. The birds only wait for this to happen, and in elegant pursuits they catch the escaping insects in the air. Field experiments conducted by the research team with birds of the Costa Rican subspecies *Myioborus miniatus comptus* (see photo) and their key prey indicated that a contrasting black-and-white tail is critical to flush-pursuit foraging success, and that subspecific variation in the extent of white in the tail reflects evolutionary adaptation to regional prey or habitat characteristics that maximizes flush-pursuit foraging performance. Thus, even though the subspecies of the Central American clade are genetically homogeneous with respect to the mitochondrial genes, analysis of tail pattern and its effect on foraging performance suggests a recent adaptive evolutionary divergence, warranting the status of separate subspecies.

The researchers conclude: "Our findings serve as a reminder that [mitochondrial DNA](#) (mtDNA) gene trees will not always succeed in

capturing all evolutionarily significant genetic change, and that manipulative field experiments can provide crucial information on the selective factors that lead to evolution of subspecies-specific morphological traits even in the absence of mtDNA diversification."

Provided by Seoul National University

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