PATTERNS OF EVOLUTION: SPECIES AND SPECIATION IN PHYLLOSCOPUS AND SEICERCUS

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Abstract: The two avian genera *Phylloscopus* and *Seicercus* are studied from a phylogenetic perspective. Based on studies of morphology, vocalisations and ecology in the field and in scientific collections the biodiversity in these groups is demonstrated to be larger than previously appreciated. Several forms treated as subspecies are shown to be independent evolutionary lineages. Two new species are described, one from Hainan Island, China (*Phylloscopus hainanus*), and one from Sichuan Province, China (*Seicercus soror*).

The genus *Phylloscopus* is difficult to define in an unambiguous way and particularly the "crowned leaf warblers" have been moved between *Phylloscopus*, *Seicercus* and *Cryptigata*. depending on which characters have been emphasised. Phylogenetic analysis based on mitochondrial DNA sequences shows that the group is not monophyletic. Furthermore, none of the previous classifications are congruent with the phylogeny presented in this thesis.

Phylogenetic analysis of *Seicercus* based on mitochondrial DNA sequences shows that the genus is not monophyletic. It is divided into three different clades which are all nested in the *Phylloscopus* clade. For one of these clades, DNA sequences from all known evolutionary lineages, with one exception, are included in the analysis. The resolution of the phylogeny is increased compared to most phylogenetic studies which commonly include only one representative of polytypic species. The most closely related terminals occupy allopatric distributions, but similar habitat. This is contrary to what is predicted for sympatric speciation, but in accordance with the expectations for allopatric speciation, which seems to be the norm for these birds. There are evidence that strict differentiation in habitat choice may be associated with early stages of secondary contact.

The use of subspecies is discouraged, as systematic studies should deal only with evolutionary entities. In all the studies included in this thesis a primary aim has been to identify terminal lineages de novo, independent of previous classifications and to study their relationships. The phylogenetic analyses show that most of the previous groupings based on morphological characters are non-monophyletic. Some of this information became available only because almost all known terminal lineages were included for some groups.

Keywords: *Phylloscopus*, *Seicercus*, phylogeny, systematics, terminal lineages, allopatric speciation.