

## THE PHYLOGEOGRAPHIC PERSPECTIVE ON EVOLUTION OF ENDEMISM IN THE CAUCASIAN AVIFAUNA: PRELIMINARY DATA

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Although Caucasus is an internationally recognized area of avian endemism there are only three species that are considered endemic to the Caucasus (Stattersfield et al. 1998). Among these three species, Caucasian snowcock (*Tetraogallus caucasicus*) inhabits high alpine habitats, Caucasian grouse (*Lyrurus mlokosiewiczzi*) and Caucasian chiffchaff (*Phylloscopus lorenzii*) inhabit subalpine habitats. Only Caucasian grouse has a sister species, black grouse (*L. tetrrix*; Drovetski 2002) whose range includes Europe. The closest relatives of the other two endemic species inhabit the mountains of western Asia. In addition to the three endemic species, Caucasus hosts numerous endemic subspecies (Stepanyan 2003). Many of these subspecies have distinct phenotypes that are easily distinguishable from their European conspecifics. From the point of view of traditional systematics such strong phenotypic differences are usually interpreted as further evidence for unique evolutionary history of Caucasian avifauna.

Alpine and forest habitats of Western Caucasus are currently separated from similar habitats in Europe by a wide belt of steppes to the north and the Black Sea to the west. Gene flow between moist grassland and forest species inhabiting Caucasus and the rest of Europe may be restricted allowing Caucasian avian communities to evolve independently.

During Pleistocene glaciations, a large part of Europe was covered by ice and Europe was recolonized from several different refugia (Hewitt 2000). Among these refugia, the Balkans appear to be the source for most European populations of vertebrates, invertebrates and plants. The two other major European mountain ranges, Pyrenees and Alps, also played an important role in shaping the distribution of genetic lineages of plants and animals within Europe. Currently, all three mountain ranges represent zones of contact for lineages that colonized Europe from different refugia.

Although Hewitt (2000) acknowledged that some central and northwestern European populations came out of unknown refugium(a) to the east, he could not include Caucasus or much of the easternmost Europe in his review for very little is known about population genetics of plants and animals in that region. Since many European species inhabit Caucasus, it could have been a refugium during Pleistocene glaciations. On the other hand, since there are many endemic forms found in the Caucasus, it could have

been isolated from the rest of the Europe with Caucasian communities evolving through colonization by European and Asian species followed by isolation.

Here we report our preliminary results on the study of genetic differences between European and Caucasian populations of six avian species. Our studies are based on mitochondrial DNA (primarily complete sequences of mitochondrial ND2 gene, 1041 bp). Detailed description of methods are provided elsewhere (Zink et al. 2002, Drovetski et al. 2003).

The difference between endemic Caucasian grouse and black grouse has been determined for two mitochondrial loci. These two species differ by 2.88% uncorrected sequence divergence in the mitochondrial ND2 gene (data from Dimcheff et al. 2002) and by 2.66% in the mitochondrial control region (data from Drovetski 2002). These divergences represent an overestimation for they are not corrected for intraspecific variation. However, they provide an important reference for comparison of Caucasian and European populations of other species.

To date we have sampled six avian species that inhabit both western Caucasus and Europe. Among these six species four have subspecies endemic to Caucasus: greater spotted woodpecker (*Dendrocopos major*), Scarlet rosefinch (*Carpodacus erithrinus*), winter wren (*Troglodytes troglodytes*), and Eurasian nuthatch (*Sitta europaea*). One species has a subspecies that is distinct from European, but is not endemic to Caucasus – white wagtail (*Motacilla alba*). Finally, the same subspecies of great tit (*Parus major*) inhabits both European part of Russia and western Caucasus. These six species can be divided into three pairs that represent three different stages of genetic differentiation between European and Caucasian populations (fig. 1).

We found no evidence of differentiation between Caucasian and European populations in the greater spotted woodpecker and great tit. The geographic distribution of haplotypes was non-random ( $F_{st}$  values were significant), but lineage sorting into European and Caucasian clades was incomplete in the Scarlet rosefinch and in the white wagtail. In the last two species, winter wren and Eurasian nuthatch, Caucasian birds were well differentiated from their European conspecifics. In both of these species lineage sorting was complete and the difference between Caucasian clades and respective European clades was 2.5% of uncorrected sequence divergence. This difference is remarkably similar to that found between Caucasian grouse and its European sister species black grouse.

Mean mismatch values for European populations were greater than that of the respective Caucasian populations in the two undifferentiated species, greater spotted woodpecker and great tit (fig. 2). This may indicate that Caucasus has been colonized by European birds relatively recently. In each of the other two species pairs, the same was true for one species, but the opposite was true for the other species. This may indicate that isolated populations had unique demographic histories in each case. The mismatch distribution of all Caucasian white wagtails combined is distinctly bimodal. This pattern is likely the result of recent colonization of Caucasus by European birds. Indeed the four individuals carrying European haplotypes were collected in the two northwestern most localities within Krasnodarskiy krai – on the northern shore of the Black Sea (Kiziltashskiy Liman), and south-eastern shore of the Sea of Azov (west of Temryuk). No wagtails carrying European haplotypes were found in the four localities to the south.

Our preliminary data show that most of the populations of Caucasian birds are differentiated from their European conspecifics. These data also indicate that some Caucasian populations, that currently are treated as conspecific with European forms, were isolated for sufficient time for completion of lineage sorting and indeed represent sister species to European taxa. A comprehensive comparative study of population genetics of Caucasian and European form is needed to elucidate the patterns of evolution of endemism in the Caucasian avifauna. We propose that a relatively large number of Caucasian bird populations may merit recognition as distinct species.

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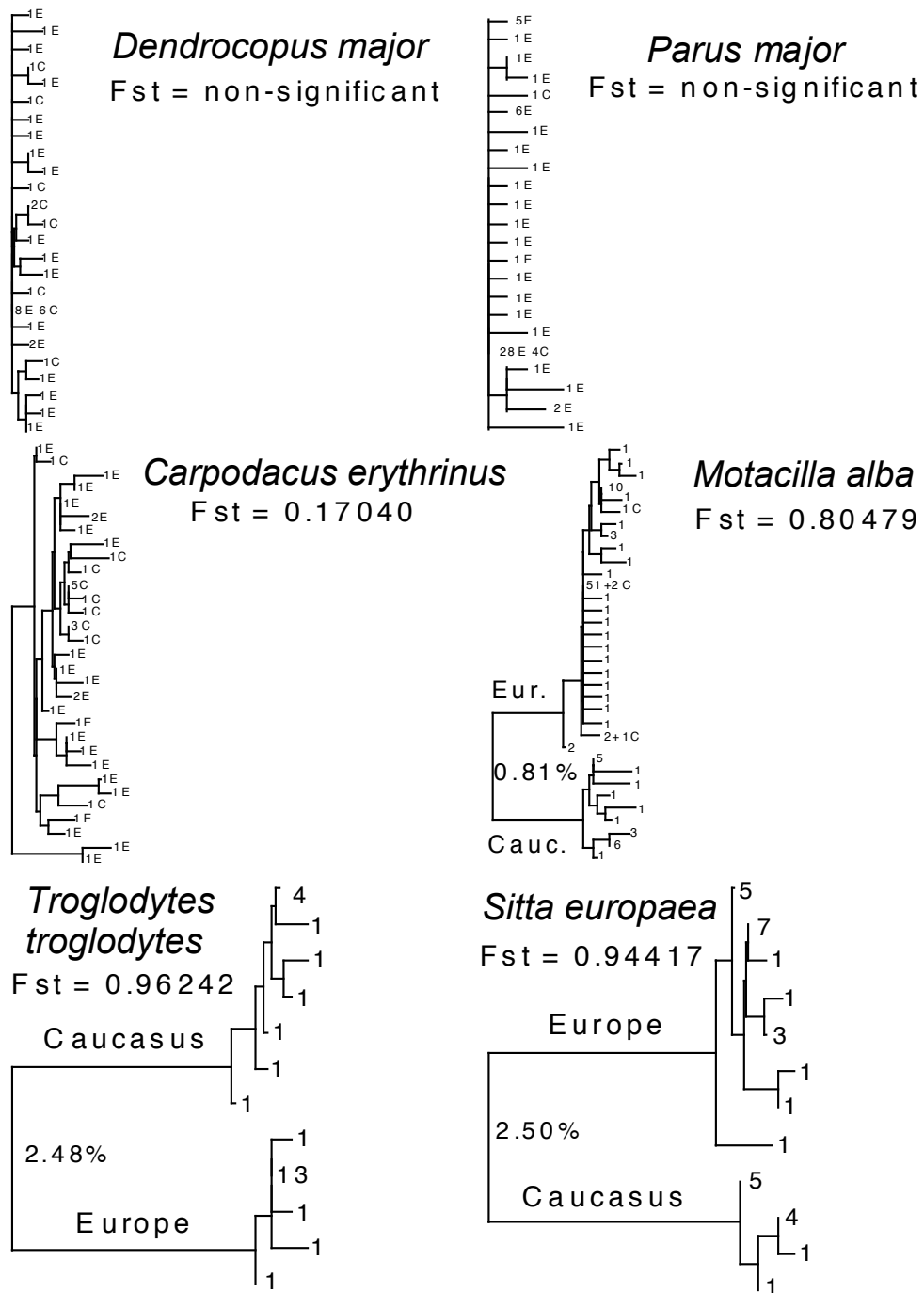


Figure 1. Phylogenetic relationship of Caucasian and European mitochondrial haplotypes (Neighbor Joining trees based on uncorrected genetic distances) in six species. All trees are drawn to the same scale. The difference between distinct clades is shown in percent of uncorrected sequence divergence. In the parts of the trees where haplotypes are not sorted between Caucasian and European clades, Caucasian individuals are identified by C next to the sample size (numbers at the tips), and European individuals identified by E.

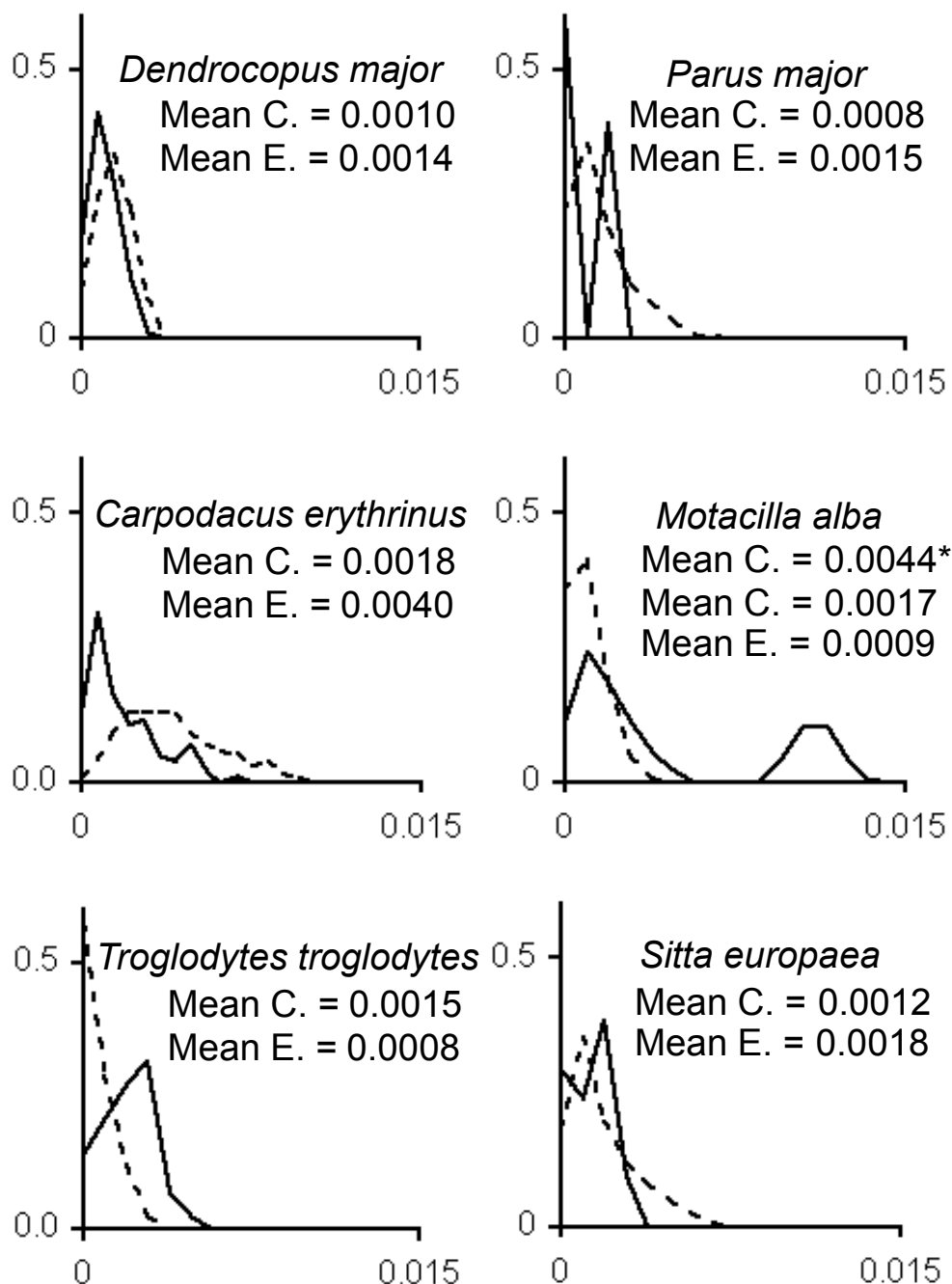


Figure 2. Mismatch distributions for Caucasian (solid line) and European (dotted line) populations in the six species. Pairwise distances (% sequence divergence) are on the horizontal axis, and their frequencies are on the vertical axis. Mean mismatch values for Caucasian and European populations are identified as Mean C. or Mean E., respectively. For white wagtail, \* after the Mean C. mismatch identifies value for all Caucasian individuals combined. The Mean C. value without \* identifies the value calculated only for individuals from the Caucasian clade.