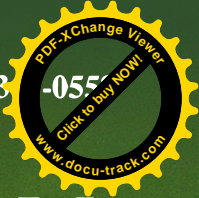


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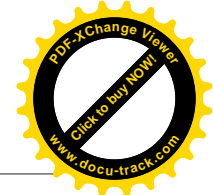
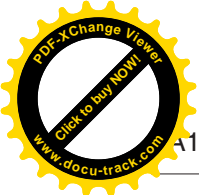


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## Phylogeography of mtDNA haplotypes and range settling in the Siberian rubythroat

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The analysis of the *cyt b* gene of mtDNA in the Siberian rubythroat (*Luscinia c. calliope*) migrating across Southern Primorye (Russian Far East) has revealed two well-differentiated phylogroups, which we call “western” and “eastern”. In our further study of breeding birds (n = 121) from 15 localities, 82 haplotypes were identified, 42.7% of which belonged to the western phylogroup (uniting *L.c. calliope* populations), and the remaining 57.3% to the eastern phylogroup. The latter in turn is separated into 2 genetic pools, about two third from which was formed from birds of the *sachalinensis* subspecies only, and the other group united individuals belonging to races *anadyrensis*, *camtschatkensis* and Sakhalin birds. A phylogenetic network of mtDNA haplotypes of *L. calliope* shows distribution of haplotypes in different taxa of *L. calliope* on various parts of the habitat. Genetic structure of populations at the north-eastern part of the habitat and Sakhalin revealed intermixture of haplotypes belonging to the western and eastern phylogroups in various proportions, while the island populations of Hokkaido and Iturup, as the most remote populations from the spatial contact with *L.c. calliope*, were represented only by haplotypes of the eastern groups. The study revealed not only different pattern of taxon-specific haplotypes distribution in the western and eastern parts of the habitat, but also showed a link between both phylogroups through *L.c. sachalinensis*. Thus, we suggested a hypothetical scheme of spreading of the Siberian rubythroat first from Siberia to Sakhalin, then to Kamchatka, to the basins of the Penzhin and Anadyr rivers with their adjacent areas of the Koryak Highlands. Further it gradually spread from Kamchatka over the Kuril Islands, eventually reaching Hokkaido. It should be emphasized that the Sakhalin subspecies, being probably the first one among all forms of the eastern phylogroup to separate, had no direct relation to the formation of populations at the Kuril Islands and Hokkaido.

