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PHYLOGEOGRAPHY AND HISTORICAL RANGE SHIFTS IN MAGPIE (*PICA PICA*):  
INSIGHTS FROM GENETIC AND BIOACOUSTIC DATA

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The Eurasian magpie *Pica pica* (Linnaeus, 1758) is a widely distributed, mostly Holarctic species occurring from Morocco and Spain to Western North America with several isolated occurrences. It lives in semi-open, semi-arid and often anthropogenic habitats. Here we present results on patterns of genetic variation in *P. pica*, particularly in its eastern Palearctic distribution, i.e., with special emphasis on populations from the Russian Far East, Japan, Korea and Taiwan. Moreover, own and published bio-acoustic data on the chatter calls of *P. pica* were compiled and the differences between populations discussed in comparison with the genetic results. Together with recent reports on the current range shifts and the spreading of the species we discuss possible ways of population expansion and settling.

The complete mitochondrial (mt) control region was sequenced in 109 individuals representing nine subspecies. Deep genetic divergence between four lineages was found: (1) a European-Siberian group, (2) a South-Far-Eastern group, (3) *P. p. mauritanica* and (4) *P. pica hudsonia*. These lineages show a clear geographic pattern and clearly correspond to single subspecies or groups of subspecies. The differentiation within the European-Siberian group (clade West) covering a huge range is rather small implying fast recent expansion. A somewhat separated lineage was detected in Kamchatka. This population, which shows clear affinity to the European-Siberian group, is very homogeneous which indicates a bottleneck/founder effect. The South-Far-Eastern group (clade East) is subdivided into two subclades which, at first sight, could be explained by distinct Pleistocene refuges of the two subspecies *P. p. serica* and *P. p. jankowskii*. Yet there is no geographic pattern and the two subspecies are randomly distributed within these two clades. We assume that this is due to postglacial range shifts and admixing of populations.

The two other lineages are separated by 4,9–6,6% average p distances from each other and the other lineages, respectively. *P. p. hudsonia* represents the sister lineage to clade west, which is known already from earlier publications. The distinct position of *P. p. mauritanica* is reported here for the first time. Unfortunately, both lineages are represented by only single individuals in our data set.

Bioacoustic data mainly coincide with phylogeographic patterns as revealed by mt sequences and are in concordance with subspecific differentiation as well as with the major split of the four mt lineages. Yet several taxa remain to be analysed. Together with the phylogeographic patterns, historical and recent reports on distribution range shifts, e.g., the fast spreading of the *P. p. jankowskii* population towards the west in Transbaikalia, and that of *P. p. leucoptera* in the opposite direction leading to a new contact zone, are summarized and discussed. The homogeneity of the Kyushu population supports historical reports on the species' introduction. The Hokkaido population originated only recently. Its unexpectedly high variation can be explained by ongoing introduction from the variable population of the South Russian Far East. In general, our data support the known scenario of divergence in geographic isolation, but ongoing expansion of distribution ranges may lead to dramatic changes in phylogeographic patterns as inferred from the mtDNA variation data presented.