

The great bustard is a key species in conservation of the European lowland dry grassland ecosystem, especially in the Ponto-Caspian steppes. We have investigated the genetic diversity, population structure and demographic history of great bustards in a regional scale by analysing mitochondrial (mt)DNA sequences (a 662 bp fragment of control region I and II) in 84 individuals sampled from the Ukraine and the Lower Volga basin (figure 1). This marker revealed moderate nucleotide ($\pi = 0.0068$) and haplotype ($h = 0.924$) diversity that could be partitioned into three matrilineage clusters scattered throughout the study area. Consequently, the amount of variation between populations was relatively low ($F_{ST} = 0.11$) indicating a weak, but significant geographical genetic subdivision in great bustard mtDNA (Table 2). Spatial analysis suggested that genetic isolation by distance has a small, but not negligible effect in the studied population. A history of allopatric population fragmentation around 100000 years (100 KY) ago followed by secondary genetic contact and past population growth (60 – 48 KY ago) accompanied by range expansion is the most likely demographic scenario (figure 2). These findings have important implications for current conservation of great bustards.

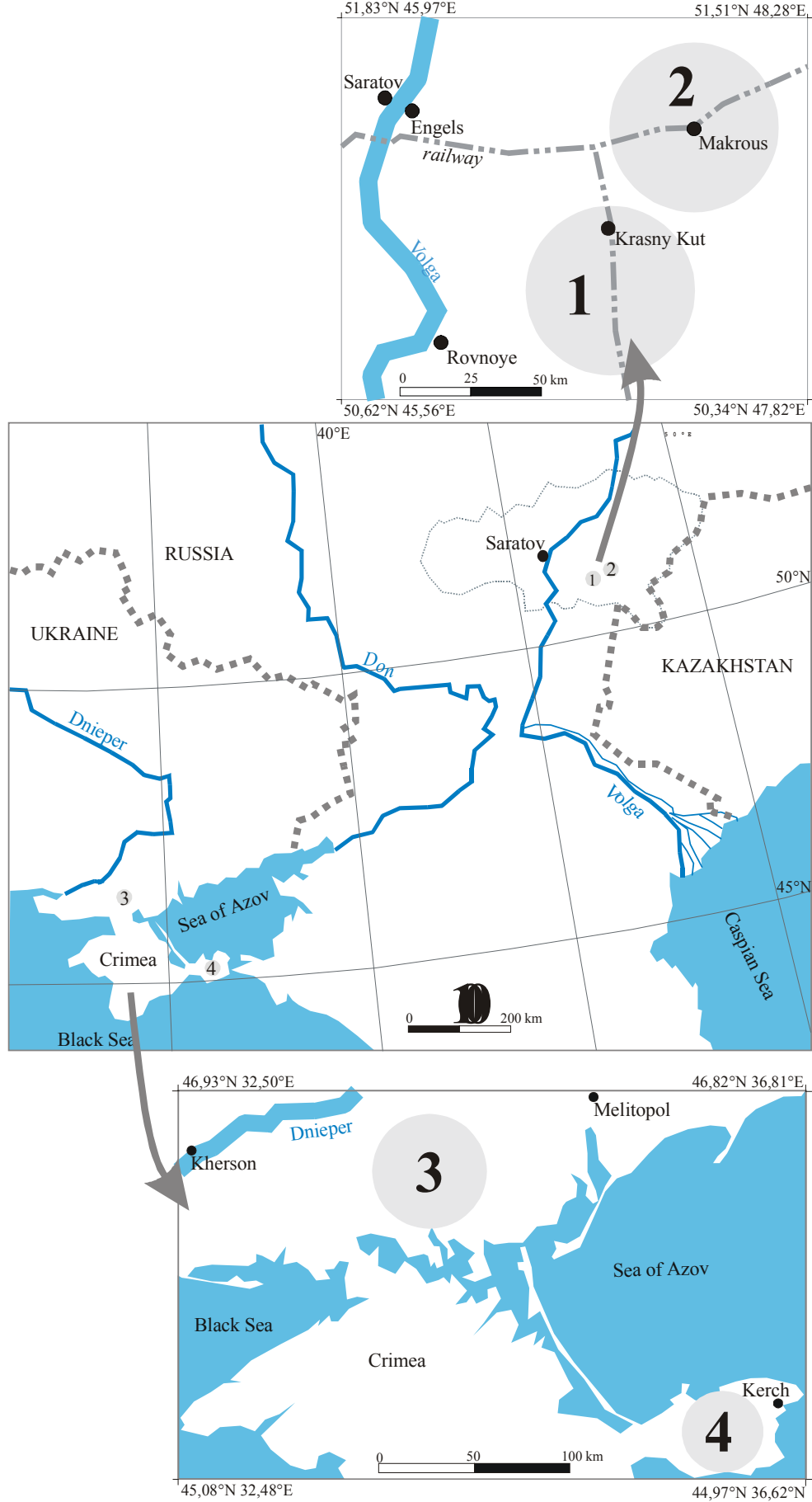


Figure 1 Map showing the localities sampled in the current study. 1 = Krasny Kut, 2 = Fyoderov, 3 = South Ukraine, 4 = Kerch peninsular.

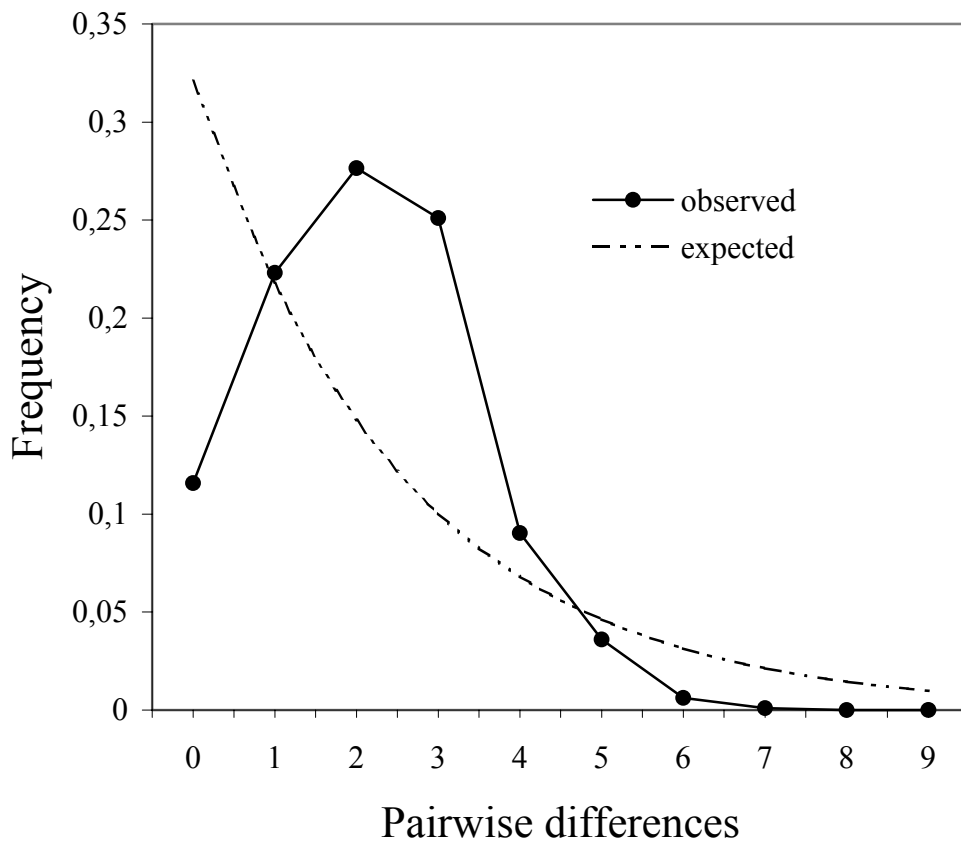


Figure 2 Mismatch distributions of the group A haplotypes shown against expectations from constant and expanding population sizes clearly demonstrate a closer fit of the data to the expectation under the conditions of past population expansion.

Table 2 Population pairwise F_{ST} values (below diagonal) and Slatkin's N_{fm} (above diagonal).

	Krasny Kut	Fyoderov	Ukraine
Krasny Kut	—	18.19942	1.78768
Fyoderov	0.02674	—	—
Ukraine	0.21856	0.21324	0.62529