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Near panmixia at the distribution-wide scale but evidence of genetic differentiation in a geographically isolated population of the Terek Sandpiper *Xenus cinereus*

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Populations from different parts of a species range may vary in their genetic structure, variation and dynamics. Geographically isolated populations or those located at the periphery of the range may differ from those located in the core of the range. Such peripheral populations may harbour genetic variation important for the adaptive potential of the species. We studied the distribution-wide population genetic structure of the Terek Sandpiper *Xenus cinereus* using 13 microsatellite loci and the mitochondrial DNA (mtDNA) control region. In addition, we estimated whether genetic variation changes from the core towards the edge of the breeding range. We used the results to evaluate the management needs of the sampled populations. Distribution-wide genetic structure was negligible; the only population that showed significant genetic differentiation was the geographically isolated Dnieper River basin population in Eastern Europe. The genetic variation of microsatellites decreased towards the edge of the distribution, supporting the abundant-centre hypotheses in which the core area of the distribution preserves the most genetic variation; however, no such trend could be seen with mtDNA. Overall genetic variation was low and there were signs of past population contractions followed by expansion; this pattern is found in most northern waders. The current effective population size (N_e) is large, and therefore global conservation measures are not necessary. However, the marginal Dnieper River population needs to be considered its

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less on mobile animal species (Munwes *et al.* 2010) or plants (Vakkari *et al.* 2009).

Conservation implications

At a global scale, the conservation status of the Terek Sandpiper is of Least Concern (BirdLife International 2017) and due to its vast distribution and large population size, both census and effective, conservation measures are not needed at a distribution-wide scale, even though the global population trend is decreasing (BirdLife International 2017). However, the Terek Sandpiper is critically endangered in the EU, based on the presence of only one small and geographically separated population in Finland (with occasional breeding in Latvia; BirdLife International 2015). The Red List assessment calls for research on migration, locating the breeding sites and estimating population parameters of the Finnish population (HELCOM 2013, BirdLife International 2015). Based on our results indicating a lack of differentiation from the main range, fairly high polymorphism in nuclear and mitochondrial markers and a higher N_e than the census population size, the Finnish population may be receiving immigrants. Indeed, colour-ringing data indicate that previously unringed displaying males are occasionally observed; however, in some years mates can be so scarce that close inbreeding is witnessed (V.–M. Pakanen pers. obs.). If immigration exists, it is possibly stochastic in nature and may be dependent on straying individuals during migration. Some Terek Sandpipers breeding in northwestern Russia migrate southwest through continental Europe and possibly also through Finland (Mauer & Ijzendoor 1987).

The isolated Dnieper River population was significantly differentiated from the main distribution (with the exception being Chuvash, although the fixation and differentiation indices were all positive and at the same level as between the other populations). Furthermore, it had homozygosity excess, the lowest allelic richness and low N_e, and there was evidence of a population bottleneck. These results fit the previous suggestion that this population is a recently founded discrete breeding population (Snow & Perrins 1998). The southern Bryansk Region, where this population is closest to the main range, is located approximately 400 km from the main range in the Voronezh and northeastern Smolensk Region, Russia (Tomkovich *et al.* 2016).

Even though Dnieper River did not possess private alleles and there was no structure based on the mitochondrial haplotypes (except for the one haplotype shared only with Finland), it is geographically isolated and differs from most of the main range populations significantly with two different markers. Therefore, it fulfils the criteria of a management unit (Moritz 1994). In addition, even though Dnieper River seems to have large enough N_e to avoid immediate risk of extinction, for example due to inbreeding (suggested threshold N_e of 50), it is not sufficient for persistence of the long-term evolutionary potential (suggested N_e of 500; Franklin 1980). Moreover, even though in Belarus the population has grown from tens to 150–200 pairs over a couple of decades (Thorup 2006, BirdLife International 2017), and the Ukrainian population has also been growing (BirdLife International 2017), local decreases have been observed. In the Middle Pripyat River in Belarus, the number of breeding pairs has declined from 20–25 in the beginning of the 21st century to only one breeding pair in 2010–2017 (Szurlej-Kielańska *et al.* 2017). The small population sizes and large distances to the main breeding range of both Finnish and Dnieper River populations make them vulnerable to genetic depletion, especially if gene flow is restricted, warranting conservation actions for preserving them (see also Almalki *et al.* 2017).

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