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Abstracts



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Major histocompatibility complex class I variability of the common tern (*Sterna hirundo*) in Europe

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Abstract

The common tern (*Sterna hirundo*) is a colonial migratory bird of the gull family (Laridae) that breeds in colonies or solitarily in the Northern Hemisphere, while spending the winter in the warmer regions of the Southern Hemisphere. Its freshwater nesting habitats include riverbanks and gravel islands, but terns also nest in estuarine and marine habitats like low-lying coasts or small uninhabited islands with sparse vegetation. Although it is listed as „least concern“ on the IUCN list, it has shown population declines in several European countries due to habitat destruction and human disturbances. The major histocompatibility complex (MHC) plays a crucial role in the adaptive immune response of vertebrates and represents an effective adaptive genetic marker in population genetics studies due to its extreme polymorphism. In particular, MHC class I genes are key for animal defence against viral infections. In this study, we analysed 273 bp of exon 3 of MHC class I genes with the aim to assess the adaptive genetic diversity of common tern populations from five European countries using targeted next generation sequencing. We successfully genotyped 271 tern samples and identified a total of 191 alleles, including 70 novel ones. We found three to eight alleles per individual. The most common allele was found in 51.7% of the samples. In the analysis of samples assigned to three groups (northern, southern marine and southern inland), the total number of alleles found per group was 113, 98 and 135, respectively, and only 47 were shared among them.

Synopsis

NA