Neutral genetic markers reveal low population genetic structure in Common Terns Sterna hirundo within Europe

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PROTECTION OF WATERBIRD HABITATS IN THE UPPER VISTULA RIVER VALLEY
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INTERNATIONAL CONFERENCE

PRESENTATION ABSTRACTS

22ND-25TH OCTOBER, 2024

KATOWICE, POLAND

Main organiser

Regional Directorate for Environmental Protection in Katowice, Poland

Co-organisers

Upper Silesian Ornithological Society, Bytom, Poland

Upper Silesian Museum in Bytom, Poland

Institute of Systematics and Evolution of Animals, Polish Academy of Sciences, Kraków, Poland

The project LIFE16 NAT/PL/00766 LIFE.VISTULA.PL
"Protection of waterbird habitats in the Upper Vistula River Valley"
is co-financed by the European Union Life programme and
the Fund for Environmental Protection and Water Management

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Genetic markers play a crucial role in avian ecology studies, offering insights into ecological and evolutionary processes. Neutral genetic markers assess genetic variations that do not appear to affect fitness or adaptive traits of an organism, meaning they are not subject to natural selection. They are commonly used to quantify genetic diversity, which is important to assess the health of populations and their resilience to environmental change, and to infer population genetic structure, aiding the understanding of migration patterns, connectivity of populations and barriers to gene flow. These genetic analyses are important for developing effective conservation strategies, particularly for long-distance migrants.

This study aimed to investigate the population genetic structure and diversity of common terns sampled across three European regions – one northern and two southern – using microsatellite markers and a fragment of the mitochondrial DNA control region. High genetic diversity was found in both marker types. Various analyses revealed weak or absent population genetic structure, indicating high gene flow between groups. The low genetic differentiation observed likely arises from differing migration patterns, particularly between the two southern groups. Our findings suggest that geographical distance between breeding colonies has minimal impact on population genetic differentiation. However, the high dispersal indicated in this study may increase the extinction risk for small populations. Therefore, conservation efforts should focus on protecting multiple breeding sites, as well as currently unoccupied but suitable areas, to preserve the genetic diversity and resilience of Common Terns in the future.

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