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Genetics • Genomics • Genetic engineering • Biotechnology • Bioinformatics

eISSN 2566-431X

Genetics & Applications

An Aspiring Interdisciplinary Journal of Genetic Research

special edition

3rd CONGRESS OF GENETICISTS IN BOSNIA AND HERZEGOVINA WITH INTERNATIONAL PARTICIPATION

The Official Publication of the
Institute for Genetic Engineering and Biotechnology
University of Sarajevo

Genetic Association in Bosnia and Herzegovina

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eISSN 2566-431x

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Book of abstracts

3rd Congress of Geneticists in Bosnia and Herzegovina with International Participation – CONGUB&H

October, 2023

Indexed/Abstracted

This journal is indexed or abstracted by:

EBSCO, *DOAJ*, *CAB Abstracts*, *Google Scholar*, *Global Health database, Crossref*, *Index Copernicus, EuroPub, Scilit and MIAR.*

The Official Publication of the
Institute for Genetic Engineering and Biotechnology
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3RD CONGRESS OF GENETICISTS IN BOSNIA AND HERZEGOVINA WITH INTERNATIONAL PARTICIPATION – CONGUB&H

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Environmental Genetics and Ecotoxicology *Oral presentation*

HIGH GENETIC DIVERSITY IN COMMON TERNS FROM EUROPE AS INFERRED FROM MITOCHONDRIAL DNA

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The common tern (*Sterna hirundo*) is a migratory seabird from the family Laridae (gulls). It breeds in the Northern Hemisphere, including the European continent, whereas it migrates to the coastal areas of the South Hemisphere during the winter. Its breeding sites cover both freshwater and marine habitats. It is currently listed as Least Concern on the IUCN Red List, but several European countries have reported declines in breeding pair numbers. The primary disturbances are habitat destruction, flooding, human disturbances as well as competition and predation. Mitochondrial DNA is a genetic marker commonly used in population genetic studies. The control region is the fastest evolving region and a great tool for assessing intraspecies relationships. The aim of this study was to assess the mitochondrial DNA control region genetic diversity of several common tern colonies in Europe categorized into three groups: Northern, Southern Inland and Southern Marine. We used blood and feather samples of 319 individuals from 12 locations in Germany, Italy, Slovenia, Hungary, and Croatia and sequenced a 709 bp-long fragment of the mitochondrial DNA control region. We found 40 haplotypes, including three that had a nucleotide insertion. The most common haplotype, Stehi03, was found in 40.13% of all samples. Overall haplotype diversity was high (0.81), with

the highest value (0.86) found in the Southern Inland group, while the Northern and Southern Marine group showed somewhat lower values (0.74 and 0.77, respectively). Overall nucleotide diversity was 0.0023. The highest nucleotide diversity was found in the Southern Inland group (0.0027), followed by the Northern and Southern Marine group (0.0018 for both groups). The haplotype network constructed to visualize relationships between the samples showed no spatial association. This indicates high connectivity between the groups, and diversity indices suggest that the Southern Inland group is the most genetically diverse group. Future research should also incorporate nuclear markers, such as microsatellite loci, to assess the possible present-day genetic structure of European common terns.

Keywords: common tern; mitochondrial DNA; control region; genetic diversity; Europe

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