

High genetic diversity in Common Terns from Europe as inferred from mitochondrial DNA

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www.ingeb.unsa.ba

Phone: +387 33 220-926

Fax: +387 33 442-891

ingeb@ingeb.unsa.ba

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

Lončar Veronika¹, Kralj Jelena², Stronen Vik Astrid³, Grgurević Marija⁴, Pavlinec Željko², Jurinović Luka⁵, Piro Simon⁶, Herrmann Christof⁷, Škornik Iztok⁸, Tome Davorin⁹, Kovács Gyula¹⁰, Preiszner Bálint¹¹, Szinai Péter^{12,13}, Volponi Stefano¹⁴, Galov Ana¹

¹Faculty of Science University of Zagreb, Zagreb, Croatia.

²Croatian Academy of Sciences and Arts, Zagreb, Croatia.

³Biotechnical Faculty, University of Ljubljana, Ljubljana, Slovenia.

⁴Kite Pharma, Hoofddorp, The Netherlands.

⁵Croatian Veterinary Institute, Poultry Centre, Zagreb, Croatia.

⁶Vogelwarte, Zoological Institute and Museum, University of Greifswald, Greifswald, Germany.

⁷Agency for Environment, Nature Conservation and Geology Mecklenburg- Vorpommern, Hiddensee Bird Ringing Scheme, Güstrow, Germany.

⁸Sečovelje Salina Nature Park, Soline Pridelava Soli d.o.o., Portorož, Slovenia.

⁹National Institute of Biology, Ljubljana, Slovenia.

¹⁰BirdLife Hungary South-Balaton Local Group, Balatonlelle, Hungary.

¹¹Balaton Limnological Research Institute, Eötvös Loránd Research Network, Tihany, Hungary.

¹²Balaton-felvidéki National Park Directorate, Csopak, Hungary.

¹³Bird Ringing and Migration Study Group of BirdLife Hungary, Budapest, Hungary.

¹⁴Italian Institute for Environmental Protection and Research, Roma, Italy

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

Presenting author's e-mail: veronika.loncar@biol.pmf.unizg.hr