Intraspecific variation and phylogeographic patterns of the grey-capped greenfinch Chloris sinica ssp. (Passeriformes: Fringillidae)

Joo-Eun Kim*a, Jong-Gil Parka,b, Kyoung-Soon Jinb, Chungoo Parkc and Dong-HaNama

*aDepartment of Biological Sciences, College of Natural Sciences, Chonnam National University, Gwangju, Korea; bBirds Research Center, Korea National Park Research Institute, Korea National Park Service, Jeollanam-do, Korea; cSchool of Biological Sciences and Technology, College of Natural Sciences, Chonnam National University, Gwangju, Korea

ABSTRACT
To study the intraspecific variation of the grey-capped greenfinch Chloris sinica (Passeriformes: Fringillidae), we sequenced complete mitochondrial (mt) genome of the C. sinica ssp. prevalent in Ulleung Island, Republic of Korea. The full length of the genome is 16,812bp, containing 37 genes (2 rRNAs, 13 proteins, and 22 tRNAs) with a putative control region (D-loop). A total of 98 single nucleotide polymorphisms (SNPs) in the full mt genome were retained for Ulleung Island population and these SNPs were greater than those of inland population compared to the reference China subspecies. The analysis of the SNPs revealed 18 SNPs for ND4 gene, with a dominant haplotype shared by Ulleung population compared to the reference China population. The phylogenetic analysis of the C. sinica subspecies showed that they are monophyletic, however, there is clear phylogenetic separation between China and Korea subspecies with strong support (100% bootstrap). These data will provide new insights into the intraspecific phylogeographical patterns of C. sinica species.

CONTACT Chungoo Park chungoo@chonnam.ac.kr School of Biological Sciences and Technology, College of Natural Sciences, Chonnam National University, 77 Yongbong-ro Bukgu, Gwangju 500-757, Korea; Dong-Ha Namdongha@chonnam.ac.kr Department of Biological Sciences, College of Natural Sciences, Chonnam National University, 77 Yongbong-ro Bukgu, Gwangju 500-757, Korea

GENEVA A.D. 2018

©This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.
inland (36 SNPs from Taean; Kim et al. in press) subspecies compared to the reference China subspecies (HQ915865).

Furthermore, using entire mt genome sequences, we performed the phylogenetic analysis to determine the evolutionary relationships among subspecies of *C. sinica*. A neighbor-joining or maximum likelihood phylogenetic tree resolves three distinct clades with significant bootstrap support (100%): China (HQ915865), and inland Korea (KM078783 and MH047559), and island Korea (MH047558; this study; Figure 1). These clades clearly correspond to the three geographic regions sampled, which is inconsistent with previous morphological studies (Won 1981; Won and Kim 2012), wherein *C. sinica* populations are separated geographically between inlands (as a subspecies *ussuriensis* from China and Korea) and islands (*minor* from Jeju Island and *kawarahiba* from Ulleung Island).

The *C. sinica* has been subdivided morphologically into three subspecies in Korean Peninsula: *ussuriensis* (inland), *kawarahiba* (Ulleung Island), and *minor* (Jeju Island). The phylogenetic relationship indicated that both inland and island populations are monophyletic, but there are two distinct geographical genetic structures between inland and island subspecies in Korea. Further research is required to differentiate the morphological variations and genetic clines in the *C. sinica* populations from a larger number of colonies including Jeju Island.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

**Funding**

This research was a part of the project titled “Development of the methods for controlling and managing marine ecological disturbance causing and harmful organisms (MEDHO),” funded by the Ministry of Oceans and Fisheries, Korea, and was financially supported by Chonnam National University (Grant number: 2014-2557) to CP. This research was also supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Science, ICT and Future Planning (grant numbers: NRF-2014R1A1A1006010 and NRF-2017R1D1A3B03034962).

**References**

del Hoyo J, Elliott A, Christie DA. 2010. Handbook of the Birds of the world. Vol. 15. Barcelona: Lynx Editions.

Kim JE, Park JG, Jin KS, Park C, Nam DH. (2018). *Chloris sinica ussuriensis* (Passeriformes: Fringillidae). Complete mitochondrial genome of the grey-capped greenfinch subspecies. Mitochondrial DNA Part B. 3(2):701–702.

Won PO. 1981. Illustrated flora & fauna of Korea: Vol. 25. Seoul, Korea: Avifauna, Ministry of Education.

Won PO, Kim HJ. 2012. The birds of Korea. Seoul, Korea: Academy book.