Available online at www.asric.org
ASRIC Journal on Health Sciences 1 (2023) 15-23

Parallel Evolution in the βA Globin Gene of Black Kite, Bar-Headed Goose and Graylag Goose: Deciphering Hemoglobin Adaptation to High Altitude Hypoxia Using Birds as Models

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Received 19 July 2022; revised 31 July 2022; accepted 3 August 2022

Abstract

Parallel evolution involving historically independent amino acid substitutions in hemoglobin (Hb) is expected among closely related lineages; however, such studies in distantly related species are limited especially from the structural point of view. Here we reported structural and phylogenetic based parallel amino acid substitutions in the β^A globin gene of the Black kite (BK), Bar-headed goose (BHG), and graylag goose (GLG) to illustrate the adaptation of hemoglobin to high altitude hypoxia and high altitude sickness in humans and animals living at extreme altitudes. Based on our data, there are five to six parallel amino acid substitutions in the β^A globin gene of BK, BHG, and GLG. Four of the parallel amino acid substitutions (Asn-β^A83-Lys, Gln-β^A90-Lys, Asp-β^A125-Ala, and Ala-β^A128-Ser) are independently evolved only among BK, BHG, and GLG. The individual Ala-β^A128-Ser substitution resulted in a significant closeness of the α1 and β1 subunits which probably stabilizes the R state of oxy-Hb at high altitude. Our data contribute to evolutionary biology by providing pieces of evidence into the parallel evolution of BK, BHG, and GLG to high altitude hypoxia and laid a foundation to studying high altitude associated hemoglobinopathies in humans and other animals.

Keywords: Parallel evolution; β^A globin gene; Black kite; bar-headed goose; graylag goose

1.0 INTRODUCTION

The study of adaptive evolution is becoming ideal as different evolutionary lineages are confronted by similar environmental dissipations. In this regard, comparative phylogenetic study is a very important component of studying the adaptive evolution of different species sharing the same environment. Specifically, the combined study of phylogenetic analysis with structural and functional information is worse useful to identify significant changes and distinguish parallel evolution in different lineages from shared ancestral traits (1-4). According to evolutionary theory, parallel evolution could be common when the number of beneficial mutations is limited by selective constraints on the structure of the protein (5). A

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