**INTRODUCTION**

Several lineages of fly and fly-flies in highland species above 3,000 masl have evolved, which requires morphological and physiological adaptations. Previous studies have focused almost exclusively on haemoglobin adaptation, revealing that highland birds have a higher concentration of the protein and an increased affinity to oxygen due to amino acid substitutions (1) and that there is convergent evolution among highland species in these adaptations to altitude (2, 3). Although mitochondrial genes participate in the cellular respiratory process, their adaptive role to high altitude has been much less studied.

Cytochrome c oxidase subunit 1 (COI) is a part of the protein complex that participates in the electron transport chain and could potentially present adaptive modifications in highland species. Previous studies showed that non-synonymous mutations in COI were found in highland insects (4) and mammals (5), but mutations that improve enzymatic kinetics of the cytochrome c oxidase complex in birds (pigeons) are not in the subunit 1 of the protein complex (6). In this context, the objective of this study is to use the large-scale COI library available as a result of the Barcode of Life project to study its adaptation to high altitude in the birds of the Americas.

**MATERIALS AND METHODS**

- **BOLD SYSTEMS**
  - Over 22,000 COI sequences of at least 600 bp from 2,000 American birds were downloaded from BOLD SYSTEMS.
  - The maximum and minimum altitudes in which it was found were determined for each of the 2,000 bird species (7).
  - Sister species pairs were established using the phylogeny of the birds of the World by Jetz et al. (8) and Hackett’s phylogeny backbone.
  - We considered as highland bird species those with a maximum altitude exceeding 2,500 masl and lowland those with a maximum altitude below 2,500 masl.
  - Sister species pairs were therefore classified into three groups: highland-highland, species, lowland-lowland, and lowland-lowland species pairs (Fig. 1)

- **RESULTS**
  - COI sequences from the three groups were aligned and analyzed in MEGA.
  - Uncorrected (p) and K2P genetic distances were estimated for each sister species pair and then used to realign the number of amino acid substitutions between species.

- **CONCLUSIONS AND FUTURE PROSPECTS**
  - We also analyze convergence among high altitude species in COI structure as a consequence of amino acid substitutions and assess intraspecific variation between highland and lowland populations.

**REFERENCES**