

Conservation Biology and Sustainable Land use can Facilitate Conservation

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Citation: Lupski M (2022) Conservation Biology and Sustainable Land use can Facilitate Conservation. *Electronic J Biol*, 18(6): 1-2

Received date: May 14, 2022, Manuscript No. IPEJBIO-22-14048; **Editor assigned date:** May 17, 2022, PreQC No. IPEJBIO-22-14048 (PQ); **Reviewed date:** May 28, 2022, QC No. IPEJBIO-22-14048; **Revised date:** June 7, 2022, Manuscript No. IPEJBIO-22-14048 (R); **Published date:** June 14, 2022, DOI: 10.36648/1860-3122.18.6.030

Description

Print and online media may reflect changing perceptions about wildlife when viewed in a historical context, as conservation programs bring about increased awareness of declining species. With a proven history of public misunderstanding and persecution, we focused on a nongame and at-risk species, the hellbender salamander (*Cryptobranchus alleganiensis*). To determine whether public perceptions of hellbenders change according to societal interests over time and to test Shaw's conservation eras, we conducted a content analysis of 288 newspaper articles over the past 153 years of coverage through Conservation Eras, including: Exploitation (1850–1899), Protection (1900–1929), Game Management (1930–1965), Environmental Management (1966–1979), and Conservation Biology (1980–2016). In addition, we examined trends in more recent online media coverage. As measured by article frame (valence values), we detected an increase in positive perceptions about hellbenders in newspapers after 1980, which coincides with the Conservation Biology Era. Many articles published within the Exploitation Era included informative natural history while articles in the Conservation Biology Era included information about the species decline or efforts to conserve and restore populations. Article frames from the Conservation Biology Era were more positive than any other era ($X^2 = 111.79$, $p < 0.001$). Conservation efforts likely impacted online media coverage (via Google Trends), which increased following the federal listing of Ozark hellbenders and their successful captive rearing by the St. Louis Zoo in 2011. Because knowledge is generated and accessed more readily than ever, and we observed media is representative of societal changes, we anticipate a new era of conservation to follow the digital information age.

Trillium Camschatcense

Trillium camschatcense is a typical polycarpic perennial rhizomatous herb distributed in China, Japan, Korea, and Russia. The species is threatened due to high ethnobotanical demand, habitat loss, over-grazing, deforestation, and peculiar life cycle. Integrating

information on its demography, reproductive success, genetics, life history, and threats to the species under various biotic and abiotic regimes will be crucial for estimating the species' long-term survival.

Generally, the taxonomists identify the avian species based on their field characters and behavior, in which several masked and similar morphological species have shown distinct species, based on the DNA barcoding techniques. Nevertheless, millions of species are yet to be described and identified because expertise in avian taxonomy amongst zoologists is dwindling globally. DNA barcoding is a practical and modern tool for taxonomists who are endowed with preparing inventory and management recommendations of the vast and altering earth biodiversity.

Indeed Hebert et al. (2004) published an article on the barcoding of birds in Central American birds using the COI gene. He has made a breakthrough in taxonomy, wherein mitochondrial DNA, rather than nuclear DNA, formed another most attractive and remarkable protocol in the molecular taxonomy of species by using a novel gene called Cytochrome c Oxidase I (COI). Globally, after Hebert's publication in 2004, several studies have been made and documented the species diversity based on COI, for example, Eurasian birds, Korean birds, Kingfishers, Palearctic birds, Scandinavian birds, Marine biodiversity, Continental patterns of avian diversification House sparrow, Avian evolutionary studies, feather mite studies, Neotropical birds and Migratory birds.

However, certain species have been identified by using COI, for example, mosquitoes (Kumar et al., 2007), Honey bees, Insects, Insects- thrips, Gobid fishes, Turtles, Wild Jungle Fowl but no studies as much as carried out on avian species particularly water birds by using DNA barcoding. Therefore, the present study intended to analyze COI gene analysis for the DNA barcoding of water birds and understand their phylogenetic relationships based on their genetic background.

Extraction of COI Gene

Extraction of COI gene, a small amount of bird tissues by using a kit is known as the Gene Elute DNA miniprep Kit, and the extraction of DNA has achieved it with the guidelines described by the Manufacturer instructions.

The tissue samples were transferred into 10 μ l of distilled water for further analysis. In the isolation of COI from the tissues, the amplification was done at the 749-bp region near the 59 termini using the following forward and reverse primers (Forward-TTCTCCAACCACAAAGACATTGGCAC and Reverse-ACGTGGGAGATAATTCCAATCCTG). Subsequently, 50 μ l of PCR reaction was prepared with the combination of 40 μ l of double-distilled water, 1.0 μ l of Taq polymerase, 2.5 μ l of MgCl₂, 4.5 μ l of 10X PCR buffer, 0.5 μ l of each primer (0.1 mM), 0.25 μ l of each dNTP (0.05 mM), and 0.5–3.0 μ l of DNA. The process of amplification was carried out in 1 min at 94 °C and followed by 5 cycles of 1 min at 94 °C, 1.5 min at 45 °C, and 1.5 min at 72 °C, and in turn by 30 cycles of 1 min at 4 °C, 1.5 min at 51 °C, and 1.5 min at 72 °C, and finally 5 min at 72 °C. The results of the PCR were visualized by using 1.2% Agarose gel electrophoresis.

The entire PCR reactions were produced a single, circa 750-bp product, and it was sequenced, and the sequencing process was carried out by using ABI 377 sequencer. The sequences of 12 waterbird species were deposited into the NCBI genbank. Nevertheless, the COI sequences of 12 species of water birds recovered without any errors and remarkably provided with the non-appearance of nuclear pseudogene amplification. In the present study, twelve different water birds were used to compare evolutionary relationships using their COI regions. The dendrogram's trunk was dichotomously branched into two main branches in which one branch constituted seven species and formed four major groups, and the second branch was organized with five species and formed two subgroups with their similar sequences.