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Birds

Challenges and Opportunities for Business, Conservation and Research

Edited by Heimo Mikkola

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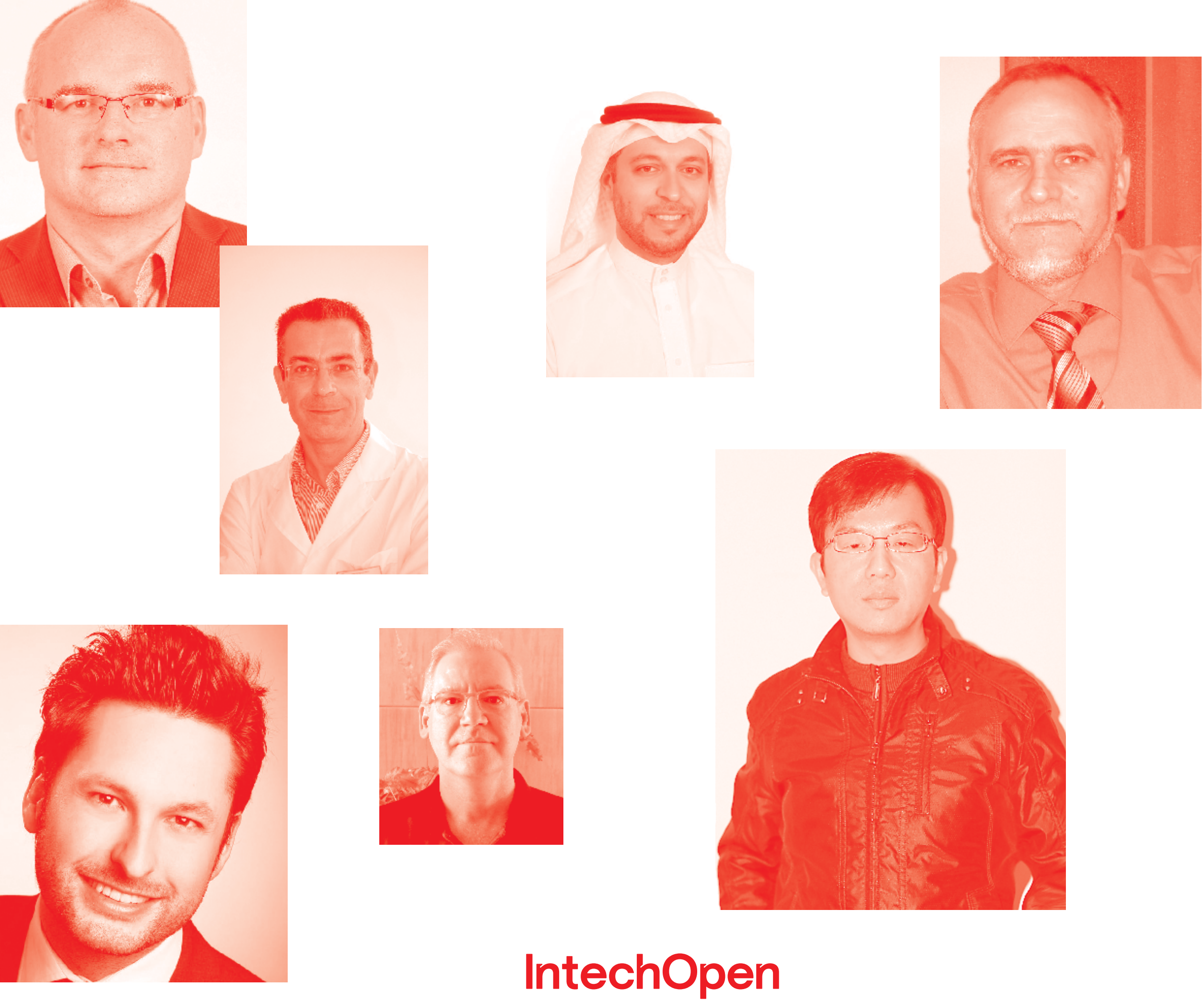

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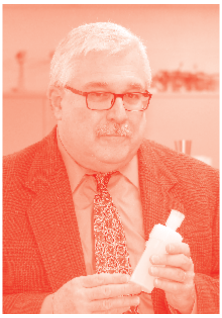

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Meet the editor

Heimo Mikkola, born in Finland in 1945, has been a bird-watcher since the age of eleven, but has concentrated on owls since 1965. His thesis for his MSc was on the great grey owl, and his Ph.D. thesis was on the ecological relationships of European owls. In 1988, Dr. Mikkola became an adjunct professor at the University of Eastern Finland. His life-long international career with the Food and Agriculture Organization (FAO) of the United Nations started in 1974 in Colombia and ended with him as the resident representative of FAO in Uruguay in 2007. In 2014, he was nominated as "Champion of Owls" in Houston, USA, mainly because of his worldwide distributed and translated owl books. Thus far, he has written some 300 papers and more than 10 books on birds. Since retirement, he has edited eight books with IntechOpen.

Contents

Preface

> *"While there are many ways how we humans are letting the numbers of bird individuals and species diminish, there is also a lot we could and should do to halt this trend and preserve avian diversity."*
>
> *Dieter Thomas Tietze, 2018.*

Birds are among the best known and studied organisms and were the first taxonomic animal group used to identify biogeographic regions, and that work continues in the most biodiverse regions on earth [1]. The popularity of birds to the public has facilitated the development of digitally accessible databases combining observations often made by non-academic birders in their local areas [2]. Freely accessible bird occurrence and ringing data explain why scientists have often been able to make sophisticated species distribution models, which have been frequently used for better conservation plans [3].

The soaring popularity of bird watching is a fast-growing hobby for millions of people across the globe. As mundane as it seems to many, it is a real passion for others. Almost 60 million Americans identify themselves as birdwatchers, whereas only 24 million Americans play basketball, 23 million play baseball, and 9 million play American football [4].

Birdwatching is an extremely healthy hobby because one is moving outside, likely reading and learning, and preferably taking notes, drawing, and imitating sounds that birds make. This engages your entire brain and keeps it healthy [5].

During the Coronavirus pandemic birdwatching gained more popularity when people experiencing lockdown looked outside and began to appreciate the colourful wildlife their windows framed, especially birds [6]. The traffic of the Audubon society website spiked 23% in March and April 2020, compared to the year prior, and one Chicago bird-related Facebook group grow 134% during the same months [6].

After this pandemic, an increasing number of birdwatchers will again be traveling to long-haul destinations to seek new bird species that cannot be seen in their own country or region. To benefit from this growing market, however, developing countries have to provide what birdwatchers demand, including safety, accessibility, infrastructure, quality of bird life, and knowledgeable guides [7].

In the United Kingdom birdwatching expenditures are estimated at 500 million USD per year. Spending of birders varies, naturally, depending on whether they participate in their hobby at or near home, within their home country, or internationally. It has been concluded that birders and other wildlife specialists spend more money than generalists, and ecotourism including birdwatching can be more lucrative for a community than other types of economic activities [7].

Many birders are willing to pay to see a particular species. In Costa Rica seeing a new species may [cost about 8-10 USD, whereas seeing a new species in the United States may cost, on average, 75 USD [8]. In addition, tiny Costa Rica offers 946 species compared to 1202 species in the vast United States [9]. However, before starting to collect new species one should learn how to identify at least the most common birds near home. No person can identify every bird at all times, but we should aim to identify most of the birds most of the time [10]. Derek Lovitch offers many interesting ways to go about identification, calling it the 'Whole Bird and More' approach. His book teaches you how to manage this complex task of identifying more species, more quickly and more of the time [10].

Ornithology, the scientific side of birding, is one of the oldest organized scientific activities [11].

For more than 200 years the public has contributed significantly to our understanding of bird identification, distribution, and abundance. Building on this tradition, eBird (http:// ebird.org/) allows volunteers anywhere in the world to submit data about the birds they see at any time and in any location [12]. The millions of observations recorded each month, logged into a central database at the Cornell Lab of Ornithology, are building a global understanding of the distribution, abundance, and movements of bird species. This information is now being used by scientists [13].

Global abundance estimates are available for 9,700 bird species, which is about 92% of all extant bird species [13]. This paper estimated that there are some 50 billion individual birds in the world at present, which is about six birds for every human on the planet. Relatively few species are very abundant. The top ten most numerous species are House Sparrow Passer domesticus at 1.6 billion; European Starling Sturnus vulgaris at 1.3 billion; Ring-billed Gull Larus delawarensis at 1.2 billion; Barn Swallow Hirundo rustica at 1.1 billion; Glaucous Gull Larus hyperboreus at 949 million; Alder Flycatcher Embidonax ainorum at 896 million; Black-legged Kittiwake Rissa tridactyla at 815 million; Horned or Shore Lark Eremophila alpestris at 771 million; Sooty Tern Onychoprion fuscatus at 711 million; and Savannah Sparrow Passerculus sandwichensis at 599 million [13].

The authors concluded that there are many rare species (1,180 species have population estimates of less than 5,000 individuals), highlighting the need to continue to refine global population estimates for all taxa and the role that global citizen science can play in this effort [13].

The taxonomy of birds complicates this hobby if taken seriously. At the moment there is a four-world list of birds, two long-established [14, 15] and two more recent offerings [16, 17]. The main differences come because the lists use different definitions of what constitutes a species [18]. Contemporary systematics attempted to take into account as many criteria as possible to delimit species, but currently the most influential approach is the use of genomic sequences. Luckily in this book, we have an excellent chapter by Emeritus Professor Michael Wink explaining the genetic reasons why we have continuously more bird species and why we may end up having 18,000 bird species in the world. The present 11,000 species is still a number relatively well to handle but soon the young people have to learn and protect 7,000 more bird species.

Evolutionary rules may make it impossible to preserve all 18,000 species forever because bird species arise, modify, and vanish. Only if we provide birds sufficient time and leave them more space can we expect to maintain so many diverse bird species, and even then the natural reasons will keep them modifying, splitting, and becoming extinct. Human impact through global climate and land-use changes force extant bird species to accelerated modifications and population splits as well as reduces the population sizes of hitherto abundant species or even lets them vanish forever [19].

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Section 1

Systematics and Taxonomy

Chapter 1

DNA Analyses Have Revolutionized Studies on the Taxonomy and Evolution in Birds

Michael Wink

Abstract

Whereas Linné aimed to classify all species of our planet by a unique binomial Latin name, later generations of taxonomists and systematicists intended to place the taxa in a natural system according to their phylogeny. This also happened in ornithology and still scientists are on the way to find the ultimate "Avian Tree of Life". Formerly, systematic relationships were studied by comparing morphological characters. Since adaptive character evolution occurred frequently, convergences could lead to misleading conclusions. An alternative to morphological characters are biochemical markers, especially nucleotide sequences of marker genes or of complete genomes. They are less prone to convergent evolution. The use of DNA sequences of marker genes for bird systematics started around 1990. The introduction of Next Generation Sequencing (NGS) facilitated the sequence analysis of large parts of bird genomes and to reconstruct the Avian Tree of Life. The genetic analyses allowed the reconstruction of phylogenetic trees and the detection of monophyletic clades, which should be the base for a phylogenetic classification. In consequence, several orders, families and genera of birds had to be rearranged. In addition, a number of species was split into several new species because DNA data could point out hidden lineages in cryptic species or in species complexes.

Keywords: systematics, taxonomy, convergence, cladistics, monophyletic clades, phylogenomics, marker genes, sequence analysis, next generation sequencing

1. Introduction

Apparently, humans always tried to classify the animals, which they saw or hunted. They gave them local names. Only during the time of classical Greek scholars, a more systematic approach emerged. The first scholar was Aristotle (384–322 BC), the known father of Natural history and Science. He described the appearance, behavior, and occurrence of more than 140 bird species [1–3]. The next progress came with Plinius (23–79 AC), a known Roman writer. Plinius analyzed the form of feet and legs to classify birds in his *Historia naturalis*. Aristotle and Plinius were the main sources of information until the Renaissance (from 1400 onwards). The Renaissance brought progress in many fields of science, including ornithology. New knowledge was no longer transmitted in hand-written books but in printed books when Johannes Gutenberg in Mainz (Germany) invented book printing around 1450 [1–3]. In consequence, many illustrated books on plants and animals were published. William Turner (1500–1568), Conrad Gessner (1516–1565), and Pierre Belon (1517–1564) were three known ornithologists in the 16th century. Gessner reported on 180 bird species in the illustrated *Historia animalium.* John Jonston (1603–1675) published the *Historiae naturalis de avibus libri VII* in 1650 illustrated by Matthaeus Merian (**Figure 1**). However, the classification was only based on morphology, leading to wrong relationships. As can be seen from **Figure 1**, bats were included in birds and the cuckoo and shrike were treated as raptors.

After 1600, the ornithological landscape quickly changed. New species were brought in from everywhere in the world by early explorers, and systematic collections of specimens were started facilitating the study of avian taxonomy. Known ornithologists of the 17th century were Walter Charleton (1619–1707), John Ray (1628–1704), and Francis Willughby (1635–1672). John Ray became famous since he produced with *Ornithologiae libri tres* a first modern ornithology handbook, based it on authentic observations [4].

Another breakthrough came in the 18th century: Carl Linnaeus (1707–1778), a naturalist and medical doctor from Uppsala (Sweden) revolutionized taxonomy by introducing a binary nomenclature, in which every animal and plant species obtained its own and unequivocal Latin name [1–3]: The Chaffinch was called *Fringilla coelebs* L.; the first name indicates the genus and the second the species. This name is exclusive for the Chaffinch. By comparing the outer morphology of animals and plants, Linné arranged species with a similar anatomy and morphology into genera, orders and classes. For birds, Linné used the morphology of feet and beaks to distinguish six orders of birds, which included 85 genera. As there are several

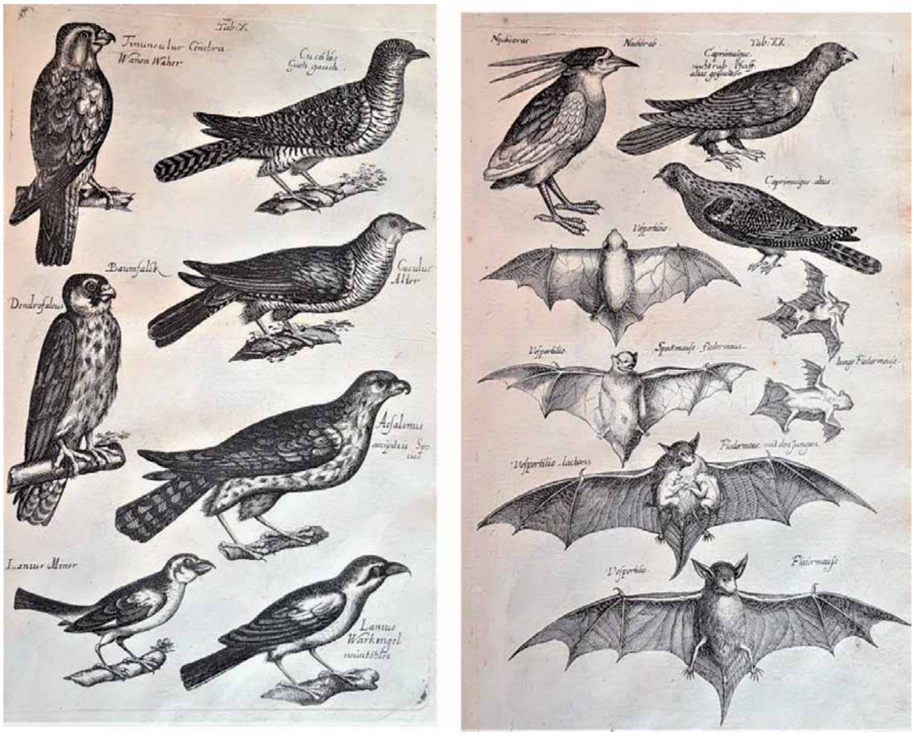

Figure 1.
Illustrations from Historiae naturalis de avibus libri VII. *As can be seen, shrikes and cuckoo were grouped with raptors because of their bill morphology. Cuckoo = Cuculus; shrike = Lanius; raptors = Tinnunculus, Dendrofalcus (a) and even bats were classified as birds because of their wings. Nycticorax= Night Heron; Caprimulgus = Nightjar; Bats= Fledermaus (b). (photo M. Wink).*

events of convergent evolution, some of his systematic assumptions were wrong and could not survive. In the 10th edition of *Systema naturae* (1758), six orders were distinguished: 1. **Accipitres**: Raptors, owls, parrots, waxwings, and shrikes; 2. **Picae**: Woodpeckers, hornbills, cuckoos, hoopoes, birds of paradise, crows, and creepers; 3. **Anseres**: all water birds, pelicans, cormorants, loons, grebes, gulls, and terns; 4. **Grallae**: Ratites, waders, flamingos, storks, herons, cranes, coots, and bustards; 5. **Gallinae**: wild fowl, guans, grouse, and quails and 6. **Passeres**: Pigeons, thrushes, larks, humming birds, nightjars, swifts, crossbills, wagtails, and tits [1].

During the 18th and 19th century, the knowledge on taxonomy and systematics of birds rapidly increased. Many explorers and travelers explored Europe, Africa, Asia, Australia and the Americas, and brought back many unknown species. Taxidermy improved [5] and specimens could be stored in skin collections, which were then created in Paris (1793), London (1881), Frankfurt, Halle, Munich, and Dresden [1, 2]. These curated collections enabled a better comparison and study of related and unrelated taxa. Already at that time, the status of species and subspecies was extensively debated.

The 19th century was strongly influenced by the new concept of evolution and phylogeny through natural selection formulated by Charles Darwin (1809–1882) and Alfred Russel Wallace (1823–1913). Species were no longer considered to be unchangeable (or created by God) but were seen in a phylogenetic context. This means, ancestral taxa had existed from which the extent taxa derived. Charles Darwin came up with the concept of a phylogenetic tree, which can illustrate the descent from common ancestors [1–3].

2. Towards a new avian classification

After Darwin, ornithologists overturned the typological species concept and tried to build up a "natural system", based on shared ancestry and comment descent. According to [6, 7], more than 40 classifications were proposed during the last two centuries. Since 1900, the order of bird families in handbooks and field guides was based on these classification systems [8–12].

Traditionally, morphology, such as plumage, beak and head shape, had been used to make inferences in systematics and taxonomy [1, 3]. Since 1900 new characters were included, coming from ecology, biogeography, and biochemistry. The main concept of classification remained overall similarity; the more similar two taxa, the more closely related they should be.

Whereas the inclusion of similar taxa into a common genus was mostly unambiguous, the circumscription of families and orders was however more difficult. In many taxa, a variation of plumage can be seen in relation to age, sex or season. Large skin collections were helpful to find out if the variable forms belonged to a single species. Several bird species (e.g. ducks and geese) can hybridize, which generate more confusion. We already noticed that adaptive characters can occur convergently. In consequence, similar adaptive features might have evolved in unrelated group of taxa. If such adaptive characters are used for taxonomy, artificial and polyphyletic groups (clades with members from unrelated lineages) may be created (**Figure 1**).

Over the last 200 years, different species concepts have also strongly influenced taxonomy and systematics [3, 4, 10]. Although ornithologists loved the typological species concept for a long time, it was substituted by Ernst Mayr by the Biological Species Concept (BSC). Presently, the "Phylogenetic Species Concept (PSC)" has been widely accepted, because it better fits the molecular data [1].

The German entomologist Willi Hennig (1913–1976) introduced the concept of cladistics. He distinguished plesiomorphic, apomorphic and synapomorphic traits to define common ancestry in clades. Clades, which comprise all descendants of a common ancestor, are termed "monophyletic". According to cladistics, a natural system of classification should be only based on monophyletic groups. If scientists obtain evidence for para- and polyphyletic clades, taxa in such groups need to be either lumped or split until all clades are monophyletic. The consequences for bird taxonomy are discussed in Part 5.

3. Impact of DNA analysis on avian systematics and phylogeny

When James Watson and Francis Crick discovered the structure of DNA in 1953 [1–3], a new era started in biology and with some delay, also in ornithology. In the decades following the discovery of DNA, new technologies emerged to study DNA and genetics: DNA sequencing was established in 1978, the polymerase chain reaction (PCR) was discovered in 1985 by Kary Mullis and Next Generation Sequencing (NGS) appeared after 2000. NGS or High-throughput Sequencing enable the parallel and concomitant sequencing of millions of DNA sequences. NGS is thus the method of choice for the analysis of complete genomes and transcriptomes [1–3, 13, 14].

3.1 DNA as a marker for phylogeny

Deoxyribonucleic acid (DNA) is a macromolecule composed of linearly coupled nucleotides. The pyrimidine bases cytosine (C) and thymine (T) have two N atoms, and the purine bases adenine (A) and guanine (G) each have four N atoms. In addition, deoxyribose (a sugar called pentose) and a phosphate group belong to a nucleotide building block. Unlike DNA, ribonucleic acid (RNA) contains uracil (U) instead of thymine and ribose (which lacks the hydroxyl group in the 2-position) instead of deoxyribose. DNA thus contains the bases A, T, G, and C, and RNA the bases A, U, G, and C. The DNA strands are complimentary and form a double helix, in which A pairs with T and G with C (**Figure 2**) [1, 3].

The DNA double helix is located in the nucleus of all eukaryotic cells as a linear, i.e. filamentous, macromolecule (**Figure 2**). Depending on the species, the nuclear genome (i.e., the DNA in the nucleus) is organized in specific number of chromosomes [1–3]. During the growth of an organism, cells have to multiply at a high rate. During cell division, the DNA of a mother cell is duplicated by a process, termed DNA replication. Consequently, daughter cells obtain an identical genome copy of the mother cell. All cells, which exist today, are never generated *de novo* but always derive from a mother cell. And this continuous flow of cell divisions must have existed since the first ancestral cell; thus all cells which exist today are connected and their DNA can be traced back to the origin of life.

Except for germ cells, all vertebrate cells have a double (diploid) set of chromosomes. All offspring receive each a haploid (single) set of chromosomes from the mother and father, respectively with the gametes (germ cells that unite at fertilization). These haploid genomes are similar, but not 100% identical. Genetic variability of individuals is generated during the generation of germ cells by a process called meiosis.

The vertebrate genome is thought to have 21,000 genes encoding proteins and another 9,000 genes encoding diverse RNAs. These genes correspond to the genotype of an individual. Since not all genes are active at the same time, but are regulated in a cell- and development-specific manner, the expression of the respective active genes is called phenotype. Epigenetic processes can influence the phenotype and phenotypic variability [3].

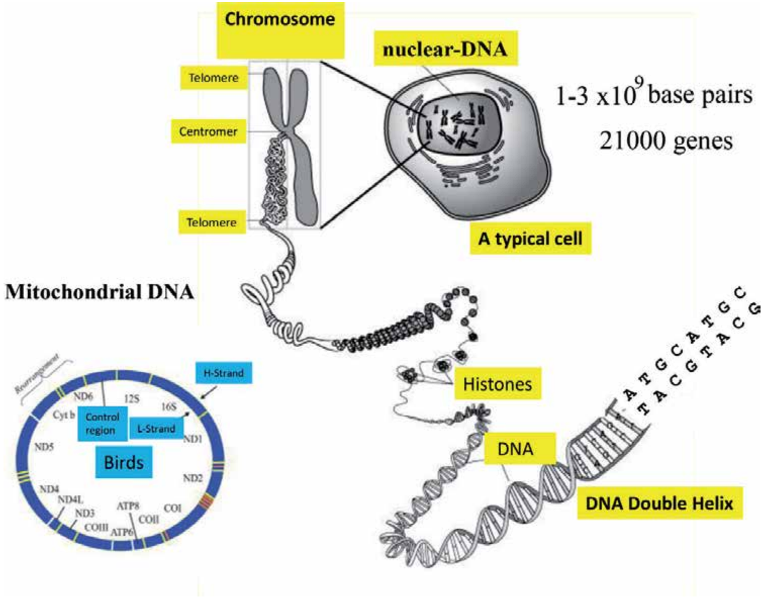

Figure 2.
Schematic view of nuclear and mitochondrial DNA in birds.

In addition to the nuclear genome (ncDNA), all animals have additional DNA in their mitochondria (mtDNA), cell organelles that originally arose from bacteria through symbiosis and whose main function is to provide ATP, the fuel for the cell [3]. Similar to bacteria, mtDNA exists as a ring-shaped chromosome and consists of approximately 16,000 to 19,000 base pairs in vertebrates. It contains 13 genes encoding enzymes or other proteins involved in electron transport, 22 genes for tRNAs (tRNA is the abbreviation for transfer RNA, which is required in protein biosynthesis), and two for rRNAs (rRNA is the abbreviation for ribosomal RNA, which is important for the structure and function of ribosomes) (**Figure 2**). Since each animal cell contains several 100 to 1000 mitochondria and each of the mitochondria contains five to ten mtDNA copies, the total number of identical mtDNA copies is several thousand per cell. The mtDNA makes up about 1% of the total DNA of a cell and is particularly suitable for research in molecular evolution and phylogenetics. In contrast to nuclear DNA, mtDNA is almost exclusively inherited maternally. Because mtDNA exhibits more sequence variation than protein coding ncDNA, the sequence analysis of mtDNA has widely used to study bird taxonomy and phylogenetics [13–16].

Most sequence differences in DNA, i.e. an exchange of one of the four DNA bases A, T, G and C, are due to point mutations. Point mutations are triggered by internal mechanisms that occur spontaneously and regularly. These include biochemical alterations of DNA bases (through depurination, deamination, dimerization, and oxidation) and the incorporation of tautomeric bases [3]. External factors for point mutations include high-energy radiation such as UV, X-ray, and high-energy ionizing radiation from radioactivity or cosmic rays, and mutagens (mutation-inducing substances). Most mutations are repaired by special enzymes before the duplication of chromosomes during cell division. This is one of the great advantages of the double helix: even if information on one DNA strand has been altered by mutation, it is still correctly present on the complementary strand and can be used by the repair enzymes as a back-up copy [3].

Most mutations are observed in somatic cells (body cells), which are not passed onto the offspring and perish with the death of the individual (somatic mutations).

Only mutations in germline cells (gametes or sex cells) can be inherited. Most mutations have no or negative consequences. Only in rare cases does a mutated gene or allele provide a carrier with a selective advantage to better adapt its bearer to its environment and thereby increase the reproductive success of its offspring. When we analyze DNA sequences or genome structures of organisms living today, we essentially see only mutations that were either neutral or had a positive selection value. Carriers of mutations with negative consequences have logically not withstood the selection pressure - they often had no or little reproductive success and just disappeared.

Only germline mutations may end up in the next generation. If they are successful, they may survive in subsequent generations. If we look at the DNA of an individual, its DNA may differ by millions of nucleotide exchanges in its genome from conspecifics, which were inherited from the ancestors. These nucleotide exchanges can be discovered by DNA sequencing and can be used to reconstruct the Tree of life. A driver for the evolution of divergent DNA sequence lineages is their geographic or ecological separation. If a population gets isolated on an island and if there is no further exchange of individuals with the ancestral population, then an independent sequence evolution sets in, as outlined in **Figure 3**. This phenomenon and feature is the base for the Tree of life.

The rate of mutations is typical for individual genes and can be used to infer the date of ancient evolutionary divergence events. This is the concept of the "Biological Clock" which is widely used in phylogenetics [3, 14].

Darwin demanded variability of traits within populations as a prerequisite for Natural Selection. We now know that this variability exists and is due to diverse mutations in protein-coding genes and in genes for transcription factors. Mutations in regulatory genes sometimes lead to more pronounced morphological changes. This variability is used, for example, in artificial selection for animal and plant breeding. Darwin already recognized the high plasticity of our genomes, from which a breeder can generate new forms in just a few generations, such as the various cabbage vegetables bred from the wild cabbage plant or domestic dogs from wolves (see [3]).

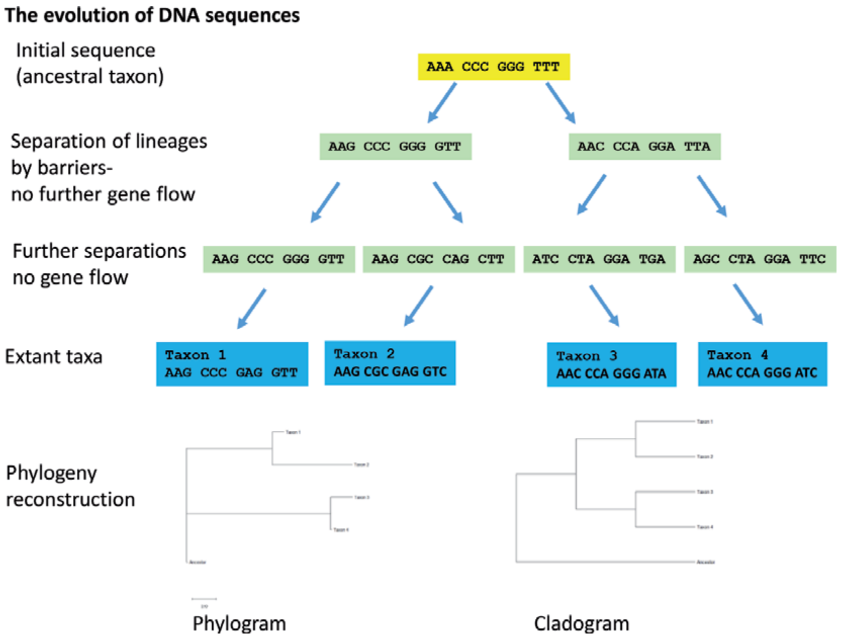

Figure 3.
Geographic or ecological separations of populations lead to sequence evolution and phylogeny.

3.2 DNA–DNA hybridization

Charles Sibley was the first scientist to utilize DNA analysis to study avian systematics. When in 1975 Sibley embarked on his DNA work, DNA sequencing was not yet invented. Sibley employed DNA–DNA hybridization analysis instead, in which DNA melting temperatures are compared. Together with Jon Ahlquist Charles Sibley investigated the DNA melting profiles of more than 1700 bird taxa. In 1990, they published their results as “Phylogeny and Classification of Birds” [7]. Sibley employed the DNA–DNA hybridization data to postulate a novel avian taxonomy, published in 1990 as “Distribution and Taxonomy of Birds of the World” [12].

Sibley and Ahlquist [12] grouped many of orders and families of birds correctly, but as we know today, they were completely wrong with others [1]. For example, New World vultures are not storks, as Sibley had assumed, but cluster at the base of the Accipitriformes. DNA–DNA hybridization has severe shortcomings, because it does not provide sufficient resolution and suffers from laboratory artifacts. Sibley and Ahlquist [7] knew the limitations of the DNA–DNA hybridization, but had no choice, because at that time, it was the only DNA method around.

3.3 DNA sequence analysis

We can isolate DNA from any bird tissue, such as blood and muscle, but DNA also occurs in feathers or in buccal swaps. Using PCR with specific primers, single genes (so-called marker genes) can be amplified and sequenced using the Sanger chain termination method. A schematic view of the procedure, how to go from DNA to a phylogeny is illustrated in **Figure 4**.

Already the sequence analysis of marker genes from mitochondria (e.g. COI, cytochrome b, ND2) or the nuclear genome is often very informative and enables informative and reliable phylogeny reconstructions. The choice of marker genes differs between animals and plants and furthermore, depends on whether one wants to study evolutionarily young or old relationships.

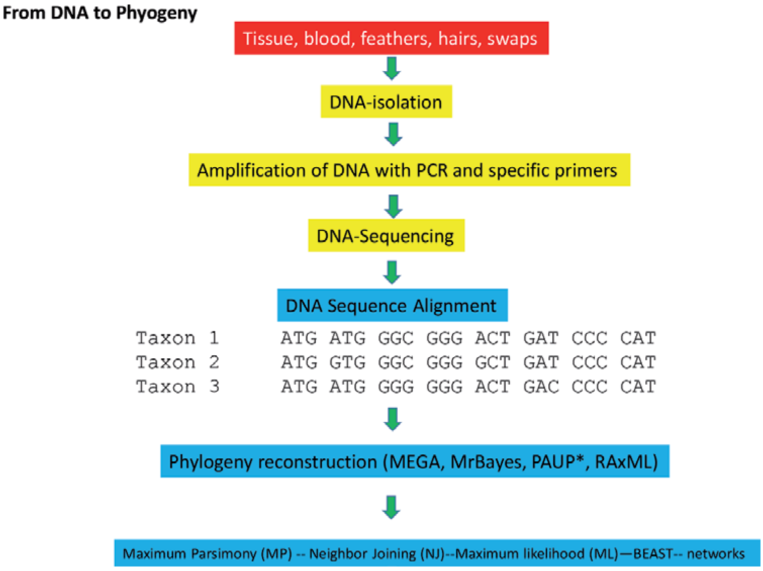

Figure 4.
From a sample with DNA to a phylogeny reconstruction.

After 2000, next generation sequencing (NGS) became available in which whole genomes are analyzed by parallel sequencing [13]. Hundreds of millions of short DNA sequences can be generated in a single NGS run. These sequences are then assembled into longer DNA segments by bioinformaticians and assigned to known genes ("annotation"). Homologous DNA sequences are aligned and, as with marker genes, evaluated using phylogeny programs. A larger and more comprehensive collection of genes or even complete genomes and transcriptomes can be sequenced by the new High-Throughput Sequencers [13, 14].

The pyrosequencer 454 from Roche represented the first generation of NGS sequencers. Several companies developed new NGS strategies and sequencers, such as Illumina, SOLiD, IonTorrent, and PacBio [1, 13, 14]. The Illumina technology is a market leader at present; these sequencers generate of up to 250 million short sequences (50 to 200 nucleotides) in a single lane. The short sequences introduce a number of problems for bioinformatics, thus new developer look sequencers that generate longer reads. 3rd generation sequencers from PacBio or Nanopore Sequencing are beginning to reach the laboratory. The longer sequences allow a localization of the sequence on a chromosome and to reconstruct complete gene assemblies including repetitive elements. Longer and high quality reads are important to reconstruct phylogenies [14].

Several thousand genome sequences are now available, mainly from prokaryotes. The number of genome sequences from animals is comparably small. But already many genome sequences are available to reconstruct the large-scale phylogenomics of animal groups, such as birds: It is foreseeable that the phylogeny of most evolutionary lineages can be reliably reconstructed via genome sequencing in a few years (see Chapter 4).

4. Towards a new "Avian Tree of Life"

Genome studies of birds started later than in other animal groups [13, 14]. Following the genome of *Gallus gallus*, the next in line were *Taeniopygia guttata*, *Meleagris gallopavo*, *Ficedula hypoleuca*, *F. albicollis*, *Falco peregrinus, Falco cherrug*, and *Anas platyrhynchos*) [13, 14, 17]. Today, several hundred genomes have been sequenced and the information is available in open databases, such as NCBI and GenBank. The initial genome data were instrumental for avian phylogenomics as the sequences could be used to assemble and align the millions of sequence snippets obtained via NGS.

The Avian Phylogenetic Consortium [18] published in 2014 a first phylogenomic Tree of life (**Figure 5**). 2015 saw a more detailed DNA analysis [19] based on target sequencing of 259 nuclear genes and a total of 394,000 nucleotides, covering 198 species in 122 families and 40 orders (**Figure 6**). The study of Prum et al. [19] can be discussed as a follow-up of Hackett et al. [14] who had sequenced 19 nuclear genes of each of the major bird families using traditional Sanger sequencing.

Simplified phylogenies [18, 19] are illustrated in **Figures 5** and **6**. Main findings include a common ancestry of swifts and nightjars, the sister-pair relationship of grebes and flamingos, the separation of falcons from diurnal raptors, inclusion of New World vultures in the raptor clade and a new clade combining falcons, parrots and passerine birds [1, 13, 14, 18, 19].

A new phylogenomic analysis covering 363 taxa from 92% of all bird families was published by Feng et al. [20]. This phylogeny contains for the first time information for many of the families within Passeriformes. The new data are combined with putative data from over 10100 bird taxa to generate a phylogeny hypothesis as

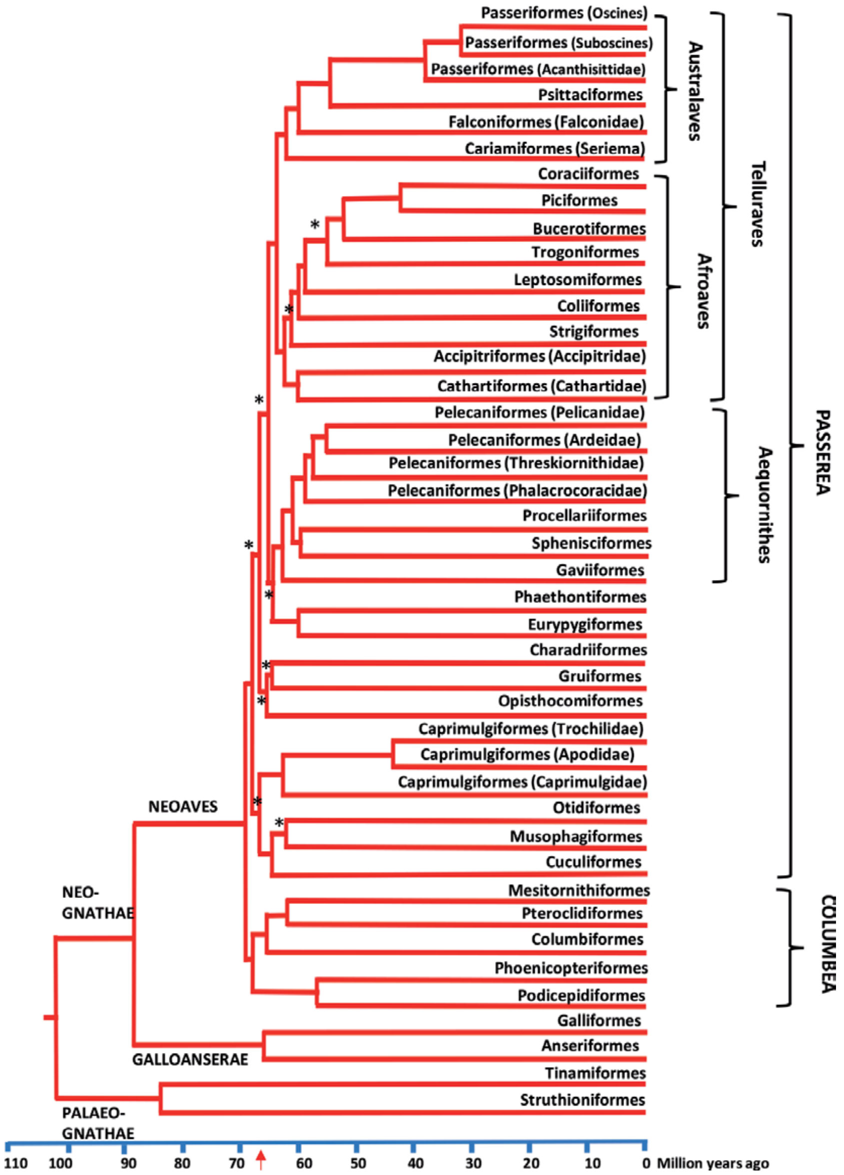

Figure 5.
The first phylogenomic avian phylogeny (modified from [18]).

shown in **Figure 7**. This analysis is preliminary and phylogenetic trees shown were reconstructed based on transposable elements. For non-passerine orders, the new phylogeny is very similar to the tree of Jarvis et al. [18] (**Figure 5**), maybe because the same taxa and genome sequences were used. For Passeriformes, the phylogeny is similar to that of Fjeldså et al. (**Figure 8**) [21].

More than 60% of all birds (6204 species) belong to the Order Passeriformes. Its systematics has seen great advantages recently. In "The Largest Avian Radiation" Jon Fjeldså, Les Christidis and Per Ericson [21] have put all evidence together to reconstruct its complex phylogeny. Passerines (also parrot and falcons) apparently evolved about 55 to 50 million years ago, just after the Cretaceous/Tertiary boundary in Australasia and then immigrated all over the world. The main radiation

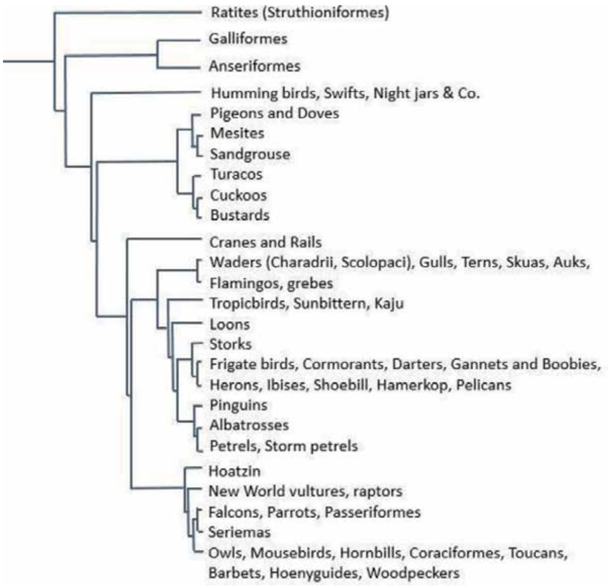

Figure 6.
A simplified phylogeny of birds according to Prum et al. [19] based on nucleotide sequences of 259 nuclear genes.

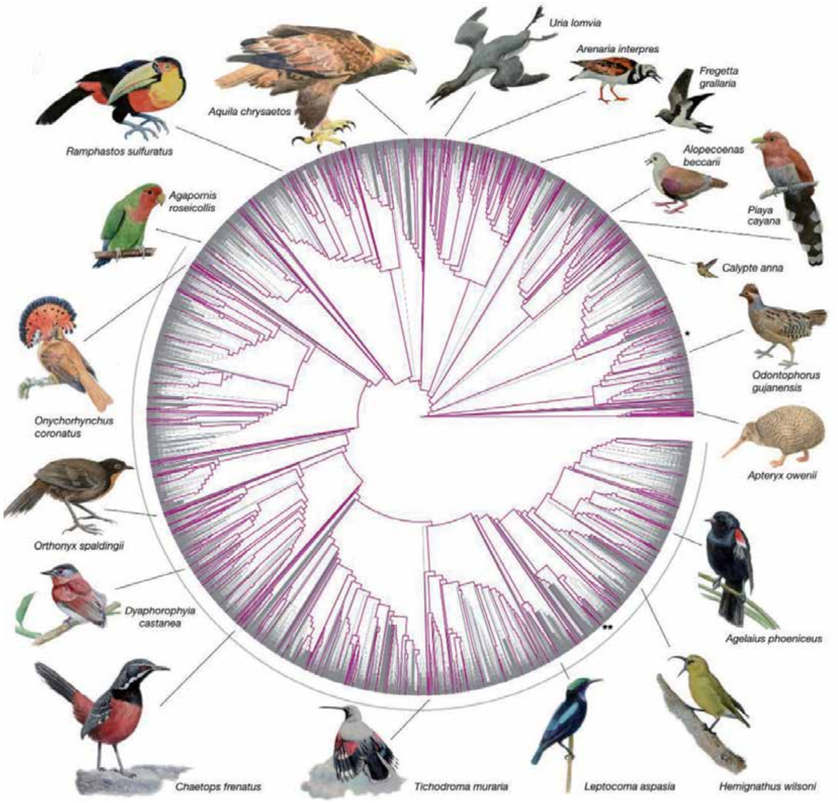

Figure 7.
A comprehensive avian tree of life [20]. (the article is licensed under a creative commons attribution 4.0 international license, which permits use, sharing, adaptation, distribution and reproduction in any medium or format).

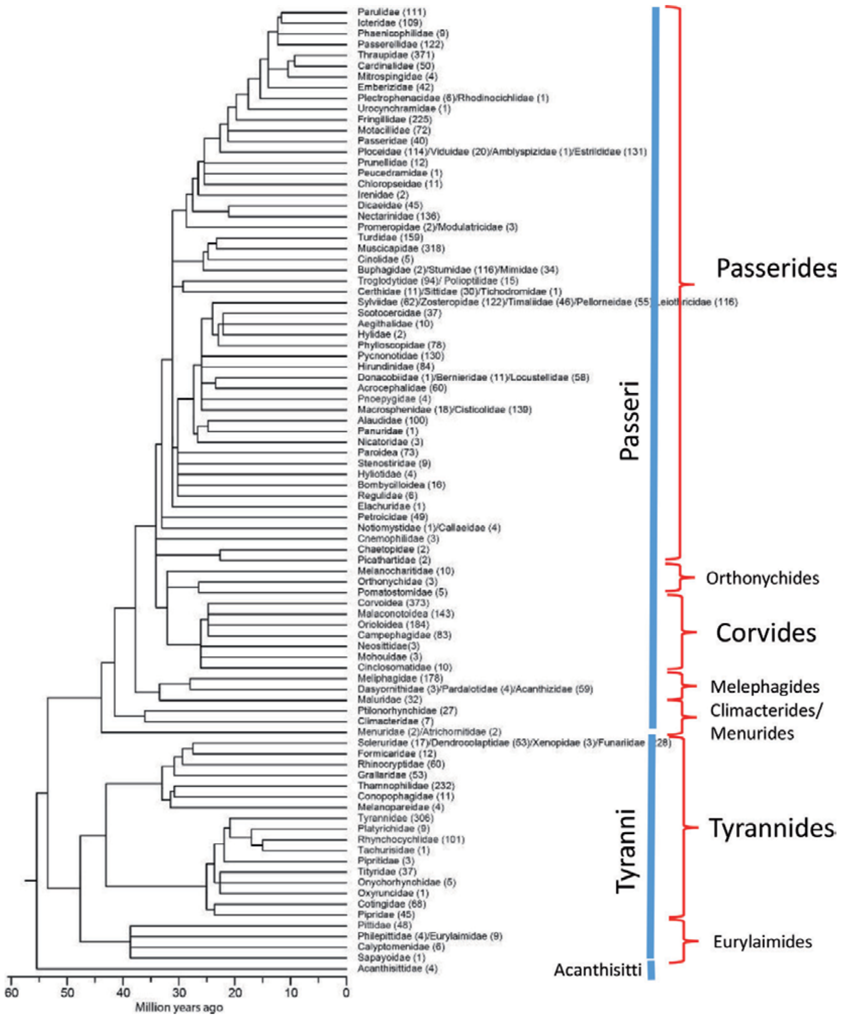

Figure 8.

A time-calibrated phylogeny of families within the Passeriformes (after [21]). Names of suborders (blue line) and infraorders (right of the red brackets).

of passerine families occurred later between 20 and 35 million years ago. The Passeriformes (**Figure 8**) are divided into three Suborders: Acanthisitti, Tyranni and Passeri. They are divided into several Infraorders and Parvorders. **Figure 8** shows a phylogeny reconstruction of the majority of families with an indication of Suborders and Infraorders. Species numbers are uneven in these groups: The Acanthisitti comprise 4 species, the Tyranni about 1290 taxa and the Passeri 4910 species. In Passeri, the largest Infraorder Corvides comprises 775 species, whereas the Passerides contain the majority of 3800 species. The book of Fjeldså et al. [21] provides phylogenies of most families of passerine birds, if available. The book is a milestone in the history of bird systematics and outlines many of the open questions.

High-throughput sequencing can also be used to study the transcriptome of birds. This information is important to understand the phenotype of an individual or adaptations to ecological or biological challenges (review in [22]). Examples are studies of the migratory phenotype of birds and the question which genes influence timing and spacing of migration events [23, 24].

5. Consequences of cladistic evaluations

Progress was not only achieved at the level of orders, but also at the level of species, genera and families. With advent of DNA sequencing, more and more bird phylogenies were reconstructed from nucleotide sequences of one or more marker genes [in the beginning only mtDNA, later mtDNA and nuclear DNA (ncDNA) were used] from each species. These phylogenies provide a good resolution at the family and genus level, but often failed to infer divergences in the far past [13, 14].

As an example for the taxonomic changes within a bird family, I would like to document our own work on owl systematics [25, 26]. In **Figure 9**, a phylogram (reconstructed from cytochrome b sequences) indicates the major groupings within Tytonidae and Strigidae. In red, I have pointed out all the taxa, where DNA data either helped to define a species or a genus. In particular, the former genera *Nyctea, Ketupa* and *Scotopelia* were lumped into the genus *Bubo*, in order to avoid a polyphyletic genus *Bubo*. The former genus *Otus* was clearly polyphyletic and was split into new genera *Megascops*, *Psiloscops* and *Ptilopsis*. *Ninox superciliaris* from Madagascar is not a member of *Ninox*, but apparently belongs to *Athene*. Linné only recognized a single species *Tyto alba* with worldwide distribution. DNA data clears distinguish between *Tyto* from Europe/Africa (*Tyto alba* complex) and the New World (*Tyto furcata* complex). The Australasian Barn owls are quite diverse with four major lineages and many new species on isolated islands. Apparently, barn owls had evolved in Australia.

Similar splits and lumpings occurred in many bird families, just to name a few (see [27]) for a comprehensive list of accepted names).

- Gulls and terns
- Petrels and albatrosses
- Bustards
- Waders
- Woodpeckers
- Swifts
- Larks
- Shrikes
- Wagtails
- Pipits
- Warblers (*Sylvia, Acrocephalus, Cisticola, Hippolais, Phylloscopus*)
- Turdids (*Saxicola, Phoenicurus, Oenanthe, Turdus*)
- Tits
- Sparrows
- Finches and buntings

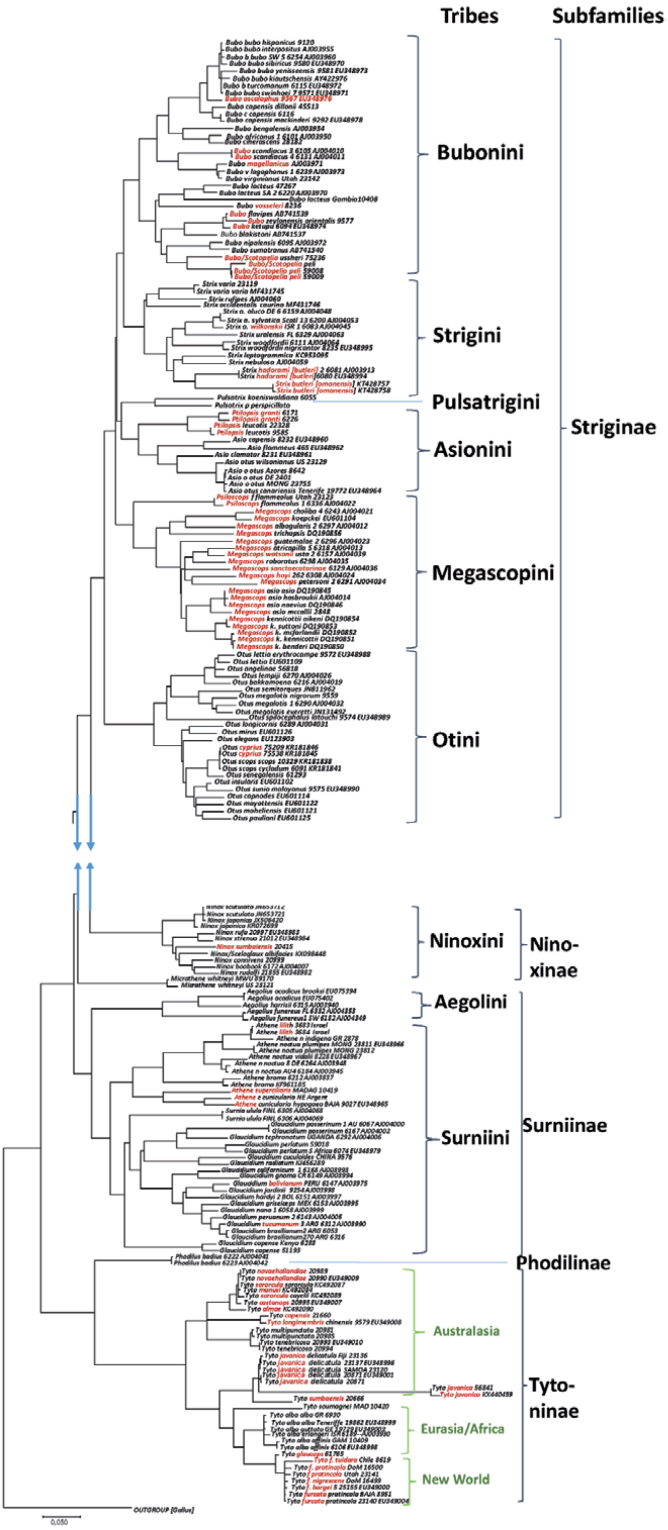

Figure 9.
Phylogeny of owls (Tytonidae, Strigidae) (after [26]). Names in red are those, which had changed because of DNA data.

Thus a birder, who started his career 40 years ago will sometimes no longer recognize the Latin names of a species and their order of arrangement in modern field guides.

All these efforts have expanded the world checklist of birds. The IOC World Bird List 11.1 [27] actually (2021) comprises **10,806** extant species (and **158** extinct species) organized in **40** Orders, **252** Families and **2,353** Genera. **19,990** subspecies, their ranges and authors are also included. The number so of new bird species is increasing continuously. It has been speculated that we will end up with more than 18000 bird species, when all of them have been sequenced and re-classified [28].

6. Phylogeography

Another area of interest is the distribution and evolution of a species over time and space. This is the realm of phylogeography [15]. In order to use DNA for such analyses, we require highly informative DNA and methods with a high degree of resolution. Although variable mtDNA is useful in many instances, a better resolution can be obtained from the analysis of microsatellite markers. Increasingly, partial (RADSeq) and complete genome analyses from High-throughput sequencing are also used to study phylogeography because we can obtain information of millions of single nucleotide polymorphisms (SNPs). In case of human evolution, such data could trace human migrations over time and ancient hybridizations with Neanderthals and Denisovans in fascinating details [3]. It will take some time, until we will have similar data for any species of birds. But, as the costs for NGS come down, it is probably only a matter of time, until we will get there.

We have analyzed the phylogeography of several birds and reptile species on oceanic islands (Macaronesia), in the Amazon region and in Eurasia. The pattern, which we discovered, differed substantially between regions. Although the Macaronesian islands (including Canary Islands, and Madeira and Azores) are sometime not far from each other, the local bird populations are resident and do not exchange between islands [29, 30]. All these oceanic islands are of volcanic origin and between 20 to 1 million years old. They are known for their richness of endemic fauna and flora.

When we studied the variation of mitochondrial DNA sequences of birds from different Macaronesian islands, we discovered, that many of them had specific and unique island haplotypes, suggesting that gene flow between islands is very low or not existing [29, 30]. As a consequence, some of the islands species obtained species rank, such as *Phyllocopus canariensis*. In *Fringilla coelebs, Cyanistes caeruleus, Erythacus rubecula, Regulus regulus, Sylvia melanocephala*, and others we could define new island specific subspecies (see references in [29, 30]). A similar diversification can be seen on the Island archipelago of the Wallace zone in Australasia [31]. However, if we look at bird population on the Aegean Islands in Greece or Turkey (except for Cyprus), little or no differentiation can be seen [32]. The Aegean islands have been connected with each other during the last few million years, which allowed gene flow among island taxa.

We also studied some bird taxa in the Amazon region and to our surprise found a strong degree of phylogeographic patterning, which correlated with the large river systems in the area. As a result, a number of morphologically similar species could be split into new taxa mostly on account of DNA data, sometimes also because of differences in vocalization [33–37].

To our surprise, we found some genetic variation in Eurasian bird species, but could often not discover a robust phylogeographic pattern. Examples are: *Lanius collurio, Merops apiaster, Upupa epops, Dendrocopus major, Tyto alba, Athene noctua, Falco peregrinus* or *Acrocephalus palustris* [38–43]. The apparent reason for this phenomenon concerns the climate in the last two million years, which saw a continuous cycle of warm and cold periods. During cold periods (ice ages) large parts of the northern hemisphere was covered by ice and bird populations, which settled these areas during warm periods, had to escape further south to climatically more favorable refugia, which existed on the Iberian peninsula, in North Africa and the Near East. In refugia, bird lineages met, mixed and then spread north again when the next warm period came. This has happened more than 10–20 times during the last 2 million years when most species of extant birds evolved. This has led to a complex mixing of genetic lineages in most Eurasian bird species (review in 44]).

The last ice age ended about 12000 years ago and gradually, woodland and wetland habitats in Central, North and Eastern Europe developed, which were then colonized from birds out of their southern refugia. When humans cleared forest and created agricultural landscapes, species of open land also settled in Europe. As a consequence, even if local bird populations are philopatric by now, the time period was too short to develop new haplotypes in different parts of Eurasia. Thus, Eurasian birds offers a great challenge for the phylogeographic analysis. However, if we would use similar markers for birds (SNPs) as used for humans, we might solve these problems.

The analysis of bird migration is still a challenge. The use of bird ringing and tracking system (geolocators, GPS sensors, satellite transmitters) have brought substantial progress. Since each individual bird carries a unique DNA profile, it should also be possible to connect a bird on migration or in the wintering grounds to its place of birth [44]. As discussed before, we need DNA markers of extremely resolution to solve this problem. MtDNA and microsatellite analyses are not informative enough in most cases [38, 45]. Genome-wide SNP analyses should help, as they did with human migrations.

7. Outlook

As a consequence of new DNA analyses and the use of cladistics, the number of extent bird species is growing from year to year. We presently recognize well over10,806 bird species; some estimates assume even more than 18,000 bird taxa if subspecies will attain species level [28]. Even if we see very good progress over recent years, it will certainly take some time until the final "Avian Tree of Life" will be published, in which the phylogenetic position and history for each of the avian species is reconstructed. A Tree of Life, will enable a better understanding of avian evolution in general, of systematics but also of the evolution of traits and adaptations.

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Conflict of interest

The author declares no conflict of interest.

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Section 2

Bird Colours and Feather Structure

Chapter 2

Haloarchaea May Contribute to the Colour of Avian Plumage in Marine Ecosystems

Rosa María Martínez-Espinosa and Javier Torregrosa-Crespo

Abstract

Some seabirds or coastal birds such as flamingos or pelicans display elegant pink or reddish colours. These colours are due to pigments that birds cannot synthesize de novo. Thus, this coloration is mainly originated from carotenoids ingested trough carotenoid rich food sources like microalgae (*Dunaliella*) or small shrimps (*Artemia*), which are microorganisms inhabiting the salty environments where the mentioned birds live. New advances in this field of knowledge have revealed that extreme microorganisms belonging to the haloarchaea group (Archaea Domain) may contribute significantly to the characteristic pink- red colour of flamingos' feathers for instance. Alive haloarchaea cells have been found on the surface of the feathers. Besides, the major carotenoid produced by haloarchaea (bacterioruberin) has also been identify within the feathers structure. This work summarizes the main contributions recently reported about this topic as well as general aspects regarding bacterioruberin as a powerful colour carotenoid. Discussions about potential role of these microorganisms in the life of seaside birds are also included.

Keywords: bacterioruberin, bird coloration, carotenoids, flamingos, natural pigments, plumage

1. Introduction

Coloration is one of the most conspicuous traits that varies among organisms. In the case of animals, colour is mainly due to: (i) the presence of pigments (carotenoids, melanin, turacoverdin, biliverdin, protoporphyrin, etc); (ii) light phenomena such as reflection/emission from animal structures (skin, feathers, etc.); (iii) the presence of microscopic structure in scales, bristles, or feathers, which give them brilliant iridescent colours (commonly named "structural colours") [1]; and (iv) general aspects related to genetics [2]. Due to these reasons, animals show different colours, which can slightly vary even between individuals belonging to the same species. Animal colorations are strongly linked to different biological roles: camouflage, sexual, social, and interspecific signalling, physical protection (against UV radiation for instance), and sexual dimorphism [3–6].

In the case of the birds, feathers play a key role in general coloration. Those that are red orange show these colours thanks to the presence of different carotenoids within their structures. Carotenoids are natural pigments widely spread in nature: chloroplasts and chromoplasts of plants, bacteria, archaea, microalgae, fungi and even phytoplankton [7–9]. All the mentioned organisms can synthesize carotenoids, but animals in general are not able to produce them *de novo* (aphids and spider mites are an exception, and it is assumed that they acquired this ability thanks to genes transferred from fungi [10]). Thus, animals obtain carotenoids from diet. After food uptake, they are mainly metabolized by the liver and intestinal epithelium [11] to be further incorporated into fatty tissues or other structures such as feathers, skin, eyes, etc.

There are over 600 known carotenoids classified into two classes: xanthophylls (which contain oxygen) and carotenes (which are hydrocarbons without oxygen). Thanks to their chemical structure, they absorb wavelengths ranging from 400–550 nanometres (violet to green light) [12]. Consequently, these pigments are deeply coloured yellow, orange or red. Some carotenoids have vitamin A activity (they can be converted into retinol) and most of them can also act as antioxidants. Recently, it has been stated that cytochrome P450 enzymes are also involved in red carotenoid coloration [13].

Red coloured birds inhabiting salted environments such as salt marshes, seaside ecosystems, salted lagoons etc. may often acquire carotenoids by ingesting small organisms or even microorganisms like yeast and algae. Thus, flamingos (*Phoenicopterus sp.*) filter-feed on brine shrimp (*Artemia salina*) and blue-green algae (*Dunaliella salina*) [14], which are high rich sources of carotenoids. They are broken down into pigments by liver enzymes and fully incorporated into tissues [15, 16].

The nature of the colour shown by red-pink feathers is one of the aspects strongly discussed during the last few years. Many works have demonstrated that the colour is due to the carotenoids obtained through the diet, whilst other studies suggested that other external factors like microorganisms or light phenomena could contribute to the final red-orange-pink phenotype. This chapter summarizes recent knowledge about the presence of alive microorganisms belonging to the Archaea domain on the surface of red-pink feathers thus may contributing to their colour. General aspects related to the carotenoids produced by haloarchaea inhabiting feathers of coastal birds are also discussed.

2. The colour of bird feathers

Bird feathers have been the aim of several works during the last two centuries. Thus, the first reports on bird plumage listed in databases like PUBMED, Web of Science or Scopus analysed aspects focused on the muscles in charge of the feathers movement [17] or their growth [18]. Other aspects of bird feathers related to biological roles like sexual selection, colonization strategies or signalling have also been extensively explored [19–23]. These aspects are intricately connected to the coloration of avian plumage.

The first detailed studies about the colour of bird feathers were published in indexed scientific journals in the middle fifties last century. Since then, around 500 manuscripts have been reported on this subject (**Figure 1**). It is worthy to note that the number of studies about the colouration of plumage significantly increased at the beginning of XXI century (**Figure 1**). However, the number of publications focused on the presence of carotenoids in bird feathers is lower compared to those related to other issues affecting the phenotype of birds (**Figure 1**). Bird coloration (mainly in feathers) is one of the most studied topics to elucidate the role of natural and sexual selection in the evolution of phenotypic diversity. Thus, the variety of vibrant plumage colours has evolved as a direct result of social and environmental pressures.

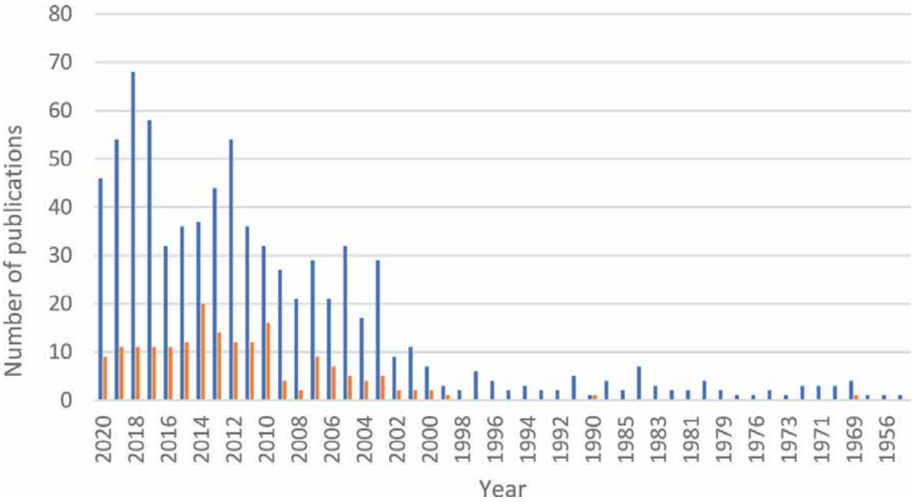

Figure 1.
Graph representation of the total number of publications per year from the database PubMed concerning the combination of the following keywords: (🟦) bird feathers AND colour; (🟧) bird feathers AND colour AND carotenoids. Revision date: 10th January 2021.

The colour of plumage and other structures in animals and plants is due to the presence of pigments (pigment-based coloration) or the presence of microscopically structured surfaces fine enough to interfere with visible light (structural coloration) [24]. Iridescence for instance, is one of the better-known examples of it [25]. In some cases, feather colours are the result of a combination of both [26, 27].

Table 1 summarizes the most representative pigments already identified as part of the colour of bird plumage. The most abundant are melanin and

Melanins		
Name	**Colour**	**References**
Eumelanin	Grey/Black	[28–31]
Pheomelanin	Brown	[28, 29, 31, 32]
Carotenoids		
Zeaxanthin	Yellow	[2, 33, 34]
Lutein	Bright Yellow	[2, 33–35]
β-carotene	Yellow	[2, 35]
β-cryptoxanthin	Yellow	[2, 35]
Canthaxanthin	Orange Red	[2, 33–35]
Astaxanthin	Red	[2, 34–36]
Rhodoxanthin	Purple-red	[34, 37, 38]
Porphyrins		
Turacoverdin	Green	[39]
Coproporphyrin III	Red Brown	[40]
Turacin	Red	[41]

Table 1.
Summary of the main features characterizing the most abundant pigments in bird feathers.

carotenoids [28, 42]. On the one hand, melanin-based coloration switches from brown to black due to the presence of phaeomelanin or eumelanin, respectively, or the number and distribution of the melanosomes [29, 30]. On the other hand, carotenoids-based colorations vary from yellow to red as previously mentioned.

The genetics of coloration in birds remains poorly described. However, it is extensively accepted that its expression is phenotypically plastic with a high sensitivity to variation in environmental conditions. Therefore, the melanin-based colour should be considered the key system to understand the molecular basis of phenotypic variations [43]. Some other pigments are only present in some species. This is the case of psittacofulvins, which are found just in a few species of parrots (*Psittacidae*) or penguins (*Spheniscidae*) [44–46] or turacoverdins, responsible for the bright green coloration of several birds of the family *Musophagidae*, most notably the turaco (*Turac*o sp.; *Musophagidae*). It is chemically related to turacin, a red pigment also found almost exclusively in turacos [39].

3. Haloarchaea

Archaea, one of the three Domains of life, make up a significant fraction of the microbial biomass on Earth [47]. It was thought that Archaea microbes were restricted to extreme environments, such as those with elevated temperatures, low or high pH, high salinity, or strict anoxia [48]. However, environmental sampling analysis based on rRNA sequences has revealed that archaea are widespread in “normal” ecosystems, including soils, oceans, marshlands, human colon, human oral cavity and even in human skin. They are particularly numerous in the oceans; thus, archaea in plankton may constitute one of the most abundant groups of organisms on the planet. From a metabolic point of view, they have evolved a variety of energy metabolisms using organic and/or inorganic electron donors and acceptors, playing important roles in the Earth’s global geochemical cycles [49].

Salty environments are dominated by organisms commonly named “halophiles” (it comes from the Greek word for “salt-loving”). They are usually classified into three groups according to their NaCl requirements: slight halophiles (2–5% or 0.34–0.85 M), moderate halophiles (5–20% or 0.85–3.4 M) and extreme halophiles (20–30% or 3.4–5.1 M) [50].

Halophilic archaea, also called Haloarchaea, are extreme or moderated halophilic species inhabiting neutral saline environments such as salt lakes, marine salterns, marshes, saltern crystallizer ponds or genuine environments like the Dead Sea [51, 52]. In those natural ecosystems, salt concentrations are around 1.5–4 M, which corresponds to 9–30% of salts (w/v). NaCl is the predominant salt and ionic proportions are like those dissolved salts in seawater.

These halophilic ecosystems harbour a large diversity of microorganisms of all three domains: small eukaryotes such the shrimp *Artemia salina*, primary producers as the green algae *Dunaliell*a [14] (**Figure 2A** and **B**), aerobic heterotrophic bacteria (mainly belonging to the family *Halomonadaceae*), anaerobic fermentative bacteria (families *Halanaerobiaceae* and *Halobacteroidaceae*) and archaeal microorganisms of the families *Halobacteriaceae* and *Haloferacaceae* (commonly named “Haloarchaea”). They are mainly characterised by their red-orange-pink colour, which is due to the pigments they produce to be protected against the high sun radiation (**Figure 3**). Salted ponds for salt crystallisation or other salty ecosystems like de Dead Sea become completely red, mainly in summer, due to microbial blooms, in which haloarchaea of the genera *Haloarcula*, *Haloferax*, *Haloquadratu*m or bacterial species like *Salinibacter ruber* constitute de major populations (**Figures 2C** and **3**).

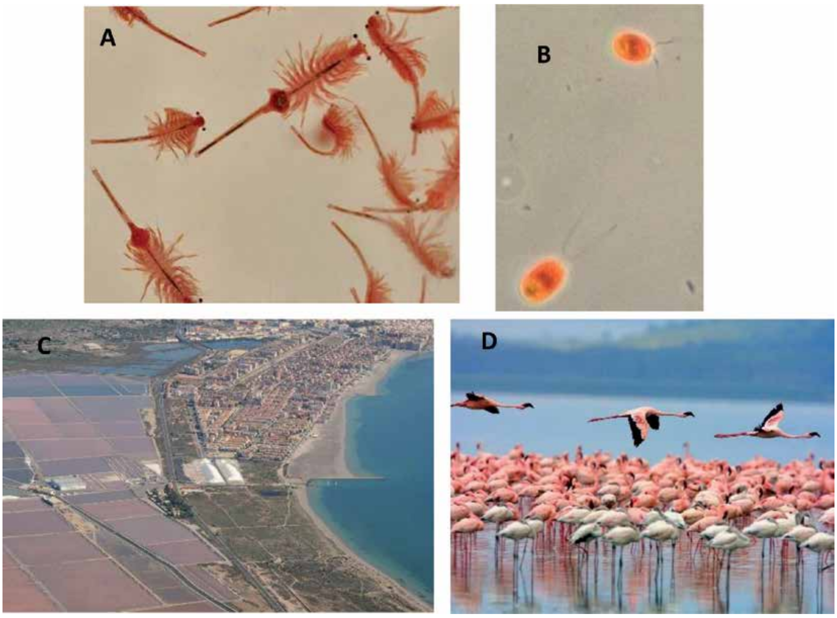

Figure 2.
(A) Artemia salina *and (B)* Dunaliella salina. *They constitute the major microbial populations in salted waters in coastal environments, salted lagoons, salty ponds from where NaCl is isolated from human consumption, etc. (C) Aerial overview of the saltern ponds located in Santa Pola city (Southeast of Spain) (http://paisajesturisticosvalencianos.com/paisajes/las-salinas-de-santa-pola-torrevieja/). This kind of ecosystems are warm places frequently inhabited by seaside birds like flamingos (D). The colour of the ponds is due to microbial blooms, which occur mainly in summer.*

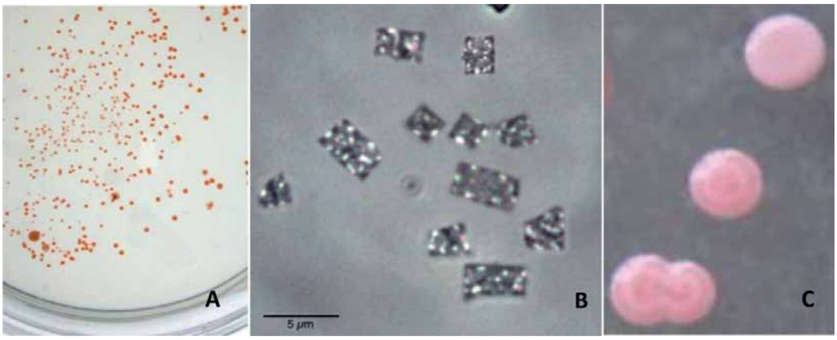

Figure 3.
(A) Haloferax volcanii *colonies; (B)* Haloquadratum walsbii *cells (picture from https://microbewiki.kenyon.edu/index.php/Haloquadra) and (C)* Haloferax mediterranei *colonies. Flamingos display haloarchaeal colours, they often frequent hypersaline lakes, and they carry haloarchaea with them on their travels around the world.*

4. Haloarchaea and their relation to avian plumage colour: the case of marine birds

Studies in the early nineties of the last century demonstrated that the carotenoids of the feathers were derived from the diet and deposited within tissues selectively [53] being the liver one of the most important organs involved in the conversion of carotenoids uptaken [54]. Some years before, other studies focused on seaside birds as flamingos stated that the major carotenoids in blood and feathers were canthaxanthin and a rare β-carotene derivative (4-keto-α-carotene) [55, 56]. Limitations on chemical and analytical techniques have contribute to the poor knowledge about carotenoids in birds up to nowadays. Fortunately, new advances in spectrometry and HPLC have made possible a significant improvement in this field of knowledge [41, 57]. Thus, during the last 15 years, several research groups worldwide have characterised the nature (and even the concentrations) of carotenoids in blood and feathers, mainly in finches [58, 59] and parrots [44, 60]. All the reported results show that the most important carotenoids contributing to the red-orange-pink colours in feathers are: canthaxanthin, astaxanthin, zeaxanthin and carotene (including its derivatives). In the case of seaside birds, it has been stated that the main rich carotenoids sources are the small shrimps and algae co-inhabiting the salty environments (*Artemia* and *Dunaliella* species, for instance) (**Figure 2**). Consequently, it is extensively assumed that the major pigments in marine bird's feathers would be those predominating in shrimps and algae (astaxanthin, canthaxanthin and carotene). However, some other studies indicate that in hypersaline habitats the birds do not feed extensively on brine shrimps *Artemia* to avoid salt stress [61]. Therefore, other carotenoid rich sources must be considered as part of the diet of marine birds to explain their pigmentation.

Recent contributions in this field have revealed that there are other important factors contributing to the red-orange-pink colour of the feathers. Between them, it is important to highlight the following: (i) genetics [2]; (ii) variation in carotenoid-protein interactions in bird feathers structures, which produces novel plumage coloration [62] and (iii) the presence of alive red-orange microorganisms on the surface of the feathers [63]. This last factor has recently been reported from flamingos growing up in captivity: viable, red-coloured archaeal strains belonging to the genera *Halococcus* and *Halogeometricum* were isolated from the surface of the plumage [63]. Apart from these viable cells, metagenomics approaches showed that cells belonging to other genera such as *Haloquadratum*, *Haloferax*, *Haloarcula*, *Halorubrum* and *Natronomonas* are also present on the surface of the flamingos' feathers. This kind of haloarchaea can produce significant amounts of bacterioruberin, a carotenoid mainly synthesised by them giving the microbial cells red-orange colours [8, 64, 65]. Besides, the analysis of the flamingo plumage pigments shows that bacterioruberin is not only in the alive microbial cells on the feathers' surface, but also found inside the flamingo feathers structure. This result directly suggests that haloarchaea are also part of the diet of flamingos. Bacterioruberin is responsible for the colour of these extremophilic microorganisms (**Figures 3** and **4**) [8, 65]. It has a primary conjugated isoprenoid chain length of 13 C=C units with no subsidiary conjugation arising from terminal groups, which contain four –OH group functionalities only (**Figure 4**).

This carotenoid is involved in several biological roles in haloarchaea: it protects the cells against the damage produced by high intensities of sun radiation, it provides aid in photoreactivation [66] and it promotes membranes stability [8, 65]. Characterisation of pure bacterioruberin samples revealed that it is more powerful than carotene as antioxidant compound [67, 68]. Due to these facts, bacterioruberin could be used in biotechnology and biomedicine for different purposes [8, 69].

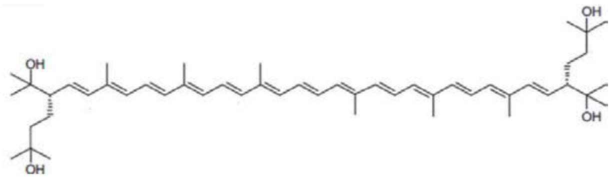

Figure 4.
Chemical structure of bacterioruberin. This compound has promising potential uses as antioxidant, antitumoral and immunomodulatory molecule for pharmaceutical and cosmetical formulations [64, 65].

Consequently, haloarchaea in general and their pigments in particular, may contribute to the orange-red colour of the feathers in two ways: (i) pink-red haloarchaea cells on the surface contribute to the pink-red phenotype in flamingos' feathers and (ii) haloarchaeal cells are part of the marine birds' diet (at least flamingos), consequently their carotenoids (mainly bacterioruberin) are ingested, metabolised and further assimilated.

5. Conclusions

New advances in the knowledge of animal pigmentation state that not only the pigments (carotenoids, melanin, etc.), but also the microstructure of the feathers as well as external factors, contribute to the final phenotype in terms of coloration. Related to birds, and particularly to seaside birds, it was thought that microalgae and small shrimps were the major sources of carotenoids so far. Nevertheless, recent results revealed that other small microbes such as haloarchaea could contribute significantly to the red-orange colours showed by birds like flamingos. In that sense, bacterioruberin becomes a new pigment to be considered to explain animal colours in marine environments. The potential influence of haloarchaea as an environmental factor determining avian plumage coloration or even protecting the microstructures of feathers against UV radiation must be investigated in further studies. Although bacterioruberin has been very well described, only few studies about its biological implications are available at the time of writing this review. Thus, more efforts must be done to explain basic aspects related to bacterioruberin metabolism and its effects on animal health and animal phenotypes. On the other hand, associations between different haloarchaeal-bird species as well as changes in these associations promoted by environmental conditions or anthropogenic actions are worthy to be analysed into detail. Hypothesis based on potential symbiotic relationship between haloarchaea and seaside birds remains unexplored.

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Conflict of interest

The authors declare no conflict of interest.

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Chapter 3

Viscous Drag Reduction and Contour Feather Geometry in Water and Land Birds

Roelof D. Coertze and Arie M. Rijke

Abstract

Water birds have contour feathers in contact with water that show in their distal one-third adaptations to water repellency, resistance to water penetration and forceful impact with water. These qualities vary according to their intimacy with open water. In this study, the geometry of this part of the feather was examined to detect additional features that would affect viscous drag in water. The length-to-width ratio was measured and used to calculate the viscous drag coefficients for 48 water birds and, for comparison, 12 land birds. The lowest values for the drag coefficient were observed for birds with foraging niches as diving and swimming, followed by plunging, surface feeding, aerial and ground feeding. Land birds with no open water in their habitat had the highest drag coefficients. Three statistical approaches were used to validate the results. Allowing for the phylogenetic relatedness of the 60 species obscured any significant differences that may exist, but a non-parametric analysis that does not assume the conditions of equal sample size and variance turned out to be the most appropriate method for our data set.

Keywords: viscous drag in water, contour feather geometry, water birds, evolutionary history

1. Introduction

The contour feathers of birds are well-known to serve a variety of functions ranging from intraspecific signaling to such physical qualities as thermal insulation [1], water repellency [2] and resistance to impact [3]. They are arranged on the bird's body in an overlapping fashion like shingles on a roof with the dorsal aspect of their distal one-third exposed to air or water. This outer part of the contour feather has the patterned structure seen in pennaceous feathers with barbs extending from the rachis, each sprouting barbules of which the distal ones have hooks that catch upon the curled, proximal barbules of the barb next more distal [4]. These structural details confer to the plumage the properties of water repellency, resistance to water penetration and resistance to forceful impact. The overall pattern is essentially the same for all regions of the body surface, but differs by location for some species. For instance, a marked difference in barb diameter and spacing was observed for the head, breast and abdominal feathers of Blue Swallows (*Hirundo atrocaerulea*) affecting the water repellency and water resistance of these regions to cope with the swallow's specific habit of foraging along misty mountain slopes [5].

Water birds that swim, dive or plunge can be expected to show adaptations in their contour feathers, compatible with their foraging niches, that are absent in land birds that have no interaction with open water as indeed they do [6]. They show a water repellency and a resistance to water penetration in their contour feathers that vary with the family's specific behavioral patterns. Surface feeders tend to have a predominantly water repellent body plumage whereas those of divers and plungers are more resistant to water penetration and forceful impact.

Birds that swim and dive will also benefit from reduced drag for their locomotion in water, a consideration that applies less to waders and shore birds and not at all to land birds. Viscous drag in water is dependent on the surface microstructure of the distal one-third of the contour feather, but also on the shape of its surface in contact with water, an aspect of feathers that has so far received little or no attention. Drag in air, such as in flight, on the other hand, has been the topic of several studies.

That the shape of the surface area in contact with water varies among bird families has been noticed in the course of previous studies. It was seen to be nearly circular in land birds with a length-to-width ratio (L/W) of approximately 1.0, but oblong with an L/W of about 4 in penguins (*Spheniscidae*), the most aquatic of families. Birds less intimate with open water showed intermediate values for L/W.

In this chapter, we consider the interface between the distal one-third and flowing water to calculate viscous drag for feather shape geometry. Assuming the flow to be parallel to the long axis of the feather, i. e. zero angle of attack, we can derive the total drag coefficient (DC), composed of viscous pressure and frictional drag, from the computational and experimental results of studies on model ship hulls of varying length-to-diameter ratios using solutions to the Reynolds-averaged Navier–Stokes Equations [7]. For the relationship between drag coefficient and L/W, we then find

$$\mathrm{DC}\left(10^{-3}\right) = 4.071\,\mathrm{e}^{-0.0595\mathrm{L/W}} \tag{1}$$

for values of L/W less than 7 which is within the range of feather geometry. The equation predicts that oblong shapes of the tips of contour feathers reduce drag facilitating swimming and diving, whereas a more circular shape would cause an increase in frictional drag. A similar reasoning could be applied to the shape of the area that the body of a swimming bird has in contact with water. If this area is assumed to be elliptical, a drag coefficient for body surface area in contact with water could be determined using the same equation.

In order to establish if niche-specific adaptations in feather microstructure exist among bird species, various statistical approaches should be considered. Generalized least squares estimation of coefficients for linear models have been commonly used to investigate traits within phylogeny [8, 9]. However, statistical inaccuracies due to high type I errors are widespread without accounting for the evolutionary relationships. A more appropriate approach, described by Adams and Collyer (2018), incorporates phylogeny under a Brownian motion model of evolution while performing ANOVA. This phylogenetic-ANOVA approach offers additional advantages by accounting for group aggregation within phylogeny which could influence results and overall conclusions.

Our hypothesis is that water birds have contour feathers that exhibit in their shapes adaptations to reducing viscous drag according to their interaction with open water.

2. Methods

The measurements on contour feathers were performed on abdominal feathers as these are considered to be most representative of interaction with water. The primary source of feathers was the same as used for earlier studies which included water bird species from 11 orders and, for comparison, land bird species from 9 orders [10]. The species entered in this study are compiled in **Table 1**, using English names and taxonomic sequence suggested by Handbook of the Birds of the World [11].

The length and the width of the closed pennaceous portion of the contour feathers of the 48 water birds and twelve land birds in this study were measured to the nearest millimeter using a traveling microscope with the mid-part of the vane taken for the width. At least three feather specimens of each species were examined. The drag coefficients, listed in **Table 1**, were calculated from L/W values using the above equation.

Grouping the bird species according to their interaction with open water can be achieved by assigning them to foraging niches as proposed by Pigot et al. [12], using a standardized protocol for foraging niche delimitation. Following this procedure, a total of thirty niches has been identified for all of the approximately 10,000 bird species of the world. Of these six major foraging niches were categorized as Aquatic with two more chosen by us to accommodate the 48 water bird species of this study. The twelve land bird species could be grouped into two niches: Ground Feeding and Aerial/Sally.

All statistical analyses were conducted using the R statistical computer software (version 3.6.0). In addition to the foraging niches proposed [12] for aquatic birds (group 1) and land birds (group 2), four more analyses were performed using the values of L/W and DC for both land and aquatic bird species (consisting of the various foraging niches) categorized as the following independent variables: aquatic versus land birds (group 3), swimmers versus land birds (group 4), waders versus land birds (group 5) and swimmers versus waders (group 6). These groupings can be visualized in the context of a phylogeny in **Figure 1** and **Table 4**. Phylogenetic trees comprising of 60 bird species representatives of the independent groups were obtained from www.birdtree.org [13]. A total of 1000 trees were generated and a representative tree was constructed using the *maxCladeCred* function from the *phangorn* package (version 2.5.3).

The degree of group aggregation was determined in order to establish if the ANOVA methodology would be affected by the association between the independent variable, i. e. foraging niche and the phylogeny. Group aggregation was performed by calculating phylogenetic variance–covariance using the *vcv.phylo* function from the *ape* package (version 5.3), which was followed by performing a two-block partial least squares analysis using the *two.b.pls* function from the *geomorph* package (version 3.2.1). The degree of group aggregation was estimated by the proximity of the R-value to either 1 or 0, where values equal to or larger than 0.6 were considered strong aggregation. Significant group aggregation was considered for p-values <0.05.

In order to determine if the foraging niches for aquatic and land birds as well as the other independent variables, explain feather microstructure while accounting for phylogenetic relationships, a phylogenetic ANOVA (*procD.pgls* function from the *geomorph* package), conventional ANOVA (*aov* function) and non-parametric (*kruskal.test* function) equivalent approaches were followed. Significance among all analyses were accepted for p-values <0.05.

ID#	Bird Name	FN Group	L/W	DC (10^{-3})
1	Jackass Penquin, *S. demersus*	Aquatic Dive	3.4	3.326
2	Magellanic Penquin, *S. magellanicus*	Aquatic Dive	4	3.209
3	Gentoo Penguin, *P. papua*	Aquatic Dive	3.33	3.339
4	Rockhopper Penguin, *E. chrysocome*	Aquatic Dive	3.4	3.326
5	Great Northern Diver, *G. immer*	Aquatic Dive	2.85	3.437
6	Little Grebe, *T. ruficollis*	Aquatic Dive	2	3.615
7	Black-necked Grebe, *P. nigricollis*	Aquatic Dive	1.73	3.673
8	Yellow-nosed Albatross, *T. chlororhynchos*	Aquatic Surface	1.87	3.643
9	Great-winged Petrel, *P. macroptera*	Aquatic Aerial	2.37	3.536
10	Blue Petrel, *H. caerulea*	Aquatic Surface	2.75	3.457
11	Gray Petrel, *P. cinerea*	Aquatic Surface	3.13	3.38
12	European Storm-Petrel, *H. pelagicus*	Aquatic Aerial	2	3.615
13	Common Diving-Petrel, *P. urinatrix*	Aquatic Dive	1.63	3.695
14	Great White Pelican, *P. onocrotalus*	Aquatic Surface	2.68	3.472
15	Pink-backed Pelican, *P. rufescens*	Aquatic Surface	2.17	3.579
17	Northern Gannet, *M. bassanus*	Aquatic Plunge	2.5	3.509
18	Cape Gannet, *M. capensis*	Aquatic Plunge	2.4	3.53
19	Cape Cormorant, *P. capensis*	Aquatic Dive	2.6	3.488
20	Darter, *A. melanogaster*	Aquatic Dive	3.14	3.377
21	Great Frigatebird, *F. minor*	Aquatic Aerial	2.28	3.555
22	Gray Heron, *A. cinerea*	Aquatic Ground	1.46	3.733
23	Black-headed Heron, *A. melanocephala*	Aquatic Ground	1.45	3.734
24	Little Egret, *E. garzetta*	Aquatic Ground	2	3.61
25	Hamerkop, *S. umbretta*	Aquatic Ground	2.33	3.544
26	Yellow-billed Stork, *M. ibis*	Aquatic Ground	2.22	3.568
27	Saddlebill, *E. senegalensis*	Aquatic Ground	1.82	3.654
28	Sacred Ibis, *T. aethiopicus*	Aquatic Ground	2.12	3.589
29	Greater Flamingo, *P. ruber*	Aquatic Ground	2	3.615
30	Horned Screamer, *A. cornuta*	H.A. Ground	1.19	3.794
31	Egyptian Goose, *A. aegyptiaca*	Aquatic Surface	1.55	3.713
32	Yellow-billed Duck, *A. undulata*	H.A. Surface	2.08	3.597
34	Coqui Francolin, *F. coqui*	Ground Feeding	1.57	3.708
35	Blue Crane, *G. paradisea*	Ground Feeding	2.69	3.469
36	Limpkin, *A. guarauna*	Aquatic Ground	2.58	3.491
37	Red-knobbed Coot, *F. cristata*	Aquatic Surface	1.5	3.724
38	African Finfoot, *P. senegalensis*	Aquatic Surface	2.89	3.428
39	African Jacana, *A. africanus*	Aquatic Ground	1.73	3.673
40	Greater Painted-snipe, *R. benghalensis*	Aquatic Ground	2	3.615
41	Crab Plover, *D. ardeola*	Aquatic Ground	2	3.615
42	African Black Oystercatcher, *H. moquini*	Aquatic Ground	2.23	3.566
43	Pied Avocet, *R. avosetta*	Aquatic Ground	2.36	3.538

ID#	Bird Name	FN Group	L/W	DC (10^{-3})
44	Spotted Dikkop, *B. capensis*	Ground Feeding	2.43	3.523
45	White-fronted Plover, *C. marginatus*	Aquatic Ground	1.78	3.662
46	Eurasian Curlew, *N. arquata*	Aquatic Ground	1.94	3.628
47	Red Phalarope, *P. fulicarius*	Aquatic Ground	2	3.615
48	Pale-faced Sheathbill, *C. albus*	Ground Feeding	2.25	3.561
49	Pomarine Skua, *S. pomarinus*	Aquatic Aerial	2.57	3.494
50	Lesser Black-backed Gull, *L. fuscus*	Aquatic Surface	2.36	3.538
51	Sooty Tern, *S. fuscata*	Aquatic Plunge	2.13	3.586
52	African Skimmer, *R. flavirostris*	Aquatic Aerial	2.01	3.613
53	Common Murre, *U. aalge*	Aquatic Dive	3.33	3.339
54	Namaqua Sandgrouse, *P. namaqua*	Ground Feeding	1.2	3.799
55	Dusky Turtle-dove, *S. lugens*	Ground Feeding	1.27	3.775
56	Brown-necked Parrot, *P. robustus*	Ground Feeding	1	3.836
57	White-browed Coucal, *C. senegalensis*	Ground Feeding	1.13	3.807
58	Rufous-cheeked Nightjar, *C. rufigena*	Aerial/Sally	1.22	3.786
59	White-rumped Swift, *A. caffer*	Aerial/Sally	1.18	3.795
60	Narina Trogon, *A. narina*	Aerial/Sally	2.2	3.572
61	Half-collared Kingfisher, *A. semitorquata*	Aquatic Perch	1.87	3.643
64	European Starling, *S. vulgaris*	Ground Feeding	1.33	3.762

Table 1.
Bird species, foraging niches (FN) and drag coefficients (DC) of the 60 species in this study. Their full scientific names are provided in ***Figure 1****.*

3. Results

The results of the various forms of analyses are collected in the **Tables 2**–**4**. In **Table 2**, the 60 species of our study are presented as four categories. The 48 aquatic birds are subdivided into swimmers and waders. Their values for DC show a viscous drag coefficient for swimmers significantly lower ($p < 0.05$) than that of waders and, predictably, land birds. In **Table 3**, these categories are further subdivided into eight aquatic foraging niches and two terrestrial ones according to Pigot et al. [12]. It is seen that divers have the lowest recorded drag coefficient increasing in order for plungers, surface feeders, aerials, herbivore surface feeders, ground feeders, perchers to herbivore ground feeders. Land birds experience an even higher drag with no significant difference between ground feeders and those that catch their prey by aerial or sally sorties.

In **Table 4**, the 60 species are divided among six groups to show the outcomes of the various statistical analyses used in this study. In the phy-ANOVA analysis, the closeness of the phylogenetic relatedness of the groups is accounted for whereas in conventional ANOVA it is not. However, the value of the latter suffers of shortcomings due to lack of equal sample size and equal variance among the populations in groups one to six. The non-parametric variant does not assume the conditions of equal sample size and variance and, for this reason, is a more appropriate method of analysis for our data set.

Group aggregations were performed to determine if phylogenetic relatedness and independent groupings could influence the reliability of the phylogenetic

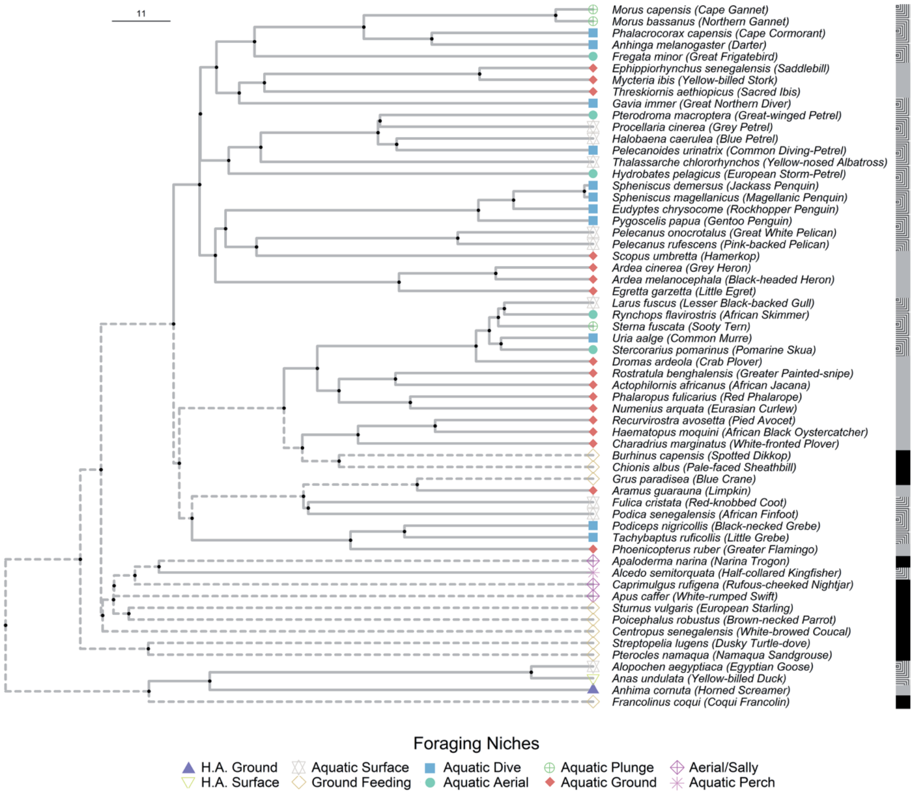

Figure 1.
Phylogenetic tree depicting the phylogenetic relationships between the 60 bird species. The various foraging niches are displayed at the tree tips. Land bird species are illustrated on the tree edges as dashed lines and aquatic birds as solid lines. Swimming characteristics are illustrated by the right-hand bar between land birds (black), waders (gray) and swimmers (dark gray).

Category	Sample Size	LW	DCf
Aquatic Birds	48	2.304 +/− 0.587	3.56 +/− 0.124
Swimmers	30	2.484 +/− 0.625	3.515 +/− 0.130
Waders	18	1.986 +/− 0.325	3.625 +/− 0.074
Land Birds	12	1.623 +/− 0.570	3.699 +/− 0.125

Table 2.
Sample size with L/W and DC values (including means (+/− standard deviation) of the various independent categories used in this study.

ANOVA analysis. The results revealed the presence of a relatively strong (r > = 0.6) and significant ($p < 0.05$) group aggregation for groups 2, 4 and 6, thus showing its limiting effect on the reliability on the outcome of the ANOVA analysis. Groups 1, 3 and 5 reveal weaker group aggregation (r < 0.6) but significance ($p < 0.05$) only for group 3.

The results of statistical significance for LW and DC values are comparable for all groups and analyses and therefore significance among groups will be discussed as a single result. Results among the various independent groupings yielded inconsistent results between the three statistical approaches. Results of the phylogenetic ANOVA approach indicated that no significance was observed for all groups

Foraging Niche	Sample Size	LW	DCf
Aquatic Dive[1]	11	2.855 +/− 0.739	3.439 +/− 0.156
Aquatic Plunge[1]	3	2.343 +/− 0.156	3.542 +/− 0.032
Aquatic Surface[1]	9	2.322 +/− 0.557	3.548 +/− 0.118
Aquatic Aerial[1]	5	2.246 +/− 0.218	3.562 +/− 0.046
H.A. Surface[1]	1	2.080 +/− NA	3.597 +/− NA
Aquatic Ground[1]	17	2.036 +/− 0.264	3.615 +/− 0.063
Aquatic Perch[1]	1	1.87 +/− NA	3.643 +/− NA
H.A. Ground[1]	1	1.19 +/− NA	3.794 +/− NA
Ground Feeding[2]	9	1.652 +/− 0.596	3.693 +/− 0.130
Aerial/Sally[2]	3	1.533 +/− 0.472	3.718 +/− 0.103

[1] *Aquatic Niches.*
[2] *Terrestrial Niches.*

Table 3.
Sample size with L/W and DC values (including means (+/− standard deviation) of the eight aquatic and two terrestrial foraging niches according to Pigot et al. [12]. ***Figure 1*** *Lists the birds that belong to each foraging niche.*

Group		Phy-ANOVA	Parametric	Non-Parametric
1	Aquatic Birds	NS	S	NS
2*	Land Birds	NS	NS	NS
3	Aquatic vs. Land	NS	S	S
4*	Swimmers vs. Land	NS	S	S
5	Waders vs. Land	NS	S	NS
6*	Swimmers vs. Waders	NS	S	S

*S: Significant (p < 0.05). NS: Non-significant (p > 0.05). *: Significant (p < 0.05) and strong (r > = 0.6) group aggregation.*

Table 4.
Summary of the outcome of the statistical analyses used in this study.

($p < 0.05$). Parametric results were highly contrasted against this result in that all groups with the exception of land birds indicated significant differences in feather microstructures. The non-parametric equivalent results in significance for groups 3, 4 and 6 and therefore corresponds with the results of phylogenetic ANOVA for groups 1, 2 and 5. The only consistent result across all analyses was group 2, the foraging niches of land birds, which indicated non-significance ($p < 0.05$).

4. Discussion

The present study has shown that adaptations in feather microstructure and body surface area in contact with water that bring about a reduction in viscous and frictional drag while swimming increase according to the bird's intimacy with open water. Swimming and diving birds, such as penguins and grebes, benefit the most from reduced viscous drag, more so than plungers such as gannets. Aerials such as terns even less so, but much more than herbivore surface feeders such as ducks.

The body feathers of ducks, in turn, appear to be better adapted to their watery habitat than those of aquatic ground feeders such as herons or kingfishers. The single herbivore aquatic ground feeder in this study, the Spotted Dikkop, is a bird of open scrubby habitat with comparatively little interaction with open water. Its drag coefficient is more in line with those of land birds in which adaptations to locomotion in water are not expected to have evolved.

Land birds do not only show drag coefficients higher than those of water birds, they also show no significant difference among the two foraging niches examined in this study. This is in line with expectation as their lack of interaction with open water and their locomotion in air only suggest that forces that foster reduced drag in water have been absent in their evolutionary history.

Of the three methods of statistical analyses, the phy-ANOVA test shows us that allowing for phylogenetic relatedness negates any differences among feather microstructure that may exist. Only for land birds would non-significance be expected. There is no doubt that group aggregation among the 48 water bird species is quite strong which detracts from the reliability of our positive and negative findings. Adding more species to the study or identifying more foraging niches could, statistically speaking, affect the results either way depending on numbers of species and their phylogenetic relatedness. Alternatively, it could be argued that relatedness is not necessarily a force that would make the evolution of an isolated trait impossible. Several examples support this notion. For instance, the Flightless cormorant (*Phalacrocorax harrisi*) is undoubtedly closely related to all other cormorants, yet a small change in the diameter and spacing of its barbs has rendered the bird better adapted to its bottom feeding habits than other cormorants are. The contour feathers of Brown pelicans (*Pelecanus occidentalis)* that, unlike their congeners, dive from the air to procure their prey, are more water repellent than those of other pelicans that catch their fish while swimming. Similar considerations apply to the differences in the contour feathers of dippers (*Cinclidae*) [6].

As argued above, a conventional statistical test while avoiding the condition of equal sample size and variance among populations, may the more suitable. Following this line of thought, the non-parametric variety of analysis would show that among group 1 consisting of all 48 aquatic birds, no significance is apparent, but when compared to land birds, it is. Subdividing into swimmers and waders shows comparison of the first group with land birds to be significant whereas that of waders with land birds is not. However, comparison between swimmers and waders is significant again indicating that, in terms of feather microstructure, waders stand between swimmers and land birds, but closer to land birds. This interpretation is entirely plausible, particularly if we assume that water birds have evolved from land birds.

In summary, the length-to-width ratio of the dorsal aspect of the distal one-third of abdominal feathers, the part that is in contact with water in aquatic birds, varies with the extent of interaction with open water as formulated by our hypothesis. This ratio and the total drag coefficient, composed of viscous pressure and frictional drag and calculated from Reynolds-averaged Navier–Stokes equations, are lowest for swimming and diving birds and increase for birds with less intimacy with open water. The highest values were found for land birds that have no open water in their habitat.

Due to the limited number of foraging niches and close phylogenetic relatedness among water bird families, statistically significant differences among water birds was not observed if allowance for phylogeny was made. However, using conventional statistical tests, in particular the non-parametric variety that does not assume conditions of equal sample size and variance, did show significant results when comparing water birds with land birds, swimming birds with land birds and swimming birds with waders, but not waders with land birds. This finding suggests, in terms of feather microstructure, a closer evolutionary relationship between waders and land birds than between waders and swimmers. In line with expectation, land birds showed no significant differences in their contour feather geometry that could be related to interaction with open water.

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Section 3

Abundances and Distribution

Chapter 4

Seabirds of the Benguela Ecosystem: Utilisation, Long-Term Changes and Challenges

Azwianewi B. Makhado, Rodney Braby, Bruce M. Dyer, Jessica Kemper, Alistair M. McInnes, Desmond Tom and Robert J.M. Crawford

Abstract

The Benguela Current is used by c. 82 seabird species, of which seven are endemic to it. Eggs and guano of formerly abundant seabirds were heavily harvested in the 19th and 20th centuries but decreases in seabird populations led to cessation of these industries at islands. Guano is still scraped from platforms. Seabird ecotourism has grown. There were large recent decreases in numbers of African Penguins *Spheniscus demersus*, Cape Gannets *Morus capensis* and Cape *Phalacrocorax capensis* and Bank *P. neglectus* Cormorants and redistributions of these other species away from the centre of the Benguela ecosystem towards its northern or eastern boundaries. In 2020, seabirds endemic to the Benguela ecosystem and albatrosses and petrels migrating into it had high proportions of globally Near Threatened or Threatened species. The primary threat to four Endangered endemic birds was scarcity of forage resources. A Vulnerable endemic damara tern was susceptible to habitat degradation and disturbance. The principal threat to visiting albatrosses and petrels was by-catch mortality. Identification and effective protection of Important Bird Area breeding and marine foraging and aggregation sites, and a suite of complementary measures, are needed to conserve the seabirds and ensure continuation of their economic and ecosystem benefits into the future.

Keywords: Benguela seabirds, conservation status, distributional changes, forage availability, guano, habitat degradation, long-term change, utilisation

1. Introduction

The Benguela Current Large Marine Ecosystem (BCLME) in the southeast Atlantic Ocean is one of the world's four major eastern boundary currents, which undergo intense upwelling of cool nutrient-rich waters that support high phytoplankton biomasses and abundant forage fish resources [1]. The forage fishes, in turn, are fed upon by numerous predators, including seabirds [2]. The BCLME ranges from approximately Benguela in southern Angola to Woody Cape at the eastern border of Algoa Bay in southern South Africa, being bounded in the north and east by the warm Angola and Agulhas currents, respectively (**Figure 1**).

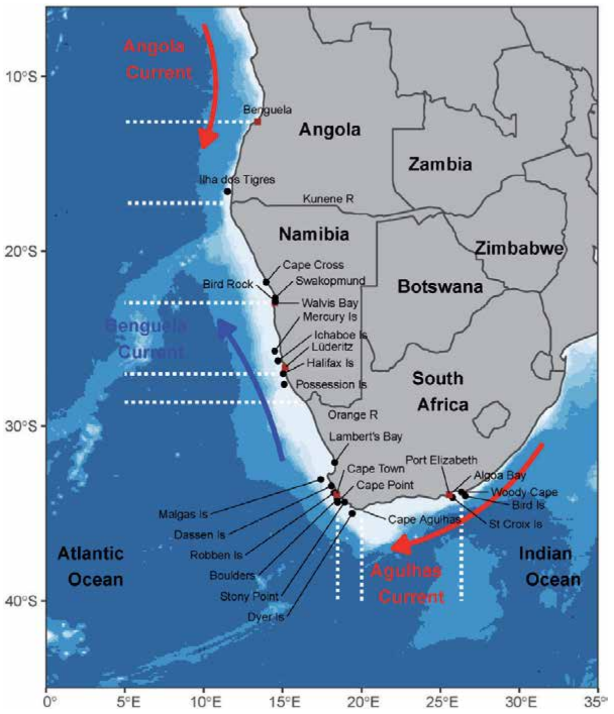

Figure 1.
A map of the Benguela ecosystem showing localities mentioned in the text. The dotted white lines demarcate the seven regions used to investigate distributional changes of seabirds and the guano they produced.

There are 16 species of seabird that breed within the BCLME. Additionally at least 4.4 million birds [3] of c. 66 other species (excluding rare vagrants) migrate to or through the BCLME (**Table 1**). Non-breeding migrants may remain within the BCLME year round.

Species	Common name	IUCN status	Population trend
Aptenodytes patagonicus	King Penguin	Least Concern	Increasing
Ardenna carneipes	Flesh-footed Shearwater	Near Threatened	Decreasing
Ardenna gravis	Great Shearwater	Least Concern	Stable
Ardenna grisea	Sooty Shearwater	Near Threatened	Decreasing
Bulweria bulwerii	Bulwer's Petrel	Least Concern	Stable
Calonectris borealis	Cory's Shearwater	Least Concern	Unknown
Calonectris diomedea	Scopoli's Shearwater	Least Concern	Decreasing
Catharacta antarctica	Brown (Subantarctic) Skua	Least Concern	Decreasing
Catharacta maccormicki	South Polar Skua	Least Concern	Stable
Daption capense	Cape (Pintado) Petrel	Least Concern	Stable
Diomedea amsterdamensis	Amsterdam Albatross	Endangered	Increasing
Diomedea dabbenena	Tristan Albatross	Critically Endangered	Decreasing
Diomedea epomophora	Southern Royal Albatross	Vulnerable	Stable
Diomedea exulans	Wandering Albatross	Vulnerable	Decreasing

Species	Common name	IUCN status	Population trend
Diomedea sanfordi	Northern Royal Albatross	Endangered	Decreasing
Eudyptes chrysocome	Southern Rockhopper Penguin	Vulnerable	Decreasing
Eudyptes chrysolophus	Macaroni Penguin	Vulnerable	Decreasing
Eudyptes moseleyi	Northern Rockhopper Penguin	Endangered	Decreasing
Fregetta grallaria	White-bellied Storm-Petrel	Least Concern	Decreasing
Fregetta tropica	Black-bellied Storm-Petrel	Least Concern	Decreasing
Gelochelidon nilotica	Common Gull-billed Tern	Least Concern	Decreasing
Hydobates leucorous (Oceanodroma leucorhoa)	Leach's Storm-Petrel	Vulnerable	Decreasing
Hydrobates pelagicus	European Storm-Petrel	Least Concern	Unknown
Hydroprogne caspia	Caspian Tern	Least Concern	Increasing
Larus cirrocephalus	Grey-headed Gull	Least Concern	Stable
Larus dominicanus vetula	Kelp Gull	Least Concern	Increasing
Larus hartlaubii	Hartlaub's Gull	Least Concern	Increasing
Larus pipixcan	Franklin's Gull	Least Concern	Increasing
Larus ridibundus	Common Black-headed Gull	Least Concern	Unknown
Lugensa brevirostris	Kerguelen Petrel	Least Concern	Decreasing
Macronectes giganteus	Southern Giant-Petrel	Least Concern	Increasing
Macronectes halli	Northern Giant-Petrel	Least Concern	Increasing
Microcarbo coronatus	Crowned Cormorant	Near Threatened	Stable
Morus capensis	Cape Gannet	Endangered	Decreasing
Morus serrator	Australian Gannet	Least Concern	Increasing
Oceanites oceanicus	Wilson's Storm-Petrel	Least Concern	Stable
Onychoprion (Sterna) fuscatus	Sooty Tern	Least Concern	Unknown
Pachyptila belcheri	Slender-billed Prion	Least Concern	Stable
Pachyptila desolata	Antarctic Prion	Least Concern	Decreasing
Pachyptila salvini	Salvin's Prion	Least Concern	Stable
Pelagodroma marina	White-faced Storm-Petrel	Least Concern	Decreasing
Pelecanus onocrotalus	Great White Pelican	Least Concern	Unknown
Phaethon aethereus	Red-billed Tropicbird	Least Concern	Decreasing
Phaethon lepturus	White-tailed Tropicbird	Least Concern	Decreasing
Phaethon rubricauda	Red-tailed Tropicbird	Least Concern	Stable
Phalacrocorax capensis	Cape Cormorant	Endangered	Decreasing
Phalacrocorax lucidus	White-breasted Cormorant	Least Concern	Unknown

Species	**Common name**	**IUCN status**	**Population trend**
Phalacrocorax neglectus	Bank Cormorant	Endangered	Decreasing
Phalaropus fulicarius	Red (Grey) Phalarope	Least Concern	Unknown
Phalaropus lobatus	Red-necked Phalarope	Least Concern	Decreasing
Phoebetria fusca	Sooty Albatross	Endangered	Decreasing
Phoebetria palpebrata	Light-mantled Albatross	Near Threatened	Decreasing
Procellaria aequinoctialis	White-chinned Petrel	Vulnerable	Decreasing
Procellaria cinerea	Grey Petrel	Near Threatened	Decreasing
Procellaria conspicillata	Spectacled Petrel	Vulnerable	Increasing
Pterodroma incerta	Atlantic Petrel	Endangered	Decreasing
Pterodroma macroptera	Great-winged Petrel	Least Concern	Decreasing
Pterodroma mollis	Soft-plumaged Petrel	Least Concern	Stable
Puffinus assimilis	Little Shearwater	Least Concern	Decreasing
Puffinus puffinus	Manx Shearwater	Least Concern	Unknown
Spheniscus demersus	African Penguin	Endangered	Decreasing
Stercorarius longicaudus	Long-tailed Jaeger	Least Concern	Stable
Stercorarius parasiticus	Arctic (Parasitic) Jaeger	Least Concern	Stable
Stercorarius pomarinus	Pomarine Jaeger	Least Concern	Stable
Sterna albifrons	Little Tern	Least Concern	Decreasing
Sterna dougallii	Roseate Tern	Least Concern	Unknown
Sterna hirundo	Common Tern	Least Concern	Unknown
Sterna paradisaea	Arctic Tern	Least Concern	Decreasing
Sterna vittata	Antarctic Tern	Least Concern	Unknown
Sternula balaenarum	Damara Tern	Vulnerable	Decreasing
Sula leucogaster	Brown Booby	Least Concern	Decreasing
Sula sula	Red-footed Booby	Least Concern	Decreasing
Thalassarche carteri	Indian Yellow-nosed Albatross	Endangered	Decreasing
Thalassarche cauta	Shy Albatross	Near Threatened	Unknown
Thalassarche chlororhynchos	Atlantic Yellow-nosed Albatross	Endangered	Decreasing
Thalassarche chrysostoma	Grey-headed Albatross	Endangered	Decreasing
Thalassarche melanophrys	Black-browed Albatross	Least Concern	Increasing
Thalassarche salvini	Salvin's Albatross	Vulnerable	Unknown
Thalasseus b. bergii	Greater Crested (Swift) Tern	Least Concern	Stable
Thalasseus maximus	Royal Tern	Least Concern	Stable
Thalasseus sandvicensis	Sandwich Tern	Least Concern	Stable
Xema (Larus) sabini	Sabine's Gull	Least Concern	Stable

Table 1.
The conservation status of seabirds that occur in the BCLME (rare vagrants have been excluded). Where known, the recent global population trend is indicated [4]. Information is sorted on genus and then species. Grey shading indicates species or races that breed only in the BCLME. The Royal Tern occurring in the BCLME has recently been reclassified as the West African Crested Tern Thalasseus albididorsalis.

This chapter summarises the former and present utilisation of the BCLME's seabirds and their products, changes in their distribution and abundance, their conservation status and factors influencing it, and future challenges if healthy seabird populations and their benefits are to be maintained. In order to investigate distributional changes, the BCLME was divided into seven regions: southern Angola, northern, central and southern Namibia, and western, southwestern and southern South Africa, as indicated on **Figure 1**.

2. Utilisation

2.1 Penguin eggs

From the late 1400s, African Penguins *Spheniscus demersus* and other seabirds in the BCLME were caught as food by early explorers, as fuel to supply ship boilers and to be rendered down for their fat [5, 6]. However, the primary attraction of African Penguins was their eggs. Collection of these on a large scale may have begun as early as 1652 [7]. Details of numbers of eggs collected at different breeding localities are available for each year from 1871–1967 (after which collections ceased) with gaps from 1879–1890, 1894–1896 and in 1904 and 1914 [7].

Annual collections averaged c. 192,000 eggs from 1871–1878, c. 537,000 eggs from 1891–1931 and c. 76,000 eggs from 1935–1967 (**Figure 2**). The overall harvest for the 80 years between 1871 and 1967 for which records were kept was c. 23.4 million eggs, with a maximum of 801,500 eggs in 1899. About 99% of the eggs were taken off western South Africa (84% from Dassen Island), with small proportions coming from southern Namibia (< 1%) and southwestern South Africa (c. 1%). Although ease of access to colonies and of gathering eggs would have influenced localities selected for collections, their geographical distribution approximated that of African Penguins at the time. In the early 1900s, Dassen Island off western South Africa was the largest colony holding an estimated 0.57–0.93 million breeding pairs between 1910 and 1930 [8, 9]. In 1956, no African Penguins bred in Angola or northern Namibia. The proportions then breeding in central and southern Namibia and in western, southwestern and southern South Africa were 5%, 25%, 62%, 3% and 5%, respectively [10].

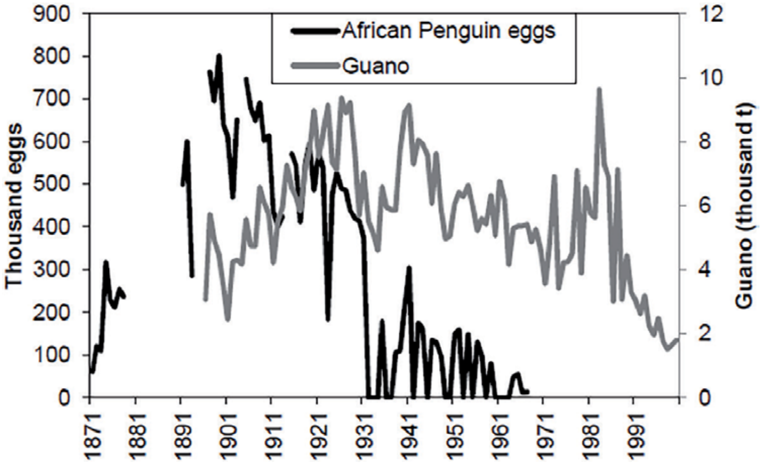

Figure 2.
Trends in total collections of African Penguin eggs and seabird guano in the BCLME, 1871–1999.

At Dassen Island, c. 48% of penguin eggs produced in the early 20th century were collected; this was unsustainable and led to an estimated decrease in the number of penguins there aged two years or older, from c. 1.45 million in 2010 to c. 0.22 million in 1956 and 0.14 million in 1967 [8].

2.2 Guano

In the 1840s, after the value of guano as an agricultural fertilizer became known, accumulated deposits of seabird guano were stripped from many southern African islands [11]. Then, from the late 1800s until the mid-1980s or early 1990s, fresh deposits of seabird guano were regularly collected at a number of islands off Namibia and South Africa. At Ichaboe Island in central Namibia sporadic guano extraction persisted until 2016. From 1896, annual records of quantities removed from different islands were maintained [12]. Most of the guano extracted from the islands was produced by Cape Gannets *Morus capensis* and Cape Cormorants *Phalacrocorax capensis*. Phosphatic sand was at times removed from African Penguin breeding areas at Dassen Island to mix with guano or to spread over breeding areas of Cape Gannets, which build their nests from guano [13]. In southern Africa, the African Penguin, Cape Gannet and Cape Cormorant became known as the 'guano-producing' seabirds, although other cormorants and Great White Pelicans *Pelecanus onocrotalus* would have contributed small amounts to guano depositions at some localities. Between 1930 and 1971 platforms were constructed by private entrepreneurs to collect guano at Bird Rock, Swakopmund and Cape Cross on the northern Namibian coast, which was mainly produced by Cape Cormorants [14]. Annual records of quantities taken from each platform were maintained [15]. Between 1900 and 1999, an average of c. 5,700 t of seabird guano (after subtraction of additions of phosphatic sand) was extracted annually in the BCLME, with a maximum of c. 9,600 t and a minimum of c. 1,500 t (**Figure 2**).

Guano extraction sometimes displaced or caused disturbance to seabirds, reducing breeding success [16]. It also created hollows on some islands, allowing rain to accumulate, which on occasion flooded nests of some seabird species and also reduced breeding success [17].

2.3 Tourism

Seabird tourism is a rapidly expanding industry in the BCLME. In South Africa, Boulders at Simon's Town, Stony Point at Betty's Bay and Robben Island provide opportunities for the public to observe African Penguins and other seabirds in their natural habitat and have become popular tourist destinations that generate socio-economic gains through gate fees, provision of jobs and benefits to surrounding areas [18]. For example, Boulders provided 885 jobs directly associated with its penguin colony and expenditure related to the colony was approximately ZAR 311 million [19]. It contributed to the overall branding of Cape Town as a popular destination for international visitors [18]. The Stony Point penguin colony received an average of 77,500 visitors p. a. from 2010–2019 [20]. The Cape Gannet colony at Lambert's Bay is an important source of revenue for that community [20]. Land tours to view breeding and roosting seabirds operate in Namibia, e.g. [21]. Boat-based seabird viewing operates out of several southern African ports, including around the largest African Penguin colony at St Croix Island [20].

It was estimated that seabird tourism contributed c. ZAR 500 million to the South African economy in 2020 [20].

3. Long-term changes in distribution and abundance

3.1 Guano

Production of guano at the platforms in northern Namibia commenced in the 1930s when the average yield was c. 450 t p.a.; it then increased to a peak of c. 3,350 t in the 1980s before a decrease in the 1990s. By contrast, yields in central and southern Namibia and western South Africa peaked in the 1920s at c. 3,500 t, 1,900 t and 2,300 t p.a., respectively, and then decreased. In southwestern South Africa, production peaked at c. 400 t p.a. in the 1910s and then decreased. In southern South Africa it increased from c. 120 t p.a. in the 1890s to an average of c. 340 t p.a. between the 1920s and 1980s (**Figure 3**). Hence, there were long-term increases in guano yields in northern Namibia and southern South Africa but

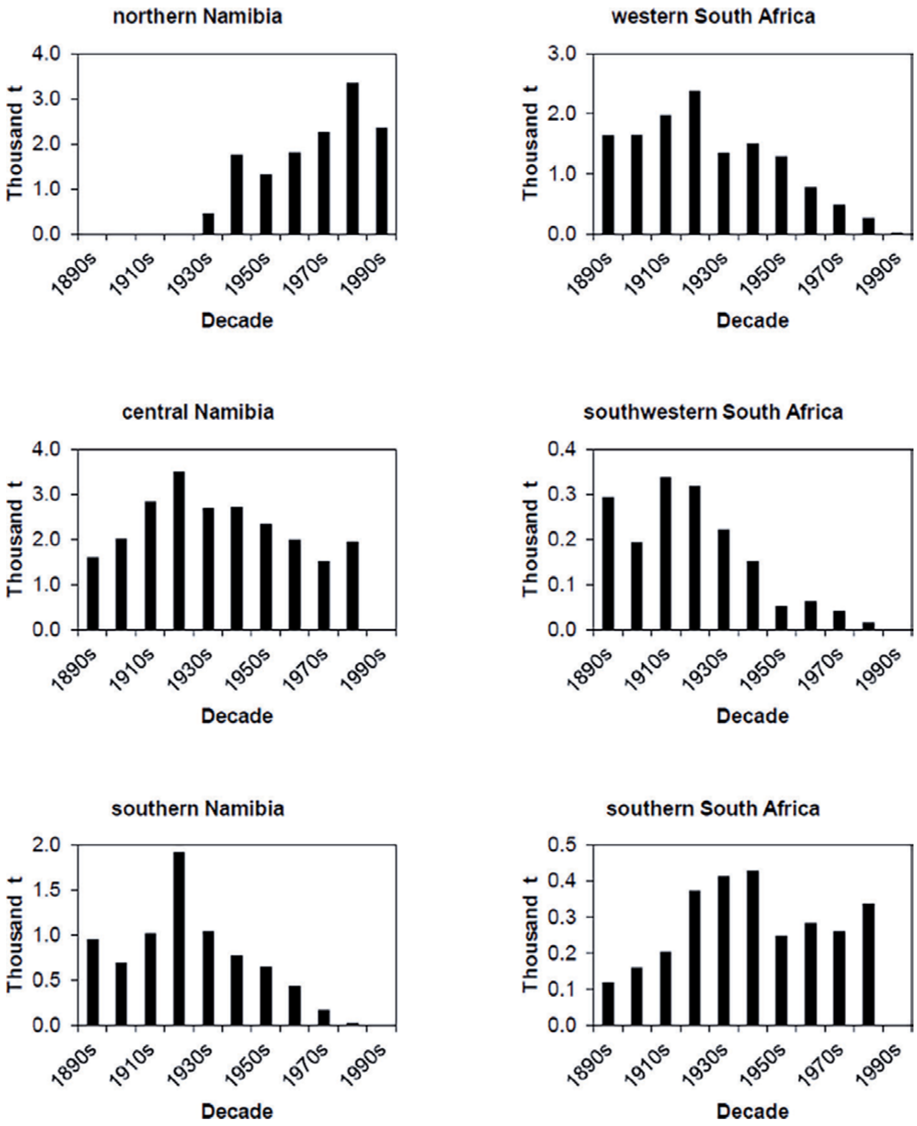

Figure 3.
Average collections of seabird guano in six regions of the BCLME over 11 decades, 1890s–1990s.

decreases in the four intervening regions. The trends after the 1920s accord with the provision of nesting habitat for cormorants in the north, and with decreases of Cape Cormorants in central and southern Namibia after the 1970s and in western South Africa after the 1980s [15, 22]. They also match decreases of Cape Gannets at colonies in Namibia after the 1950s and in western South Africa after the 1990s, but an increase in the Cape Gannet colony at Bird Island, Algoa Bay in southern South Africa [23]. Guano extraction at islands was gradually halted to minimize its adverse impacts on dwindling seabird colonies [24].

3.2 'Guano-producing' seabirds

Average numbers of the BCLME's three 'guano-producing' seabirds that bred in each of the selected regions were determined for seven decades from the 1950s to the 2010s. Information was collated from [25, 26] for African Penguins, [23] for Cape Gannets and [15, 22, 27, 28] for Cape Cormorants. Unpublished data held by the Benguela Current Convention (BCC) were also utilized. Methods used to estimate numbers of breeding birds are described in the afore-mentioned sources. Aerial photography was frequently applied for large surface-nesting colonies of the three seabird species, whereas ground surveys were employed for smaller colonies or when nests were on cliffs, under boulders or vegetation, or in burrows.

For all decades, averages were obtained for each breeding locality and summed for all localities in a region. In the 1960s, there was no reliable information on numbers of African Penguins that bred in South Africa or on numbers of Cape Cormorants that bred in Namibia and southern South Africa, so these values were interpolated from information for the 1950s and 1970s. Various small colonies of African Penguins and Cape Cormorants were not counted in all decades. However, except as detailed above, reliable estimates were available for all major colonies and the absence of information for some minor colonies is not expected meaningfully to influence the trends that are shown in **Figure 4**.

In the period under consideration, no African Penguins bred in southern Angola or northern Namibia. Cape Gannets only bred at Mercury and Ichaboe islands in central Namibia, Possession Island in southern Namibia, Lambert's Bay and Malgas islands in western South Africa and Bird Island, Algoa Bay in southern South Africa. Cape Cormorants bred in all seven regions.

Estimates of the number of Cape Cormorants breeding in northern Namibia increased between the 1950s and the 1970s, when there were c. 75,000 pairs, and then decreased. Cape Cormorants were first recorded breeding in southern Angola in the 2000s and c. 16,000 pairs bred there in 2017 [28]. About 40,000 pairs bred in southern Angola and northern Namibia between the 1980s and 2010s (**Figure 4**). In the 1950s, central and southern Namibia held c. 200,000 and c. 50,000 pairs of 'guano-producing' seabirds, respectively. By the 2010s, the average numbers breeding had decreased in central Namibia by c. 85% and in southern Namibia by c. 95%. There were large decreases of African Penguins and Cape Gannets in both these regions (**Figure 4**).

In western South Africa, average numbers of the 'guano-producing' seabirds fell by c. 75% from c. 200,000 pairs in the 1950s to c. 50,000 pairs in the 2010s. As in central and southern Namibia, there were large losses of African Penguins. There also was a severe decrease of Cape Cormorants (**Figure 4**). In southwestern South Africa, average numbers of the 'guano-producing' seabirds increased from c. 7,500 pairs in the 1950s to c. 60,000 pairs in the 1970s, as a result of increases of both African Penguins and Cape Cormorants. Numbers then decreased to an average of c. 30,000 pairs in the 2010s, following a large decrease in African Penguins after the 1970s (**Figure 4**). In southern South Africa, average numbers of the

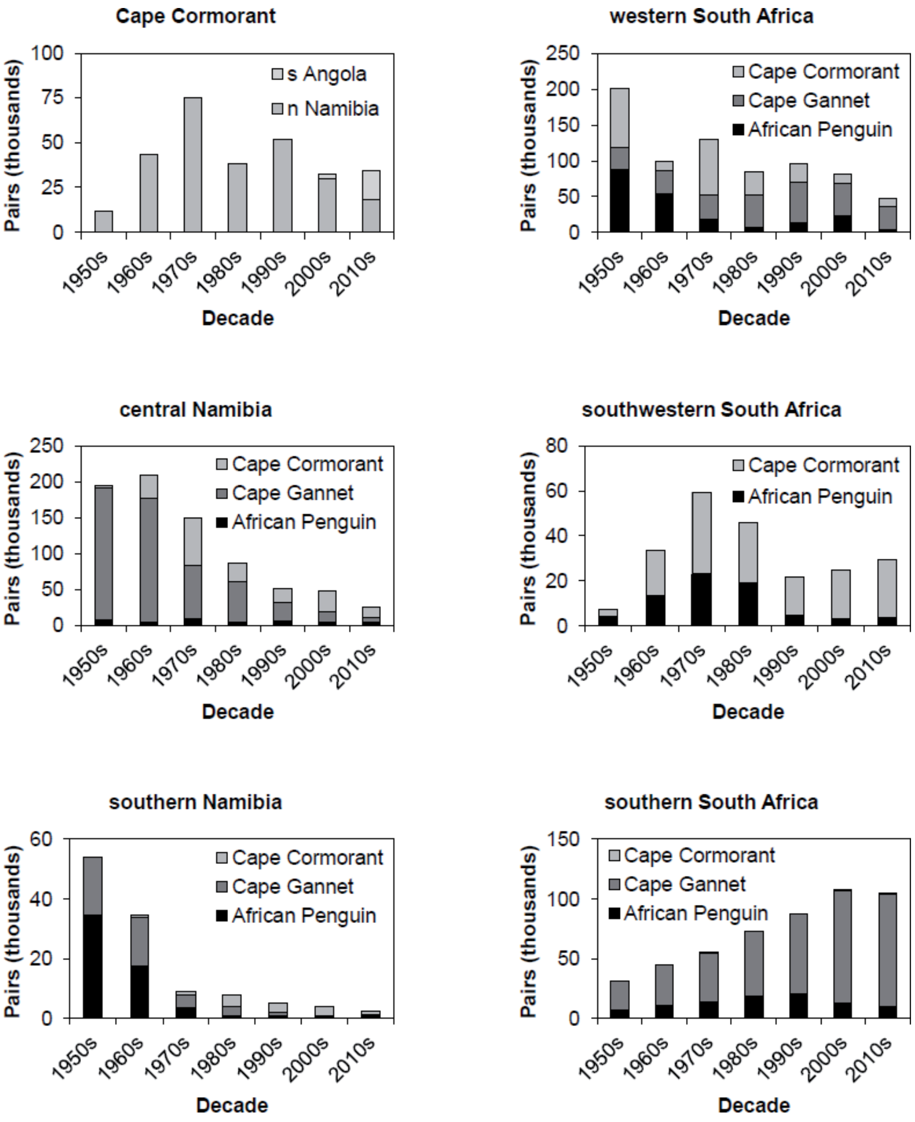

Figure 4.
Average estimates of breeding pairs of African Penguins, Cape Gannets and Cape Cormorants in seven regions of the BCLME over seven decades, 1950s–2010s. Of these species, only Cape Cormorants bred in the northernmost two regions where average numbers breeding are shown in the top left box.

'guano-producing' seabirds trebled from c. 30,000 pairs in the 1950s to >100,000 pairs in the 2000s and 2010s, primarily as a result of a large increase in the number of Cape Gannets (**Figure 4**).

In summary, in the BCLME between the 1950s and 2010s there were substantial increases in numbers of Cape Cormorants in northern regions and of Cape Cormorants and Cape Gannets in southern regions, but large decreases of these two species and of African Penguins in central regions. Construction of platforms in northern Namibia facilitated a northern expansion of Cape Cormorants and the species also colonized Ilha dos Tigres in southern Angola [28]. Cape Cormorants likewise established several new colonies in the south, both at islands and mainland localities [22]. Cape Gannets were unsuccessful in attempts to form new colonies, but greatly enlarged their southernmost colony at Bird Island in Algoa Bay [23]. African Penguins formed three new colonies in the south and attempted to initiate another southern colony, but were unable to offset huge decreases at central colonies [25]. The average numbers of the three 'guano-producing' seabirds taken together fell by 50% from c. 500,000 pairs in the 1950s to c. 250,000 pairs in the 2010s. Over the same period, average numbers for African Penguins decreased by c. 84% from c. 141,000 pairs to c. 23,000 pairs and for Cape Gannets by c. 49% from c. 259,000 pairs to c. 133,000 pairs. Average numbers for Cape Cormorants increased from c. 100,000 pairs in the 1950s to c. 250,000 pairs in the 1970s [15] and then decreased to c. 91,000 pairs in the 2010s.

3.3 Other seabirds

In South Africa, in addition to shifts to the south and east of the three 'guano-producing' seabirds reported in the previous section, there were decreased proportions of birds breeding in the north and increases in the south for Bank Cormorant *P. neglectus*, White-breasted Cormorant *P. lucidus*, Crowned Cormorant *Microcarbo coronatus*, Kelp Gull *Larus dominicanus*, Greater Crested (Swift) Tern *Thalasseus bergii* and Damara Tern *Sternula balaenarum* [29–35]. There is little or no competition by White-breasted and Crowned Cormorants, Kelp Gulls and Damara Terns with fisheries for forage resources [36], so environmental change may have influenced the redistributions of the seabirds [33].

In Namibia, in addition to the northward expansion of Cape Cormorants mentioned above, the proportion of Bank Cormorants that bred north of Ichaboe Island increased from 28% in 1995–1997 [37] to 84% in 2010 [38].

Overall there were large decreases in Bank Cormorants after the 1970s [30, 38]. In South Africa there were also decreases of Damara Terns after the 1990s [34] but populations of the other four seabirds showed stability or increased [33].

3.4 Other biota

Off South Africa, in the 1990s and 2000s there were shifts to the south and east in the distributions of three important forage resources heavily exploited by commercial fisheries: Cape rock lobster *Jasus lalandii* [39], anchovy *Engraulis encrasicolus* [40] and sardine *Sardinops sagax* [41]. The shifts may have been influenced by localised overfishing [39, 41] and environmental change [40, 42]. At the same time, an increased contribution of bearded goby *Sufflogobius bibarbatus* to the diet of Bank Cormorants off western South Africa suggested a southward expansion of the Namibian stock of this fish species [43]. When Namibia's sardine stock collapsed in the 1960s, its range contracted to the north [44] and it was largely replaced by bearded goby, jellyfish and possibly Cape horse mackerel *Trachurus capensis* [45, 46].

4. Conservation and management

4.1 Conservation status

The conservation status of the 82 seabirds that breed in or visit the BCLME was assessed in 2018 or 2019 by the International Union for Conservation of Nature (IUCN) and is shown in **Table 1**, along with the species' population trends [4]. Sixteen seabird species breed in the BCLME, of which seven are endemic to it and for two others the local races are endemic (**Table 1**). All nine endemic taxa and three wider-ranging species (Leach's Storm Petrel *Hydobates leucorous*, Australian Gannet *M. serrator* and Roseate Tern *Sterna dougallii*) breed only along the coastline, whereas the other four non-endemic species (Great White Pelican, White-breasted Cormorant, Grey-headed Gull *L. cirrocephalus* and Caspian Tern *Hydroprogne caspia*) also breed at suitable inland localities. Four of the endemic seabirds feed to a large extent on forage resources that are targeted by commercial fisheries: African Penguin, Cape Gannet and Cape Cormorant on sardine and anchovy; Bank Cormorant on rock lobster [36]. Food scarcity was a major driver of recent large decreases of these species [24], which led to all being listed by the IUCN as Endangered (EN) [47]. The other three endemic seabirds do not compete with fisheries for prey. The Crowned Cormorant population was stable but relatively small and is currently listed as Near Threatened (NT) [47], whereas Damara Tern decreased on account of disturbance at, or loss of, breeding habitat and is currently listed as Vulnerable (VU) [47–49]. The loss of breeding habitat also influenced other Benguela seabirds [24]. In 2020, Hartlaub's Gull (endemic to the BCLME) and the wider-ranging Great White Pelican, Australian Gannet, which in the BCLME hybridises with Cape Gannet [6], White-breasted Cormorant, Kelp and Grey-headed gulls, Greater Crested, Roseate and Caspian terns were globally Least Concern (LC); Leach's Storm Petrel, which mainly breeds in the northern hemisphere and has decreased, was VU [47]. However, in South Africa the small and isolated populations of Leach's Storm Petrel (c. 5 pairs) and Roseate Tern (c. 125 pairs) were regarded as Critically Endangered (CR) and EN, respectively, and the small populations of Great White Pelican (c. 2,500 pairs) and Caspian Tern (c. 310 pairs) as VU [50]. Leach's Storm Petrel and Roseate Tern have not been recorded breeding in Angola or Namibia. In 2020, six of the seven seabirds endemic to the BCLME were EN, VU or NT. Of the other nine species that breed in the BCLME, globally one was VU but regionally four were CR, EN or VU.

The 66 seabird species that migrate to the BCLME are made up of four penguins, 13 albatrosses, three prions, 18 petrels and shearwaters, five storm petrels, three tropicbirds, two boobies, two phalaropes, five skuas or jaegers, three gulls and eight terns. One pair of one of the terns (Sandwich *T. sandvicensis*) bred at Halifax Island in 2014 [51]. Three *Eudyptes* penguins were classified as EN or VU (**Table 1**). However, threats to these penguins occur mainly outside the BCLME [47]. In 2020, the Tristan Albatross *Diomedea dabbenena* was CR and the Amsterdam *D. amsterdamensis*, Northern Royal *D. sanfordi*, Sooty *Phoebetria fusca*, Atlantic Yellow-nosed *Thalassarche chlororhynchos*, Indian Yellow-nosed *T. carteri* and Grey-headed *T. chrysostoma* albatrosses were all EN. Three of the other albatrosses were VU and two were NT. The Atlantic Petrel *Pterodroma incerta* was EN, all three *Procellaria* petrels were VU or NT and two *Ardenna* shearwaters were NT. All the other migrant seabirds were LC (**Table 1**). Incidental by-catch in fisheries was a major cause of mortality and a driver of population decreases for several albatrosses and large petrels [52, 53] and is the main at-sea threat faced by such species in the BCLME [54–57]. The introduction of invasive mammal predators, such as mice, on sub-Antarctic islands, e.g. Marion and Gough islands, has had a significant impact on populations of some albatrosses and petrels that visit the BCLME, e.g. [58].

4.2 Conservation challenges

Amongst challenges facing seabirds that breed in the BCLME are geographical shifts of forage resources that led to mismatches in the distributions of the birds' breeding localities and their prey and, as a consequence, to reduced sizes of many colonies and, in instances, to one or a few localities holding large proportions of certain species' populations.

Small colonies may suffer from Allee effects, or inverse density dependence, which increase their chances of extinction [59]. For example, African Penguins that feed in groups have a greater catch per unit effort than solitary birds [60], but diminishing colonies may become too small for sufficient foraging groups to form [59]. Dwindling colonies also mean that higher proportions of birds nest near colony edges, where eggs and chicks are at a greater risk of predation [61]. Amongst African Penguins taken to a rescue centre, females had higher mortality rates than males [62]. If a similar sex-biased mortality exists in the wild, it may skew sex ratios at small colonies. Empirical information on the performance of 41 discrete colonies of African Penguins showed that only one of 28 colonies that had fewer than 250 pairs survived for 40 years, compared to 50% of colonies with 500–1,000 pairs, 67% of those having 1,000–5,000 pairs and all larger colonies [63]. This makes it imperative to maintain colonies at sizes sufficient to have reasonable longevity.

In 2010, Mercury Island held 72% of the global population of Bank Cormorants [38] and 73% of Namibia's African Penguins [25]. In 2018, c.70% of the Cape Gannet population was at Bird Island, Algoa Bay at the eastern boundary of the BCLME [23]. In the 2010s, 54% of South Africa's Cape Cormorants bred at Dyer Island [22]. Such congregations of large proportions of a species at a single locality may offset Allee effects but render the species highly susceptible to local catastrophic events such as oil spills [64].

As indicated above, major threats to seabirds that breed in the BCLME include food scarcity, which has resulted from altered distributions of prey and overfishing, and disturbance at, or a loss of, breeding habitat. At a global perspective, a priority identified for seabird conservation was effective protection of Important Bird Area (IBA) breeding and marine IBA feeding and aggregation sites, as part of networks of Marine Protected Areas (MPAs) [52]. IBA and MPA initiatives should mitigate both the loss of breeding habitat [65] and food scarcity. Around African Penguin colonies commercial fishing of forage resources decreased numbers breeding [66], whereas closures to fishing reduced energetic costs of foraging [67] and improved chick condition and breeding success [68, 69]. Numbers of Bank Cormorants breeding showed a positive response to local availability of rock lobsters and modelling suggested that prohibition of commercial lobster catches around colonies would benefit this bird [70].

A second measure that could enhance food availability is the identification and implementation of thresholds (below which fishing would be disallowed) of forage fish abundance (or availability) that are necessary to maintain adequate reproduction and survival of dependent predators [71–73]. In addition to abundance and availability of food, quality of prey is an important consideration if energetic requirements of seabirds are to be met [43, 74, 75]. A third means to achieve sufficient food is to offset mismatches in the distributions of breeding localities and prey of seabirds through the establishment of colonies nearer to the food supply. Guano platforms in Namibia served this purpose for Cape Cormorants and an attempt to establish a new African Penguin colony in South Africa has been initiated [76].

Other threats to seabirds that breed in the BCLME include competition for breeding space [77] and high mortality from predation [78], disease [79, 80] and pollution [81]. Marine developments and operations, such as ship-to-ship bunkering, finfish aquaculture and proposed offshore windfarms, are emerging as further threats to the BCLME's breeding seabirds. Given that 63% of these seabirds are globally or regionally CR, EN, VU or NT, it will be necessary to control all factors impacting their populations.

A second priority identified for seabird conservation at a global scale was reduction of by-catch to negligible levels [52, 53]. Substantial strides have been made in mitigating seabird by-catch in South African and Namibian fisheries [54–57]. South Africa has recently committed to eradicate the house mouse *Mus muscullus* from Marion Island in 2023. If successful, this is likely to reduce losses of some albatrosses and petrels that visit the BCLME.

4.3 Ecosystem role

When breeding, seabirds are central-place foragers that bring large quantities of nutrients from the ocean to their colonies. This influences the functioning of island and headland ecosystems through increasing algal growth and changing the structure of intertidal communities, which in turn increases the population sizes of some shorebird species [82]. Inputs by seabirds of nitrogen (N) and phosphorus (P) are substantial, with concentrations per unit of surface area among the highest measured on the Earth's surface. Furthermore, an important fraction of the total excreted N and P is readily soluble, increasing the short-term bioavailability of these nutrients in coastal waters [83]. Not only do seabirds have such beneficial bottom-up impacts but they may exert valuable top-down control by removing substandard individuals, thus aiding long-term survival of prey populations [84]. Seabirds also facilitate feeding by other species; e.g. African Penguins herd prey shoals upwards making them available to birds restricted to feeding near the surface [85].

5. Conclusions

The productive waters of the Benguela upwelling system provide foraging opportunities for large numbers of seabirds, including 16 species that breed in the BCLME and c. 66 species that visit it.

In the 1800s and 1900s collections of penguin eggs took place over almost 100 years but proved unsustainable. Seabird guano was extracted over >100 years but purse-seine fisheries initiated after World War 2 depleted forage resources and led to decreases of guano-producing seabirds. Recently seabird ecotourism in the BCLME has been expanding.

After the 1950s guano production decreased in the central BCLME but increased in the north and was stable in the south until the cessation of extractions at islands. After the 1970s there were decreases of and shifts to the north or south in distributions of the three 'guano-producing' seabirds. There were similar redistributions of several other seabirds. The altered distributions likely resulted from both intensive fishing and environmental change.

The conservation status of seabirds breeding in the BCLME has deteriorated. Main threats to these species include food scarcity and loss of breeding habitat, which need to be controlled if socio-economic and ecosystem benefits of seabirds are to be maintained. Although fishery by-catch and invasive mammalian predators are important threats to several seabirds that visit the BLCME, South Africa and Namibia have taken steps to mitigate these.

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Conflict of interest

The authors have no conflict of interest to declare.

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Chapter 5

Avifauna in Relation to Habitat Disturbance in Wildlife Management Areas of the Ruvuma Miombo Ecosystem, Southern Tanzania

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Abstract

Understanding of relative distribution of avifauna provides insights for the conservation and management of wildlife in the community managed areas. This study examined relative diversity, abundance, and distribution of avifauna in selected habitat types across five Wildlife Management Areas of the Ruvuma landscape in miombo vegetation, southern Tanzania. Five habitat types were surveyed during the study: farmland, swamps, riverine forest, dense and open woodland. Transect lines, mist-netting, and point count methods were used to document 156 species of birds in the study sites. Descriptive statistics and Kruskal-Wallis tests were used to compare species richness and diversity across habitat types. We found differences in avifaunal species distribution in the study area whereby farmland had the highest abundance of avifauna species and lowest in the riverine forest. These results suggest that variations of avifauna species abundance, diversity, and distribution could be attributed by human activities across habitat types; due to the reason that habitats with less human encroachment had good species diversity and richness. Therefore, to improve avitourism and avoid local extinction of species, we urge for prompt action to mitigate species loss by creating awareness in the adjacent community through conservation education on the importance of protecting such biodiversity resources.

Keywords: Avifauna, diversity, conservation, habitat destruction, wildlife management areas, miombo

1. Introduction

The miombo ecosystems are known worldwide for their higher biodiversity [1, 2]. Woodlands in the miombo ecosystems are dominated by trees of the genera *Brachystegia*, *Julbernardia*, and *Isoberlinia* Leguminosae, subfamily Caesalpinioideae [1, 3]. The woodlands cover between 2.7 and 3.6 million km^2 in 11 African countries [2, 4–6]. In Tanzania, this vegetation type covers more than 90% of forested land

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[4, 7–10], and some of the miombo woodlands are found within several of the iconic protected areas including Selous Game Reserves and the Mikumi, Ruaha, Nyerere National Park as well as the Ruvuma Landscape in southern Tanzania. The ecological services it provides include: the provision of forage for wild and domestic animals, nesting sites for birds, water catchments, carbon sequestration, and biodiversity conservation in general and is archived due to the presence of habitat heterogeneity in particular flora diversity that exists in the miombo areas [3, 4].

Floral species compositions are a very important component to determine the distribution and diversity of avifauna communities [11]. Bird species diversity in savannah landscapes increases with an increase in vegetation/habitat heterogeneity in the miombo woodlands [5, 6]. In heterogeneous habitats, some avian species tend to show preference on certain habitat types, which also influence avifaunal diversity, abundance, and distribution across landscapes [7, 8, 12]. For example, miombo pied barbet (*Tricholaema frontata*), miombo rock thrush (*Monticola angolensis*), stierling's wren warbler (*Calamonastes stierlingi*), racket-tailed roller (*Coracias spatulatus*) and white-tailed blue-flycatcher (*Elminia albicauda*) prefer miombo woodland, only stierling's wren warbler and racket-tailed roller were observed during data collection other species listed here were not recorded during this study possibly due to habitat degradation.

The Ruvuma landscape in Tunduru District, in southern Tanzania encompasses five Wildlife Management Areas (WMAs) namely: Mbarang'andu, Kimbanda, and Kisungule in Namtumbo District, Nalika and Chingoli WMAs in Tunduru District (**Figure 1**). It borders the Selous Game Reserve and Nyerere National Park in the north and the Niassa National Reserve (Mozambique) to the south. The Ruvuma River forms an international boundary between Tanzania and Mozambique within Namtumbo and Tunduru districts [13]. The two protected areas rely on the presence of the five Wildlife Management Areas as they provide dispersal and movement area (corridor) to Niassa National Reserve in Mozambique and to Nyerere National Park. Habitat destruction by humans is a serious threat that alters the integrity of ecosystems [8], also affects vegetation cover. It is possible that human activities occurring in the miombo woodland resulted in land cover change [7, 9, 10, 14, 15]. Currently, the Wildlife Management Areas (WMAs) of the Ruvuma region in southern Tanzania undergo fragmentations caused by human activities which include uncontrolled wildfires, collection of fuel wood, charcoal, timber, illegal hunting, cattle grazing, and agriculture. In this area, communities have formulated the Wildlife Management Area (WMA), which is the form of community-based conservation which ensures villagers or communities rich in wildlife sustainably conserve, utilize and benefit from wildlife. Wildlife Management Areas are formed within village land from which villagers set aside a piece of land purposely for sustainable conservation and utilization of wildlife resources. The Tanzania government actualized WMAs for the local community to participate in wildlife management and conserve wildlife habitats in the communal land.

Apart from the study investigated on abundance, nesting and habitat of the white-browed sparrow-weaver (*Plocepasser mahali*) conducted by Ngongolo and Mtoka [16] no other study attempted to describe the diversity, abundance, and distribution of avifaunal species across the habitat gradient, and assess the implication of ongoing human activities to the conservation of avifauna species across the Ruvuma Landscape. This gives an opportunity to assess avifauna diversity and distribution in relation to habitat disturbance and how avifauna responded to this habitat destruction. Studying avifauna in Ruvuma landscape will open a room for avitourim activities and conserve from habitat degradation. Therefore, this chapter aimed at presenting the diversity of avifauna species in the Wildlife Management Areas in the Ruvuma Landscape in relation to human activities. It is predicted that

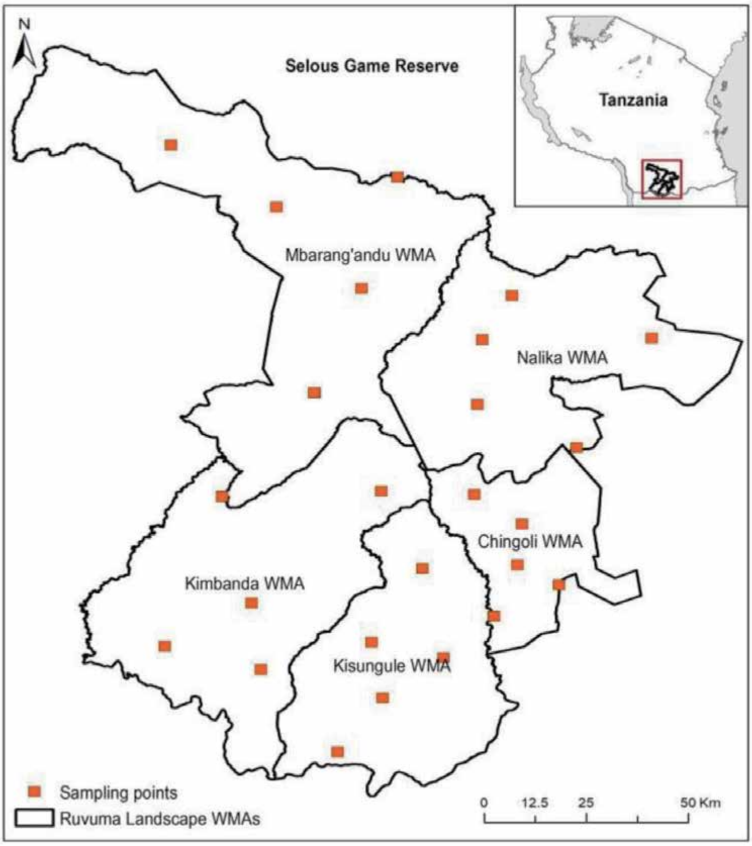

Figure 1.
Map of Ruvuma WMAs showing the location of the sampling sites.

avian species diversity and abundance would be higher in protected habitats inside WMA than in areas dominated by human activities namely farmlands.

In this study we treated the presence of farmlands in WMAs where they are not supposed to be as disturbance, because all WMAs in Tanzania have land use planning. The land use planning in all WMAs provides guidelines by zoning communal land where different activities can be conducted, such cattle grazing, settlements, farming and wildlife conservation area (tourist areas). All plots selected in this study were from wildlife conservation zones where also farms existed. Potential actions for intervention have been highlighted.

2. Methods and materials

2.1 Climate and vegetation types

The rainfall pattern is unimodal spanning from late November to May with a mean annual rainfall of 800–1200 mm in a north–south gradient. The mean annual temperature is 21°C, following the Köppen system [17]. The area consists of extensive miombo woodland, including *Brachystegia* sp., *Julbernardia* sp., *Isoberlinia* sp., *Afzelia quanzensis*, *Pterocarpus angolensis*, and rare and threatened plant species such as *Dalbergia melanoxylon,* which forms dense miombo along the hills and rivers [18]. Also, there are seasonal and permanent wetlands (swamps), riverine forests along numerous perennial and seasonal streams. Due to the increasing anthropogenic activities, the area currently has farmlands and patches of wooded with scattered trees and grazing land.

2.2 Sampling design

Five sites of 200 m x 200 m were established in each WMA, making a total of 25 sites. We selected different habitat types for each of the five sites, namely miombo woodland (open and dense), farmland, swamps, and riverine forest.

2.3 Avifauna survey

Each site was sampled using three complementary methods to maximize the sample size. First, in each habitat type, avifauna counts were carried out using the point transects technique [6, 19]. This method consists of standing at a particular point or walking slowly across the site back and forth several times, to detect cryptic and skulking species in the area. These counts were repeated for 3 days, based on results from our pilot study, and the numbers for each site were averaged. A 20-minute counting period was used at each site, and the starting time (between 6:30 and 10:30 h) was rotated among the sites to reduce bias. Avifauna was identified by both sight and call, and numbers were recorded [20].

Secondly, the transect method was used. Three transects 40 km in length each were established in every WMA using existing roads. The locations of all transects were based on accessibility and were sampled using a vehicle driven at a speed of 20 km/hr. or less that stopped for each individual or group of birds encountered [21]. Two observers sighted and recorded all avifauna on either side of the vehicle and notes on habitat type were also taken [21].

Thirdly, mist-netting was used to the targeted cryptic, understory, and lower canopy avian species. Nets were erected and checked every 15 min in the early morning (between 6:30–10:30 h) and late afternoon (between 16:00–18:00 h). The total number of each species caught, and the associated habitat type was recorded. Each bird was marked with a drop of red permanent spray paints at the base of its toes on the right tarsi for verification, if recaptured, to avoid double counting [22].

2.4 Statistical analysis

The biodiversity indices in different habitats or within these WMAs were obtained following Magurran [23]. This index uses three biodiversity indices including, diversity, richness, and abundance. A non-parametric Kruskal-Wallis test was used to assess whether there were significant differences in mean species abundance among five WMAs, and across each habitat type [24]. Differences in mean bird numbers between habitats in each WMA were tested using Mann–Whitney tests to assess whether the number of species was significantly lower in human-encroached habitat (farmland), i.e., farmland, compared to riverine forest, and dense and open miombo woodland habitats. Statistical tests were computed using the software package PAST [24]. For all these analyses, farmland habitat in this study represented human encroachment into protected areas and was used to compare with other habitat types found in the WMAs. We further calculated the Jaccard similarity index (Ji) between different habitat types to determine the level of similarities in species composition using the formulae [24]:

$$\text{Jaccard similarity coefficient (J)}; \mathrm{J} = \mathrm{A}/(\mathrm{A}+\mathrm{B}+\mathrm{C}) \qquad (1)$$

Where A = number of species found in both communities, B = number of species only found in community 1 and C = number of species found in community 2. The equation returns a number between 0 and 1, where a number close to 1 indicates a higher similarity in species composition [23]. We then multiplied J by 100 to obtain a percent, to easily interpret the results.

3. Results

3.1 Avian species diversity, distribution, and richness

A total of 156 avian species representing 18 orders and 61 families were recorded in the five WMAs. The overall avian species Shannon diversity (H′) for all the habitat types ranged from 2.28–4.08, except for dense miombo woodland which had H′ = 1.69 (**Table 1**). Riverine forest habitat had higher species richness (n = 101 species), representing almost 45% of the total recorded individuals (**Table 1**). Avian species diversity was highest in riverine forest and lowest in dense miombo woodlands (**Table 1**; **Figure 2**). The Shannon Index of diversity revealed that species evenness for the five habitats surveyed was relatively low ranging from 0.29–0.59 (**Table 1**).

Values bearing different letters within column are significantly different ($p < 0.05$) and values with similar letters within column are not significantly

Habitat type	Number of avian species	Overall abundance	Mean abundance	Shannon diversity (H′)	Shannon evenness (E_H)
Dense miombo	14	105	7.50 ± 3.91	1.69	0.39
Farmland	40	580	14.50 ± 5.82	2.46	0.29
Open miombo	98	1338	13.65 ± 2.08	3.9	0.51
Riverine forest	101	759	7.52 ± 0.97	4.08	0.59
Swamp areas	20	188	9.40 ± 3.26	2.28	0.49

Table 1.
Avian species diversity, abundance, and evenness in different habitats of WMAs in Ruvuma landscape (± standard error).

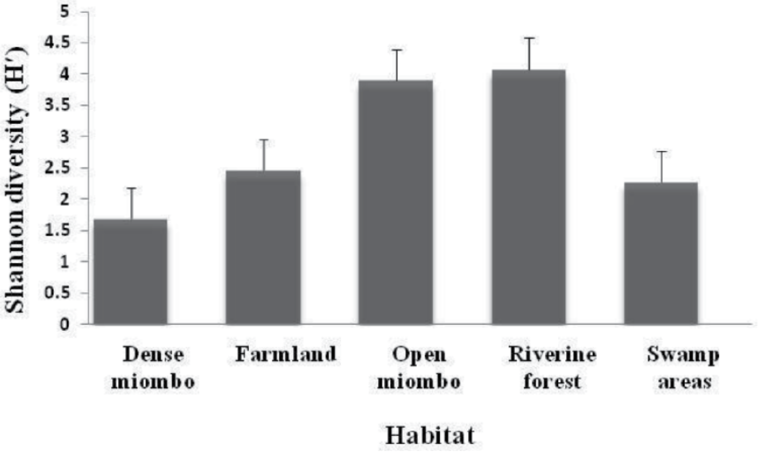

Figure 2.
Avian species diversity in different habitats.

different ($p > 0.05$; **Table 2**). Dense miombo woodland, farm and swamp exhibited higher number of birds per point count than in open miombo woodland and riverine forest implying that the avian species were more scattered in open miombo woodlands and riverine forests.

The overall mean abundance of avifauna in the WMAs differed significantly (Kruskal-Wallis test, $\chi^2 = 50.13$, df = 4, P = 0.03). Kimbanda had the highest mean abundance of species followed by Kisungule (**Figure 3**). There was a significant difference in the mean abundance of avifauna across the five habitats (Kruskal-Wallis test, $\chi^2 = 13.18$, df = 4, P = 0.010). Mean abundance of species was significantly higher in farmland than in dense miombo (Mann–Whitney tests, U = 19, $P < 0.0001$), open miombo woodland (U = 66.5, $P < 0.0003$), riverine forest (U = 157, $P < 0.019$) and swamps (U = 93.5, $P < 0.004$) (**Figure 3**).

The distribution of the 2970 avifauna species recorded in the five habitat types is given in (**Table 1** above; **Figure 4**). Some species were found in more than one habitat type, a total of six species with bronze mannikin (*Lonchura cucullata*) the most abundant (**Figure 5**). Tawny-flanked prinia (*Prinia subflava*), blue-spotted wood dove (*Turtur afer*), common bulbul (*Pycnonotus barbatus*), violet-backed starling (*Cinnyricinclus leucogaster*), and Jameson's firefinch (*Lagonosticta rhodopareia*) were observed in four habitat types, except swamp habitat (see **Figure 5**; Appendix **Table A1**). Southern cordon-bleu (*Uraeginthus bengalus*) was observed in three habitat types and was the second most abundant species recorded

Habitats	Average bird count
Dense miombo woodland	6.18a
Farm	6.11a
Open miombo woodland	3.71b
Riverine forest	3.45b
swamp	6.48a

Table 2.
Average number of birds per point count in different habitats.

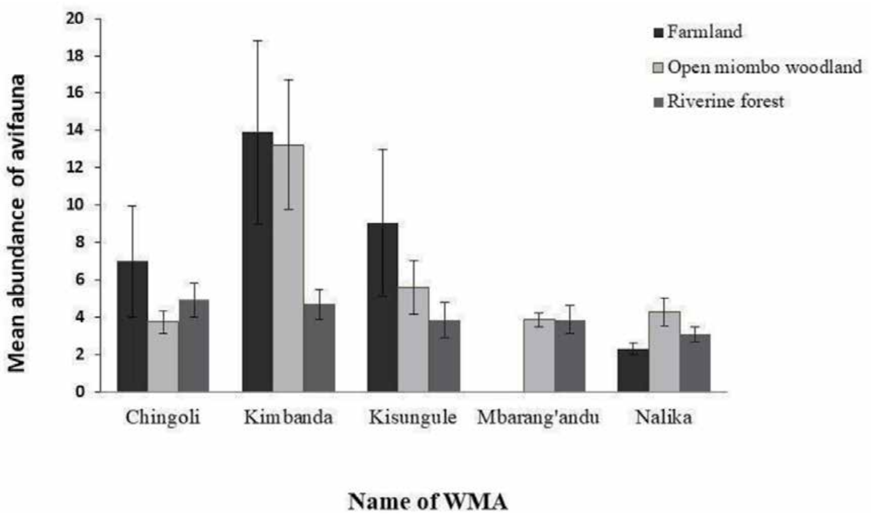

Figure 3.
Avian abundance in different habitats of wildlife management areas in southern Tanzania.

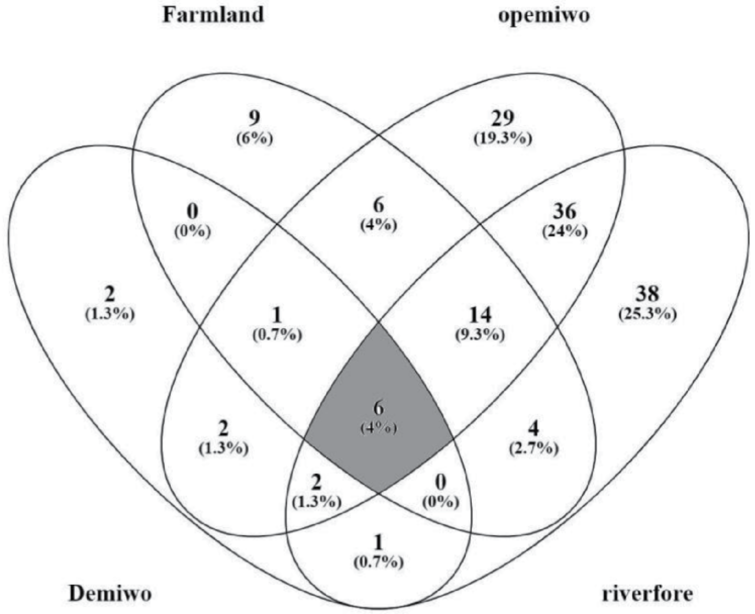

Figure 4.
Avifauna species observed foraging in different habitats. Definition of abbreviation used (Demiwo = dense miombo woodland, riverfore = riverine forest, farmland = farmland habitat, opemiwo = open miombo woodland).

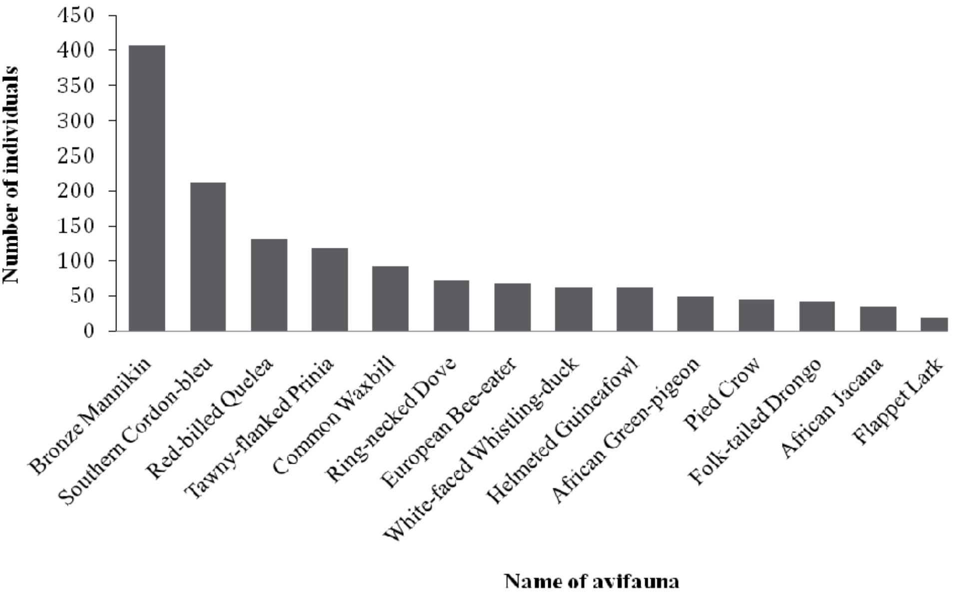

Figure 5.
Distribution of avian species in different habitats within WMAs of the Ruvuma landscape in southern Tanzania.

during this study (**Figure 5**). Other species including pied crow (*Corvus albus*), brown-headed parrot (*Poicephalus cryptoxanthus*), and red-necked francolin (*Pternistis afer*) were observed in three habitat types (see Appendix **Table A1**) whereas black-faced waxbill (*Estrilda erythronotos*) and African pied wagtail (*Motacilla aguimp*), were observed only in farmland areas.

Cryptic species like African broadbill (*Smithornis capensis*) and red-capped robin-chat (*Cossypha natalensis*) and understory bird species including red-throated twinspot (*Hypargos niveoguttatus*) were observed only in the riverine forest using mist-nets and point count methods (Appendix **Table A1**). Palearctic migrants including European nightjar (*Caprimulgus europaeus*), European swift (*Apus apus*), and European bee-eater (*Merops apiaster*) were also recorded. Trumpeter hornbill (*Bycanistes bucinator*) is a bird of conservation status that was observed during the study in forest patches.

3.2 Species composition and similarities between different habitat types

We found strong contrast in species composition among habitat types (**Table 3**). The highest species similarities were between open woodland vs. Riverine forest (41%), Farmland vs. Open woodland (24%) and Farmland vs. Riverine forest (21%)

Habitat types	Dense woodland	Open woodland	Farmland	Riverine	Swamp area
	—	—	—	—	—
Open woodland	11	—	—	—	—
Farmland	15	24	—	—	—
Riverine forest	8	41	21	—	—
Swamp area	0	1	2	5	—

Table 3.
Jaccard species composition similarity index (J) between habitat types of the WMAs in Ruvuma landscape, in southern Tanzania. In this table the similarity presented in percentage (%).

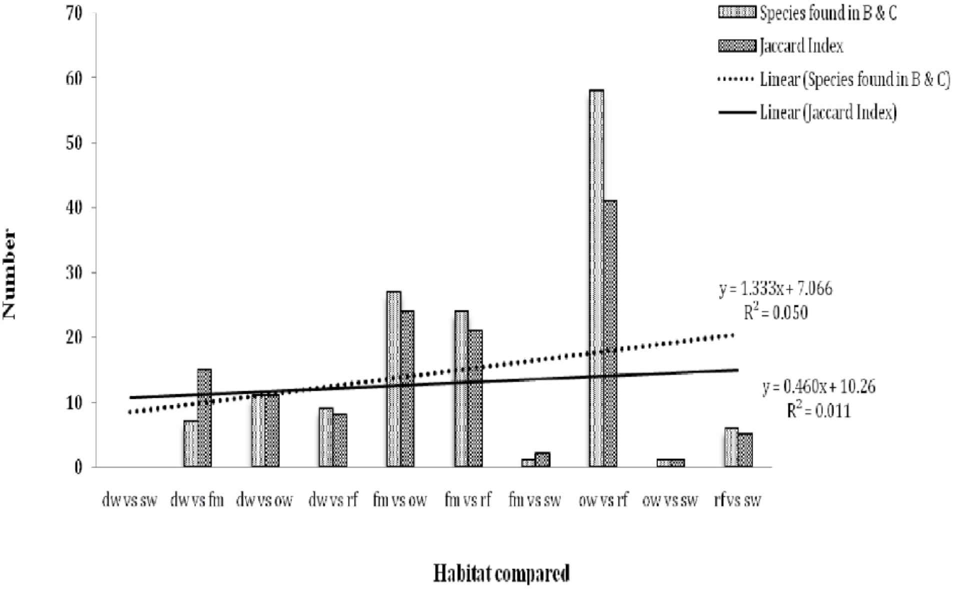

Figure 6.
Plotted trend line to show species composition similarities between habitat types of the WMAs in Ruvuma landscape, in southern Tanzania. Definition of abbreviation used (dw vs. sw = dense woodland vs. swamp area; dw vs. fm = dense woodland vs. farmland; dw vs. ow = dense woodland vs. open woodland; dw vs. rf = dense woodland vs. riverine forest; fm vs.ow = farmland vs. open woodland; fm vs. rf = farmland vs. riverine forest; fm vs. sw = farmland vs. swamp area; ow vs. rf = open woodland vs. riverine forest; ow vs. sw = open woodland vs. swamp area; rf vs. sw = riverine forest vs. swamp area).

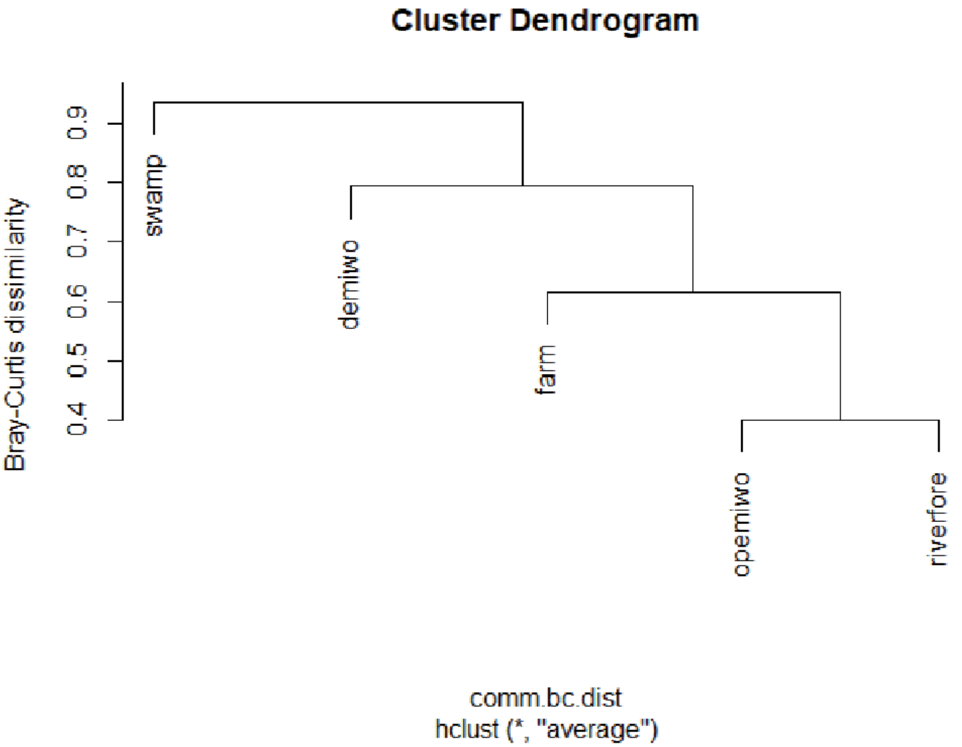

Figure 7.
Cluster analysis of different habitat types based on bird species composition (presence/absence). Definition of abbreviation used (Demiwo = dense miombo woodland, riverfore = riverine forest, farmland = farmland habitat, opemiwo = open miombo woodland).

while dense woodland vs. Swamp areas had no similarity in composition (0%), Open woodland vs. Swamp area (1%) and Farmland vs. Swamp area (2%; **Table 3**). The Jaccard similarity indices among various pairs of habitat types compared (**Table 3**; **Figure 6**).

From the results, avian species adapted to open miombo woodlands and those adapted to riverine forest were very closely related and far from avian species adapted to swamps (**Figure 7**). Avian species adapted to swamps were separated from all other avian species adapted other habitats (**Figure 7**). Indeed, this entails a need for conservation of swamps to avoid local distinction of swamp adapted species.

4. Discussion and conclusion

4.1 Avian species diversity, distribution, and richness

Farmland habitats were observed in all WMAs except in Mbarang'andu where we did not encounter cultivated areas inside the core WMA. Possibly due to the presence of an anti-poaching office established inside WMA by Tanzania Wildlife Management Authority (TAWA, formerly Wildlife Division). In our study, we predicted that there would be higher avian diversity, richness, and abundance in WMAs than in human-modified areas named here as farmlands. We found strong support for this prediction for the species diversity and richness of avifauna but not for abundance. This suggested that the differing occurrence of avifauna species across given habitats could be attributed to some reasons including food requirement as well as heat tolerance [25].

The richness and diversity imply a variety of taxa that exist in an area, many taxa should, therefore, survive in habitats that have a variety of favorable conditions and resources such as the presence of food, nesting areas, shade and water that might contribute to higher species richness and diversity. Therefore, low species diversity in the farmland might be contributed by the insufficient supply of food as well as insufficient cover for birds to hide against predators, lack of shade to hide from diurnal temperature [12, 26] low food supply compared to forests and woodlands. Suggesting that farmlands have reached maximum disturbance, as in lower farmlands heterogeneous vegetation offer foods and shelter for birds encouraging higher diversity and abundance [8]. Thus the granivores which are largely seed eaters such as the bronze mannikin, southern cordon-bleu, and red-billed quelea were dominant in farmlands than in other habitats because farmlands were rich in seed types vegetation, in line with the findings of others [12, 26]. Furthermore, for similar reasons, the abundance of the granivores species was also higher in open miombo where grassland patches are dominant than in forest areas. Birds that preferred mixed habitat of tree-covered vegetation and open areas chose forest and woodlands but are not water-bound and avoided farmlands such as red-throated twinspot, pygmy kingfisher and red-capped robin-chat, they co-existed in riverine forest and woodland, together with birds that prefer evergreen or lowland forest, dense deciduous thickets, or other dense woodlands such as black-throated wattle-eye and the African broadbill.

4.2 Species composition and similarities between different habitat types

The presence of higher species composition and similarities among habitat types suggests that miombo woodlands harbor unique avifauna species. Some avian species are observed to occur in more than one habitat type indicating that avian species are not habitat specialists. In this study, such patterns were observed; some species existed in more than 4 habitat types suggesting areas visited they provide similar resource abundance, types, and habitat heterogeneity.

Therefore, under no intervention strategies, the Ruvuma Landscape will result in a marked loss of avian richness and diversity. This suggests that measures that will reduce land clearance for agriculture need to be promptly implemented to reduce the ecological impacts on avifauna. Wildlife management areas should involve adjacent communities that are the key stakeholders of the habitats and species biodiversity conservation. Such measures can enhance the resilience of wildlife management areas and complement the goals of community-based conservation measures [27, 28]. Unfortunately, any proposed measures may be challenged by increasing human pressure due to agricultural intensification needs as well as a rapidly changing climate that may be beyond the WMA's management control. Examining the links of these threats to avian biodiversity and addressing such in an urgent manner is likely to abate current human disturbance in the WMAs of Ruvuma region.

Acknowledgements

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Conflict of interest

The authors have not declared any conflict of interests.

Appendix

No.	English name	Species name	Habitat type						
			Dense miombo woodland	Farmland	Open miombo woodland	Riverine forest	Swamp areas	Grand Total	Ratio
1	Bronze mannikin	*Spermestes cuculiata*	56	222	56	72	0	406	0.137
2	Southern (Blue-breasted) cordon-bleu	*Uraeginthus angolensis*	3	85	123	0	0	211	0.071
3	Red-billed quelea	*Quelea quelea*	0	15	115	0	0	130	0.044
4	Tawny-flanked prinia	*Prinia subflava*	18	27	38	34	0	117	0.039
5	Common waxbill	*Estrilda astrild*	0	9	63	20	0	92	0.031
6	Common bulbul	*Pycnonotus goiavier*	5	1	37	33	0	76	0.026
7	Ring-necked dove	*Streptopelia capicola*	0	21	51	0	0	72	0.024
8	European bee-eater	*Merops apiaster*	0	3	51	8	6	68	0.023
9	Violet-backed starling	*Cinnyricinclus leucogaster*	2	4	45	17	0	68	0.023
10	White-faced whistling-duck	*Dendrocygna viduata*	0	0	0	0	62	62	0.021
11	Helmeted guineafowl	*Numida meleagris*	0	0	59	2	0	61	0.021
12	Blue-spotted wood-dove	*Turtur afer*	5	7	26	11	0	49	0.016
13	African green-pigeon	*Treron calvus*	0	2	42	4	0	48	0.016
14	Pied crow	*Corvus albus*	0	30	10	5	0	45	0.015
15	Fork-tailed drongo	*Dicrurus adsimilis*	0	2	35	5	0	42	0.014
16	Arrow-marked babbler	*Turdoides jardineii*	0	0	12	26	0	38	0.013
17	Gray-backed (bleating) camaroptera	*Camaroptera brevicaudata*	0	0	6	32	0	38	0.013

No.	English name	Species name	Habitat type						
			Dense miombo woodland	Farmland	Open miombo woodland	Riverine forest	Swamp areas	Grand Total	Ratio
18	Little greenbul	*Eurillas virens*	0	0	2	36	0	38	0.013
19	African jacana	*Actophilornis africanus*	0	0	0	2	33	35	0.012
20	Black-crowned tchagra	*Tchagra senegalus*	0	4	26	5	0	35	0.012
21	Lesser striped swallow	*Cecropis abyssinica*	0	13	0	21	0	34	0.011
22	Wire-tailed swallow	*Hirundo smithii*	0	34	0	0	0	34	0.011
23	Rufous-naped lark	*Mirafra africana*	0	0	32	0	0	32	0.011
24	Brown-headed parrot	*Poicephalus cryptoxanthus*	2	0	25	2	0	29	0.010
25	Lesser blue-eared starling	*Lamprotornis chloropterus*	0	0	25	3	0	28	0.009
26	Black-backed puffback	*Dryoscopus cubla*	0	0	10	16	0	26	0.009
27	Black-headed oriole	*Riolus larvatus*	0	1	18	6	0	25	0.008
28	Collared sunbird	*Hedydipna collaris*	1	0	9	15	0	25	0.008
29	Mosque swallow	*Cecropis senegalensis*	0	6	12	6	0	24	0.008
30	Pied kingfisher	*Ceryle rudis*	0	0	0	6	18	24	0.008
31	Mottled spinetail	*Telacanthura ussheri*	0	0	0	23	0	23	0.008
32	Purple-crested turaco	*Gallirex porphyreolophus*	0	0	15	8	0	23	0.008
33	Pennant-winged nightjar	*Caprimulgus vexillarius*	0	0	19	2	0	21	0.007
34	Rattling cisticola	*Cisticola chiniana*	4	0	0	17	0	21	0.007
35	Tropical boubou	*Laniarius aethiopicus*	0	0	7	14	0	21	0.007
36	White-headed black chat	*Myrmecocichla arnotti*	0	0	17	4	0	21	0.007
37	African paradise-flycatcher	*Terpsiphone viridis*	0	3	12	5	0	20	0.007
38	Gray-headed bush-shrike	*Malaconotus blanchoti*	0	0	6	13	0	19	0.006
39	African palm-swift	*Cypsiurus parvus*	0	19	0	0	0	19	0.006
40	Brown-crowned tchagra	*Tchagra australis*	0	4	7	7	0	18	0.006

No.	English name	Species name	Habitat type						
			Dense miombo woodland	**Farmland**	**Open miombo woodland**	**Riverine forest**	**Swamp areas**	**Grand Total**	**Ratio**
41	Flappet lark	*Mirafra rufocinnamomea*	0	2	10	6	0	18	0.006
42	Pale-billed hornbill	*Lophoceros pallidirostris*	0	0	2	16	0	18	0.006
43	Red-throated twinspot	*Hypargos niveoguttatus*	0	0	0	18	0	18	0.006
44	Gray-headed kingfisher	*Halcyon leucocephala*	0	0	15	2	0	17	0.006
45	Jameson's frefinch	*Lagonosticta rhodopareia*	2	2	5	8	0	17	0.006
46	Red-necked francolin	*Pternistis afer*	0	6	3	8	0	17	0.006
47	Yellow bishop	*Euplectes capensis*	0	0	8	9	0	17	0.006
48	African golden oriole	*Oriolus auratus*	0	2	14	0	0	16	0.005
49	Black-faced waxbill	*Estrilda erythronotos*	0	15	0	0	0	15	0.005
50	White-rumped swift	*Apus caffer*	0	3	0	12	0	15	0.005
51	Yellow-breasted apalis	*Apalis flavida*	0	0	3	12	0	15	0.005
52	Black-throated wattle-eye	*Platysteira peltata*	0	0	0	14	0	14	0.005
53	African firefinch	*Lagonosticta rubricata*	0	6	4	3	0	13	0.004
54	Green woodhoopoe	*Phoeniculus purpureus*	0	0	13	0	0	13	0.004
55	Spotted flycatcher	*Muscicapa striata*	0	0	12	1	0	13	0.004
56	Orange-breasted bush-shrike	*Chlorophoneus sulfureopectus*	0	0	8	5	0	13	0.004
57	White-backed duck	*Thalassornis leuconotus*	0	0	0	0	12	12	0.004
58	White-browed sparrow-weaver	*Plocepasser mahali*	0	0	12	0	0	12	0.004
59	Yellow-fronted canary	*Crithagra mozambica*	0	0	12	0	0	12	0.004
60	African darter	*Anhinga rufa*	0	0	0	0	11	11	0.004
61	Kurrichane thrush	*Turdus libonyana*	0	0	9	2	0	11	0.004
62	African gray hornbill	*Lophoceros nasutus*	0	2	3	5	0	10	0.003
63	Böhm's spinetail	*Neafrapus boehmi*	0	0	0	10	0	10	0.003

No.	**English name**	**Species name**	**Habitat type**						
			Dense miombo woodland	**Farmland**	**Open miombo woodland**	**Riverine forest**	**Swamp areas**	**Grand Total**	**Ratio**
64	Common squacco heron	*Ardeola ralloides*	0	0	0	0	10	10	0.003
65	Coqui francolin	*Peliperdix coqui*	0	0	10	0	0	10	0.003
66	Shelley's sunbird	*Cinnyris shelleyi*	0	0	3	7	0	10	0.003
67	Reichenow's woodpecker	*Campethera scriptoricauda*	1	0	9	0	0	10	0.003
68	African broadbill	*Smithornis capensis*	0	0	0	9	0	9	0.003
69	Black crake	*Zapornia flavirostra*	0	0	0	2	7	9	0.003
70	Green-capped eremomela	*Eremomela scotops*	0	0	6	3	0	9	0.003
71	Striped kingfisher	*Halcyon chelicuti*	0	0	7	2	0	9	0.003
72	Little bee-eater	*Merops pusillus*	0	0	6	2	0	8	0.003
73	Little swift	*Apus affinis*	0	8	0	0	0	8	0.003
74	Pied wagtail	*Motacilla aguimp*	0	8	0	0	0	8	0.003
75	Senegal lapwing	*Vanellus lugubris*	0	0	8	0	0	8	0.003
76	Amethyst sunbird	*Chalcomitra amethystina*	0	0	0	7	0	7	0.002
77	Greater honeyguide	*Indicator indicator*	0	0	7	0	0	7	0.002
78	Racket-tailed roller	*Coracias spatulatus*	0	1	6	0	0	7	0.002
79	Red-faced cisticola	*Cisticola erythrops*	0	0	0	4	3	7	0.002
80	Rufous-bellied tit	*Melaniparus rufiventris*	0	0	5	2	0	7	0.002
81	Broad-billed roller	*Eurystomus glaucurus*	0	0	5	1	0	6	0.002
82	Brown-hooded kingfisher	*Halcyon albiventris*	0	0	6	0	0	6	0.002
83	Dark chanting-goshawk	*Melierax metabates*	0	1	4	1	0	6	0.002
84	Eastern bearded scrub-robin	*Tychaedon quadrivirgata*	0	0	2	4	0	6	0.002
85	Great white egret	*Ardea alba*	0	0	0	0	6	6	0.002
86	Southern ground-hornbill	*Bucorvus leadbeateri*	0	0	6	0	0	6	0.002
87	Livingstone's turaco	*Tauraco livingstonii*	0	0	6	0	0	6	0.002

No.	**English name**	**Species name**	**Habitat type**						
			Dense miombo woodland	**Farmland**	**Open miombo woodland**	**Riverine forest**	**Swamp areas**	**Grand Total**	**Ratio**
88	Red-cheeked cordon-bleu	*Uraeginthus bengalus*	0	0	0	6	0	6	0.002
89	Southern gray-headed sparrow	*Passer diffusus*	0	0	6	0	0	6	0.002
90	Swallow-tailed bee-eater	*Merops hirundineus*	0	0	6	0	0	6	0.002
91	Trumpeter hornbill	*Bycanistes bucinator*	0	0	0	6	0	6	0.002
92	White-crested helmetshrike	*Prionops plumatus*	0	0	6	0	0	6	0.002
93	Willow warbler	*Phylloscopus trochilus*	0	0	6	0	0	6	0.002
94	Common hoopoe	*Upupa epops*	0	0	0	5	0	5	0.002
95	Black cuckoo	*Cuculus clamosus*	0	0	0	5	0	5	0.002
96	Black kite	*Milvus migrans*	0	2	3	0	0	5	0.002
97	Common sandpiper	*Actitis hypoleucos*	0	0	0	3	2	5	0.002
98	Golden-tailed woodpecker	*Campethera abingoni*	0	0	4	1	0	5	0.002
99	Little sparrowhawk	*Accipiter minullus*	0	0	4	1	0	5	0.002
100	Pale (East coast) batis	*Batis soror*	0	0	2	3	0	5	0.002
101	Pygmy kingfisher	*Ispidina picta*	0	0	0	3	2	5	0.002
102	Red-chested cuckoo	*Cuculus solitarius*	0	0	0	5	0	5	0.002
103	Miombo wren warbler	*Calamonastes stierlingi*	0	0	5	0	0	5	0.002
104	Wattled lapwing	*Vanellus senegallus*	0	0	0	3	2	5	0.002
105	White-bellied sunbird	*Cinnyris talatala*	0	0	3	2	0	5	0.002
106	White-breasted cuckoo-shrike	*Ceblepyris pectoralis*	0	0	5	0	0	5	0.002
107	Yellow-bellied greenbul	*Chlorocichla flaviventris*	0	0	2	3	0	5	0.002
108	Cardinal woodpecker	*Dendropicos fuscescens*	1	0	3	0	0	4	0.001
109	African pipit	*Anthus richardi*	0	0	3	0	2	5	0.002
110	Hamerkop	*Scopus umbretta*	0	0	0	4	0	4	0.001
111	Lilac-breasted roller	*Coracias caudatus*	0	0	2	2	0	4	0.001
112	Pearl-spotted owlet	*Glaucidium perlatum*	0	0	4	0	0	4	0.001

No.	English name	Species name	Habitat type						
			Dense miombo woodland	**Farmland**	**Open miombo woodland**	**Riverine forest**	**Swamp areas**	**Grand Total**	**Ratio**
113	Red-capped robin-chat	*Cossypha natalensis*	0	0	0	4	0	4	0.001
114	White-browed coucal	*Centropus superciliosus*	0	0	2	2	0	4	0.001
115	White-browed robin-chat	*Cossypha heuglini*	0	0	0	4	0	4	0.001
116	Black cuckoo-shrike	*Campephaga flava*	0	0	1	2	0	3	0.001
117	Böhm's bee-eater	*Merops boehmi*	0	0	0	3	0	3	0.001
118	Brubru	*Nilaus afer*	0	0	3	0	0	3	0.001
119	Cabanis's bunting	*Emberiza cabanisi*	0	2	1	0	0	3	0.001
120	Crested barbet	*Trachyphonus vaillantii*	0	0	1	2	0	3	0.001
121	Crowned hornbill	*Lophoceros alboterminatus*	0	3	0	0	0	3	0.001
122	European swift	*Apus apus*	0	0	0	3	0	3	0.001
123	African fish eagle	*Haliaeetus vocifer*	0	0	0	1	2	3	0.001
124	Hadada ibis	*Bostrychia hagedash*	0	0	0	0	3	3	0.001
125	Harlequin quail	*Coturnix delegorguei*	0	0	0	3	0	3	0.001
126	Namaqua dove	*Oena capensis*	3	0	0	0	0	3	0.001
127	Speckle-throated woodpecker	*Campethera scriptoricauda*	0	0	3	0	0	3	0.001
128	Parasitic weaver	*Anomalospiza imberbis*	0	0	3	0	0	3	0.001
129	Red-fronted tinkerbird	*Pogoniulus pusillus*	0	0	0	3	0	3	0.001
130	Red-headed weaver	*Anaplectes rubriceps*	0	0	3	0	0	3	0.001
131	Speckled mousebird	*Colius striatus*	0	0	0	3	0	3	0.001
132	Stripe-breasted seedeater	*Crithagra striatipectus*	0	0	3	0	0	3	0.001
133	White-browed scrub-robin	*Cercotrichas leucophrys*	0	0	1	2	0	3	0.001
134	Wood sandpiper	*Tringa glareola*	0	0	0	0	3	3	0.001
135	Black-headed heron	*Ardea melanocephala*	0	1	0	1	0	2	0.001

No.	English name	Species name	Habitat type						
			Dense miombo woodland	Farmland	Open miombo woodland	Riverine forest	Swamp areas	Grand Total	Ratio
136	Black-winged stilt	*Himantopus himantopus*	0	0	0	2	0	2	0.001
137	Brimstone canary	*Crithagra sulphurata*	0	0	2	0	0	2	0.001
138	Egyptian goose	*Alopochen aegyptiaca*	0	0	0	0	2	2	0.001
139	Fiscal shrike	*Lanius collaris*	0	2	0	0	0	2	0.001
140	Golden-breasted bunting	*Emberiza flaviventris*	2	0	0	0	0	2	0.001
141	Retz's helmet shrike	*Prionops retzii*	0	0	0	2	0	2	0.001
142	Scarlet-chested sunbird	*Chalcomitra senegalensis*	0	0	0	2	0	2	0.001
143	Tambourine dove	*Turtur tympanistria*	0	0	0	2	0	2	0.001
144	African barred owlet	*Glaucidium capense*	0	0	1	0	0	1	0.000
145	Piping cisticola	*Cisticola fulvicapilla*	0	0	3	0	0	3	0.001
146	Red-eyed dove	*Streptopelia semitorquata*	0	0	0	3	0	3	0.001
147	Beautiful sunbird	*Cinnyris pulchellus*	0	1	0	0	0	1	0.000
148	Black coucal	*Centropus grillii*	0	0	0	1	0	1	0.000
149	Brown snake-eagle	*Circaetus cinereus*	0	0	0	1	0	1	0.000
150	European nightjar	*Caprimulgus europaeus*	0	0	1	0	0	1	0.000
151	Gray heron	*Ardea cinerea*	0	0	0	0	1	1	0.000
152	Olive sunbird	*Cyanomitra olivacea*	0	0	0	1	0	1	0.000
153	Saddlebill	*Ephippiorhynchus senegalensis*	0	0	0	0	1	1	0.000
154	Spectacled weaver	*Ploceus ocularis*	0	0	1	0	0	1	0.000
155	Spotted creeper	*Salpornis salvadori*	0	0	0	1	0	1	0.000
156	Woodland kingfisher	*Halcyon senegalensis*	0	0	0	1	0	1	0.000
	Grand Total		105	580	1338	759	188	2970	

Table A1.
List of avifauna species observed in different habitats of WMAs in Ruvuma.

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Chapter 6

The Limit to the Density of Species (A Reflection on Human Intervention in Conservation and Its Effects)

Luis Fernando Basanta Reyes, Manuel Calderón Carrasco and Ángel Rodríguez Martín

Abstract

Human actions on the natural environment cannot always be considered as impacts resulting from their behavior to survive. Many of these activities have caused irreversible damage and changes in the landscape, flora, and fauna. By contrast, several actions, carried out "a priori" with the best intention, to help in the conservation of species considered in danger, have caused a dangerous decompensation. Aid for the recovery of some species of birds has led to their overpopulation. The artificial contributions of food, always in the same places, have caused an excessive increase in the number of griffon vultures (*Gyps fulvus*), which has produced the reduction of other endangered species, such as the black stork (*Ciconia nigra*) and the Bonelli's eagle (*Aquila fasciata*), which have been displaced from the rocks in which they nested due to the harassment of a greater number of vultures. Besides, vultures are attacking domestic livestock at the most defenseless times, such as during calving. Greater flamingo (*Phoenicopterus roseus*) has become out of control in numbers in Europe. The two classic breeding areas, La Camargue (France) and La Laguna de Fuente de Piedra (Spain) have produced an enormous annual number of individuals that are distributed among the few lagoons of Mediterranean Europe. The wetlands are devastated by the flamingo, which removes the mud and prevents sunlight from reaching the underwater vegetation, turning these lagoons into dead water, having to be abandoned (temporarily) by most aquatic species, including the flamingo. The shortage of food resources of natural origin, for such a disproportionate number, has caused the flamingo to invade the rice fields, accepting its grain as a substitute for the invertebrates that it habitually consumed, and which are now scarce. The same is the case with the white stork (*Ciconia ciconia*) in southern Europe. The increase in their population has reduced the number of reptiles and amphibians, bringing several of their species to the brink of extinction. Storks have varied their prey spectrum, consuming carrion, and preying on Montagu's harrier (*Circus pygargus*) brood. In these cases, and many others, the theory of "the more the better" is not valid. If we want to make the protection of some species compatible with the conservation of others, it seems necessary to redirect some situations …

Keywords: density of species, overpopulation, human intervention, conservation effects, species affectation, endangered species

1. Introduction

It could be thought, initially, that this chapter will be one more that deals with the impact that certain invasive species cause on the biota of a certain area, region, or country. Not exactly, though too. It is necessary to recognize that this matter - much approached and treated at different levels - still leaves ample room for suggestions and debates. In the text that follows, several examples of intervention in favor of a specific bird species are shown, to increase its populations and "remove" it from a classification "critically endangered" or remarkably close to it.

The measures implemented by different public administrations and/or conservation entities, to try to recover a specific species and avoid its classification as endangered, near endangered, etc., have provoked, and still do, a series of reactions both target species in question, such as related species or prey species; even on those that we would never have believed could be affected by the recovery plans of the former.

Admittedly, some of these reactions were not easy to predict, others were not. In some cases, political or personal "honor" criteria have prevailed, in an apparent maelstrom or race, to have more individuals than another "competing" region or nation.

Also, shortcuts have sometimes been sought. Some original, others of questionable ethics, with reasonable doubts to be protected by scientific criteria.

At times, there has been a sin of precipitation and rapid search for striking results, rather than the application of biological knowledge, and of considering a probable long-term projection.

"A wild population is defined as a set of individuals of a species that inhabits a certain area". "Density is the number of specimens per spatial unit (surface or volume). It is often more useful than the absolute size of the population since density determines and conditions fundamental aspects such as competition for resources" [1].

"Traditionally, indicator species have been considered those that, by being present in a certain system, indicate that said ecosystem is healthy, from the physical, chemical, or biological point of view (or, by the on the contrary, that it is deteriorated, as occurs with the species of aquatic invertebrates that indicate contamination). They are usually species that are easy to detect and "monitor" so that the demographic changes of their populations can be detected in time and interpreted in terms of other variables of conservation interest that are more difficult to measure" [2].

Dedicating all efforts to the recovery of a species, you can avoid the symptoms that warn us of its risk situation, but not end with its origin or, what is worse, camouflage the situation of other less striking species, but in a similar situation. "No species serves to indicate anything about its ecosystem of origin when it is kept in captivity, or conditions of probation, away from enemies and provided with food" [2].

Recovery involves much more than just increasing population numbers. Density can and should have a limit.

These premises constitute the basis on which this chapter will work: The growth in the number of specimens/surface unit of a specific species, which has been "helped" in different ways, is affecting other populations in such a way that it has displaced or eradicated them from specific areas, endangering their existence.

Not all cases of increase in population density in birds are due to human intervention, through the execution of direct intervention measures, to intentionally favor a certain endangered species. However, behind most animal overpopulations - not just birds - are human actions that, consciously or unconsciously, have caused them.

The examples discussed below refer to situations that occurred in Spain. We know of multiple similar actions in other countries. The reader will be able to relate and apply each case to its environment but will agree with us that a limit to the density of the species is necessary.

2. The case of …

2.1 The griffon vulture (*Gyps fulvus*)

Traditionally, raptors have been considered "harmful" in a simplistic dichotomous classification, in contrast to "beneficial birds." The diurnal raptors have been especially "persecuted", for predating on rabbits (*Oryctolagus cuniculus),* red-legged partridges (*Alectoris rufa*), and other species, which man uses for his consumption.

Birds of prey were considered protected species, in Spain, from the year 1973. However, their habitats were not protected until several years later. It could be the paradox that an imperial eagle (*Aquila adalberti*) would fly over the entire Spanish territory without risk of being shot, but, incoherently, it would starve because its habitat had been destroyed, it did not have preys, or it could not rest safely or reproduce, because there are no trees on which to build the nest.

The custom of poisoning carrion and eggs did not cease with the law. Raptors continued to perish due to the "silent" effect of strychnine, a situation that also affected corvids. The secondary poisoning of scavenger birds occurred by ingesting the corpses of mammals considered vermin, such as foxes, which had been poisoned, or even wild boars, which had eaten the deadly bait intended for foxes.

There was another important decrease in the populations of griffon vultures due to the use of the tractor in agriculture, because it marked the end of the use of animals to plow and harvest agricultural fields: animals that were a basic contribution to their subsistence.

Traditionally, the corpses of domestic cattle were abandoned in the field, in the same place where they died (in the case of extensive livestock) or transferred to a point away from the facilities if they were housed animals.

In the case of the herds in the extensive regime, the location of the corpses depended completely on chance, so the ethological patterns of the search flights of the vultures did not suffer alterations.

The European Union, with the emergence of the bovine disease, called spongiform encephalopathy, which is transmissible to humans, issued regulations that prohibited these practices, making it mandatory to hire incineration services for carcasses. Suddenly, the most important source of food for scavengers was eliminated, which from then on only had carcasses from hunting. In some localities, points of deposit of carcasses of cattle were authorized, in which the animals were eviscerated (being buried or incinerated these carcasses).

During that time, vultures attacked disadvantaged animals, such as during parturition, tearing of genitalia and killing the calf or lamb [5]. Situations that, until then, had been exceptional, but continues occurring on more frequent occasions today (**Figure 1**). As a contrast [3–5], as follows: "A sheep of my property died in childbirth, I dragged it to a clearing where the vultures could see it better, they fell on it and almost ate it completely but they did not touch the corpse of the dead lamb as well and cause the sheep to die. It is the case of a dead animal" [4] and "A cow disappeared from a farm in Portezuelo, a town very close to Acehúche. It was found almost eaten by vultures and suddenly we saw something moves on the corpse; it was a calf that had not been touched and left ahead. In this case they were able to attack the mother even before she was dead, but we are not sure" [4].

Figure 1.
Vultures on the prowl. Sheep in a protective attitude towards lambs. Photo M. Calderón.

To alleviate the decrease in food in the field, many public and private initiatives (NGO's) were carried out, consisting of preparing fixed feeding points for scavengers. The contributions of remains were made, in general, with constant periodicity (**Figure 2**).

In 2011, the EU standard was transposed into Spanish legislation, once again authorizing the abandonment of carcasses in the field, after the pertinent analyzes.

In an area of the La Serena region (Badajoz), at the end of the last century, there were 150 breeding pairs of griffon vultures. In 2020 the census was of more than 400 couples. There are no feeders for vultures there, but the extensive sheep herd

Figure 2.
To alleviate the decrease of food in the field,fixed feeding points for scavengers were prepared. Photo M. Calderón.

has increased enormously, from the moment that EU aid began to be paid per head of cattle and not per farm, as was done previously [3].

The attention and care of these sheep have decreased a lot or is almost non-existent. The death of several heads does not seem to worry the farmer, always compensated by the EU subsidy. The vultures, logically, take advantage of the corpses and increase their number of reproductive pairs.

Species such as the griffon vulture increase their population density, constituting new breeding colonies, while other birds of prey, as important as they, decrease in number due to the pressure of the vultures when competing for nesting platforms on the rocks.

Griffon vultures, in certain areas, are seriously compromising the viability and existence of several species of raptors and other gliders, which exist in much smaller numbers of population and are truly vulnerable or are vulnerable or in danger, such as the golden eagle (*Aquila chrysaëtos*), the Bonelli's eagle (*Aquila fasciata)* and the black stork (*Ciconia nigra)* [3, 4].

At the end of the 20th century, in the rocky areas of Hornachos (Badajoz) or any other area in the area, a golden eagle could expel three pairs of griffon vultures from a ledge to install their nest there. At present, the highest platforms and ledges, the best ones, are occupied by griffon vultures aided by the much higher number of specimens, can displace the eagle and forcing it to live in less secure rocks, and even, not to breed [3].

This situation has been repeated with Bonelli's eagle, forced by the pressure of the vultures to abandon the rocky cuttings of Cabeza del Buey (Badajoz). Only a single nest remains, at low height, far from its usual rocky platform, with a high risk of attack by predators, and located between two recent colonies of vultures that, in a very few years, will force it to leave the area permanently (**Figure 3**) [3].

Vultures perch on the same rocky platform where black stork's nest is located, and some vultures have been observed aggressively stretching their necks against the black stork in its nest [3].

Egyptian vulture *(Neophron percnopterus)* has been definitively expelled from the Sierra de las Cabras, at La Serena (Badajoz) [3].

In the Monfragüe National Park (Serradilla, Jaraicejo, Malpartida de Plasencia, Serrejón, Toril and Torrejón el Rubio, Cáceres province), the problem with

Figure 3.
Bonelli's eagle adult and chick in the nest. Photo M. Calderón.

Figure 4.
Griffon vulture on black vulture nest after expelling the owners. Photo A. Rodríguez Martín.

reference to the griffon vulture has similarities with what happened in the La Serena region, mentioned above.

At the end of the last century, the population of griffon vultures in Monfragüe was about 250 breeding pairs, which nested on the numerous cliffs on the banks of the Tagus and Tiétar rivers that cross the national park, and on the steep slopes of its mountains. In 2020, the census of breeding pairs of griffon vultures was 700 and 350 of black vulture (*Aegypius monachus*) [4].

In recent years, griffon vultures have expelled exactly 75 pairs of black vultures (*Aegypius monachus*) from their nests and have occupied them with their spawn. Black vulture pairs have been displaced from their platforms (tree nests) by the pressure exerted by the high number of griffon vulture pairs (**Figure 4**) [4].

The black vulture is a species classified as vulnerable due to its low population. The griffon vulture is not included in the catalog, because it is a species without conservation problems.

The griffon vultures of the Monfragüe National Park have traditionally been feeding on the carcasses of deer, wild boar, and domestic cattle, existing in the farms adjacent to the park, maintaining a population with a little upward trend. In recent years, their number has increased, due to the greater availability of food. Two farms, located in the nearby village of Acehuche, and some others arround, deposit the corpses of pigs and chickens that die in their facilities, in landfills set up for this purpose (**Figure 5**).

In addition to the “upheaval” in the griffon vulture population, caused by these permanent contributions, another ghoulish species has changed its wintering quarters, conditioned by the food source. It is the egyptian vulture that gathers an important nucleus of wintering individuals: between 125 and 140 specimens. For the egyptian vulture to nest in the park, it has been necessary to intervene by adopting some ledges and caves (reducing the entrance hole), to prevent the vultures from also displacing them from their nests. The conditioning of Egyptian vulture nests so that the griffons cannot enter, or at least it is more difficult for them, has been carried out throughout Extremadura [4].

Black stork is pressured by griffon vultures in other places. An example: a black stork nest located on a pine tree, which had been used annually since 1977. In 1990 it moved and built a new nest on a rock, next to the Alcántara water reservoir. There

Figure 5.
Farmers deposit the corpses of pigs and chickens that die in their facilities, in landfills set up for this purpose. Photo A. Rodríguez Martín.

it raised 4–5 years until a couple of vultures occupied the nest and was breeding in it for years. The pair of black storks did not reproduce for 4 years. In the fifth year they settled on a pine tree where they stayed for a few years. Again it goes to another rock near the reservoir, surrounded by breeding griffon vultures, it was successful for another 4–5 years and in the end it was also displaced by griffons, this has happened 3 years ago and we have not located the nest of this couple or their descendants [4].

In this case, the difference in the breeding season gives an advantage to the vultures that begin to reproduce in January, while black storks do not return to Spain, from Africa, until the middle of March (**Figure 6**).

There are 7 pairs of Bonelli's eagle in the Monfragüe area. Four of them reproduce on trees. Problems with Bonelli's eagle nests due to its occupation by griffon vultures have occurred frequently in Extremadura, especially those found in the rocks. In Monfragüe, in particular, there was an even more striking case because a

Figure 6.
Vultures begin to build their new nests in January. Photo M. Calderón.

Figure 7.
Vulture fight. Photo M. Calderón.

Bonelli's nest installed in a cork oak, tucked between the branches where it seemed that the vultures could not reach, but the nest was occupied by vultures [4].

The density of the vulture population in Spain already seems excessive. The SEO/Birdlife Census of the year 2018 [6], calculates in more than 100,000 specimens This number has been reached by the creation of feeders for scavengers. There is not so much carrion in the field to feed such a population. If it were not for the artificial help of the feeders, the population would maintain numbers more in line with the natural availability of food and its behavior would not have been stamped, dedicating itself to waiting for daily or weekly food, without search effort or natural selection of specimens for playback.

It is common, from what has been observed, that initiatives to support a specific animal species have a beginning, but not an end. We think it should not be so complicated to close the project and start a new one to help a different species. A rethinking of the role of artificial feeders is necessary. The negative impact on other endangered birds is being caused, now, by the same vultures that are being helped, due to lack of control of their density and the unlimited growth of their populations (**Figure 7**).

The times of hunting and dispersing poisons, which seriously harmed scavengers, are over (with a few sneaky exceptions). The logic of redirection and modification of permanent aid measures is imposed on griffon vulture populations, with control and limit to their density, based on calculations of space availability, and minimization of interference with other species of raptors. The policy of the more the better should not be continued.

The vultures have become artificially fed "urban park pigeons". Not so harmless, because they no longer fear the human.

2.2 The case of the greater flamingo

The greater flamingo (*Phoenicopterus roseus*), which nests in various colonies around the Mediterranean on the NW Africa, has increased its population a lot, thanks to the actions carried out in the two largest colonies in the area: La Camargue (France) and the Laguna de Fuente de Piedra (Málaga, Spain), and which have led to the expansion of the species and the creation of breeding colonies in Delta del Ebro, Castilla-La Mancha, and Alicante.

With the perspective that elapsed time gives, it is easy to judge the actions carried out years ago, undoubtedly done with the best intention because then, it was impossible to foresee the development of the events and the impacts caused.

In the Camargue (France), techniques of attraction and habitat management were used to secure the colony of flamingos that, for decades, had visited the Rhone delta and installed their colonies annually, with variable success. Among other measures, an island was built specifically designed for the installation of a large breeding colony, carrying out steps to achieve its settlement, such as the preparation of hundreds of mud cones, imitating the beginnings of nests, distributed throughout the artificial island, which it was a claim accepted by the birds [7, 8].

In Fuente de Piedra, [9] *quotes verbatim*: "According to [10] this species was not particularly abundant in the past in this area, and the management measures aimed at promoting its breeding in Fuente de Piedra [11] the disappearance of nearby wetlands that they formerly used, such as the Lantejuela lagoon [12] and the creation of the extensive fish farming farm at Veta la Palma, have been able to contribute to the increase in population. of flamingos from Fuente de Piedra and their presence in the Doñana National Park. ICONA bought the lagoon …

The specific objective of the Fuente de Piedra nature reserve was the increase in the flamingo population [13, 14] "something unprecedented and probably unthinkable in the case of much more threatened species (but not so big and pretty)" [15].

They followed in the footsteps of La Camargue, conducting, creating and adapting the island of Senra and making and installing a certain amount of clay cones to attract flamingos.

The flamingos of the Fuente de Piedra colony have no sufficient food resources, neither in the lagoon nor in the surroundings. They must make a flight of about 350 km (round trip) to the marshes, rice fields and lagoons of Doñana, to meet their needs and bring food to their chickens. These flights are performed at night [16].

"Since the 1960s, the density of flamingos has doubled in Spanish wetlands due to the combination of species management (including measures to ensure nesting, more frequently than would be natural for this species) and destruction of many wetlands outside the breeding season. The destruction of submerged macrophyte grasslands harms ducks and coots" [15] (**Figure 8**).

Figure 8.
The density of flamingos has doubled in Spanish wetlands. Photo A. Amor.

"Since the eighties of the last century, monitoring and management of the species have been carried out in our country, which has contributed to reproductive success and, therefore, to a notable increase in the population" [17]. Breeding colonies were started in Doñana, Marismas del Odiel, Delta del Ebro and in some lagoons in Albacete and La Mancha.

In the Mediterranean biome, because of climate change and desiccation caused by human action, there is a significant reduction in the surface of wetlands and the duration of their hydroperiod "This fact, together with conservation policies and exploitation by flamingos from alternative artificial habitats such as rice fields or aquaculture ponds, has caused an increase in flamingo populations in the south of the Iberian Peninsula [18]. The traditional resources of the flamingo (*Daphnia sp*. and other small aquatic invertebrates) are insufficient. The flamingo has explored and found in rice, a magnificent new source of nutrients.

"In the case of the greater flamingo, their way of feeding, trampling, and stirring water and sediments, produces changes in the turbidity and distribution of

Figure 9.
Flamingo's way of feeding, trampling, and stirring water and sediments, produces changes in the turbidity of the water. Photo A. Amor.

nutrients [19] and reduces the cover of submerged plants, promoting a change of waters clear (dominated by submerged macrophytes) to cloudy waters (dominated by phytoplankton) [20]). Therefore, an increase in the density of flamingos or geese can cause (rather than indicate) major changes in wetlands (**Figure 9**) [15].

In 2020, 6,030 young were born in the colony of greater flamingos in the Fuente de Piedra lagoon, with a total of more than 10,000 reproducers. "Between the years 1984 to 2019 the flamingos have bred in 28 seasons and have not, due to insufficient rainfall, in eight. In that time, 388,046 breeding pairs have been established in the lagoon and 221,157 young have been born [21].

It seems clear that we do not have lagoons for all the flamingos that are born every year, not in Spain, but any of the Mediterranean coastal countries.

The increase in the flamingo population in Spain could harm, among many other aquatic birds, to marbled duck (*Marmaronetta angustirostris*), a critically endangered duck. As they coincide in a good part of its distribution area in Spain, the flamingo, "kicking" and stirring the funds to filter its food, produces the reduction of the "meadow" of submerged plants, which is the area where marbled ducks feed [10, 12, 22, 23].

"Besides, due to the particular way the flamingo feeds, it can mobilize the pathogenic bacteria found in the sediments while carrying out this activity, being able to promote the appearance of epidemics suffered by the marbled ducks and other aquatic birds in El Hondo in the last years." [23]. El Hondo is a reservoir located in the province of Alicante, close to the Mediterranean coast, 400 km to the east of Fuente de Piedra, which is used by flamingos as a wintering area, with censuses close to 2000 specimens.

In the Spanish region of Castilla-La Mancha, located in the center of the peninsula, the presence of flamingos in its network of endorheic lagoons has been testimonial until recent times (**Figure 10**).

The runaway increase in population density has led the flamenco to disperse through other lagoons in the center, taking with them environmental problems and deteriorating the already poor quality of its waters.

According to the calculations of the NGO Ecologistas en Acción, a total of 9,000 flamingos are distributed by the lagoons of Castilla-La Mancha. "It is a species that can alter lagoons, destroying submerged plant communities. They are altering the monitoring of the lagoons and the plant communities". "They destroy aquatic vegetation …" [24].

Figure 10.
Flamingos starting a new colony in the Manjavacas lagoon in Central Spain. Photo J. Porrero.

Its presence was relatively scarce until the end of the nineties, with colonies in the Pétrola lagoon, in the province of Albacete. In 2010, a breeding colony was installed in the Manjavacas lagoon (Cuenca), with a total of 2,500 adult specimens that produced 450 young.

According to [25]: "Physical alterations are evident in the case of the greater flamingo which is one of its forms of feeding behavior, leaves obvious craters of approximately one meter in diameter at the bottom of the wetlands it occupies. This modification of the sediment topography, in addition to hydrological changes, can affect aquatic vegetation ..." (**Figure 11**).

An important opinion indicates [15]: "the density of flamingos has doubled several times in Spanish wetlands, due to the combination of species management (including measures to ensure nesting more frequently than would be natural for this species) and the destruction of many wetlands used outside the breeding season. The destruction of submerged macrophyte meadows by flamingoes, harms ducks, coots (*Fulica atra, F. cristata*) and other birds that depend on them, but may favor waders that prefer to feed in open water areas [12]. In part, this could explain the positive correlation between the abundance of flamingos and waders".

The increase in the density of the greater flamingo in Spain, and the Mediterranean area, is higher than what has been announced. The destruction of lagoons by the excessive number of flamingos is an indisputable fact, but it goes unnoticed. The turbidity of the waters after the flamingo flocks' search for food is something that cannot be seen from the shores.

The case of the flamingo is another example of management, in favor of a species, that has overflowed, causing enormous damage to especially fragile ecosystems such as wetlands.

It has never been a real endangered species. The interconnection between the Mediterranean and Northwest African colonies has been ensuring their survival and causing their overpopulation. This is another wrong case of "the more the merrier". Intervention is essential to limit the population of this species and to do it very soon.

Figure 11.
Flamingos leave obvious craters of approximately one meter in diameter at the bottom of the wetlands it occupies. Photo J. Porrero.

2.3 The case of the white stork

The white stork population in Spain decreased notably in the second third of the 20th century, after the closure of landfills in small rural towns, the centralization of waste treatment at the county level and, most likely, due to the increased use of Organochlorine insecticides such as DDT, which decreased the number of invertebrates in the field and could affect the fertility of storks.

The 1984 census of nesting pairs was 6,753 nests, with a decrease of 8% concerning the 1974 census and 47% regarding the 1957 census [26, 27]. Starting in 1984, the population grew again at a good pace, reaching the figure of 16,643 in the 1994 census, which meant a percentage increase of 146% [28]. There was a new increase in the 2004 census, reaching 33,217 breeding pairs: population growth of 100% (**Figure 12**) [29].

The changes produced in agricultural land, the use of insecticides and herbicides, the intensification of crops, the disappearance of puddles and small wetlands, have caused a change in the behavior of storks, at least in the province of Badajoz, both in their methods and places of hunting as in the specific object of their diet [3, 5].

There is an increase in the density of the white stork population in the province of Badajoz, coinciding with the figures from the censuses. A large part of that population no longer migrates. It remains in its breeding territories all year round. Winters are milder, due to climate change, and you have food

Figure 12.
Stork chicks just fed by the adult. Photo. M. Calderón.

Figure 13.
A decade ago this would be a flock of premigratory storks, now it is a pre-wintering flock. Photo M. Calderón.

resources at your fingertips, so you neither need nor compensate for migration to Africa (**Figure 13**) [3, 5].

The white stork hunting system is solitary during the breeding season. During the migratory season, and in winter, in their African territories, the group hunt in line, beating fields in search of prey [30].

As many specimens remain in Extremadura during the winter, without migrating, they use the same hunting technique as in Africa. In the La Serena area, it is common to observe, in recent years, groups of 40–60 storks in a line, advancing in unison, capturing any animal that moves in their path.

This hunting system - it is being observed - they have begun to use it also in the breeding season. In previous years, storks hunted in cereal crops, until the plants reached a height like their tarsi, not returning till after harvest.

Currently, they have been observed hunting, among wheat or barley plantations that exceed their height, to the point that they already dare to prey on Montagu's harrier young which they capture directly in the nests of this raptor located on the ground [3]. It is another proof of the stork's change in feeding strategy. Previously, it had been observed preying on the nests of smaller birds, such as the lark (*Alauda arvensis)* and, exceptionally, house sparrow adults (*Passer domesticus/hispaniolensis*) that install their nests in the vicinity of the white stork nests [5].

These new predatory behaviors may be due to the scarcity of common prey (Orthoptera, Coleoptera, amphibians and reptiles), being forced to increase the spectrum of prey.

The increase in the density of storks in Extremadura, due to various causes in which man has always intervened, has caused an ecological problem of great importance but truly little visible: it is the enormous decrease in amphibians and reptiles, even when they keep in the small ponds in which the first ones reproduce. The constant predatory pressure of white storks on amphibians in humid areas, which are rare in the region, has led to the virtual extinction of these groups, with no specimens being observed or heard in areas where, until about 7 or 8 years ago, were relatively abundant (**Figure 14**).

As an example, a case followed in detail: This is a section of the Ortigas river as it passes through the municipality of La Guarda (Badajoz).

Figure 14.
Stork hunting alone. Photo M. Calderón.

Until 2012, there was a variable number in that stretch of the river, 9 stork nests in the trees of the river and 3–5 on the roof of the village church. In spring and summer, the nocturnal songs of toads, toads and frogs were heard, according to their different periods. In 2014 another colony of storks was installed with 8 new nests. Since that year, the silence of the amphibians is permanent.

A quick and reliable way of dating the abundance of reptiles and amphibians in that area was to travel a 6 km stretch of the road that connects the town of La Guarda with Campanario (10 km.), With little traffic of vehicles during the day, and width of 5 m, noting the snakes run over and those that cross from one side to the other (*Malpolon monspesulanus, Zamenis scalaris*). Upon return, several stops were made to observe, at different preset stations, the density of ocellated lizards (*Timon lepidus*.) in the rocky areas near the road [31].

The same road can serve as a measurement and sampling unit for the density calculations of some amphibians (*Epidalea calamita, Pelobates cultripes).* To do this, a night in April had to be chosen, after a rainy day. The transit of amphibians between small ponds, in search of a mate, reached such densities that, in some sections, it was impossible to continue driving, being necessary to travel the road on foot, so as not to kill dozens of amphibians by crushing [31]. Some data for the years 1973–1990 reached 3 snakes/km and 20 amphibians/km, with some concentration points of 78 amphibians/100 m.

At present, with a somewhat higher frequency of passage of cars, the finding of a snake run over is anecdotal, and the passage of amphibians is imperceptible or non-existent.

The trophic chain must be conserved based on the proportional balance between the species that make it up. An increase in predators means a decrease in prey. When the number of predators is excessive, the usual prey disappears, being replaced by others that are not prepared for the new threat, entering a disadvantage. In the case of the white stork, its predation, in such high numbers, is causing the disappearance of amphibians and reptiles in surrounding areas.

This situation could be extrapolated to the rest of the Spanish territory. There is a lack of studies that quantify it, urgently, so as not to be too late, as usual …

Figure 15.
Cattle heron on a sheep. Photo F. del Río.

2.4 The case of the cattle heron on the Island of Lanzarote (Las Palmas Province, Canary Islands, Spain)

Cattle heron (*Bubulcus ibis*) makes migratory movements from Africa to spend the winter in the Canary Islands, due to the lack of food at that time in Africa, returning to the continent to reproduce.

Accidentally a wounded specimen could be cared for by a human and attracted a couple, getting to reproduce on the island of Lanzarote and starting a breeding colony on the island, which reaches 1,500 individuals (**Figure 15**).

This population, that nest in the city of Arrecife, the island's capital, is seriously endangering the conservation of endemic reptile species, which they capture as the basis of their diet. The authorities do not solve the problem firmly. They are allowing the disappearance of reptiles and causing damage to other species of birds on the island (**Figure 15**).

An island is a very sensitive ecosystem. Not acting is irresponsible [32].

2.5 The case of the northern raven on the Island of Fuerteventura (Las Palmas province, Canary Islands, Spain)

The population of northern raven (*Corvus corax canariensis),* an endemic subspecies of the Canary Islands, "reaches 1,300 specimens, according to the General Directorate of the Environment of the Canary Government, which rejects that they cause significant damage to livestock" (**Figure 16**).

"According to the study carried out in these four years by the General Directorate for the Fight against Climate Change and the Environment of the Government of the Canary Islands on the population of crows in Fuerteventura and the control of the damages produced in the field and livestock, the number of

Figure 16.
The northern raven (canary race) has reached overpopulation on the island of Fuerteventura. Photo F. del Río.

specimens would be around 1,300 with a density fluctuation between 0.81 and 0.96 individuals per square kilometer. In terms of damage, only six incidents per year have been reported in a total of 163 livestock farms, which indicates a 'very limited' incidence [33].

The incidence of ravens, "not so limited", occurs on endemic populations of reptiles, which are experiencing such loss of numbers that their survival is in danger. It is urgently necessary to establish limits to the density of the raven population [32].

Ornithologists residing on the island indicate that the increase in the density of this species has its origin in the contributions of farm animal remains, which are carried out weekly at two specific points on the island. The productivity of the breeding pairs of crows is currently maximum (4–5 chicks per nest). The high number of specimens, causes them to no longer find places to install their nests, even building them at an exceptionally low height, on fig trees. They warn of the impact they are causing on endemic reptile populations, seriously compromising their continuity [32].

The contribution of food by man has produced the desired effect, in its day, which was to increase the population of this subspecies of raven. However, a limit to its density has not been established. Once the recovery program has started, it has not been marked where to stop. If now the weekly contributions to the dumps were stopped abruptly, the ravens would have a much greater impact on their captures of reptiles, reaching a certain extinction. It seems urgent and essential, a biological control of the raven, to establish a number, in order to allow to maintain the subspecies and, at the same time and level, the endemic reptiles of the island.

In none of the above cases can the "the more the better" be validated.

There is no shortage of examples of very worrying situations, which reach this qualification due to the inaction of governments and "animalistic" civil society, which treats and grants animals the same rights as humans, and even more¨:

The case of "escapes" from private collections and zoos; the case of the release of pets, by individuals; the case of domestic and feral cats; the case of … so many cases …

3. Conclusion

"We are surrounded" is a phrase that indicates the imminent of losing a battle.

The fever of a new fondness for nature and the trafficking of exotic species, leads to conservationism and the authorities, to inaction in situations caused by alien populations of animals that have been introduced into the natural environment, intentionally (as experiments), by escapes from captivity or liberations due to thought and militancy, such as the American mink, in Europe.

We wish this epilogue is not the last cry for help in favor of various species, endangered by well-intentioned human actions, that have not foreseen the "collateral damage", or yes, in programs or actions for the recovery or reinforcement of populations animals, and that they do not seem to present a clear reading of the problems caused, nor do they seem to set limits to the density of the species.

Any project, or monospecific conservation program, must consider the effects that it may cause to other populations, set temporary limits, in the short term, in which the impact caused to other species is reviewed, and the performances reduced or suspended.

As humans, we have intervened and altered so many balances and ecosystems that we have a responsibility to mitigate the damage caused. 150 species are going extinct every day. We have lost forever, thousands of species without having come to know them. This is sad and irresponsible. It would be sadder, still, to allow those that we already know to be lost and not get to know those that remain to be discovered.

We have a lot of work to do. We have a lot of problems. We are surrounded ...

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Chapter 7

Rhea americana Distribution: Range Expansion and Introductions of America's Largest Bird

Everton B.P. de Miranda

Abstract

Species distribution is a good predictor of several important traits, including threat status. Additionally, species expanding out of their original range can become invasive and this trend must be evaluated objectively. The greater rhea (*Rhea americana*) is a flightless large-sized avian species that thrives on open landscapes of South America. The species has been affected by the conversion of their savanna habitat into cropland and pastures, as well as benefited from forest conversion into fields at neighboring ecoregions. I propose to evaluate those range expansions, contractions and extirpations, as well as to depict the current species distribution. Here I show that greater rheas have expanded their range out of the "dry lands diagonal" into degraded portions of forested ecosystems—more extensively on the Amazon Forest—while persisting in human-altered landscapes of their historical range. This suggests that the species is faring well regarding conservation, which does not justify its current status at IUCN. Additionally, the potential ecological interactions of the species in newly colonized environments must be investigated. The faunal savanization undergoing in the Neotropics accounts on many new ecological interactions, of which greater rheas are a relevant part. Future actions of management may improve the species conservation profile.

Keywords: Amazon, Arc of Deforestation, game bird, grassland, Greater rhea, restinga, savannization, soybean farming

1. Introduction

Species distribution mapping and modeling has been described as "measuring, weighting and studying the behaviour of ghosts" [1]. Subjected to natural and anthropic range contraction or expansions—besides anthropic extirpations—makes species ranges a shapeshifting subject that challenges scientific inquiry [2, 3]. The greater rhea (*Rhea americana*) is a species described as occurring in the "Neotropical Dry Diagonal" of open savanna landscapes in South America [4–6], composed by the Caatinga, Cerrado, Chaco and Pampa [4, 6]. Given that those ecosystems are under high rates of destruction [7], and that the surrounding close canopy forests are also being cleared by the expansion of cattle ranching [8, 9] leading to the savannization of their faunas [10], the understanding of greater rhea reaction to those drivers is of great interest. For instance, other species associated with open landscapes, such as the maned wolf (*Chrysocyon brachyurus*), have expanded their distribution towards the degraded sections of Atlantic Forest and Amazon Forest [11, 12]. Greater rheas by their time are known to have successfully established populations out of their range, most notably in Germany [13].

Greater rheas are the biggest birds in the Americas averaging 1.4 m and 23 kg, reaching 40 kg in large males [14]. They lay eggs during the dry season from June to September, which hatch in the beginning of the rain season from September to November [15]. Males are polygynous while females are polyandrous: females will move around during breeding season, mating and depositing their eggs with a male, and then mating with other males [16]. Males are sedentary, incubating and raising the hatchlings on their own [16]. Each nest is thus visited by several females, containing up to 80 eggs; each female lay 5–10 eggs per breeding season [17]. The average clutch size is 26 eggs per nest, laid by seven females on average [17]. Nests are shallow depression on soil, cleaned of vegetation debris [17]. Out of the breeding season, both sexes are social, and form flocks up to a 80 individuals [18], which facilitate vigilance toward predators [19].

As many large-sized species [20], greater rheas are of ecological importance. Feeding mainly on broad-leaved herbs, they occasionally eat fruit and invertebrates [21]. They are seed predators for many plant species in Cerrado, while dispersing seeds in a few cases [22]. They are occasional prey for pumas (*Puma concolor*), jaguars (*Panthera onca*) and solitary eagles (*Buteogallus coronatus*) [23, 24], while their eggs serve as food for several armadillo species [25]. Association with pampas deer (*Ozotocerus bezoarticus*) and guanacos (*Llama guanicoe*) is common on open fields for predator vigilance [26–28]. The species is considered Near Threatened by IUCN, because of habitat loss to agriculture and cattle ranching, which makes little sense (since the species occur in both pastures and plantations) and by poaching [29]. Furthermore, greater rhea distribution as shown by IUCN is grossly mistaken, showing the species occurring all over the Atlantic Forest [29].

The greater rhea is of high cultural importance in South America. Princess Therese of Bavaria [30] mentions the species' occurrence in a public garden of northeastern Brazil as early as 1888, and greater rheas remains nowadays as ornamental wildlife in Alvorada Palace, Brazil's presidential residence [31]. Greater rhea was an important source of feathers for dusters historically [5], and name a Brazilian national park [32], inspired music and several popular expressions.

In this paper, my aim is to describe the current distribution of rheas in South America, including their range expansion, introductions and extirpations. With this, I hope to provide basis to management and conservation activities dedicated to the species. An accessible, handy, single-source database approaching the species current distribution range is still missing from scientific literature, and is of prime interest in the context of wildlife conservation in anthropic landscapes.

2. Methods

2.1 Databases

I collected records of greater rheas with geographic references for all five countries that encompass their historical distribution: Brazil, Bolivia, Paraguay, Uruguay and Argentina. I used the three Citizen Science databases to obtain the data: WikiAves.com, EBird.org and INaturalist.org, chosen by the amount of available data and ease to extract it. Since my aim is to depict the species current distribution, I used recent records from 2003 to 2021. The greater rhea is easy to visualize and photograph, thus common in those databases. Consequently, I rarefied the data to one record per county per database (i.e. maximum of three records per county). I scrutinized the data for duplicated records, removing these. I inspected records on the southwestern limit of the species occurrence with attention for lesser rheas (*Rhea pennata*), which were removed. I did the same procedure for captive individuals labeled as wild. Individuals living in fenced or partially fenced areas such as large urban parks, if not dependent of supplementary feeding, were included in de database as wild. All records and their geographic coordinates can be found in Mendeley Data https://data.mendeley.com/datasets/fvwcwhwt9v/1.

2.2 Criteria for defining populations as native, introduced, or range expansion

I defined all population living within the diagonal of dry areas in South America (Caatinga, Cerrado, Chaco and Pampas domains [4, 6]) as native even if resulting from accidental or purposeful reintroductions if and only if within native range [33–35]. I made exceptions for individuals living in restingas (coastal savannahs over sand dunes) were the species did not occur historically. These populations on restingas were labeled as introduced. I used the same criteria for other populations outside of the dry area's diagonal, unless the population could result from natural emigration. Populations resulting from emigration towards forest domains—arising from forest degradation—were labeled as range expansion. Populations within ecotone areas were labeled as native, since several open-field species occur within grassland enclaves in a matrix of forest (e.g. marsh deer *Blastocerus dichotomus*, pampas deer, and greater rheas themselves [36–38]).

2.3 Mapping and vegetation cover

I collected vegetation cover maps for depicting canopy closeness from MOD44B.v006, representing areas currently covered by tall wood vegetation, not appropriated for rheas. The MOD44B.v006 image layer in the MODIS Vegetation Continuous Fields product provides a continuous, quantitative representation of global tree cover (greater rhea non-habitat) at a 250 m spatial resolution [39]. I used vegetation ecoregions from WWF categorization [40], chosen because it defines ecoregions as relatively large landscapes, each containing a distinct assemblages of species, with boundaries similar to the original extent of natural communities—prior to modern land-use change.

3. Results

I collected a total of 777 occurrences. The largest number of records came from WikiAves (496), followed by EBird (205) and then INaturalist (76). Most data are fairly recent, with the average year being 2017 and the modal year being 2019. Nine records refer to introduced populations, 68 to range expansion, and 700 to native populations. The current distribution of the greater rhea throughout the Neotropics is shown in **Figure 1**. Our map suggests that the diagonal of dry areas in South America is still a stronghold for the species. The northern Cerrado scrubland to wooded savanna macromosaic, mainly located in central Brazil, has an extensive patch of greater rhea populations. Important habitat extensions remain in Pampas (Argentina, Uruguay and Brazil), Beni savannas (Bolivia), and Caatinga arid lands in northeastern Brazil.

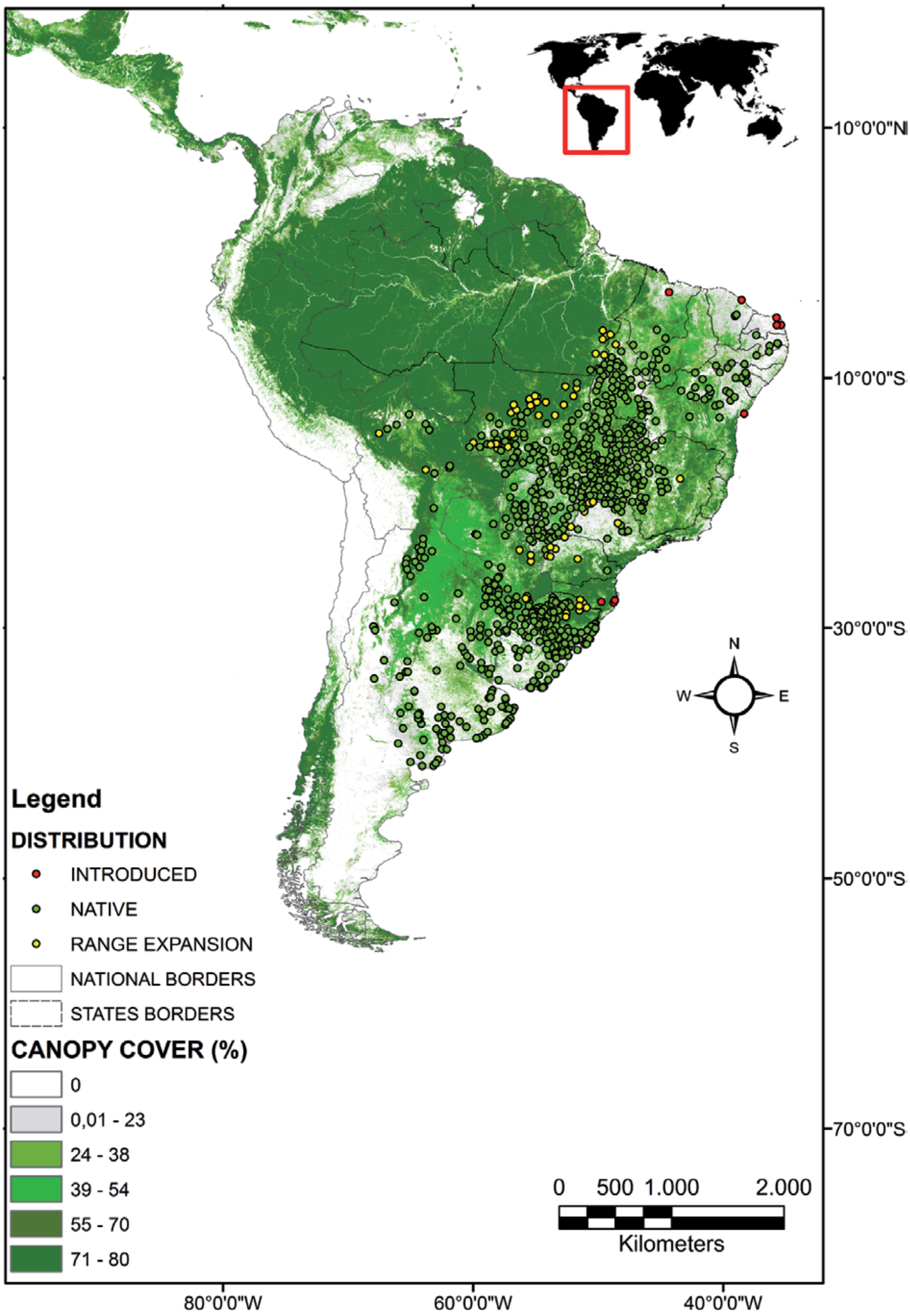

Figure 1.
Greater rhea distribution overlapped with the canopy closeness in South America. Both areas naturally open (as the Caatinga, Cerrado, Chaco and Pampa) offer natural habitat to the species, while deforested areas within formerly forested ecoregions (as the Atlantic Forest and the Amazon Forest) are occupied by range extensions.

Introductions of greater rheas have been recorded mainly within the restingas (coastal savannas over dunes) over Brazilian coast (**Figure 2**). Although out of greater rhea native range, the species thrive on such ecosystems as they present similar characteristics of their native savannas. Some of those records present individuals within enclosed areas, while other are free ranging, and others nowadays present vanished populations.

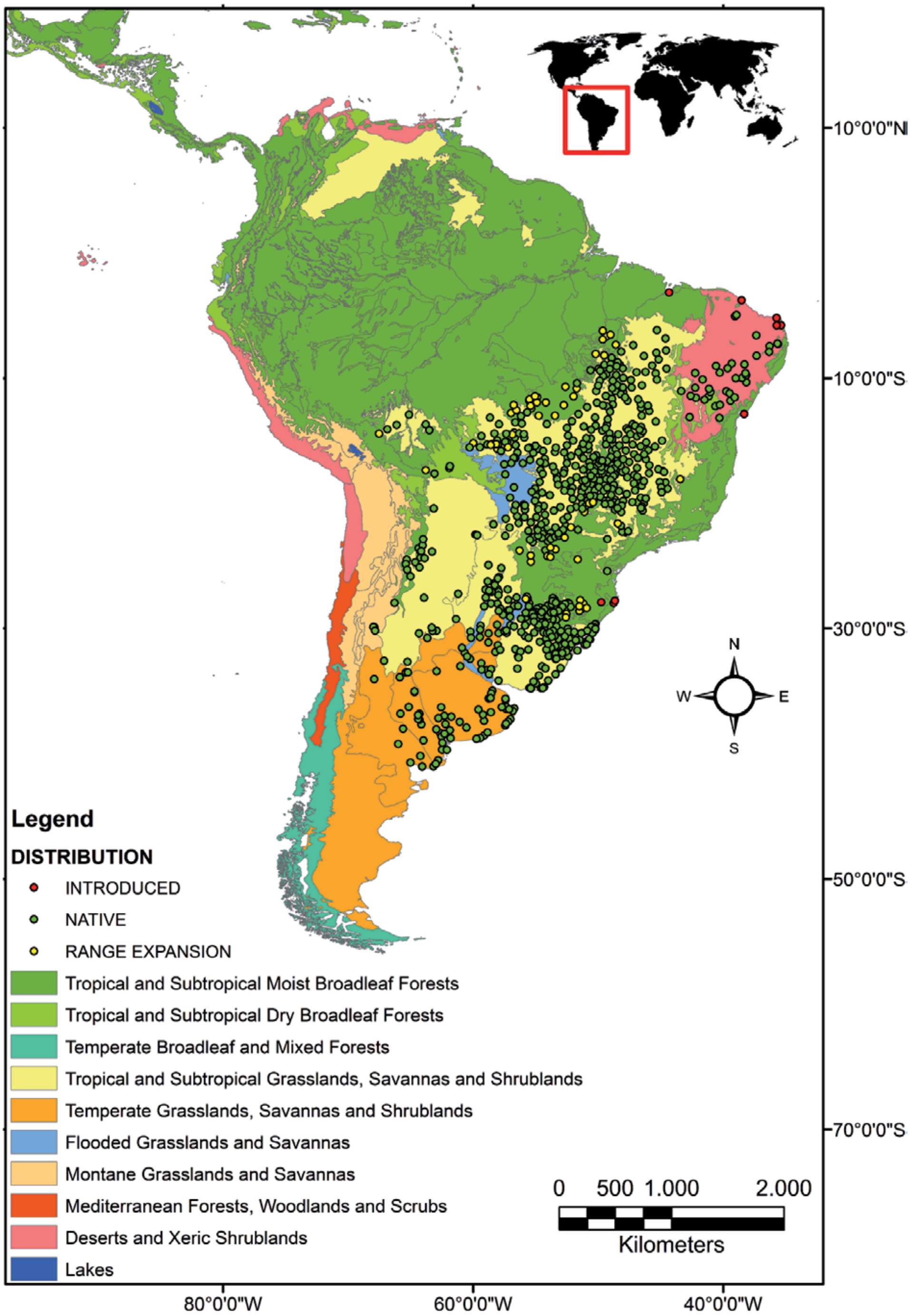

Figure 2.
Greater rhea current distribution shown overlapped with South America ecoregions. The species is frequently associated with savanna-like formations, and expanded its range towards forested regions after forests where degraded to give space to pastures and grain cultivation.

Range expansions are recorded on several savanna-forest transition zones, some of which allowed the greater rhea to expand up to 500 km towards formerly forested regions (**Figure 2**). An extensive area recently colonized by greater rheas is the southeastern section of the Arc of Deforestation, where greater rheas ride on the expansion of soybean farming. They are also found on degraded pasture, expanding from their natural habitat in the savannas bordering the Amazon Forest.

Extinctions of greater rhea happened over much of the savannas (Cerrado ecoregion) within the state of southeastern Brazil, as Minas Gerais and São Paulo. Both states have lost their rheas populations in areas where intensive agriculture—as sugarcane, eucalyptus and other non-open field crops—have been implemented. Hundreds of years of unregulated hunting, together with poaching after Brazil established wildlife protection laws, may also have presented a role over these range contractions.

4. Discussion

Greater rheas are present over much of their historical range, successfully adapting to human-modified landscapes. This adaptability allowed greater rheas to expand their range naturally, and thrive after introductions. Citizen-science databases continue to prove their usefulness, providing up-to-date data on species distribution that would be unfeasible if provided by traditional field-collection activities. Even after trimming, hundreds of recent records of greater rheas are readily available. Those records allow us to infer that the species continues to be present over much of its historical range over South America's "diagonal of dry areas". Additionally, they have been introduced into several spots at coastal Brazil, where some populations thrive. Besides these, large-scale range expansions exist in several parts of their range, with emphasis on the Amazon Forest. Those results are of prime importance for the species management and conservation.

One first element I call into attention is about the global status of the greater rhea at IUCN: the species is currently considered Near Threatened [29]. Pointing habitat loss as a problem seems a mistake, since the species is expanding range, including both soybean plantations and degraded pastures as habitat. Evidence towards this can be drawn from the fact that the species still presents big populations even within sections of central Brazil that have been dominated by farming (as Goiás state), where greater rheas subsist between cultivated fields, pastures and private reserves (as required by Brazil forest code [41]). On the other hand, poaching in northeastern Brazil seems to have limited the populations in Caatinga [42]. Since this is one of the poorest regions of Brazil [43], and at the same time one of the arid region of highest population density on Earth [44], the underlying reasons become obvious. This is especially worrisome because these animals appear to be under relatively isolation regarding the populations on Cerrado, and have potential to represent a subspecies endemic to the arid lands of Northeastern Brazil. Whereas they have been under the name of *R. a. americana* under old-fashioned taxonomy [45], this topic deserver further attention. The species global range and threat status deserves a reevaluation.

On the other hand, greater rheas have disappeared from several important protected areas in Brazil, which have been curiously less efficient in maintaining populations than the aforementioned private lands. Some of the more emblematic examples come from: (i) Águas Emendadas Ecological Station and Brasília National Park, both well-managed protected areas in Brazil capital where feral dogs and poaching eliminated the species [46]; (ii) Serra da Capivara National Park, where poaching and woody-vegetation encroaching eliminated the species [42]; and (iii) the Itirapina Ecological Station, where the reasons also seems related with poaching and feral dogs [47]. A tantalizing historical record of the species—which have been putatively attributed to Campos dos Goytacazes—is presented on an illustration at Rugendas *Magnum Opus* "*Malerische Reise in Brazilien*" [48]. Campos dos Goytacazes presents open habitat enclave in within the Atlantic Forest dense woodlands, conceptually known as Campos dos Goytacazes Gap [49]. With sandy soils and a rainfall limited to ~1000 mm/year [50], the region was originally covered by open vegetation ("campos" means field in Portuguese), and had historical attributes to hold a greater rhea populations. As described on the illustration itself, hunting may have caused the species demise in the region. Regarding modern species extirpations, the lack of management for feral dogs [51, 52] combined with the poor management of fires, lacking prescribed fires and consequently easing wild fires [53] seems to be worsening the species habitat transforming open field into encroached woodlands inside savanna protected areas.

Greater rheas present high management potential for its meat [54, 55], feathers [5, 54], hunting rights [55] and importance as a subsistence source of food [55, 56]. They should therefore be prioritized within the current discussions regarding wildlife management in Brazil [57, 58], a country that has no forms of wildlife use [59] and is watching several species of high potential to fade away through careless poaching [60]. Under the opposite paradigm, Germany has developed sustainable practices for hunting the greater rheas after few years of greater rheas invasion [13]. This can be a tool to trim the populations within the portions of the range where the species is expanding. Hunting can also stimulate reintroduction by the government or hunting associations within the former range. Similar phenomena have happened to other game bird species, such as the turkey (*Meleagris gallopavo*) [61]. Wildlife management is strongly present wherever larger wildlife is thriving [62], with South Africa, USA and Europe frequently cited as good examples.

One aspect of the species range expansion and introductions is the ecological meaning of greater rheas as seed predator and seed dispersers [22]. While the species seems strongly restricted to pastures and croplands within the Amazon, never being observed in forests or forest borders, populations in the coastal savannas probably interact extensively with native plant communities, which provide interesting research opportunities. Greater rheas and their eggs can also present a role as prey species for big cats and mesopredators on these systems. Checking out those interactions in the context of the savannization of forest ecosystems [10] may provide useful insights regarding ecological interactions of these areas. The introductions shown here may not sound as unusual as the species presence in Germany [13], but range expansions and introductions are known for several large, terrestrial paleognates such as the ostrich (*Struthio camelus*) [63] and the emus (*Dromaius novaehollandiae*) [64].

I consider the distribution presented here to be a work in progress, since I may have missed some previously documented occurrences, or listed some that are no longer considered valid since the species went locally extinct. Continuous updates of the list I provide, with subsequent editions as new information comes to researcher's attention, will provide a better basis for future work. I encourage my readers and colleagues to improve this checklist by providing information and references for any oversights or possible misinterpretations, as well as new published information as it becomes available. Another limitation is that I used the counties to prune the data and avoid crowding the map. Since county density varies widely, I emphasize that all states where the species currently occur have similar county density, except for northern Brazil (Amazonas and Pará) which are regions currently out of major rhea distribution.

5. Conclusion

In conclusion, I present evidence that greater rheas have been adapting well to man-made landscapes and is of minor relevance regarding conservation in most of its range. Populations within Caatinga in northeastern Brazil are an exception regarding this trend. Additionally, the species have expanded its range, most expressively in the Amazon forest, with unknown consequences. Introductions in several restinga locations also exist. Additionally, the species present potential as game, and this can contribute to their conservation. Finally, the open landscapes within South America are important refuges for the greater rhea, an under-studied, emblematic species of the savannas region in the Neotropics.

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Conflict of interest

There is no conflict of interest to be declared.

Appendices and nomenclature

A complete list of coordinates can be found in Mendeley Data (http://dx.doi.org/10.17632/fvwcwhwt9v.1).

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Section 4

Management and Conservation

Chapter 8

Management of the Barnacle Goose (*Branta leucopsis*) in Finland: Conservation versus Hunting

Heimo Mikkola

Abstract

The Barnacle Goose (*Branta leucopsis*) has had recent uncontrolled population increase in all of its northern distribution areas and is now one of the three most abundant goose species in the world. Not many birds, other than this have had such a naming mystery and a long time it was not known if the Barnacle Goose was a bird or a fish. So no wonder that also its conservation or possible hunting divides the opinions of people and authorities. This chapter is suggesting well regulated, sustainable, springtime hunting of these geese in such agriculture fields they will cause most serious crop losses. To be effective and meet public social approval, management actions must have a strong scientific basis and include an efficient monitoring programme. Necessary decisions to reach a consensus among stakeholders are discussed.

Keywords: Barnacle Goose, folklore, population increase, agriculture crop losses, hunting as a management tool

1. Introduction

The Barnacle Goose, *Branta leucopsis,* is one of the very few species of birds endemic to the north-east Atlantic region [1]. Nests have been found at heights of as much as 1,000 feet above sea level on steep faces of coastline. In these conditions, the parent birds are very successful in defending their eggs against predators explaining partly the success of this goose [1]. It belongs to black geese genus, *Branta*, with largely black colour separating them from the grey *Anser* species. First, the Barnacle Goose and the close relative Brent (or Brant) Goose, *Branta bernicla,* were previously seen as one species, but modern genetic analysis has shown that it is an eastern derivate of the Cackling Goose *Branta hutchinsii* lineage [2].

All Barnacle Goose populations are increasing, and growing geese foraging on cropland leads to serious challenges for many farmers. To prevent geese damage to agriculture farmers are seeking different tools to protect their crop. In Finland, the size of the migrating Barnacle Goose flocks are causing increasing human-wildlife conflicts (**Figure 1**). This chapter seeks a sustainable solution between conservation and hunting.

Figure 1.
Barnacle goose flock landing like the African locusts to feed everything on the farmer's field in Finland. Photo: Courtesy of Esko Rajala.

2. Barnacle Goose—a bird or a fish

A very old myth from 12th century in the western British Isles and Ireland said that this 'bird' is spawned from the goose barnacle ('Shellfish' genus *Lepas*) living on seawater [3]. According to the myth, the barnacles, which seemed to grow out of driftwood steeped in sea, were developing geese. And, indeed, people saw goose feathers in the barnacles' cirri which are feather-like feeding appendages the barnacle opens up in water into a fan-shape to catch food particles [4]. So the goose barnacle was giving the Barnacle Goose its English name and the scientific name, *Branta bernicla,* for the Brant or Brent Goose [5]. This myth persisted until the end of the 18th century. Somehow it is easy to see the logic of this myth as in those days these geese or their goslings were never seen in the UK or Irish summer, and so they were assumed to develop underwater in the form of barnacles. And fall gales often blew ashore driftwood full of barnacles just when the annual appearance of geese started through migration from their remote summer breeding grounds north of the Arctic Circle [4].

It seems clear that the well known Swedish taxonomist, Carl von Linné, also knew this old Middle Age myth, for he named the genus *Lepas* and two local species *L. anatifera* Linnaeus 1758 and *L.anserifera* Linnaeus 1767 ('duck-bearing' and'goose-bearing' correspondingly), and these pedunculate barnacles continue to be called goose barnacles [4].

Until relatively recently, Catholics in Contai Chiarrae (=County Kerry) in Ireland, who abstained from meat on the fasting days of the Church could still eat the Barnacle Goose because it was considered as fish [6]. These people did not know or care that Pope Innocent III (in 1215) had explicitly prohibited eating of these geese during Lent, arguing that despite their unusual reproduction, they lived and fed like ducks and so were of the same nature as other birds [7].

3. Distribution and population

Barnacle Geese breed mainly on the Arctic islands, Greenland, Svalbard, and Novaya Zemlya. Small numbers of feral birds, also breed in the Northern European countries and since 1971 a new population originally from the Novaya Zemlya has started to breed on the islands and coasts of the Baltic Sea [8]. Principal range states have been listed as: Belgium, Denmark (Including the Faroe Islands and Greenland), Estonia, Finland, Germany, Holland, Iceland, Ireland, Latvia, Lithuania, Norway, Russia, Sweden and the UK (Scotland) [9].

The Arctic Russia breeding population is migratory, the temperate Baltic breeding population, including the Norwegian Oslo Fjord breeding population, is also migratory but another temperate North Sea population, breeding in the Belgium, Holland, Germany and south-west Denmark is considered to be sedentary [9].

4. Global population estimates

Estimated population was 1960 ca. 30,000 individuals [10] but a worry was expressed that what happens to those birds after the nuclear tests of the Soviet Union started in Novaja Zemlja in autumn 1961. However, the size of the Barnacle Goose population has increased from 112,000 in the 1980s to well over 1.4 million in the 2010s [9]. Of all three populations listed above, the Russia, Germany and Holland population is currently the largest and it is expected to grow from 1.2 million in 2014 to 8.7 million birds by the next few years. Such an increase in population size is set to place further pressure on ecosystems, human health and air safety [9].

5. Barnacle Goose in Finland

The oldest observations known are 18 July 1840 from Sipoo and an adult male shot on July 1841 in Åland. After that more birds were seen in different parts of the country but one-third of these observations were made in the autumn [11]. Slowly the numbers started to increase and about 150 birds of this species were seen between Oulunsalo and Hailuoto between 24.-30.May 1954 [12].

During the spring migration 2,000 birds were seen in two days of May 1961, in Loviisa and 3,300 unidentified geese but some likely Barnacle Geese. The largest flocks were about 250 birds when other years before the flocks were much smaller [10].

In Finland, the Barnacle Goose has been breeding since the early 1980s [13]. The population size is now more than 14,000 individuals. Birds breeding in Finland head south later in the autumn than arctic breeders, and return north sooner in the spring [13]. A total of 3,421 have been ringed 1913–2019 (**Table 1**) and about half of those were goslings. There are 2,458 recoveries and 96% of those come from Finland. Some 80 per cent have been recovered alive, mainly by reading the ring number with binoculars or telescope. Before 2011 there were 11 recoveries from Holland, five from Germany, two from Russia, and one from Sweden [15]. Both of the geese shot in Russia were ringed as goslings in Helsinki and Kotka. The natal site fidelity is high as 13 goslings were recovered in subsequent summers on average 3 km distance (range 0–152 km). The longevity record for Finnish Barnacle Geese is 22 years 4 months and 17 days [15].

5.1 Remarks on other goose in Finland

Before the conservation and the management options concerning the Barnacle Geese it is important to see the situation of the other goose species in the country.

5.2 *Anser albifrons*

White-fronted Goose or Greater White-fronted Goose has holarctic distribution, predominantly in the tundra but to some extent also in the boreal climatic

Species	Ringed	Recoveries/Controls
Anser albifrons	8	0
Anser anser	1037	581
Anser brachyrhynchus	40	27
Anser erythropus	167	65
Anser fabalis	1618	9103
Anser indicus	15	44
Branta bernicla	25	3
Branta canadensis	891	691
Branta leucopsis	3421	2458
Branta ruficollis	2	4

Table 1.
Goose ringing in Finland 1913–2019 [14].

zone. This species shows a remarkable similarity in behaviour with the Greylag Goose and in the south, their breeding ranges are immediately adjacent [1]. White-fronted Goose does not breed in Finland but Siberian birds are seen in the country on migration, especially in autumn, sometimes in large flocks. The birds that migrate over Finland spend the winter around the North Sea [16]. The number of these migrants varies between 250,000 and 400,000 individuals [17]. Ringing results reveal that most of the breeding birds from western Greenland on their autumn migration cross both the interior of Greenland and the wide stretch of the Atlantic Ocean to winter in Ireland and western parts of Scotland and England [1]. Global estimates rank this goose the third most numerous goose in the world with some 3 million birds [17, 18]. Hunting is popular and given the size of the population the daily bag limit for White-fronted Geese was recently increased from two to three birds in the US Central and Mississippi Flyways [18]. Japan has the largest population of Greater White-fronted Geese wintering in eastern Asia [19]. Recent flocks of up to 100,000 birds are starting similar discussion on agriculture damages as the Barnacle Geese are causing in Finland [20].

5.3 *Anser anser*

The Greylag Goose is the ancestor of the domestic goose and in the historic times, the species nested over the whole of Europe, and even in northeastern Algeria [1]. Still, in the 18th century, the Greylag Goose nested on all the sea coasts of Finland. The increased traffic, cultivation of the suitable breeding grounds and direct nest disturbance were thought to be responsible for the great reduction in numbers of this species [11]. Therefore, it has ceased to breed over the great part of the earlier distribution area. Already in the 1920s, this goose was not breeding regularly in the Gulf of Finland and the bottom of the population was probably in the 1940s when only three pairs nested in the Gulf of Finland and 20 pairs in the Archipelago Sea [11]. After the species was given full protection in 1947 the slow increase started and in 1950 the population was estimated to be 150 pairs and 1955 already 250 pairs [11]. Then Greylag Geese started to return to breed along the entire coastal stretch of Finland but the majority of the population was found in the Gulf of Bothnia. The population kept growing and the full protection was withdrawn in 1960 [21]. In 1974 alarm bells were ringed again:" The populations of the Greylag Goose are alarmingly small and may be in serious need of protection" [22].

However, in 2010 the population was estimated to be 5,000–6,000 [23]. Nationwide surveys have not been very reliable but the population growth is believed to have continued until 2017 [21] when the breeding population was between 7,000 and 9,000 pairs [17]. After that, the population has started to decrease up to 20% per year as the hunting pressure has been too heavy. According to hunting statistics, 8,700 Greylag Geese were killed in 2017, and 2018 before the end of July already 6,300 had been shot [21].

A total of 1037 Greylag Geese have been ringed in Finland between 1913–2019 (**Table 1**). Some 25 per cent of the recoveries have been made alive. The Finnish Greylag Geese migrate to central and western Europe, as far as the Mediterranean region. Three birds have even reached northern Africa, two in Algeria and one in Tunisia [15]. The longest distance, 3,774 km, was covered by a goose ringed at Liminka Bay near Oulu and shot in southern Spain. Hunting accounts for 92 per cent of the known death causes [15].

No goose species can tolerate hunting pressure heavier than 20 per cent of the total population. In the case of Greylag Goose, this limit is now reached so the hunting should not be allowed from the fields in August before the normal hunting season. In 2018 almost 60 per cent of the Greylag Geese were hunted from the fields [21].

5.4 *Anser brachyrhunchus*

Historically, the Pink-footed Goose was considered as a subspecies of *Anser fabalis* but based on the mitochondrial DNA studies it was classified as a separate species [24].

Two biogeographical populations of Pink-footed Geese have been recognised: The western Iceland/East Greenland population wintering in the British Isles and the eastern Svalbard population staging in Norway and wintering in Denmark, the Netherlands and Belgium. Especially the western population has increased dramatically, approximately 10-fold between the 1950s and 1999 when the population was estimated to be 200,000–250,000 [25]. The population trend in the UK shows a 124 per cent increase between 1992/93–2017/18 and 67 per cent increase from 2007/08–2017/18 [26]. The late UK winter population estimates have been well over 500,000; in 2015 even 537,000 birds [27].

Similarly but only on the three-fold scale, the easter population has increased over the last decades on the high-arctic archipelago of Svalbard. In 1999 eastern population size was on the order of 32,000–37,000 individuals [28] when in 2011 it was already 80,000 [29]. Coinciding with the recent population increases, the wintering ranges of the western and eastern populations have come closer, possibly increasing the current rate of exchange between the populations [30]. The population increase and the change in the migration routes bring continuously more Pink-footed Geese in the Western part of Finland [17]. From the total European population of 80,000 birds, some 10,000 are estimated to migrate through Finland. The largest flocks during the spring have been more than 2,000 birds [17]. The continued growth of the Svalbard population is a conservation success story, yet its increasing population size, along with other goose species, has progressively brought them into conflict with agricultural interests as well as having other environmental and social implications. In particular, an increase in conflicts has been noted in Norway during spring. Furthermore, there is concern about degradation of vulnerable tundra vegetation in Svalbard due to increasing goose grazing intensities [31].

Management plan [32] is aiming that the eastern population size should be around 60,000 ensuring sustainable hunting in Norway and Denmark. New scientific evaluation could change the target population size following 'wise use' principals. The western population is huntable during open season in Iceland and the UK. The harvest rates are recorded in Iceland where ca. 15,000–24,000 Pink-footed Geese were shot annually between 2008–2019 [33]. The UK statistics are not so well kept (no bag reporting system in place to monitor hunting) but the indirect estimation of the Pink-footed Geese hunting in Britain indicated that about 25,000 birds have been shot annually [34]. Obviously, these hunting numbers had no negative impact on the Pink-footed Geese population as it still kept growing rapidly (67% in the last 10 years as shown above).

5.5 *Anser caerulescens*

The Snow Goose is native North American species but occasionally some individuals stray into Europe. Birds found in Europe are known to have nested in several countries and, for example, in the UK a few nestings have been witnessed almost every year in the 21st century [35]. In Finland, Snow Goose breeding was ensured for three consecutive years in the same Kirkkonummi archipelago between 1982 and 1984. In the 1980s, the species was in Finland more common than ever before or later. During the Atlas period, 2006–2010 only one breeding time sighting was made in Hailuoto [36]. **Table 2** shows that between 2008 and 2019 Snow Geese have been recorded 0–9 times annually, and no further breedings are known.

5.6 *Anser erythropus*

The Lesser White-fronted Goose resembles a small form of the White-fronted Goose, and undoubtedly these species are closely related, but the degree of mutual relationship is not clear [1]. The Lesser White-fronted Goose was once globally a common bird and the main wintering grounds at the Caspian Sea in Iran used to have at least 50,000 birds in the 1930s. In 1980 the amount went down to 4,000 to 5,000 individuals [15]. Enormous massacres of these birds have taken place in the wintering grounds in Japan, in consequence of which the species has become rare in eastern Siberia [1].

Before 2nd World War, the breeding population in Finland was estimated to be 2,100 individuals [17] when in 1955 same estimation was 200 pairs [11] and 1980 only 10–12 pairs [15]. The whole Fennoscandian population was earlier 10,000 pairs and was estimated to be only 15–25 pairs in 2008 [23]. The reasons for this drastic decrease are not well known but some changes in agriculture practices like the use of pesticides and strong industrial development in the wintering grounds are mentioned [23]. Despite the heavy decrease, the hunting was banned only in 1969 when there were no geese left for hunting.

Table 1 shows that 167 birds have ringed between 1913 and 2019. Three birds ringed as goslings in 1994–1995 were shot in Russia (one) and Kazakhstan (two) during their first autumn. The main cause of death has been hunting but only 11 wild birds have been ringed before 2011 [15]. One adult bird ringed in May 2006, in Norway was shot in Kerkinilake, an internationally known bird and biodiversity area (IBA), in Greece despite hunting is illegal in that area [37].

5.7 *Anser fabalis*

The taxonomy of the Bean Goose is still not fully resolved but current view divides the species into four subspecies: *A.f.fabalis, A.f.middendorffii, A.f.rossicus* and *A.f.serrirostris* [38]. The subspecies are also grouped into breeding forms that inhabit different habitats in Fennoscandia and Russia. The tundra breeding forms

Species	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019
A.c.	1	2	5	5	9	2	2	5	3	4	4	0
A.i.	45[1]	27	13	15[2]	11	9	8	15	14	7	9	11[3]
B.b.	9	4	6	15	8	4	10	3	4	7	8	3
B.r.	15	5[4]	14	5	18	16	18	12	21	44	18	40

A.c. = Anser caerulescens; A.i. = Anser indicus, B.b. = Branta bernicla hrota, and B.r. = Branta ruficollis.

[1] *Very good year for the Bar-headed Geese with 45 records, very early in the spring and late in the autumn, including first sure breeding in Finland. Kemijärvi parents with 4 young ones 14/06/2008 [66].*

[2] *A good year - 15 birds seen in 2011 [62] – the same report mentions that 2006–2008 was seen 40, 52 and 45 Anser indicus in Finland.*

[3] *Bar-headed Geese are now interpreted to be of natural origin, monthly numbers being April – 1, May – 8, June – 4, July – 3, August – 2, September – 11 and October 8. Liminka 6 individuals 13.9–1.10.*

[4] *2009 was a low year for the Red-breasted Goose – 5 records (mentions that 2008 15, 2007 9, 2006 7 and 2005 6 records).*

Table 2.
Rare goose recorded in Finland between 2009–2019 [54–65].

(*rossicus* and *serrirostris*) inhabit open tundra when the taiga forms (*fabalis* and *middendorffii*) inhabit open or wooded mires. Two forms differ slightly in colour, size and shape, especially bill colouration and morphology but the visual identification of each subspecies is not easy. Thus, the subspecies are not recorded in goose counts or hunting statistics [38].

The Bean Goose breeds mainly in northern parts of Finland, but occasionally nests have been found in bogs in Central Finland. The Finnish population estimated at 1,000–2,500 pairs [39]. The population has declined in the south due to heavy hunting from the fields [40]. A total of 1,618 Bean Geese have been ringed. The main cause of death is hunting, 89 per cent of the known causes of death. Twenty geese were predated. Out of the nine known predators, Golden Eagle is to be accounted for eight cases and White-tailed Eagle for one case [15].

The Taiga Bean Goose population was very low several years and the hunting was banned six years ago. Last year hunting started again in Lapland 20–27 August but only one bird per hunter and season are allowed and a bag reporting has to be made for each bird [40]. In the eastern part of the country, Tundra Bean Goose is much more common than the Taiga Bean Goose due to the migrating birds from Russia. These birds can be hunted from October to November but the catch has to be reported like in Lapland [40]. The genomic analysis has shown that over half of the Finnish Bean Goose bag consists of the declining Taiga Been Geese, which is far too many considering the fast decline of this subspecies [38]. The hunting of the Tundra Bean Goose with a large and stable population could be acceptable as long as it does not affect the Taiga Bean Goose population [38].

5.8 *Anser indicus*

The Bar-headed Goose breeds normally in Central Asia in colonies of thousands near high altitude mountain lakes and winters in South Asia, as far south as peninsular India (**Figure 2**). The grey goose genus *Anser* has no other member indigenous to the Indian region. The Bar-headed Goose is often kept in captivity, as it is

Figure 2.
The Bar-headed goose is one of the world's highest-flying birds and normal breeding areas often above 4,000 metres. Has recently bred in Finnish Lapland. Photo from Qinghai, China, courtesy of Coke and Some Smith <naturetraveler@msn.com>.

considered beautiful and breeds readily. Breeding feral populations have become established in Norway and England, where the feral population is believed to be declining due to over-hunting [41]. Recent observations in Finland and the first breeding in Kemijärvi in Finnish Lapland [42] are shown in **Table 2**. The Finnish breeding population varies from zero to two pairs and that of Europe from 10 to 30, respectively [17].

5.9 *Branta bernicla*

The Brent Goose is a rare breeder in Greenland (100–150 pairs), Svalbard (500–1500) and the Russian Arctic (400–600) [43]. Its European wintering population used to be large (> 240,000 individuals), and it did increase between 1970–1990 [44]. However, more recently the species has undergone a large decline (> 30%) overall and is now evaluated as vulnerable [43]. It is not known if the enormous increase of the Barnacle Geese would somehow explain the decrease of the Brent Goose. Indeed, there seems to be a possibility for the extensive food competition between these two species at least on the wintering grounds where they share the same tidal zone with coastal meadows, mudflats, or sand-banks [1]. It was interesting that in 1965 I only saw the Light-bellied Brent Geese in Kapp Linné, Svalbard, while now there would be more Barnacle Geese [45].

In Finland, the Brent Goose has never been common but in May 1954 a total of 20,000 were counted near Oulu [10] and that time the wintering population was estimated in Britain and West Europe to be only 26,500. Almost all of the birds seen in Finland are the nominate race *Branta bernicla bernicla*, though there are occasional sightings of the Eastern Siberian race *B.b. nigricans* which has a brownish-black belly and pale flanks [44]. There are also regular but few annual sightings of light-bellied *B.b.hrota* race from Greenland and Svalbard (**Table 2**).

5.10 *Branta canadensis*

The Canada Goose is estimated to be the most abundant goose species in North America, already in 2000, the population was between 4 and 5 million birds [46]. In recent years, the populations have grown substantially making it the most common goose in the world. The US goose harvest for 2013/14 reported over 1.3 million Canada Geese taken [47]. The Canada Goose was introduced to Sweden in 1930s – first shot in Finland 1955 in Hailuoto was thought to have arrived from Sweden [13]. Later it was also brought to Finland as a game animal in the 1960s but a self-sustained population developed much later, 1970s [15]. Nowadays 9,000–10,000 pairs are breeding mainly in the southern parts of the country [48]. The Canada Goose is well adapted to living in Finland and can even winter in Finnish waters. More commonly it migrates to winter in the southern parts of the Baltic Sea and Sweden, with a few birds migrating as far as Denmark or Holland [49]. In some areas, many consider them pests for their droppings, bacteria in their droppings, noise, and confrontational behaviour [49]. In Finland, these problems have been noted, particularly on the golf courses, in public parks and beaches, and planned communities. and pastures in the country. Hunting in Finland takes place from 10 August to 31 December and during the last twenty years, some 5,000 birds have been shot annually [50].

5.11 *Branta ruficollis*

The Red-breasted Goose breeds in a relatively confined area on the tundra of central Siberia east of the River Ob as far as the Taimyr Peninsula [51]. A large part

Figure 3.
An original Red-breasted geese papyrus painting from the Dr. Ragab's papyrus institute, Giza, Egypt. Photo: Heimo Mikkola 1982.

Range State	Compensation	Subsidies	Derogation and derogation shooting	Hunting	Other measures [1]
Belarus				X[2]	
Belgium	X		X	X	X
Denmark			X	X	X
Estonia	X		X	X	X
Finland	X			X	X
France			X	X[2]	
Germany	X	X	X	X	X
Holland	X		X	X	
Iceland	[3]			X	X
Latvia	X			X	X
Norway		X	X[4]	X	X
Sweden	X	X	X	X	X
Ukraine				X	X
United Kingdom	X	X	X	X	X

[1] *Other measures include for instance different scaring methods, providing alternative foraging areas for geese etc.*
[2] *In France, geese are hunted for recreational used only, and hunting is not related to agricultural conflicts.*
[3] *A compensation scheme is under development negotiation.*
[4] *Norway is not a member of the European Union and has a specific regulation rooted in the national game law.*

Table 3.
Management tools used for geese in European goose management platform range states [68].

of the population traditionally wintered in Kirov Bay in the Caspian Sea, but when vineyards and cotton replaced the cereal crops in the 1960s, the geese were forced to alter their migration strategy. Now the remaining population (less than 40,000 birds) winter in suitable habitats in Hungary, Bulgaria and Romania [52]. This may not be the first time when this species had to alter its wintering site, as during the antiquity the Red-breasted Goose occurred more frequently in Egypt [53] and is featured on ancient Egyptian paintings (**Figure 3**).

The first know record from Finland is from 6/10/1879 when one individual was caught in a snare in Sääminki [11]. **Table 2** shows that this species is becoming more common every year since 2005 but still there are no breeding attempts [54–65].

From the rare geese in Finland, the real expanders have been only the Red-breasted Goose and to some extent the Bar-headed Geese which are now counted as the natural origin birds in Finland. However, none of these species in **Table 3** could tolerate any hunting or other human disturbance [54–66].

6. Conservation

The Barnacle Goose conservation is regulated under the EU Birds Directive and it is also listed on Appendix II of the Bern Convention [67]. So the species is protected from hunting. An International Single Species Management Plan for the Barnacle Goose covers all three populations: (1) The East Greenland/Scotland & Ireland population, (2) the Svalbard/South-West Scotland population and (3) the Russia/Germany & Holland population [9]. This report aimed to provide a framework to coordinate management measures in the Range States in a manner that is consistent with their legal obligations (**Table 3**).

Table 3 shows that nine out of 14 countries use various forms of financial tools to reduce economic losses due to goose foraging. Twelve countries are using also other measures such as different scaring methods or provision of alternative foraging fields for geese. Eight countries practice derogation or derogation shooting. All the Range States have an open season for goose hunting [68].

7. Sustainable hunting

With population sizes still rising, the IUCN lists the species' conservation status being of Least Concern (LC) [69]. However, as at present, the Barnacle Goose has the protection of endangered species based on the Nature Conservation Act. The coverage of monitoring of agricultural damage and conflicts is poor. Information is merely based on annual compensations applied and paid to farmers.

The authorities should declare the Barnacle Geese as overabundant and allow a sustainable spring harvest which should be allowed only on farmlands to attenuate goose damage to crops at that time. The spring harvest could be considered also as a conservation strategy to protect the goose habitats. It is expected that very soon the rapidly increasing population will exceed the carrying capacity of their breeding areas and in winter some marshes heavily used by the Barnacle Geese become completely denuded (cf. [70]).

Sustainable hunting is defined as" the use of wild game species and their habitats in a way and at the rate that does not lead to the long-term decline of biodiversity or hinder its restoration" [71].

Knowing that far more than 800,000 Barnacle Geese are feeding during the spring migration the valuable crops, especially in eastern Finland, it would not be too much to hunt 15,000 birds to compensate the crop losses. That would not reduce the total population more than two per cent even if assuming that each killed bird would have got two goslings next breeding season in the north. With the same assumptions (50:50 sex ratio, two flyable young/pair, and 10% predator losses from the total population) the autumn population would be 1,059,750 individuals despite the proposed spring harvest in Finland. If we would plan to establish a target spring population between 750,000 and one million, this calculation shows that there is a safe room for the autumn harvest of some 60,000 birds.

It is a common opinion in Finland that only two most common geese species can and should be hunted. These species are Canada Goose and Barnacle Goose. Hunting of these two species would not cause any identification problems, as more rare and fully protected Brent Goose has no white in the head and all *Anser* species are grey distinguishing them from the largely black *Branta* genus.

There is now an official petition for the people to sign on the internet to demand the government to reconsider its decision not to allow the hunting of the Barnacle Geese in Finland although it is the far most common geese in the country and causing a lot of problems to the farmers, golf courses and city parks etc.

Same time the hunting of the much less common Greylag Goose and Taiga Bean Goose could be terminated until the population will recover also [21].

New management actions must have a scientific basis, result from a consensus among stakeholder, and include an efficient monitoring programme (cf. [70]). Different stakeholders should include representatives of farmers, hunters, birdwatchers, conservation associations, and local, regional and national authorities. These people should meet annually to share current information about the Barnacle Goose population and to discuss their respective concerns (cf. [70]).

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Chapter 9

The Conservation of European Goldfinch in North Algeria

Bara Mouslim

Abstract

This chapter presents the conservation status and threat of the European goldfinch *Carduelis carduelis* in Algeria. Many selective pressures run into this passerine, mainly human pressure due to keeping and hatching the birds in captivity. Illegal trading is actively carried out between countries of North Africa (mainly the pathway Morocco – Algeria – Tunisia). This situation is clearly expounding a threatened status of this songbird. A scientific survey was done in north center of Algeria to assess the captivity rate of goldfinch. Systematic sampling was done in several houses of Bouira district. Goldfinch breeder's age varies between 20 and 40 years. No income and no fixed job are the main reasons for these breeders. Results exposed serious threat of this species in center of Algeria. Management plan and conservation directions have been proposed for this species.

Keywords: Algeria, conservation, status, goldfinch, *Carduelis carduelis*

1. Introduction

The human-animal relationship is defined as the degree of proximity or distance between animal and human, this mutual perception which develops is expressed in their mutual behavior [1]. We are currently living in an area marked mainly by a drastic erosion of biological diversity, although we do not know the real number of species inventoried in our planet. Their rate of extinction is estimated to the order of 100 to 1000 times greater than normality. In addition, several thousand endangered wild animals are poached by humans for: furs, tusks, scientific experiments, and domestic collections. Many species are endangered, according to the IUCN report: every day around the world 15% of all species are threatened [2]. There have always been species that have disappeared throughout the history of the earth (such as mammoths, dinosaurs, ammonites or more recently dodos and great penguins) and other current species that are in danger of disappearing like pandas, gorillas, orangutans, tigers, rhinos, and several species of birds. For example, it has been estimated that 50,000 monkeys, 350 million fish, 10 million reptile skins, 15 million mammal skins and 5 million birds are sold each year [2]. 47% of the wildlife captured for illegal trading come from South America, while the United States is the main market for this trade. A scientific report published in 2014 concluded that in 40 last years, more than half of the wild animals of the planet have faced this brutal situation. Alarming findings are well exposed in this report, because of the changes in the method of calculating the LPI (Living Planet Index) which offer a more faithful representation of the global distribution of vertebrate species [2]. The rest of the report is just as alarming, indeed, between 1970 and 2016, the monitoring of 21.000 mammals, birds, reptiles, amphibians, and fish population showing a decline rate of 68% [2].

An endangered species is defined by scientific authorities as: a species whose number of individuals has fallen sharply or will decline in future years if nothing is done to protect it. Depending on the greater or lesser danger in which a species is found, it is classified into one of three categories: critically endangered, endangered, or vulnerable [3]. Throughout ancient history, the evolution in social organization, human race has been articulated around two vital elements: water and food. In contemporary history, biodiversity has taken on a more important dimension in the space of human exchanges, linked to growth and reverse on the availability of biological resources and their sustainability. In contrast, we are currently living a new shift in concepts, and according to the eminent American environmentalist and writer Edward O. Wilson (1975): "The 'backbone' of biodiversity is being eroded. A small step up the Red List ladder is a giant leap towards extinction. This is just a snapshot of the ongoing losses globally".

Several scientists are proposing other regional indices for species conservation for more efficiency and more meaning. Among the animals that are experiencing a decline in their status and population, birds have experienced several forms of extinction and several species are disappearing each year. The European goldfinch *Carduelis carduelis* which was the subject of this study is critically endangered in Algeria and classified in the Bern Convention (Annex 2 - strictly protected species). In the contrast, its global status according to the IUCN red list is least concern "LC" [3].

In Algeria, population size of the European goldfinch has been declining gradually for several years. In East of country (mainly in Guelma and Souk Ahras forests), this passerine was known as a regular breeder [4, 5]. According to Algerian Forest Department report, the goldfinch which attracts by coloring of its plumage and its songs, is threatened by intensive hunting/poaching, and remains captured in cages for human pleasure of the ears and eyes. Poaching (during the breeding season) for domestic breeding of European goldfinches have been the main causes of the collapse of their numbers in the wild and the drop in their nesting success rate [5]. In addition, it is still considered as a cage bird which has caused its regression nationwide [6].

In 1970, need to reverse the trend of biodiversity erosion, many countries legislated creation of national parks. Since 1983, Algerian environment department started the creation of national parks and natural reserves. In 2002, during National parks of North Africa and the Middle East direction meeting, Algeria held first place in terms of the number of protected areas classified in these regions [7]. Indeed, Algeria has created eleven national parks to conserve heritage specimens in variety of ecosystems such as landscapes and forests. The creation of these protected natural environments aims to find sustainable balance between the biotopes and biocenosis that constitute them.

2. General view on the European goldfinch

2.1 Geographical distribution of the species

The geographical distribution of this goldfinch is very wide, it extends from the Atlantic (Ireland) through the Iberian Peninsula, the Madeira Islands and the Canary Islands, North Africa to Lake Baikal in the east of the continent, and this in a band centered on the temperate latitudes. In the north, the species reaches southern Finland and Scandinavia and follows southern Siberia. In the south, this population is fragmented in the extreme northeast of Africa and only becomes continuous from Asia Minor (Turkey). The species bypassing the Caspian Sea from the south linked in southern Central Asia and then joins Siberia via the Altai. An extension takes place in the western Himalayas. There are 12 subspecies that share this large area. Continental Europe is occupied by the subspecies "*carduelis*", which is known to be sedentary in most of its range. On the other hand, it has been successfully introduced in Australia, Bermuda, and the Azores [8, 9]. In the United States, its introduction dates to the early 1852s in Greenwood Cemetery (Brooklyn, New York) (**Figure 1**) [6].

2.2 Description of the goldfinch

The goldfinch has been raised in cages for an exceptionally long time for its beautiful plumage and remarkable songs. In some places, notably in the Mediterranean Basin (and mainly in Algeria) it is the subject of a real local culture, which has a negative effect on its ecological condition and conservation status. The impulsive attitude and spontaneous behavior, in fact hide some factors that illustrate its vulnerability. The destruction of the laying and the rejection of the chicks also add to the fate of the species in captivity. This songbird is easily suitable to the restricted space, but it is better off in an equipped aviary (trap doors/specific cage) where it can evolve and set up its breeding success.

Breeding is mostly done in pairs, but a triplet (male × female × female) can be attempted for better conservation of the species. The opposite case of breeding (male × male × female) is rejected due to territoriality. On the other hand, a conservation problem within the species arises in the case of informal breeding, in fact, the extrinsic hybridization of the species pairs quite easily, not only with the domestic canary (*Serinus canaria domestica*) but with other native or exotic finches, such as European greenfinch (*Chloris chloris*), European siskin (*Spinus spinus*), Eurasian bullfinch (*Pyrrhula pyrrhula*), common linnet (*Linaria cannabina*), even common chaffinches (*Fringilla coelebs*) and common crossbills (*Loxia curvirostra percna*) [11].

2.3 Anthropic pressure and threatened species

Thousands of species are endangered around the world due to natural habitats destruction, overexploitation, invasive species, climate change and pollution. All activities are linked to human activities. Thus, the main reason for species erosion is the illegal trading (**Figure 2**) [12].

The issue of illegal trading is treated almost systematically as an environmental problem, before being considered as criminal and transnational. It is run by

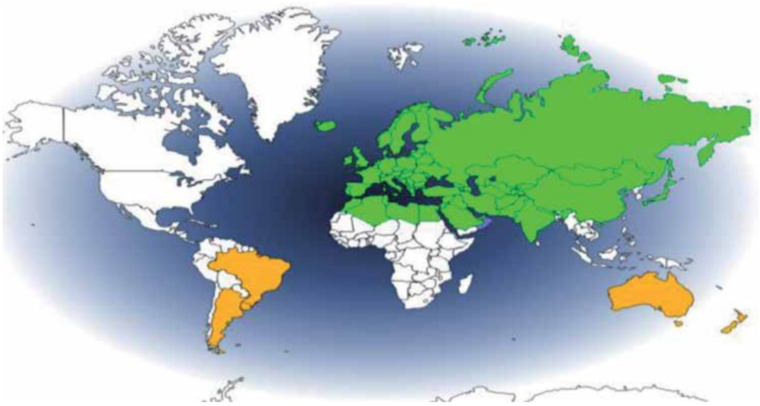

Figure 1.
Geographical map of European goldfinch distribution around the world and phenological status. Green part: Breeding species, blue part: Occasional species, Brown part: Introduced species [10].

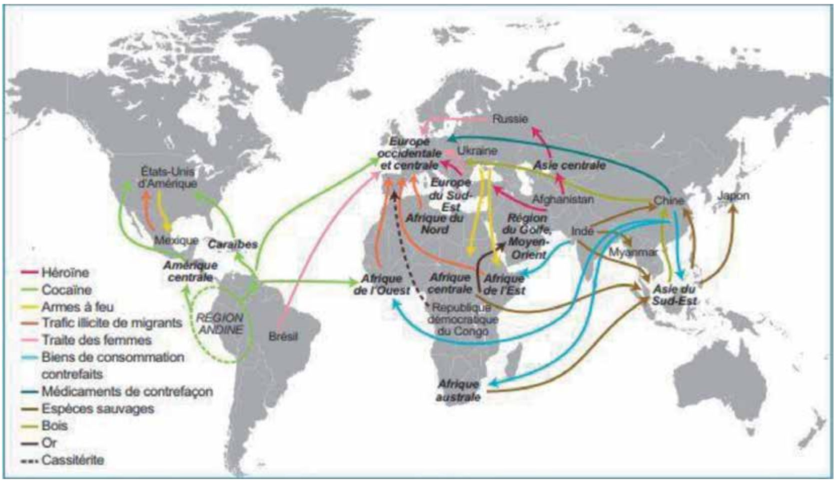

Figure 2.
International network of transnational organized crime way [13].

extremely well-organized networks of poachers, wholesalers, middlemen, smugglers, and retailers. Through these networks, the derivatives of illegal wild species find their way into the commercial chain, with prices increasing from links of this chain [14]. This illegal trade is estimated at 19 billion dollars per year [2]. United States is the first importer of exotic species, and then follows European continent and China [15]. **Figure 2** illustrates a simplified international way taken for various illegal activities, including illegal wildlife trading.

Specialized organizations prevent this illegal trading to conserve species by legal way of trading species (controlled process). This is the main aim of the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES), signed in 1973. This convention is one of the best known and most important environmental conventions. And often serves as an example, especially given the large number of signatory States. It seems obvious that a transnational problem such as this trading, a global action involved many international community parts is necessary. Non-governmental organizations (NGOs) have also established themselves as key players in CITES and participate in the conference as a part to this convention.

Recently, the United Nations is becoming actor to this process, by adopting a historical resolution on July 30, 2015 (resolution A/RES/69/314), which is related to illegal trade monitoring and taking measures against this [16].

2.4 Legal framework

Conservation of birds in Algeria is relatively recent since the first text relating to the protection of non-domestic animal species was dated on August 20, 1983. This action was subsequently consolidated, with laws about environment and hunting, i.e., the framework law of January 17, 1995 relating to non-domestic animal species protected in Algeria and the law n ° 04–07 August 1, 2004 relating to hunting.

3. Analysis of poaching and illegal trading of goldfinch

In Algeria, it has been noted that all captive goldfinches are originating from neighboring forests. This conclusion was reported in [17], where 70% of captive goldfinch were poached from TIKAJDA forest. The main species found in this town are becoming from local forest (Bouira, Boumerdes, Bejaia, Medea and Algiers). On the other hand, few proportions of *Carduelis* in center of country are becoming from West part of Algeria (smuggling network started from Spain and Morocco). Many scientific studies reported that Spanish or Moroccan goldfinch were observed in center and east of Algeria.

Scientific survey of goldfinch breeder's age shows that the age category interested in this bird varies between 20 and 40 years. Difficulty in social status no income and no fixed job are the main reasons for these breeders (**Figure 3**).

Many data on social classes of European goldfinch breeders in Algeria shown that unemployed persons are doing this poaching and illegal trading (**Figure 4**). This activity is less often done by students or retired persons.

This illegal trading is generating a high turnover. For example, in Bouira the price varies between 5000 DZD and 7500 DZD per individuals. This price never goes below 5000 DZA and in certain cases some individuals are sold at prices going up to 10.000 DZD or more. The European goldfinch trading in Bouira for one day can generate a parallel and informal market which is equal to more than 1.077.500 DZD and does not undergo any form of financial monitoring and control. This sum corresponds to 7000 Euro per day [17].

Social class is a deterministic parameter in the captivity growing of goldfinches in Algeria. The causes are multiple, due to social level of Algerian population and as well as to the intellectual development and responsibility of persons in preserving nature and protect wildlife species.

Algerian forest department said that a young breeder person, could aim to sell 5000 goldfinch individuals at Boumati market (El-Harrach – Algiers) for the price of 4000 DZD, while he acquired them at only 200 DZD from Maghnia market (Tlemcen) situated in Algerian Moroccan border.

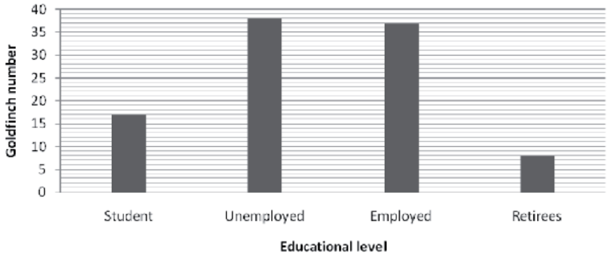

Figure 3.
Age distribution of the European goldfinch breeders in Algeria (Bouira) [17].

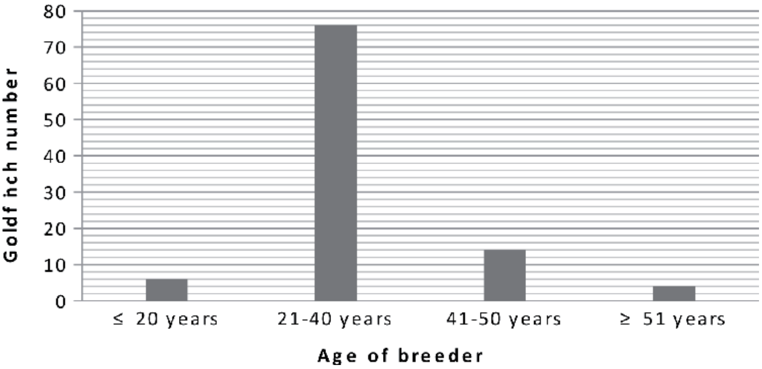

Figure 4.
European goldfinch breeder's educational level in Algeria (Bouira) [17].

The sum of 1.241.000 DZD shows that the trading of this songbird has generated a parallel and informal market which is illegal, and without any form of financial monitoring and control. All bird individuals supplied to the Algerian market are often sold wholesale to less than 20 MAD per unit by the Moroccan smuggler networks who transport them illicitly to Algeria. There the final price can reach up to 15.000 DA (around 1.400 MAD). On the Moroccan market, the single goldfinch is sold between 70 and 100 DH. The cost varies according to the talent of the bird and its age. An adult bird in Oujda market (Morocco) is sold 70–100 MAD, then transported to Algeria for selling between 20.000 DZD (corresponds to 1360 MAD). The young birds' price in Oujda varies between 30 and 50 MAD and selling price in Algeria is around 2.000 DZD (corresponds to 136 MAD) [17].

Warning results on this species and the number of birds in cages approved the causes of its extinction, indeed, during these last ten years the population of this passerine has been under a strong selective pressure and a decline in nature population. Many observations done by ecologists from Guelma university reported that in Guelma, Souk Ahras, Bouira and Algeirs forests the European goldfinch is almost missing [18]. According to Algerian forest department, an unemployed young person, had a project, to sell 5000 individuals in illegal market of Boumati (El-Harrach – Algiers) at 4.000 DZD, while he acquired them at 200 DZD only from the markets of Maghnia (Tlemcen) situated in Algerian Moroccan border [17].

Poaching and wild hunting decimated 80% of the goldfinch species in our region (Algeria). This problem is done by different techniques: poachers place a female goldfinch inside a cage to seduce the males who easily fall into the trap, the head dead, this technique allows non-selective capture of no less than 20 birds at a time [19] and the birds are captured also by glue. Bedhiaf and Kharoubi [20] report that the crossing of goldfinch in captivity is more successful with canary. This cross bird is highly regarded for its beauty and strong voice. The Environmental Protection committee proposed reducing this poaching by authorization certificate during the hunting season. Each breeder is not allowed to hunt more than ten goldfinches per trip which should protect this species [20].

4. Conclusion

The sum of 1.241.000 DZD shows that the European goldfinch trading generated a parallel and informal market, which is illegal, also without any form of financial monitoring and control. The goldfinch individuals who supply Algerian market are often sold at less than 20 MAD per unit to Moroccan smugglers networks. All birds are transported illicitly to Algeria. Their final price can reach up to 15.000 DZD (around 1.400 MAD). On the Moroccan market, the simple goldfinch is sold between 70 and 100 MAD. The cost varies according to the song and age of the bird. For example, the selling of this species in Oujda market (Morocco) varies between 70 and 100 DH. In Algeria, the selling price is reaching up to 7.000–15.000 DZD. The price of the young goldfinch individuals is between 30 and 50 MAD, then traded around 2.000 DZD (135 MAD) in Algeria.

Globally, annual data compiled by nature conservation authorities and non-governmental organizations estimate that the wildlife trade market (and among them the European goldfinch) generates an annual turnover of over USD 20 billion. Placing this traffic in third place after drug trafficking and arms trafficking [21]. These illegal practices are apprehended by the competent authorities whether it is the elements of the Algerian customs or the agents of Algerian forestry department.

Figure 5.
Thousands of goldfinch individuals resulting from illegal trading apprehended in the north-western region of Algeria near the Moroccan border [22].

Theses authorities organize each year the release of these birds confiscated from this traffic to maintain the natural population (**Figure 5**). The birds were observed in 2016 in Djurdjura National Park (TIKJDA sector) when 80 individuals were released [23].

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For many humans, birds are the most fascinating group of animals and they are definitely among the best-known and studied organisms. Thanks to global citizen science data, we know that there are some 50 billion individual birds in the world at present, which is about six birds for every human on the planet. Birds have an important role as indicators of the state of the environment, giving them high public value. Human-related global impacts such as climate changes and accelerating urbanization force extant species to continuous adaptations, population modifications, or even outright extinction. This book includes nine chapters covering such topics as bird genetics, the colour of avian plumage, conservation problems, sustainable hunting, habitat disturbance, range expansion and introductions, and long-term bird population changes and challenges. A key chapter explains the genetic rules and reasons why we have continuously more bird species in the world and why we may end up having 7,000 species more than the present 11,000 species.

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