

Indian Birds

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Aims & Objectives

- To publish a newsletter that will provide a platform to birdwatchers for publishing notes and observations primarily on birds of South Asia.
- To promote awareness of bird watching amongst the general public.
- To establish and maintain links/liason with other associations or organized bodies in India or abroad whose objectives are in keeping with the objectives of the Trust (i.e. to support amateur birdwatchers with cash / kind for projects in ornithology).



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Blue-breasted Quail
©Anwaruddin Choudhury

Front cover: Changeable Hawk-Eagle *Spizaetus cirrhatus* [Photo: S. Ramakrishnan. Southern India, October 2005.]. **Inside back cover:** Field sketch: Changeable Hawk-Eagle *Spizaetus cirrhatus* [Artist: Lester Perera (Sri Lanka)]. **Back cover:** Verditer Flycatcher *Eumyias thalassina* [Photo: Sumit Sen].

Taxonomy for birders: a beginner's guide to DNA and species problems

Norman Maclean, Martin Collinson & Richard G. Newell

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ABSTRACT The use of molecular data has revolutionised taxonomy. As a result, there is upheaval within national and regional bird lists, with new species splits and lumps and, perhaps more disruptively, alterations to the sequence in which families and species are listed. These changes, sometimes based on esoteric genetic or mathematical data, affect ornithologists and birders. In this paper, some of the basics of modern taxonomic practice are explained, and we show how these principles may be applied to genetic data to generate molecular phylogenies. Examples are used to illustrate how genetic data may resolve complex taxonomic problems, and also to show some of the reasons why DNA does not offer a simple resolution to the 'species problem'. There are no simple rules to determine species boundaries, and the use of molecular data does not yet change this. There are cases where different DNA sequences tell different stories, which can be different again from phylogenies based on morphological data.

Taxonomy allocates all birds to hierarchical groupings (e.g. orders, families, genera, species and subspecies) on the basis of the perceived evolutionary relationships between them (see reviews in Greenwood 1997 and Newton 2003). Conventionally, taxonomists have to draw conclusions on the basis of what, at some level of analysis, birds or other organisms 'look like', not only with respect to their morphology, but also how they sound and behave. It is tempting to assume that birds which look, behave or sound most similar are closely related. This is usually valid – but one problem is that distantly related animals or plants might look like each other because they live in similar environments. One simple example might be cetaceans, penguins and fish; they are all pointed at the front end and have smooth contours because they face the same environmental problem – moving through water without too much drag. Ignoring the possibility of so-called 'convergent evolution' may give false impressions of close relationships.

Modern taxonomy arranges organisms into groups – **clades** – largely on the basis of the presence of '**shared-derived characters**' (or '**synapomorphies**') (see Ridley 1986 for review). These are characters that several (but not all)

members of a species group have inherited from a common ancestor during the evolution of the group. For example, if a group of six closely related species (A–F) is thought to have evolved from a single red-legged ancestral species, and four of these species (A–D) have red legs, whereas two (E and F) have yellow legs, the yellow legs would be a shared-derived character – i.e. a new characteristic that has evolved by mutation from the red-legged ancestors (see fig. 1). In a cladistic classification, and in the absence of contrary information, it would be assumed that yellow legs evolved only once, in a common ancestor of E and F, and hence that both E and F are more closely related to each other than to any of species A–D. Of course, leg colour by itself does not prove anything, but if E and F also share other characters which the others do not (perhaps they both have a wing-bar while the other species do not), then bit by bit the evidence mounts that they really have evolved from a recent common ancestor.

To understand how cladistic taxonomy works, it is also necessary to understand the concept of **monophyly**. Any taxonomic clade (species, genus, family, etc.) should conventionally be **monophyletic**, which means that all members of the group should be

descended from a single common ancestor, and should contain all the descendants of that ancestor (see Collinson 2001). For example, the six species in fig. 1 form a monophyletic clade. In contrast, a taxonomic grouping is said to be **paraphyletic** if some of the descendants of the common ancestor are now excluded from the grouping. If species A, C, D, E and F in fig. 1 were in one genus (X), and species B was classified as belonging to another genus (Y), then genus X would be paraphyletic, since as one of the known descendants of the common ancestor of the genus would now be excluded. By convention, paraphyletic groupings are not allowed. Nor, conventionally, are **polyphyletic** groupings, where all the different members of a genus or higher taxonomic rank have evolved from a number of more distantly related ancestors. To a first approximation, polyphyletic groupings are a mishmash of distantly related animals, grouped together to the exclusion of more closely related animals. An example would be if we attempted to group cetaceans, penguins and fish together in an Order of 'swimming things' – in effect an extreme version of paraphyly.

Many superficial characters, such as leg colour or wing length, may change rapidly – indeed too rapidly and too

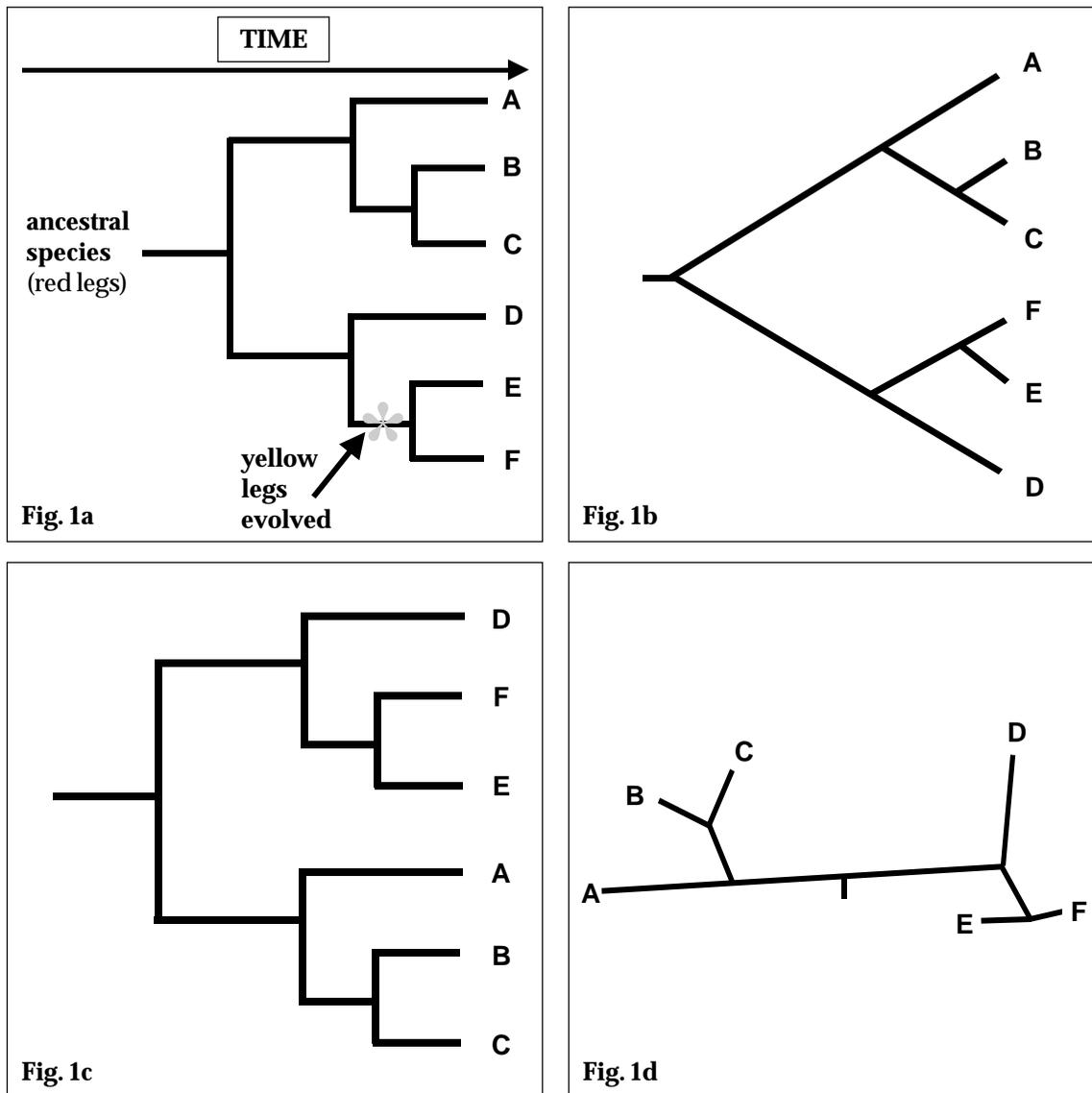


Fig. 1a. Phylogenetic figure adapted from Baldauf (2003), showing the relationships among six hypothetical species of bird, A–F (see also text). It postulates that a single ancestral species split into two separate species over evolutionary time. One of these species was the ancestor of A–C, the other was the ancestor of D–F. The A–C group and the D–F group may be regarded as separate clades (see text for definition). In the A–C clade, the ancestor of A–C split into two further species, one of which went on to become present-day species A, while the other subsequently underwent a further split to become species B and C. An identical process of evolution occurred in the D–F clade. Every branching point on the figure represents (in this case) a speciation event, and is called a node. The branches are internodes. Some methods of resolving the phylogeny (but not all) may allow the lengths of the branches to represent the evolutionary distance between the species (i.e. a rough measure of the length of time they have been separated).

The yellow legs of species E and F are a shared-derived character (synapomorphy), as explained in the text. This is evidence that they are sister species and would be used as such in the construction of the tree. If one of the taxa, say B, had green legs, this would be a unique-derived character (**autapomorphy**), but this is phylogenetically rather uninformative as it gives no clue to which of the other taxa are its closest relatives. The red legs of A–D are a retained ancestral character (**symplesiomorphy**) and are also phylogenetically uninformative (within this species group).

Fig. 1b–d. Note that the exact shape of the branches is of no consequence, such that figs. 1b and 1d present exactly the same qualitative phylogenetic information as fig. 1a. It is also possible to rotate the nodes without changing the phylogeny at all; fig. 1c carries identical information to fig. 1a.

All the trees in this figure have a root – the single earliest branch representing the common ancestor of species A–F. Roots can only be indicated if an **outgroup** (a taxon that is only distantly related to species A–F) has been included in the analysis (but not, in the cases above, explicitly shown on the tree). For example, if A–F were species of tit *Parus*, the outgroup taxon might be a species of flycatcher *Ficedula*. If an outgroup has not been included, it is not possible to indicate a root for the tree, but it is perfectly acceptable to construct and display an unrooted tree.

often to tell us anything useful about the evolutionary history of the birds. Experienced 'conventional' phylogeneticists are generally able to recognise which morphological or behavioural characters are likely to be phylogenetically useful. Nonetheless, the potential for physical characters to mislead phylogeneticists never really goes away. The use of molecular evidence (proteins and, especially now, DNA-sequence data) helps to get round this by offering an array of data that are closer to the underlying genetic base of the birds.

Species concepts and phylogenetic trees

Species concepts, as they apply to birds, have been reviewed extensively (Cracraft 1997; Collinson 2001; Helbig *et al.* 2002; Newton 2003; Parkin 2003) and we do not intend to repeat the arguments here. In broad terms, these can be divided into: '**biological**' species concepts in which species are defined primarily on the basis of present-day reproductive behaviour (a tendency not to hybridise); and '**phylogenetic**' or '**evolutionary**' species concepts in which species are defined according to their evolutionary history.

Phylogenetic trees, such as those presented in fig. 1, are reconstructions of the perceived evolutionary history of the taxa involved, based on evidence which can normally be obtained only from the present day. Whatever the species concept used, any speciation event where one species evolves into two species which no longer breed with each other can be represented by a node ('**branching point**') in a phylogenetic tree. Speciation may be due to range fragmentation (see Tokeshi 1999 for review). For example, many remote islands have endemic bird species, probably resulting from the chance arrival of vagrants and the subsequent evolution and divergence of these 'founders' away from their ancestral stock, with which they no longer breed. The separation of two species into different evolutionary lineages in a phylogenetic tree does not necessarily preclude the possibility of ongoing hybridisation. Over 10% of bird species have been known to hybridise with at least one other species in the wild (Grant & Grant 1992). Sometimes, especially when related species are fortuitously or

unwittingly) brought together, this hybridisation may be quite extensive. For example, Ruddy Ducks *Oxyura jamaicensis* breed freely with White-headed Ducks *O. leucocephala*. Hybridisation between Hawaiian Ducks *Anas wyvilliana* and Mallards *Anas platyrhynchos*, following the introduction of the latter, is apparently leading to the virtual extinction of the original form of Hawaiian Duck (US Fish & Wildlife Service 1999). These are extreme cases, where the species pairs did not meet in the past and have done so now only through human intervention. Nonetheless, the possibility for gene flow (hybridisation) between different species is ever-present, and may confuse genetic analysis of species boundaries. The rest of this paper deals with the analysis of the genetic structure within and between species. First, it is necessary to introduce the genetic material – DNA.

An introduction to DNA

Deoxyribonucleic acid (DNA) is the heritable genetic material. Every cell in our bodies carries copies of the DNA we inherited from our parents. It is the 'instruction manual' for the cells, known as the **genome**, the so-called 'book of life', which is written with a code using only four letters – the chemical bases adenine, thymine, cytosine and guanine (A, T, C and G). Hanging off a repetitive sugar-phosphate 'washing line' is the 'laundry' of As, Ts, Cs and Gs; the order in which these letters occur along the line underlies the genetic code and makes us what we are. The sequence of letters – genes – can be read by molecular machinery in the cell that tracks along them and puts proteins together on the basis of the instructions it sees in the DNA (see the extensive review text in Lewin 2002). The familiar double helix of DNA consists of two complementary 'washing lines' of bases, bonded to one another across the strands, such that T always bonds with A and G always bonds with C. Although DNA is generally extremely stable, sometimes, these A, T, C and G bases may fall off, or be chemically changed, or new bases may be added, or big chunks of DNA may break off, or turn round – these are the processes of mutation (reviewed in Majerus *et al.* 1996). Mutation usually arises as a result of accidental damage

or mistakes in replication of DNA, sometimes due to radiation or exposure to environmental chemicals. Mutations occur randomly in all our cells all the time, but as described below, may cause disadvantageous changes. Usually our cellular repair proteins spot mutations and correct them. In the time it takes you to read this paper, over 20 potentially lethal mutations will occur somewhere in the cells of your body, and you have to hope that they are repaired.

Proteins carry out all the important jobs required to keep body cells working, and are clearly critical to survival. If the coding regions of DNA, which provide the template for these proteins, are defective, as a result of mutation, then the proteins may not work. If that happens, there is a good chance that the mutant animal will not survive so, over evolutionary time, these DNA sequences do not change much. There are also regulatory regions of DNA that do not themselves make proteins, but control where and when different proteins are made in which different cells of the body, for example building bone cells or brain cells in the right places. Regulatory regions are critical too. Nonetheless, mutations in regulatory or coding regions of DNA can still occur because not all changes are necessarily bad. So, over evolutionary time, mutations may build up in and around genes that enable us to distinguish different individuals and species.

The DNA in a typical vertebrate cell includes about six billion base pairs, enough to provide for about one million genes, but most vertebrates have only about 20,000–30,000 genes (Genome Sequencing Consortium 2001). Therefore, the bulk of DNA in higher organisms appears not to do anything. Many of these bits of DNA may have had functions in the past – the minority are recognisable as genes that are no longer functional. Some are, or were, viral sequences that were integrated into the DNA and never left, and are now inactive. Other, very similar bits of DNA may occasionally replicate and move about within the DNA ('**jumping elements**'), with or without causing any harm. Some are strings of repeated sequences that are the product of mistakes during DNA replication. For example, molecular studies of bird taxa are frequently carried out by exploiting

microsatellite DNA sequences. These are non-coding and consist of a long series of short (usually two to six bases) motifs (Majerus *et al.* 1996). Many different microsatellites are spread throughout the genome of most organisms and may be used as indicators of variation between individuals or populations. Being non-coding, they also evolve quickly. Whatever their origin, these areas of DNA comprise vast strings of 'nonsense'. These apparently non-functional 'neutral' sequences of DNA can mutate freely, because mutation of nonsense, to make more nonsense, has no adverse effect (Kimura 1983).

For genes that encode proteins which affect key metabolic processes like respiration, mutations that change the proteins are likely to be lethal and are soon eliminated from the population – these areas of DNA change relatively slowly. They are said to be highly conserved. Bits of DNA that have no apparent function may be free to acquire mutations very rapidly. This is an important consideration; if a phylogeneticist is studying closely related taxa that diverged from each other only recently, there is little point in looking at slowly evolving, highly conserved parts of DNA – they will be too similar in the different taxa to tell us anything useful about their evolution. Conversely, when studying old evolutionary events, it is better to use these highly conserved stretches of DNA, for which informative mutations are likely to have built up over millions of years. The non-conserved, variable bits of DNA will have mutated so much that it is impossible to compare them among the relevant taxa. It soon becomes clear that DNA-based approaches to taxonomy are potentially extremely complex.

The mechanics of molecular evolution

Most mutations are repaired. Some, however, are not repaired, and persist. Mutations in sperm or egg cells may be passed on to the next generation, meaning that different individuals in a single species are genetically different. For example, humans may have red, blond or black hair, and blue, brown or green eyes – these are genetic differences within a single species. Although we all carry the same genes, there are many slightly different versions (**alleles**) of

these genes in the population as a whole, thanks to mutations. All animals carry pigment genes, but because individuals may have different alleles of these genes, they are differently pigmented, e.g. dark- and light-phase Arctic Skuas *Stercorarius parasiticus*. Mendel's famous peas (Mendel 1866) were selected on the basis of having different alleles of the same gene giving, say, wrinkled or smooth coats on the seeds. When scientists talk about the genetic variation within a population or a species, they are referring to the number and proportion of different alleles they can find for any single gene or other stretch of DNA.

There are several forces that can change the genetic structure of a species. Mutations are ultimately the source of all genetic variation, and the occurrence of different mutations in different populations of a single species is the raw material of speciation. Mutations persist or are eliminated partly as a result of **natural selection**, which changes the genetic structure of a population either by allowing the survival of a newly arisen mutation that confers a survival advantage to the bearer, or by eliminating individuals that are disadvantaged. Because the environment plays a major role in natural selection, populations of one species which lives in different environments may, through natural selection, evolve to look or behave differently. Random processes can also change the genetic structure of a population; for example, when a cow treads on a lark's nest, the nestlings will perish irrespective of genetic traits (whether 'fit' or 'unfit'). Such random mortality is inevitable, and may lead ultimately to genetic differences between different populations of a single species, or it may lead to the accidental loss of useful mutations purely by chance (**genetic drift**).

Random dispersal of individuals between populations may slow down divergence; the permanent movement of individuals from one population to another is called '**migration**' by population biologists (distinct from the seasonal movement of individuals between breeding and wintering areas more familiar to birders). Dispersive 'migration' may often work against speciation (but not always; see the study

of Great Tits *Parus major* by Garant *et al.* 2005). Perhaps counterintuitively, sex may also work against speciation. Sexual reproduction provides a mechanism for new gene alleles or gene combinations which arose in one population of a species to spread through other populations of the same species, and is a great homogenising factor. Sex also allows for hybridisation, by which gene sequences may be shared between different species.

At the level of a single DNA base pair it can be seen that there are several forces at work, either increasing or reducing divergence between individuals within a species. When the necessary mathematics are performed, the homogenising forces (e.g. sex, dispersal) tend to win (Dover 1982). Thus, unless there are special natural or sexual selective circumstances that maintain unusually high diversity, individuals of a species in an interbreeding population tend to have very similar (but not usually identical) DNA.

So, if there are large fixed (consistent) DNA differences between two populations or subspecies of a single species, it indicates that there has been little or no interbreeding. When two or more taxa no longer interbreed, gene flow between them can no longer occur. So the DNA sequences of reproductively isolated populations are free to diverge, by mutation, with respect to each other. Taxa that stopped interbreeding only recently will have very similar DNA sequences; taxa that have been reproductively isolated for many millions of years will have very different DNA sequences. The ability of scientists to read the same bits of DNA sequence in individuals of different taxa, to analyse how similar they are and decide, on the basis of sequence comparisons, which taxa are most closely related to which others, is the basis of DNA-based molecular phylogeny. While the mathematics are complicated, the principles are not dissimilar to classical morphology-based attempts to reconstruct phylogeny – those taxa that are closely related will tend to look most similar, and can be arranged into clades on the basis of shared-derived mutations in their DNA.

Nuclear and mitochondrial DNA

The vast majority of the DNA that all animals, plants and fungi carry in their cells occurs in the cell nucleus. At fertilisation, the nucleus of the sperm, carrying one complete 'set' of DNA (**chromosomes**), fuses with the nucleus of the egg, carrying another complete set of DNA, to form an embryo that is **diploid**, i.e. it carries two complete sets of chromosomal DNA – one from each parent. This means that every cell in our bodies has two copies (alleles) of every single gene and every bit of non-coding or 'junk' DNA. Normally, both alleles of any particular gene will be functional. However, a benefit of being diploid is that if one allele of the gene, say the one inherited from the father, is mutated and not working, the other copy, from the mother, is likely to be functional – there is back-up. Note also that, while an individual may possess two variant alleles of any one nuclear gene, within a population, there may be a large number of different alleles of the same gene. This is what is meant by the term '**gene pool**'.

Some DNA resides outside the nucleus in structures such as chloroplasts (responsible for photosynthetic processes in plants) or mitochondria (the 'batteries' of the cell, responsible for producing energy). Mitochondrial DNA (mtDNA) is a relatively small circular molecule (the ends are connected), and carries a small number of genes, not directly related to external morphology, but to energy production (see Lewin 2002).

Although both sperm and eggs carry mitochondria, the sperm mitochondria do not enter the egg at fertilisation, and are quickly broken down. This means that for birds (and all other animals), mitochondria are inherited only down the female line. That is, although all the cells in our bodies contain nuclear DNA from both our parents, we have only our mother's mitochondrial DNA, whether we are male or female.

Mitochondrial DNA is subject to random mutation just like nuclear DNA but the mutation rate of the mtDNA is substantially higher, not least because mutations are not efficiently repaired. Mutations may be passed from mother to offspring and hence, over time, different taxa that no longer interbreed develop sequence differences in their

mtDNA. The use of mtDNA for building evolutionary trees is so widespread, at least in part, because:

- 1) It is an abundant, fairly small molecule that is easy to isolate. Every cell has many mitochondria, each with several or many copies of (usually) identical mtDNA.
- 2) It carries mutations only through the female line with virtually none of the

mixing (recombination) of maternal and paternal chromosomes that complicates analysis of nuclear DNA.

- 3) It has genes for respiratory enzymes (e.g. *cytochrome b*) that are highly conserved and which mutate fairly slowly. It also has regulatory regions, e.g. certain parts of the control region, which mutate very quickly.

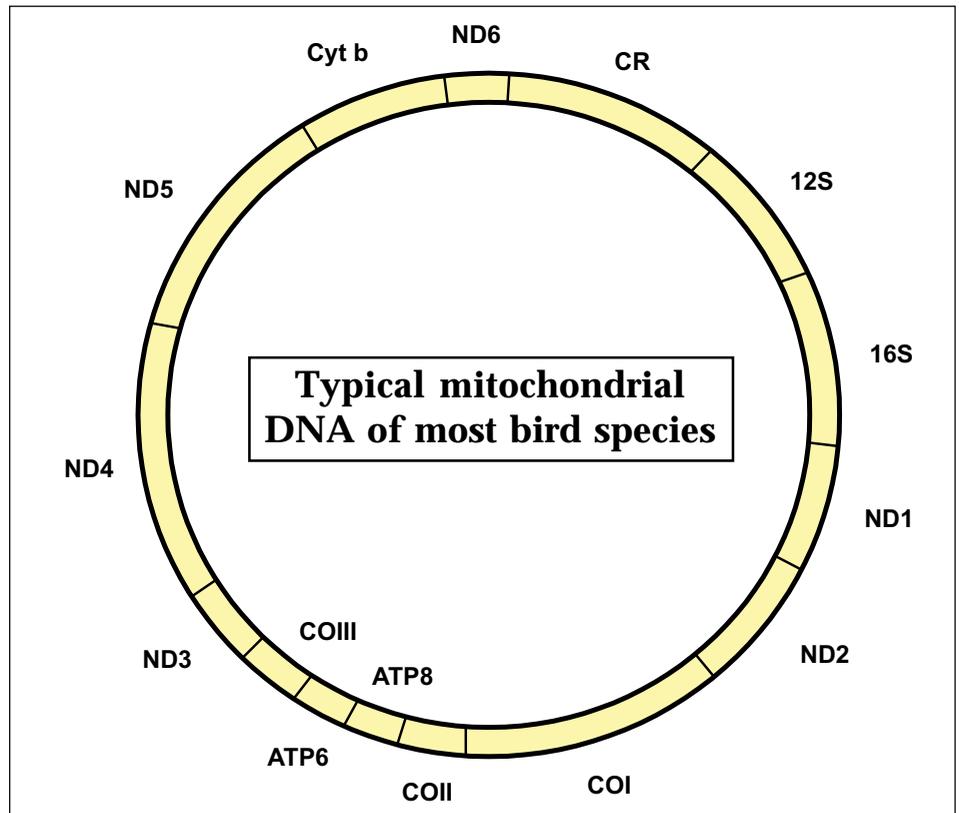


Fig. 2. Diagram of the mitochondrial DNA of a bird. This is the most common form, found in the domestic chicken *Gallus gallus* and most other birds. A slightly different form is found in some bird groups such as falcons (Falconidae) and woodpeckers (Picidae); see Mindell *et al.* (1998). The mitochondrial-DNA molecule consists of a closed circle, consisting of about 17,000 base pairs (compared with about 3,000 million base pairs in the nuclear DNA).

In the diagram, the genetically significant parts are labelled. 12S and 16S are genes coding for ribosomal RNA; ND1–ND6 are genes coding for subunits of a large protein called NADH dehydrogenase; *cytochrome b* is a gene coding for the enzyme *cytochrome b*; and CO I, II, and III are genes coding for cytochrome oxidases. ATP6 and ATP8 are genes coding for subunits of the protein adenosine triphosphate. CR is the control region containing the sequences where DNA replication is initiated – the origin of replication. Any of these regions of DNA may be used to extract phylogenetic information – some mutate slowly and are of use for determining ancient phylogenetic events, whereas others, such as the control region, have very quickly mutating (hypervariable) sequences that can be used to resolve recent evolutionary events, such as the radiation of the large white-headed gulls *Larus argentatus-fuscus-michahellis-cachinnans*.

[NB 'RNA' is ribonucleic acid – a nucleic acid found in all living cells that is essential for the manufacture of proteins according to the instructions carried by genes; a 'ribosome' is a subcellular particle consisting of RNA and associated proteins concerned with the manufacture of proteins.]

Consequently, different bits of the mitochondrial genome can be analysed to determine evolutionary patterns between recently diverged (closely related) or distantly related species (fig. 2).

What rates of divergence in mitochondrial DNA should we expect? Calibration of the amount of divergence expected over, say one million years, can be achieved by looking at the percentage DNA differences between taxa whose divergence can be dated to known geological events. For example, Hawaiian honeycreepers (Drepanididae) are believed to have speciated by occupying and diversifying on new islands as these appeared following undersea volcanic activity (Fleischer & McIntosh 2001). The times of appearance of the different islands in the chain is known, thus allowing determination of when new honeycreeper species evolved. The estimates are that in one million years of evolution, the mitochondrial *cytochrome b* sequence has diverged by about 1.6% on average, and the whole mitochondrial sequence has diverged by about 2%. Most of the latter variation is, of course, concentrated in the faster evolving bits.

As discussed by Newton (2003), different subspecies of a single species do not usually show more than about 2.5% divergence in the sequences of their mitochondrial *cytochrome b* gene, whereas different sister species may show up to 10% divergence or more in this sequence. Similar calculations would apply to some other mitochondrial gene sequences (examples in Helbig *et al.* 1995). But, as emphasised by Newton (2003), not all species fit in with these expectations. Some populations of birds that display good species separation on other grounds may show <1% divergence in sequence (e.g. Blue-winged Teal *Anas discors* and Cinnamon Teal *A. cyanoptera*), and some subspecies may have more than 2.5% divergence (e.g. Mountain Chickadee subspecies *Parus gambeli gambeli* and *P. g. baileyae*). So, it is of little value to say, in isolation, that 'DNA studies indicate a 3% difference' either in support of or against a proposed species split, and such arguments based on percentage divergence are dangerously circular

anyway.

The mechanics of molecular analysis

DNA can be extracted from tiny amounts of fresh tissue (e.g. blood, muscle, feathers, faeces) and is even recoverable from museum specimens. To perform a molecular analysis, DNA is isolated from individuals of all the taxa under study, and either directly sequenced or subjected to some other chemical procedure which cuts up (**restricts**) or makes copies of (**amplifies**) sections of it using the **polymerase chain reaction (PCR)**. Genes such as *cytochrome b* are best analysed by direct sequencing of the series of As, Ts, Cs and Gs. Various pieces of non-coding repetitive sequence, such as microsatellites, are usually analysed indirectly by restriction or amplification, producing a series of DNA bands of different sizes that are characteristic of the taxon.

Once the DNA has been sequenced, cut or amplified by PCR into an analysable form, the actual processes of analysis are not in principle much different from those employed for conventional morphological or behavioural analyses. Taxonomists look for informative mutations – shared-derived characters (synapomorphies) that can be used to link taxa together. For example, if there are six species A–F, and at position 123 of their *cytochrome b* gene, all of them have a thymine base ('T'), this does not help to resolve their phylogeny. If however, A–D have a 'T', but E and F have a guanine base 'G', this may be taken as evidence that E and F are closely related. By itself, this is not strong evidence, but if several different parts of the *cytochrome b* gene tell the same story, then the evidence gets stronger. Mathematical algorithms are used to determine, on the basis of DNA sequences, which species are most similar, and to build evolutionary trees. Different methodologies determine those trees requiring the minimum amount of mutation (**maximum parsimony**), or those trees that are most likely on the basis of prior knowledge about how DNA mutates (**maximum likelihood**) or those that progressively clump together the most similar species (**neighbour-joining**) (full review in Nei 1987). These techniques are described more fully in Appendix 1.

Sibley and Ahlquist exploited DNA–

DNA hybridisation to classify the bird families of the world (Sibley *et al.* 1988; Sibley & Ahlquist 1990). Their method did not analyse the genome sequences in detail. Instead, it was assumed that if the DNAs of two different species of bird are very similar, they will bind very tightly together because of complementary pairing of the As with Ts, and Cs with Gs, as described earlier. Conversely, if two species are only distantly related, their DNAs will be more divergent, so when mixed together they will not bind very tightly (rather like a zip-fastener with a lot of missing teeth). Sibley and Ahlquist's technique measured the melting temperature (the temperature at which the two complementary strands fall apart) of the hybridised DNA. The more similar the sequences in the compared samples, the more tightly they will combine and the higher the temperature needed to induce separation. The technique showed, for example, that New World barbets (Capitonidae) have closer molecular affinities to toucans (Ramphastidae) than to the barbets of the Old World (Megalaemidae and Lybiidae). The technique is at best only suited to broad-based taxonomic studies.

Problems with DNA

If DNA methods are so powerful, we should ask why answers to all of the outstanding taxonomic questions are not quickly forthcoming. DNA analysis is in practice probably no more objective than other analyses. Determining a phylogenetic tree from a DNA sequence is not simple. The same mutation may occur independently in distantly related species, giving a false impression of a close relationship. Similarly, over time, a mutated DNA base may randomly mutate back to its original state, giving a false impression of no mutation. The assembly and alignment of DNA sequences from several species of bird may require some heavy-duty computer work. Mistakes here seriously bias the data. Subsequent treatment of the data, whether by different analyses (neighbour-joining, maximum parsimony, etc.) compounded by uncertain assumptions about frequencies of different sorts of mutations, may result in several plausible-looking phylogenies from one dataset. On the other hand, if different

Box 1. Can a DNA sequence serve as a bar-code for species identity?

The idea of using a short DNA sequence as a 'bar-code' to allow molecular categorisation of every species was originally proposed by Hebert *et al.* (2003), using a 650-base-long sequence of the mitochondrial CO1 gene. This idea has now been applied to a study of 260 species of North American birds by these authors (Hebert *et al.* 2004). All species had a different bar-code (some had more than one), and differences between related species were about 18 times higher than those within species. Some interesting anomalies were revealed, all of which serve to support the idea of using this sequence as a species bar-code. In four exceptional cases (Solitary Sandpiper *Tringa solitaria*, Eastern Meadowlark *Sturnella magna*, Marsh Wren *Cistothorus palustris* and Warbling Vireo *Vireo gilvus*), there were deep sequence divergences within a species. Interestingly, all but the sandpiper have been proposed for possible splitting by some taxonomists, so these species may well include other cryptic molecular species. Thirteen species within four genera revealed rather low levels of molecular differentiation. These included seven species of large white-headed gulls *Larus*, the two North American oystercatchers *Haematopus bachmani* and *H. palliatus*, Mallard *Anas platyrhynchos* and Black Duck *A. rubripes*, and American *Corvus brachyrhynchos* and Northwestern Crow *C. caurinus*, all of these being species with known levels of hybridisation or recent allopatric divergence.

treatments of the DNA data produce the same, or very similar, phylogenetic trees, we can have more confidence that the correct picture is emerging.

Analysis of any gene or other sequence from mitochondrial or nuclear DNA of a group of species produces only a phylogeny of the gene (or whatever part of the DNA was analysed), for which each node in the tree is a point at which a mutation occurred. It is usual to assume that the phylogeny of the gene in these different species accurately reflects the evolution of the species that carry the gene. This is probably normally a reasonable assumption, but it need not necessarily be the case, especially for groups of species (or subspecies) that have separated only recently. More than one mtDNA lineage may exist within one species population. Trees inferred from various parts of the nuclear genome will not necessarily be congruent to trees from the mtDNA. Using any of these trees, based on a single gene or other DNA sequence as a dependable guide for the species tree, can be dangerous.

Discrepancies between morphological and genetic divergence

New species may evolve rapidly over comparatively short time spans (Fryer & Iles 1972). The best-known avian examples are Darwin's finches (Emberizidae) on the Galapagos and Hawaiian honeycreepers, which must have evolved over thousands rather than millions of years because geological evidence shows that the volcanic archipelagos on which they live were created only recently – see Sato *et al.* (1999). Conversely, some organisms, e.g. ginkgo trees (Ginkgoaceae) and

coelacanths (Latimeriidae), have remained morphologically almost unchanged for about 300 million years. Ospreys *Pandion haliaetus* look morphologically remarkably uniform across a virtual world range, while Common Chaffinches *Fringilla coelebs* and Wrens *Troglodytes troglodytes* have many described subspecies, with local song variations even within the UK, as well as clinal plumage variations across continents and discrete isolated or island forms (Vaurie 1959; Catchpole & Rowell 1993).

The morphology of a species is determined largely by its genes. Morphology is also influenced by the environment, however, and when the environment changes rapidly, morphology may change rapidly. On the other hand, animals or plants that live in constant, unchanging environments, such as the deep ocean, may show very little morphological change over geological timescales, even though mutations in their DNA are inevitably piling up. This has implications for genetic analysis. Groups of species which have evolved rapidly and recently may all be genetically uniform; their evolution may be difficult to resolve using DNA. Yet single species with a large and long-standing world range may show high intraspecific genetic variation; for example, all Barn Owls *Tyto alba* have a similar appearance but they exhibit a fairly complex genetic structure, so they must have spread across the planet some considerable time ago (König *et al.* 1999).

The strongest reason for the frequent lack of concordance between molecular and morphological approaches to taxonomy is that the molecular data are

almost never drawn from the genes controlling aspects of morphology that are conventionally used to delimit species. The normal analyses of fast-evolving and selectively neutral non-coding sequences, or of slowly mutating metabolic or respiratory enzymes like *cytochrome b*, are fine for measuring the time elapsed since the divergence of two taxa, but give no indication of the often rapid changes in morphology and reproductive behaviour which may drive speciation. Thus, while the Barnacle Goose *Branta leucopsis* is, on the basis of the molecular sequences analysed, closely related to the Lesser Canada Goose *B. hutchinsii*, its morphology and plumage have changed quite dramatically (Paxinos *et al.* 2002; see discussion below). Although this may appear to be a bad thing, it is in fact the strength of genetic analysis – DNA mutation allows a direct analysis of evolution without the complications that result from the influence of the physical and biological environment on external morphology. Molecular analyses could be based on genes which are involved in morphological evolution important to speciation, but relatively few of these sequences have been characterised and none have been studied sufficiently to confirm they give reliable phylogenetic data.

Some examples of the use of DNA

While advising caution for birders in the interpretation and application of DNA data, we do not want to paint an unnecessarily bleak picture. The rest of this paper demonstrates how DNA has contributed to our understanding of some interesting species issues, describing cases where it has provided

a clear phylogenetic signal, and cases where it has not.

Phylogenies based solely on DNA sequences may reveal species boundaries that were not obvious solely on the basis of morphology. For example, it is now largely accepted that Western *Phylloscopus bonelli* and Eastern Bonelli's Warblers *Ph. orientalis* are separate species, based largely on differences in their calls, and also on the DNA evidence, which showed that they may have diverged several million years ago. The species have remained separate in spite of continued occasional opportunities to hybridise (Helbig *et al.* 1995). More recently, DNA evidence has suggested other splits, based both on the absolute genetic distance between taxa that were previously assumed to be closely related, and on the relationship of those taxa with other species. Bearing

in mind that any taxonomic grouping (species, genus, family, etc.) should be monophyletic, one of the arguments for splitting Eurasian *Anas crecca* and Green-winged Teals *A. carolinensis* was that, on the basis of mtDNA, *carolinensis* appeared to be genetically closer to a South American species, Specked Teal *A. flavirostris*, than to *crecca* (Johnson & Sorenson 1999). There were two possible taxonomic arrangements that could satisfy the requirement for monophyly in the taxonomic arrangement of these teals, both different from the traditional arrangement: either lump all three taxa into one species (which would be bizarre, given the highly divergent plumage of *flavirostris*) or split them into three species (Sangster *et al.* 2001). It was suggested that, at some stage, there was a single Holarctic ancestral teal with separate populations which diverged

into Palearctic and Nearctic species. This may have been followed by range expansion of the Nearctic species into South America. The North American *carolinensis* maintained an appearance close to the Palearctic *crecca* but, in isolation and under its own selective pressures, the South American *flavirostris* evolved into something that looked superficially quite different. On the other hand, is it a mere coincidence that the Yellow-billed Pintail *Anas georgica*, sympatric with Speckled Teal, shares traits with *flavirostris* not present in the other teals? Has hybridisation caused *flavirostris* to look quite different from *crecca* and *carolinensis*?

Canada Geese

A similar situation may exist with respect to the Canada Geese *Branta canadensis*. Morphologically, these may be divided into 'small' and 'large' subspecies. Paxinos *et al.* (2002) published a phylogeny based on mtDNA sequences of two large subspecies ('Dusky' *B. c. occidentalis* and 'Giant' Canada Goose *B. c. maxima*) and three small subspecies ('Cackling' *B. c. minima*, 'Richardson's' *B. c. hutchinsii* and 'Taverner's' Canada Goose *B. c. taverneri*), and also included other *Branta* species in the analysis (see fig. 3). They showed that the traditional 'Canada Goose' species was paraphyletic – Barnacle Goose *B. leucopsis* appeared to be closely related to the small Canada Geese while the Hawaiian Goose *B. sandvicensis* (with other extinct Hawaiian geese) was suggested to be closely related to the large Canada Geese. In contrast, small and large Canada Geese were more distantly related to each other. Barnacle and Hawaiian Geese are clearly different species from Canada Goose, so the requirement to maintain monophyly demands that Canada Goose should be split into two species, Greater *B. canadensis* and Lesser Canada Goose *B. hutchinsii* (Banks *et al.* 2004). It is possible that, assuming that the mtDNA data represent the true phylogeny of these goose taxa, their last common ancestor had plumage resembling modern-day Canada Geese, but that two isolated ancestral populations at the extreme edges of the range, Hawaiian and Barnacle Goose, evolved rapidly into different species with quite different

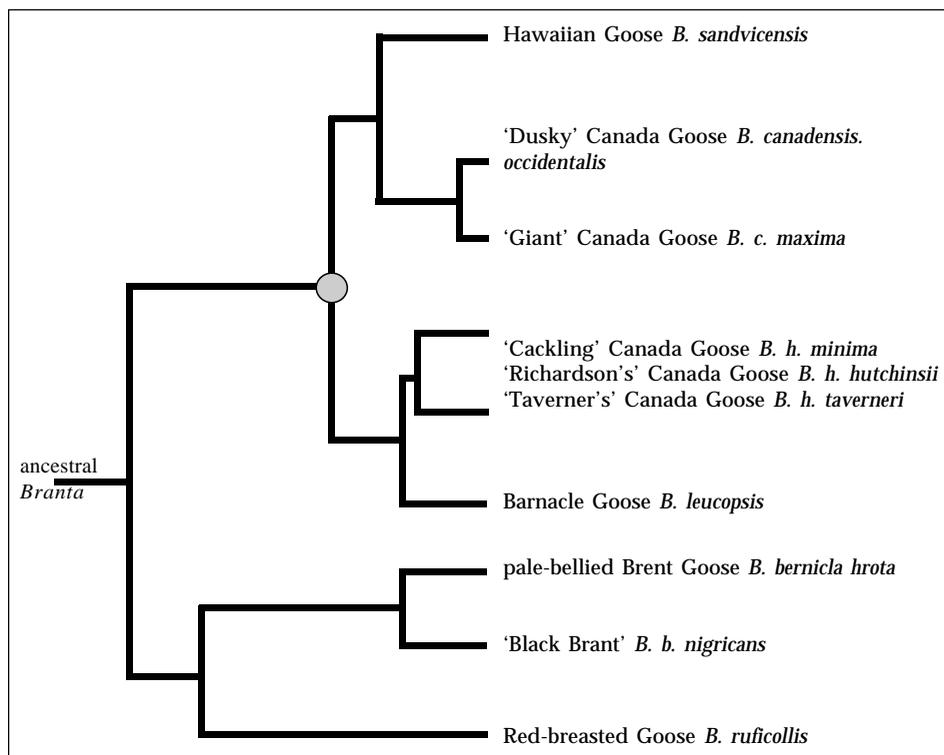


Fig. 3. Relationships among the black geese *Branta*, adapted from Paxinos *et al.* (2002), based on mtDNA sequences. The tree suggests that Hawaiian Goose is the sister taxon of the large Canada Geese ('Dusky' and 'Giant') and that Barnacle Goose is the sister species of small Canada Geese ('Cackling', 'Richardson's' and 'Taverner's'). The last common ancestor of the 'traditional' Canada Goose (marked as a red node here) also gave rise to Hawaiian Goose (and other extinct Hawaiian taxa not shown here) and Barnacle Goose, which are both different species. The traditional Canada Goose assemblage is, therefore, paraphyletic.

Splitting large and small Canada Geese recreates 'acceptable' monophyly, wherein each species is descended from one common ancestral taxon, and all the descendants of that taxon are included in the species. Note that this figure is diagrammatic only, and that branch lengths have been altered slightly.

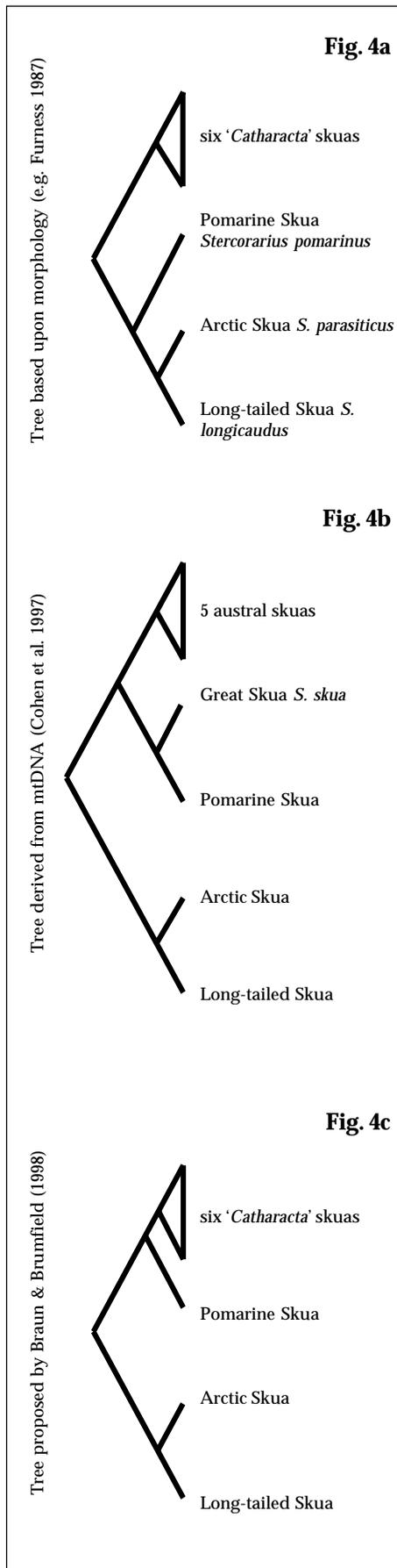


Fig. 4. Different interpretations of skua *Stercorarius* taxonomy – see text for details and discussion.

plumage patterns. Situations where molecular data do not accord with phylogenies based on morphology or plumage are, however, hard to interpret. Ideally, each line of enquiry – nuclear and mtDNA and morphology – should give the same result.

Skuas

The skuas *Stercorarius* provide a good example of the difficulties that taxonomists face in trying to unravel evolutionary history. Morphological analysis produces an unambiguous phylogenetic tree with two well-separated clades, consistent with the separation of skuas into two genera, *Catharacta* and *Stercorarius* (fig. 4a; Furness 1987), representing the 'large' and 'small' skuas respectively. On the other hand, Cohen *et al.* (1997) reported the results of several independent studies which analysed nuclear DNA, mtDNA and ectoparasites, with supporting evidence from behaviour and structure. These data implied that Pomarine *S. pomarinus* and Great Skuas *S. skua* are more closely related to each other than either is to its congeners. A phylogenetic tree, based solely on the analysis of mtDNA, grouped Pomarine and Great Skuas together, forming a sister clade to the 'austral' skuas: South Polar *S. maccormicki*, Chilean *S. chilensis* and Brown Skuas *S. antarcticus* (fig. 4b). This tree is inconsistent with the traditional grouping of two genera for the large and small skuas, because both genera would be paraphyletic.

But there is a difficulty with the Cohen *et al.* (1997) tree because, depending upon the assumptions made about the morphology of the original ancestral skua, either the 'large skua' ('*Catharacta*') morphology (of Great, South Polar, Brown and Chilean Skuas) or the 'small skua' morphology (of Pomarine, Arctic *S. parasiticus* and Long-tailed Skuas *S. longicaudus*) must have evolved independently twice, something which is believed to be highly unlikely. They explored several hypotheses to explain this, though popular attention settled on the possibility that Pomarine Skua is a result of past hybridisation between a large '*Catharacta*' skua species and a small *Stercorarius* skua population.

Braun & Brumfield (1998) reanalysed the data of Cohen *et al.* (1997). They

looked at the results from nuclear DNA, which suggested that Great Skua is closer to South Polar Skua than it is to Pomarine Skua, and proposed an alternative tree, with Pomarine basal to the '*Catharacta*' clade. This tree has a much more plausible explanation, which is that the ancestral skua species split into two lineages, one of which evolved into Arctic and Long-tailed Skuas while the other evolved into Pomarine Skua and all the large '*Catharacta*' skuas (fig. 4c). The Braun & Brumfield tree implies that the ancestral skua had small-skua-type morphology; it is attractive because it does not rely on 'far-fetched' explanations such as inter-generic hybridisation to explain skua evolution. However, it does not really explain why Pomarine and Great Skuas have such similar mtDNA and ectoparasites. Andersson (1999) calculated a phylogenetic tree based upon the ectoparasite species found on skuas, used as a taxonomic indicator of their hosts, and this tree was similar to that generated from mtDNA. It is highly unlikely that this concordance between the two trees could occur fortuitously, or by convergent evolution, so Andersson concluded the most likely explanation was that hybridisation *had* occurred. The evidence indicates that Great Skua perhaps evolved from a (presumably very small) population of migrant male austral skuas that lingered in the north and could not find mates of the same species and so, in desperation, took the best mates that they could find – female Pomarine Skuas! Given the uncertainty about skua evolution, the best solution at present seems to be to place all skuas, large and small, in a single genus, *Stercorarius*. In any case, there is no protocol to deal with the constraint of monophyly when a taxon derived by hybridisation is interposed between two otherwise perfectly good monophyletic groupings.

Greenish Warblers

Greenish Warbler *Phylloscopus trochiloides* shows a clinal gradation from northwest Europe through Central Asia, forming (notwithstanding a 1,000-km gap in China) a 'ring' around the Himalayas (Irwin 2000, 2001, 2005; reviewed in Collinson 2001, Collinson *et al.* 2003). In the area of overlap they behave as two species: 'Two-barred

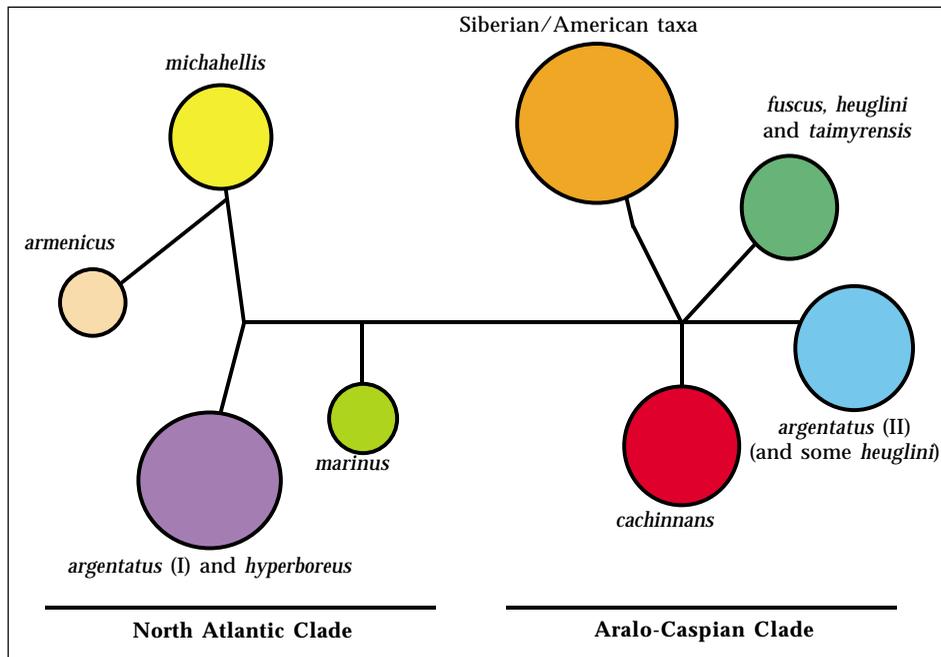


Fig. 5. Pictorial representation of the genetic relationships between 'large white-headed gulls'. The lines represent genetic distance, the lengths of the lines being roughly proportional to the number of DNA mutations differentiating among the taxa. The filled circles represent a cluster of individual gulls with very similar or identical mtDNA sequences. The orange circle representing 'Siberian/American' taxa contains individuals of Iceland Gull *Larus glaucooides*, Glaucous-winged Gull *L. glaucescens*, American individuals of Glaucous Gull *L. hyperboreus*, Slaty-backed Gull *L. schistisagus*, as well as individuals of *smithsonianus*, *taimyrensis*, *mongolicus*, *vegae* and *heuglini*. The figure is based on Liebers *et al.* (2004), but very much simplified and with several anomalies removed. The occurrence of European and British Herring Gulls (*argentatus/argenteus*) with mtDNA sequences that fall within either clade may be due either to past hybridisation or to retention of ancient DNA sequences that were present in the ancestors of all the gulls.

and American Herring Gull *L. ?a. smithsonianus* to the palest birds, European Herring Gulls *L. a. argentatus/argenteus* (Mayr 1963; Grant 1986). Early attempts to determine the evolutionary relationships between these gulls, and the more southern 'yellow-legged' taxa *atlantis*, *michahellis*, *cachinnans*, *barabensis* and *mongolicus*, were difficult to interpret because the DNA sequences analysed did not mutate fast enough to resolve their apparently rapid evolution. Crochet *et al.* (2002, 2003) and Liebers *et al.* (2001, 2004) analysed DNA sequences from both the *cytochrome b* gene and the fast-mutating hypervariable region of mtDNA from 'Herring Gull' and other white-winged and Siberian/Pacific taxa. It was found that the deepest genetic split divided gulls broadly into a 'North Atlantic' clade (containing well-differentiated groups of DNA sequences from individuals of *michahellis*, *armenicus*, *argentatus* but also containing a group of DNA sequences from Great Black-backed Gulls *L. marinus* and European individuals of Glaucous Gull *L. hyperboreus*) and an 'Aralo-Caspian' clade, containing everything else (see fig. 5). If the mtDNA evidence truly reflects the evolution of these gulls, then the Herring Gull is not monophyletic, but has both Aralo-Caspian and North Atlantic origins.

The large white-headed gulls probably evolved against a background of periodic glaciations which restricted northern birds to isolated refugia, splitting once-widespread species into smaller subpopulations where they then evolved in isolation. During warmer interglacial periods, their ranges would expand again (see Collinson 2001). Birds from the North Atlantic refugium, the possible ancestors of the subspecies *atlantis*, expanded into the Mediterranean and along both the European and the American Atlantic coasts, and differentiated to form Armenian Gull *L. armenicus*, Yellow-legged Gull *L. m. michahellis/atlantis*, European Herring Gull and Great Black-backed Gull. Birds from the Aralo-Caspian refugium migrated north and west, where they evolved into *heuglini* and the Lesser Black-backed taxa; and east, where they evolved into other Siberian and Pacific taxa. Several interesting points emerged from the

Greenish Warbler' *P. t. plumbeitarsus* does not interbreed with *P. t. viridanus*. On vocal and morphological grounds, there is no point in the ring at which one can say where a Greenish Warbler turns into a Two-barred Greenish Warbler, so they are classified as one species (see further detail in Newton 2003). DNA analysis demonstrates that there are eastern and western genetic clades, but that these genetic clades do not correspond with any morphological or other biological distinction between any of the taxa. This is perhaps the best avian example of a ring species, where classifying *P. t. viridanus* and *P. t. plumbeitarsus* as either subspecies on one hand, or separate species on the other, does not in either case fully describe the subtlety of the evolving biological scenario – a case of a rigid nomenclature being unable to describe what is going on in the real world. It would appear that the ancestral 'greenish warbler' evolved along the

southern rim of the Himalayas, and moved north during interglacial periods, undergoing selection pressure for more complex songs as it did so. On top of this, it is possible that periodic range fragmentation allowed for development of clearly separate eastern and western genetic clades.

Large white-headed gulls

On the other hand, the best available DNA evidence has probably torn apart another erstwhile example of an avian ring species, that involving the large white-headed gulls. The circumpolar distribution of northern Herring *Larus argentatus* and Lesser Black-backed Gull *L. fuscus* taxa was interpreted as an example of a ring species, based on an apparent cline in mantle and wing coloration of adults; from the darkest birds (Lesser Black-backed), east through Heuglin's *L. ?f. heuglini*, Taimyr *L. ?f. taimyrensis*, Vega *L. ?a. vegae/birulai*

analysis. In particular that the American Herring Gull *smithsonianus* is not closely related to European Herring Gulls *argentatus/argenteus*, but is a member of the Siberian group of gulls descended from the Aralo-Caspian refugium. This suggests that the original interpretation of a ring species was wrong, because if 'Herring Gull' was a ring species, *argentatus/argenteus* and *smithsonianus* would have to be closely related. Similarly Caspian Gull *L. a. cachinnans* and Yellow-legged Gull are apparently not closely related – they have also evolved from different refugial populations.

Another interesting point was that the 'herring gull' phylogeny contained other non-controversial 'good' species embedded within it, such as Great Black-backed Gull, but also (within the 'Siberian' group), individuals of Glaucous-winged Gull *L. glaucescens*, Iceland Gull *L. glaucoides* and Slaty-backed Gull *L. schistisagus*. This suggests that the rapid evolution of morphology and reproductive isolation in gull taxa is not well correlated with genetic distance between the taxa – new species may be able to evolve very rapidly in the absence of much genetic change (even in the highly variable bits of their mtDNA). This was rather counterintuitive, since one might expect that if these gulls were well-formed species, then the clades of similar DNA would correspond to morphologically recognisable species or subspecies; but this was not always the case. Among the Siberian/American group, for example, individuals from nine different taxa representing five uncontroversial species had virtually identical mtDNA.

The concept of a ring species of northern 'herring gulls' is not entirely dead, but it now excludes European Herring Gull *L. argentatus*! The pattern of DNA divergence of the 'Aralo-Caspian'-derived clade is consistent with a 'broken ring', from Lesser Black-backed Gulls in northwest Europe, with no undisputed species boundaries along the (stepped) cline of *fuscus-heuglini-taimyrensis-vegae-smithsonianus*. If Lesser Black-backed Gulls *L. f. graellsii* continue their colonisation of northeast North America and breed alongside *smithsonianus*, then some sort of ring-like species scenario may once again be

completed.

Lots of other interesting and as yet unresolved hypotheses about gull taxa can be postulated on the basis of recent genetic data. These gulls demonstrate that any simplistic approach to analysing their DNA is not going to reveal their true phylogeny. Much more work needs to be done, perhaps with nuclear DNA, before there is any chance of uncovering the whole story.

Wagtails

It is perhaps not a coincidence that another group of closely related taxa, the wagtails *Motacilla*, which share some aspects of their glacial evolutionary history with the gulls (i.e. recent interglacial expansion from southern refugia), also share a confusing mtDNA phylogeny. Furthermore, their mtDNA, nuclear DNA and morphology all tell different stories, though results from morphological studies are closer to those from nuclear DNA (Voelker 2002; Pavlova 2003; Odeen & Bjorklund 2003; reviewed in Alström *et al.* 2003). Analysis of both nuclear and mtDNA suggested that there is a genetic divide between the eastern and western forms of Yellow Wagtail *M. flava*, which mostly correlates with marked differences in their vocalisations. In terms of their genetics, 'eastern' yellow wagtails include *M. f. tschutschensis*, *taivana* and *macronyx*, whereas 'western' subspecies are *flava*, *flavissima*, *iberiae*, *cinereocapilla*, *pygmaea*, *feldegg*, *lutea*, *leucocephala* and probably *thunbergi* (although eastern populations of 'Grey-headed Wagtail' *M. f. thunbergi* may fall within the eastern clade). Furthermore, the phylogeny derived from mtDNA shows that the conventional 'Yellow Wagtail' species turns out to be paraphyletic, because subspecies of Citrine Wagtail *M. citreola*, Grey Wagtail *M. cinerea* and the White Wagtails *M. alba*, and possibly other taxa, are nested within and between the eastern and western clades of *M. flava*. Interestingly, there is little if any genetic evidence for splitting 'Black-headed Wagtail' *M. f. feldegg* from other 'western' yellow wagtails. A case could be made for splitting at least the eastern and western *M. flava* clades, even though each group has forms with morphology similar to the other. This has been done by the

American Ornithologists' Union (Banks *et al.* 2004), but Alström *et al.* (2003) considered that more research is needed before taking such a step. It is suggested that the Yellow Wagtails evolved their bewildering variety of male plumages, in the absence of much genetic change, as a result of unpredictable forces of sexual selection as pioneer birds advanced northwards during interglacials (Voelker 2002; Odeen & Bjorklund 2003). Under these conditions of low population density and perhaps reduced natural selective forces, male plumage evolution was driven rapidly by the sexual 'whims' of the females.

DNA sequence from the control region, 12S ribosomal and the ND2 gene suggested that the *citreola* and *calcarata* subspecies of Citrine Wagtail were not closely related (Odeen & Bjorklund 2003), and if we acted on this evidence, they would have to be split. However, nuclear DNA (from the CHD1Z gene) produced a more 'sensible' phylogenetic tree, which placed these two taxa next to each other, as close relatives. This illustrates how cautious we have to be when interpreting genetic studies; major taxonomic changes can be adopted safely only when supported by multiple lines of evidence. Birds may carry the 'wrong' mitochondrial DNA as a result of previous hybridisation with other taxa.

If wagtails and gulls demonstrate how plumage variation and reproductive isolation may evolve rapidly without leaving a clear, or even particularly meaningful, genetic paper-trail, then perhaps even more extreme examples may ultimately rewrite the speciation textbooks.

Galapagos finches and Crossbills

The species cluster of 'Darwin's finches' *Geospiza*, *Camarhynchus*, *Certhidea* and *Pinaroloxias* has been regarded for many years as a classic example of island species evolution (see Grant 1986 for a general account). The cluster consists of 14 well-described species, of which 13 live on the Galapagos Island archipelago and one on Cocos Island, almost 800 km to the northeast. They are all apparent descendants of a single ancestral mainland species, presumed to be a relative of the Dull-coloured Grassquit *Tiaris obscurus*.

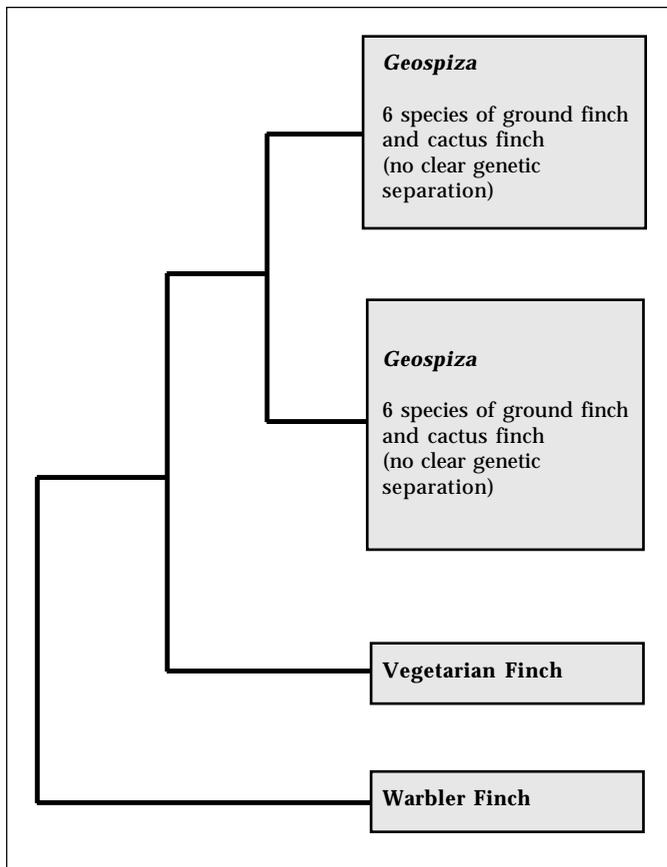


Fig. 6. Molecular phylogeny of Galapagos and Cocos Island Finches, simplified from Sato *et al.* (1999).

Sato *et al.* (1999) published the results of a substantial study of all of these birds using two distinct mitochondrial sequences for comparison, the *cytochrome b* region and the control region. They confirmed that the Cocos Island Finch *Pinaroloxias inornata* belongs with the Galapagos finch grouping, supporting a line of descent from a common ancestor with the Dull-coloured Grassquit; and they identified the Warbler-Finch *Certhidea olivacea* and Vegetarian Finch *Camarhynchus crassirostris* as being slightly distant from the main group of tree finches. Indeed, the Warbler Finch seems on molecular grounds to be basal to the Darwin's finch assemblage (fig. 6).

In contrast, the six species of ground finch *Geospiza* continue to hybridise frequently, and are not well-separated genetically. This was something of a surprise, although an earlier study based on protein **allozyme** (allozymes are differing forms of an enzyme encoded by different alleles at the same locus) variation had also suggested this (Yang & Patton 1981).

pressure may act to eliminate birds with suboptimal bill sizes.

The Medium Ground Finch *Geospiza fortis* recently gave a dramatic demonstration of just how fast a population can evolve. When, in 1977, a serious drought caused plants yielding smaller seeds (the food supply of smaller individuals) to fail, on Daphne Island the mean body size and bill size of the population increased significantly within one year (Boag & Grant 1981). Most of the smaller birds died as they could not cope with larger and tougher seeds. In subsequent seasons, however, with the return of the small-seed food supply, mean body size slowly decreased again. Had the drought lasted sufficiently long, then alleles for small size could have been eliminated completely and the mean size would not have decreased again so quickly, if at all.

The situation of this finch, where the processes driving speciation occur rapidly, all the time, may give some insights into the evolutionary relationships among the crossbills

The different species of ground finch differ in body size and bill depth, and are presumably adapted for different food items. However, long-term research has suggested that in most years there may be such an abundance of easily accessible food that selection in this respect may be weak, and that virtually all birds may survive, whatever their bill size or shape. In these conditions, there may be little or no selection against hybrids, and even relatively rare hybridisation would allow for gene flow between species, obscuring their molecular phylogenies. In years of drought, however, when food is scarce, strong selection

pressure may act to eliminate birds with suboptimal bill sizes. Based on nuclear microsatellite DNA and mitochondrial control regions, there are no clear differences among the DNA of any of the three currently recognised west European species, Parrot *L. pytyopsittacus*, Scottish *L. scotica* and Common Crossbill *L. curvirostra* (Pieltney *et al.* 2001), somewhat similar to the lack of genetic differentiation among *Geospiza* finches. These three crossbills are diagnosable only by mean body size, bill shape and call. As in the case of the bills of Galapagos ground finches, the three mean bill sizes of these crossbill taxa may be optimal for different sizes of cone, but this does not restrict their feeding most of the time, when cones are abundant. It is possible that bill size is selected strongly only when cones are scarce or if the environment is particularly harsh. Their preferences for different-sized cones are sufficient to restrict, but not eliminate, the gene flow between them so that bill size never becomes distinctly different in each form.

A comparable lack of genetic differentiation was reported among redpoll *Carduelis* taxa (Ottvall *et al.* 2002). For redpolls, in common with crossbills, it may be that the different species have evolved recently. Furthermore, their nomadic lifestyles (which allow for gene flow across large geographic distances), combined with generally large populations (which make it difficult for new mutations to spread throughout the populations), and occasional hybridisation, prevent very much genetic differentiation becoming established, even between good morphological species.

Cuckoos

There are other avian examples where genetically distinguishable forms are not necessarily different species. One fascinating example of this is the female Common Cuckoo *Cuculus canorus*. Female Common Cuckoos are genetically distinguishable according to their host species (Gibbs *et al.* 2000); however, males are not similarly distinguishable, and they will mate with a female of any kind. The different host-specific females are known as **gentes** (singular gens). Present evidence suggests that the gene which determines egg colour is in the female-specific W-chromosome. The ability to lay eggs in nests of the right

host is learned behaviour (imprinting). Apart from the W-chromosome, a Meadow Pipit *Anthus pratensis* Cuckoo female can pass its nuclear genes to a Reed Warbler *Acrocephalus scirpaceus* Cuckoo granddaughter via a male son. For a full account of the cuckoos, see Davies (2000).

Where does the future lie?

Most of the easy taxonomic decisions in ornithology have probably already been made. It is a fact that more significance is given to the rank of species than to any other rank, whether by birdwatchers, professional ornithologists, or government environmental ministries. This is a pity, as the importance of each classifiable form should be assessed independently of whether current taxonomy considers them species or not (Collinson 1999). Bird taxonomy is in perpetual flux. This is normal and perhaps desirable, if it is a symptom of discovery of new relevant facts by continuing research. Ornithologists in the Western Palearctic have perhaps forgotten this, having been spoilt by the stability engendered by the Voous List of Holarctic birds. Stability becomes stagnation when it stifles the application of relevant research. While there are perhaps some arguments for managing the pace of taxonomic change for practical reasons, stability *per se* is not a good thing. We would argue that, while unnecessary change is to be avoided, unnecessary stability may be equally harmful to ornithology. Nor is it always 'safer' to lump than to split, for the same reasons. Furthermore, taxonomic decisions are *hypotheses* – it is not necessary to wait until the evidence becomes overwhelming before proposing a taxonomic change; it is sufficient that the proposal is justified after taking into account all the relevant known facts or, alternatively, to await more facts when the conclusion looks improbable.

What we hope we have shown in this paper is that although the advent of DNA studies and other molecular techniques has enabled enormous strides in determining the inter-relationships between species and higher-level categories, DNA is not a panacea. There are some sets of species that have indistinguishable DNA, at least on the basis of the sequences so far

analysed, for example the crossbills, as well as single species which have highly diverse DNA in their gene pools. Thus it is necessary to apply the same standards of critical evaluation to molecular evidence as for evidence based on aspects of morphology, vocalisations, behaviour, ecology and physiology.

Taxonomy is a science; but it is performed by humans and its end-product, classification, is, at least in part, for humans. The challenge for taxonomists is to get their science and their judgements right, in a climate of political pressure. When Fea's *Pterodroma feae* and Zino's Petrels *P. madeira* were split (Bourne 1983), the scientific underpinnings of the decision were perhaps of less immediate significance than the subsequent attention directed to the plight of these two relict populations. More recently, proposed splits of albatross species (e.g. Shirihai 2002) may well attract attention for the same reason. And what would be the consequences of lumping Scottish Crossbill (Britain's only endemic bird species) with Common Crossbill (or even with both the other west European species) on the conservation status of the forests in which they live? We are not advocating political taxonomy, but the political consequences of taxonomic decisions are sometimes far-reaching.

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Appendix 1

A 'cheat-sheet' for those trying to understand the primary literature

Constructing phylogenetic trees from DNA sequence data

This appendix describes the basics of phylogenetic analysis, based on direct sequencing of DNA, to reveal the sequence of As, Ts, Cs and Gs, as described in the text. Many of the principles described here are, however, also applicable to other methods that analyse the lengths of DNA fragments without identifying the exact sequences.

(i) Sequence the same region of DNA in individuals of all the taxa you wish to include in the analysis

There are, at the first level of analysis, two problems here. The first is to ensure that you are really sequencing the same (orthologous) bit of DNA in all taxa. During evolution, DNA duplication events have led to extra copies of genes being created. Sometimes, these extra genes remain functional (gene families), with different members accumulating different mutations. Sometimes the extra genes may become non-functional and accumulate new mutations rapidly – they look somewhat like functional genes, but have no role ('**pseudogenes**'). Some mitochondrial genes may have lookalike copies in the cell nucleus. At the molecular level, it is possible to get all these variants confused, and if the same single gene is sequenced in, say, five taxa, but by accident a mutant pseudogene is sequenced in a sixth closely related taxon, the molecular analysis is going to suggest, erroneously, that this sixth species is only distantly related to the other five. For this reason, phylogenetic papers will often describe the precautions taken to ensure that orthologous sequences were compared, usually by looking hard for non-orthologous copies and making sure that, if they were present, they were found and identified.

The second problem is that, as explained in the text, different individuals from the same taxon will often have slightly different DNA sequences (different alleles). The scientist needs ideally to sample several individuals from the same species or subspecies to quantify the intra-taxon variation. It may be necessary to produce a 'consensus' (average) sequence for each taxon. Ideally, the intra-taxon variation should be small compared with the variation among the taxa to be analysed.

(ii) Line up of DNA sequences ready for analysis

If one has a DNA sequence from one taxon (for example ten bases ATCGATCGAG), then the power of phylogenetic analysis is maximised only when it is possible to be confident that each base can be compared with the equivalent base in other taxa. This would be easy if no bases were ever gained or lost. If there were only ever going to be ten bases in the orthologous sequence in other taxa, then if a sequence from another species or subspecies of ATCGATGGAG was derived, we would know that there had been one mutation in the second taxon (a C to G substitution at position 7). As described in the main text, however, it is also possible, within the normal range of mutations, to lose bases (**deletions**) or gain them (**insertions**). If, in a third taxon, the C at position 7 has been deleted, we get a sequence of ATCGATGAG. Lining that up simply against the first sequence gives the impression

that in fact four mutations (40% divergence!) have occurred – three base substitutions and a deletion, i.e.

```
ATCGATCGAG
ATCGATGAG–
```

The phylogeneticist, or his computer, has to spot that, in fact, it is more parsimonious to assume that only one mutation has occurred, the deletion at position 7 (a 10% divergence), and line up the sequences accordingly.

```
ATCGATCGAG
ATCGAT–GAG
```

This is the process of sequence alignment, and is critical to the process of obtaining reliable phylogenetic information. While this may seem obvious, it has to be mentioned here because sequence alignment can be extremely tricky when more than about five sequences are compared. Furthermore, the last step in this largely computerised process remains to check them and adjust by eye. If the sequence alignment produces an unexpected phylogenetic tree, it may be necessary to go back and realign the sequences. This is an obvious source of subjectivity and potential error.

Insertions or deletions, leading to gaps in sequences, are a biological big deal. They often lead to a gene becoming completely inactive, so conceptually the creation of a new gap is rarer than a simple swapping of one base for another in the DNA. So, although sequence comparisons may ignore sites with gaps (see below), the presence or absence of different gaps in different taxa is a valuable source of phylogenetic information; if two taxa in a family share a derived gap in sequence that is not shown by their other relatives, it is extremely strong evidence that they are sister taxa. Indeed, it is possible to create large phylogenies based on the presence or absence of gaps (Fain & Houde 2004). For the purpose of sequence analysis, however, gaps and the bases immediately adjacent to them are normally ignored.

(iii) Analysis of the sequence homology

If the sequence alignment has been performed correctly, the phylogeneticist should ideally be left with complete orthologous sequences of the same length from all the taxa to be examined. These sequences can now be fed into a computer to determine which are the most similar, and/or what phylogenetic tree linking the taxa can best explain the observed pattern of mutations in the DNA. The mathematics are complicated, and the details of no interest to the average birder, but the methods can be classified broadly into two groups (Nei 1983).

Analyses that link the most closely related sequences together and piece by piece build up a tree of 'sister groups' are called **distance-matrix methods** – they appear in papers as 'Unweighted Paired-group Means Analysis' (UPGMA), 'Fitch-Margoliash method', or 'neighbour-joining'. Put simply, they measure the genetic divergence between different

sequences and put the most similar ones together.

The second set of analyses, **discrete data methods**, regard each position in a set of sequences from the different taxa as a small piece of information about the evolutionary history of the taxa, and build a tree on the basis of a consensus of sum total of all these little pieces of information from all the orthologous positions in the sequence. They make certain assumptions about the nature of mutation – which mutations are rarer than others, for example – and reconstruct a tree based on the minimum amount of evolution required to explain the observed sequences ('maximum parsimony'), or which phylogenetic tree is most likely, given what we think we know about the processes of molecular change ('maximum likelihood').

If analyses of the same data by two or more methods, from both classes of analysis described above, give the same results, this increases our confidence in the conclusions.

(iv) Testing the phylogenetic tree

Once the computers have done their work, the resulting tree is meant to reflect the relationships between the taxa included in the DNA analysis. But how do we know whether the tree is reliable? Were the molecular data clear-cut, such that the computer could really reconstruct only one plausible tree; or were the DNA sequences so confusing that the computer could not really sort them out, and has just made the best of a bad job? Each phylogenetic tree needs testing for reliability, and the most universal way of doing this is by a technique known as '**bootstrapping**'; so called because it can obtain reliable statistical information out of almost any dataset, hence 'pulling it up by its bootstraps'.

If 100 bases of DNA sequence have been compared among, say, four taxa, then in fact there are 100 independent pieces of

information, each suggesting a phylogeny. The consensus phylogenetic tree is the combined 'voice' of these 100 parts. For example, the preferred phylogenetic tree may suggest that two species, A and B, are sister taxa, more closely related to each other than to any other taxa. If this result is clear-cut and obvious from the 100 base-pair sequence comparison, then it is argued that it should also be quite obvious from a subset of the data – so if, instead of taking 100 pieces of information, we take 50, then A and B should still emerge as sister taxa. This is essentially what bootstrapping does. Thus for a 100 bp sequence, the computer would pick 100 random numbers between 1 and 100 (note that, like rolling a dice six times, some numbers might come up more than once, and some not at all) so that a subset of unique sites in the sequence is derived. The phylogeny would then be reconstructed using *only* the DNA bases at those randomly selected positions. The process might be repeated 100 or 1,000 times, and the percentage of times that A and B emerge as sister taxa on the basis of these random subsets of the data is calculated. This percentage can be presented unmodified as 'bootstrap support' and shown on the consensus phylogenetic tree at the node (branch point) between A and B. If the relationship between A and B is robust, we would expect bootstrap support of 90–100%, and certainly more than 70%. Anything less than 70% has to be looked at critically; it suggests there are other arrangements of taxa in the phylogenetic tree that might equally be plausible.

Ideally, in published molecular phylogenetic trees using methods that are open to bootstrapping, the bootstrap support for each node will be shown. The closer the number is to 100, the more you can believe it.

This appendix is based loosely on Baldauf (2003).

Waterbird surveys along coastal Myanmar

Thet Zaw Naing

Naing, Thet Zaw. 2006. Waterbirds survey in mouth of Yangon River and Ayeyarwaddy (Irrawaddy) delta. *Indian Birds* 2 (3): 65-71.
Naing, Thet Zaw, Secretary, Myanmar bird and Nature Society. Email: sst@mptmail.net.mm.

ABSTRACT In December 2005 and March 2006, waterbirds surveys were conducted at various points in the mouth of Yangon River and in the Ayeyarwaddy (Irrawaddy) Delta. One new species and one new subspecies for Myanmar were recorded namely: Great Frigatebird *Fregata minor* and Long-tailed Shrike *Lanius s. schach* respectively. In addition, three globally threatened species—Spotted Greenshank *Tringa guttifer*, Lesser Adjutant-Stork *Leptoptilos javanicus*, and Greater Spotted Eagle *Aquila clanga*—and four Near-threatened species—Darter *Anhinga melanogaster*, Painted Stork *Mycteria leucocephala*, Oriental White Ibis *Threskiornis melanocephalus* and Brown-winged Kingfisher *Halcyon amauroptera*—were also recorded.

Introduction

The wetlands of Myanmar include rivers and streams, shallow fresh water lakes and marshes, water storage reservoirs, fish ponds, seasonal flooded cultivated plains, and estuaries with extensive mangrove swamps. With a 2,278 km long coast, most wetlands in Myanmar are directly or indirectly associated with river systems, several

very large estuarine and delta systems and numerous offshore islands. There are an estimated 517,000 ha of mangrove forest in Myanmar, mostly located in Ayeyarwaddy (Irrawaddy) Delta, on the Tanintharyi and Rakhine coasts and offshore islands.

The Ayeyarwaddy Delta covers an estimated 1,100,000 ha and is located in Ayeyarwaddy and Yangon (Rangoon)

divisions. The mouth of the Yangon River is situated in Yangon division in the gulf of Mottama. These sites fall within the southern part of the ornithological regions in Myanmar (Robson 2000). These areas have been very poorly covered by ornithological surveys (Armstrong 1876; Inskipp et al. 2001, 2003; Salter 1982; Naing & Aung 2002; van der Ven & Naing 2005).

Methods

In December 2005 and March 2006, we surveyed waterbird species in the mouth of Yangon River and Ayeyarwaddy Delta. A major objective of our survey was to record the diversity and determine the numbers of waterbird species present in the study area. We observed not only waterbirds but also other bird species. During the survey, the presence of different species of birds was determined by direct viewing and by listening to and identifying their calls (for forest birds). Eleven coastal sites, except Bogalay Royal Lake, were surveyed (see Map). Details of the sites are presented in Table 1. Motorised boats were used to reach survey sites while observations and counting were done on foot. Conservation status follows BirdLife International (2001) criteria.

Results

During the survey a total of 38,235 waterbirds comprising 69 species were counted. In addition, 24 species of other birds were also recorded (see Appendix). Of these, one is a new record for Myanmar, two are new records for southern Myanmar, one is Globally Endangered, two are Vulnerable and four are Near-threatened. The status of each species in southern Myanmar (Robson 2000) is shown in the Appendix. The following records are significant.

Darter (Near-threatened): Two birds were seen at Pyinsalu Island on 25.ii.2006.

Painted Stork (Near-threatened): A single bird was seen flying at Thante on 11.i.2006.

Lesser Adjutant-Stork (Vulnerable): A total of ten were recorded at five sites – three at Meinmahla Kyun Wildlife Sanctuary, two at Kadonkani Reserve Forest, three at Pyinalan Reserve Forest, one at Puinsalu Island and one at Thante.

Oriental White Ibis (Near-threatened): A total of 252 birds were recorded at 11 sites. 12, 42, 33, 28, 36, 4, 3, 76, 11 and 7 individuals were recorded at Meinmahla Kyun Wildlife Sanctuary, Pyindaye Reserve Forest, Kadonkani Reserve Forest, Pyinalan Reserve Forest, Kaing Thaug Island, Pyinsalu

Island, Kyakankwin Pyauk Reserve Forest, Let Khoke Kone Beach, Thante and Meepya respectively.

Bar-tailed Godwit *Limosa lapponica*: This is only the sixth record for Myanmar. It was first recorded in 2001 (Inskipp et al. 2001). Subsequent records were as follows: Naing & Aung (2002), Inskipp et al. (2003), van der Ven (2004) and Naing (2005). 247 birds were recorded at four sites, namely, Meinmahla Kyun Wildlife Sanctuary, Pyindaye Reserve Forest, Pyinalan Reserve Forest and Thante.

Spotted Greenshank (Endangered): This species was rediscovered in Myanmar after a gap of almost 129 years. A total of 28 Spotted Greenshanks were recorded at three sites. Two and three individuals were recorded on a muddy shore in Thante, (16°29'N 96°23'E) on 11.i.2006. A total of 14 birds (four, seven and three respectively) were recorded on a mixed muddy-and-sandy shore in Kaing Thaug Island (15°43'05"N 95°03'16"E) on 21.ii.2006. A group of nine individuals were recorded on a mixed sandy-and-muddy shore in Pyinalan Reserve Forest, (15°45'58"N 94°59'05"E) on 22.ii.2006. The only earlier record of this species was Armstrong's sighting at Ayeyarwaddy Delta in 1875 (Armstrong 1876) and again at Kayin State (Amherst) in 1877 (Smythies 1953).

Hume (Armstrong 1876) thought that Armstrong had discovered a new species and it was named *Totanus haughtoni* Armstrong, 1876, in honour of the latter's friend, "the Rev. Professor Haughton, of Trinity College, Dublin, whose labors have done so much to enlarge the field of Natural History research," (Armstrong 1876, p.345). In fact, Smythies (1953, p.499) called it 'Armstrong's Sandpiper'! But the taxon had been described earlier as *Totanus guttifer* Nordmann, 1835.

Great Frigatebird: One juvenile Great Frigatebird was recorded at Meepya on 12.xii.2005. This is first confirming record for Myanmar.

Brown-winged Kingfisher (Near-threatened): One bird was spotted at Meinmahla Kyun Wildlife Sanctuary on 9-10.ii.2006.

Hen Harrier *Circus cyaneus*: This is a first

record for south Myanmar. One male Hen Harrier was seen at Meinmahla Kyun Wildlife Sanctuary on 10.ii.2006.

Greater Spotted Eagle (Vulnerable): One Greater Spotted Eagle was recorded at Pyindaye Reserve Forest on 14.ii.2006.

Long-tailed Shrike: This subspecies of Long-tailed Shrike is a new record for Myanmar. Three individuals were seen at Let Khoke Kone Beach on 7.ii.2006. One was again seen at the same site on 8.ii.2006.

Indian Great Reed-Warbler *Acrocephalus stentoreus*: A total of 6 birds were recorded at Let Khoke Kone Beach on 7.ii.2006. This is the second record of the species for south Myanmar, the first being that of Inskipp et al. (2003) from the same locality.

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Table 1. Details of survey sites

Sites, Coordinates & Abbreviations	Habitat	Surveyed date	Location
Meinmahla Kyun Wildlife Sanctuary (15°51'N 95°14'E): MK	Mudflats, MG	9-10.ii.2006	AD
Pyindaye Reserve Forest (15°46'N 95°28'E): PD	M, MSS, MG, F	11-17.ii.2006	AD
Kadonkani Reserve Forest (15°48'N 95°06'E): KD	MSS, MG	8, 18-20.ii.2006 & 1-2.iii.2006	AD
Pyinalan Reserve Forest (15°45'N 95°59'E): PA	MSS, MG	22-25, 27-28.ii.2006 & 1.iii.2006	AD
Kaing Thaug Island (15°43'N 94°03'E): KT	MSS, MG	21.ii.2006	AD
Pyinsalu Island (15°47'N 94°46'E): PS	MSS, MG	25-26.ii.2006	AD
Kyakankwin Pyauk Reserve Forest (15°50'N 94°41'E): KP	MSS, MG	26-27.ii.2006	AD
Bogalay Royal Lake (16°17'N 95°23'E): BR	F	7.ii.2006	AD
Let Khoke Kone Beach (16°19'N 96°09'E): LK	MSS, MG	6-8.ii.2006	AD & YR
Thante (16°29'N 96°23'E): TT	MS	11.i.2006	YR
Meepya (16°31'N 96°19'E): MP	MS	12.xii.2005	YR

Key

AD = Ayeyarwaddy Delta; F = Freshwater lake; M = Mudflats; MG = Mangrove; MS = Muddy shore; MSS = Muddy and sandy shores; YR = Mouth of Yangon River.

Appendix
Bird species recorded during the survey
 (Key to abbreviations at end of table)

Species	Status	MK	PD	KD	PA	KT	PS	KP	BR	LK	TT	MP
WATERBIRDS												
Little Grebe <i>Tachybaptus ruficollis</i>	R	12										
Little Cormorant <i>Phalacrocorax niger</i>	R	18	83	12	1		7			11	1	4
Darter <i>Anhinga melanogaster</i> —NT	R						2					
Great Frigatebird <i>Fregata minor</i>	NRM											
Little Egret <i>Egretta garzetta</i>	FR	76	216	169	96	61	33	47	1	30	32	2
Grey Heron <i>Ardea cinerea</i>	FR	6	43	11	24	16	5	16		16	3	
Purple Heron <i>A. purpurea</i>	FR		16									
Large Egret <i>Casmerodius albus</i>	FR	19	98	33	46	32	8	5		12	6	1
Median Egret <i>Mesophoyx intremedia</i>	FR		5					2			8	3
Cattle Egret <i>Bubulcus ibis</i>	R	17	150	8	106		5			10	185	48
Pond-Heron <i>Ardeola</i> spp.	R	94	222	181	178	26	43	11		93	53	32
Little Green Heron <i>Butorides striatus</i>	R	8	13	3	1	3						
Black-crowned Night-Heron <i>Nycticorax nycticorax</i>	R	34	50		71					27		
Painted Stork <i>Mycteria leucocephala</i> —NT	M										1	
Asian Openbill-Stork <i>Anastomus oscitans</i>	M				11							
White-necked Stork <i>Ciconia episcopus</i>	R	1										
Lesser Adjutant-Stork <i>Leptoptilos javanicus</i> —VU	R	3		2	3		1				1	
Glossy Ibis <i>Plegadis falcinellus</i>	M	10		4	2							
Oriental White Ibis <i>Threskiornis melanocephalus</i> —NT	M	12	42	33	28	36	4	3		76	11	7
Lesser Whistling-Duck <i>Dendrocygna javanica</i>	R	670	40	2,493			36		297	1		
Brahminy Shelduck <i>Tadorna ferruginea</i>	M	26	278	31	27					141	138	17
Cotton Teal <i>Nettapus coromandelianus</i>	R								6			
White-breasted Waterhen <i>Amaurornis phoenicurus</i>	R	5	3	2	1		1					
Ruddy-breasted Crake <i>Porzana fusca</i>	R		2	4	3							
Watercock <i>Gallix rex cinerea</i>	R			1								
Common Moorhen <i>Gallinula chloropus</i>	R		3						32			
Pheasant-tailed Jacana <i>Hydrophasianus chirurgus</i>	R								6			
Pacific Golden-Plover <i>Pluvialis fulva</i>	M		247	58	70	146	1			36	1	
Grey Plover <i>P. squatarola</i>	M		12		36	28	15	10		8	8	
Long-billed Ringed Plover <i>Charadrius placidus</i>	M		190	7	88	84				206	3	6
Little Ringed Plover <i>C. dubius</i>	R		28	8	27	3	16			22	2	
Kentish Plover <i>C. alexandrinus</i>	M		1,106	434	1,924	69	250	96		620		16

Species	Status	MK	PD	KD	PA	KT	PS	KP	BR	LK	TT	MP
Greater Coucal <i>Centropus sinensis</i>	R	X	X	X					X	X		
Lesser Coucal <i>C. bengalensis</i>	R	X	X	X						X	X	
Oriental Scops-Owl <i>Otus sunia</i>	R	X	X									
Brown Fish-Owl <i>Ketupa zeylonensis</i>	R			X								
Spotted Owlet <i>Athene brama</i>	R			X								
Large-tailed Nightjar <i>Caprimulgus macrurus</i>	R	X	X	X								
Asian Palm-Swift <i>Cypsiurus balasiensis</i>	R		X	X	X		X	X	X	X	X	X
Small Blue Kingfisher <i>Alcedo atthis</i>	R	X	X	X	X		X	X		X	X	X
Blue-eared Kingfisher <i>A. meninting</i>	R			X		X						
Brown-winged Kingfisher <i>Halcyon amauroptera</i> —NT	R	X										
White-breasted Kingfisher <i>H. smyrnensis</i>	R	X	X	X	X	X	X	X	X	X	X	X
Black-capped Kingfisher <i>H. pileata</i>	M	X	X	X	X	X	X	X		X	X	X
Collared Kingfisher <i>Todiramphus chloris</i>	R	X		X								
Small Bee-eater <i>Merops orientalis</i>	R		X	X	X	X	X	X	X	X	X	X
Blue-tailed Bee-eater <i>M. philippinus</i>	R	X	X	X					X	X	X	X
Chestnut-headed Bee-eater <i>M. leschenaulti</i>	R	X										
Indian Roller <i>Coracias benghalensis</i>	R	X	X						X	X	X	X
Oriental Broad-billed Roller <i>Eurystomus orientalis</i>	R		X									
Coppersmith Barbet <i>Megalaima haemacephala</i>	R								X	X	X	X
Grey-capped Pygmy Woodpecker <i>Dendrocopos canicapillus</i>	R	X										
Fulvous-breasted Pied Woodpecker <i>D. macei</i>	R	X										
Common Golden-backed Woodpecker <i>Dinopium javanense</i>	R		X									
Greater Golden-backed Woodpecker <i>Chrysocolaptes lucidus</i>	R	X	X									
Oriental Skylark <i>Alauda gulgula</i>	R		X	X						X	X	X
Barn Swallow <i>Hirundo rustica</i>	M	X	X	X	X	X	X	X	X	X	X	X
Red-rumped Swallow <i>H. daurica</i>	M									X		X
Striated Swallow <i>H. striolata</i>	M									X		
Asian House Martin <i>Delichon dasypus</i>	M										X	
Forest Wagtail <i>Dendronanthus indicus</i>	M			X								
White Wagtail <i>Motacilla alba</i>	M		X						X	X	X	X
Yellow Wagtail <i>M. flava</i>	M			X					X			
Grey Wagtail <i>M. cinerea</i>	M		X	X								
Richard's Pipit <i>Anthus richardi</i>	M									X		
Paddyfield Pipit <i>A. rufulus</i>	R		X							X	X	X
Black-winged Cuckoo-shrike <i>Coracina melaschistos</i>	M	X										
Small Minivet <i>Pericrocotus cinnamomeus</i>	R	X										
Bar-winged Flycatcher-Shrike <i>Hemipus picatus</i>	R	X	X									
Red-whiskered Bulbul <i>Pycnonotus jocosus</i>	R	X	X	X	X		X	X	X	X	X	X
Red-vented Bulbul <i>P. cafer</i>	R	X	X			X			X	X	X	
Streak-eared Bulbul <i>P. blanfordi</i>	R		X	X			X	X	X	X	X	X
Common Iora <i>Aegithina tiphia</i>	R	X	X						X	X	X	X
Brown Shrike <i>Lanius cristatus</i>	M	X	X	X	X	X			X	X	X	X
Long-tailed Shrike <i>L. s. schach</i>	?									X		
Grey-backed Shrike <i>L. tephronotus</i>	M								X		X	X
Blue Rock-Thrush <i>Monticola solitarius</i>	M	X										
Eyebrowed Thrush <i>Turdus obscurus</i>	M	X										
Oriental Magpie-Robin <i>Copsychus saularis</i>	R	X	X	X	X	X	X		X	X	X	X
Common Stonechat <i>Saxicola torquata</i>	M								X	X	X	X
Pied Bushchat <i>S. caprata</i>	R								X	X	X	X
Spotted Babbler <i>Pellorneum ruficeps</i>	R	X		X								
Yellow-breasted Babbler <i>Macronous gularis</i>	R	X	X	X					X			
Red-capped Babbler <i>Timalia pileata</i>	R	X										
Yellow-eyed Babbler <i>Chrysomma sinense</i>	R								X			
Streaked Fantail-Warbler <i>Cisticola juncidis</i>	R	X		X	X	X			X	X	X	X
Franklin's Prinia <i>Prinia hodgsonii</i>	R	X	X	X								
Yellow-bellied Prinia <i>P. flaviventris</i>	R	X	X						X			
Plain Prinia <i>P. inornata</i>	R	X	X	X	X	X	X	X	X	X	X	X
Oriental Great Reed-Warbler <i>Acrocephalus orientalis</i>	M		X						X	X		
Indian Great Reed-Warbler <i>A. stentoreus</i>	NS									X		
Common Tailorbird <i>Orthotomus sutorius</i>	R	X	X	X	X	X	X	X	X	X	X	X
Dusky Warbler <i>Phylloscopus fuscatus</i>	M		X	X					X	X	X	X

Species	Status	MK	PD	KD	PA	KT	PS	KP	BR	LK	TT	MP
Yellow-browed Warbler <i>P. inornatus</i>	M	X	X	X	X					X		
Greenish Leaf-Warbler <i>P. trochiloides</i>	M									X		
Striated Marsh-Warbler <i>Megalurus palustris</i>	R						X			X		
Sooty Flycatcher <i>Muscicapa sibirica</i>	M										X	
Red-throated Flycatcher <i>Ficedula parva</i>	M	X	X	X		X			X	X		
Verditer Flycatcher <i>Eumyias thalassina</i>	?	X	X							X	X	
Black-naped Monarch-Flycatcher <i>Hypothymis azurea</i>	R	X		X								
White-throated Fantail-Flycatcher <i>Rhipidura albicollis</i>	R	X	X	X		X		X	X			
Mangrove Whistler <i>Pachycephala (cinerea) grisola</i>	M			X								
Great Tit <i>Parus major</i>	R	X		X		X						
Scarlet-backed Flowerpecker <i>Dicaeum cruentatum</i>	R	X							X			
Ruby-cheeked Sunbird <i>Chalcoparia singalensis</i> ¹	R	X		X								
Brown-throated Sunbird <i>Anthreptes malacensis</i>	R	X		X								
Olive-backed Sunbird <i>Nectarinia jugularis</i>	R	X	X	X		X			X	X		
Oriental White-eye <i>Zosterops palpebrosus</i>	R	X	X	X	X				X			
Yellow-breasted Bunting <i>Emberiza aureola</i>	M										X	
Red Munia <i>Amandava amandava</i>	R									X		
White-rumped Munia <i>Lonchura striata</i>	R	X							X			
Spotted Munia <i>L. punctulata</i>	R		X						X	X	X	X
Black-headed Munia <i>L. malacca</i>	R									X	X	
House Sparrow <i>Passer domesticus</i>	R		X	X	X				X	X	X	X
Plain-backed Sparrow <i>P. flaveolus</i>	R									X		
Eurasian Tree Sparrow <i>P. montanus</i>	R	X	X	X	X	X	X	X	X	X	X	X
Streaked Weaver <i>Ploceus manyar</i>	R								X	X		X
Baya Weaver <i>P. philippinus</i>	R	X							X	X		
Grey-headed Starling <i>Sturnia malabarica</i> ¹	R					X			X			
Asian Pied Starling <i>S. contra</i> ¹	R	X	X	X	X	X	X	X	X	X	X	
Vinous-breasted Starling <i>S. burmannica</i> ¹	R									X		
Common Myna <i>Acridotheres tristis</i>	R	X	X	X	X	X	X	X	X	X	X	X
Jungle Myna <i>A. fuscus</i>	R	X	X	X	X	X	X	X	X	X	X	X
Black-naped Oriole <i>Oriolus chinensis</i>	M								X	X		
Black Drongo <i>Dicrurus macrocercus</i>	M	X	X	X	X	X	X	X	X	X	X	X
Ashy Drongo <i>D. leucophaeus</i>	M	X								X		
Ashy Woodswallow <i>Artamus fuscus</i>	R	X	X	X					X	X		X
Racket-tailed Treepie <i>Crypsirina temia</i>	R	X	X	X								
House Crow <i>Corvus splendens</i>	R		X	X	X	X	X	X	X	X	X	X
Jungle Crow <i>C. macrorhynchos</i>	R	X	X	X	X	X			X	X	X	X

¹ After Rasmussen & Anderton (2005).

KEY

Threat

EN = Endangered
 NT = Near-threatened
 VU = Vulnerable

Status (in southern Myanmar vide Robson 2000)

R = Resident
 M = Migrant
 FR = Former Resident (current status uncertain / unknown)
 ? = Status uncertain / unknown
 NR = New record for Myanmar
 NS = New record for South Myanmar

Site

MK = Meinmahla Kyun Wildlife Sanctuary
 PD = Pyindaye Reserve Forest
 KD = Kadonkani Reserve Forest
 PA = Pyinalan Reserve Forest
 KT = Kaingya Island

PS = Pyinsalu Island

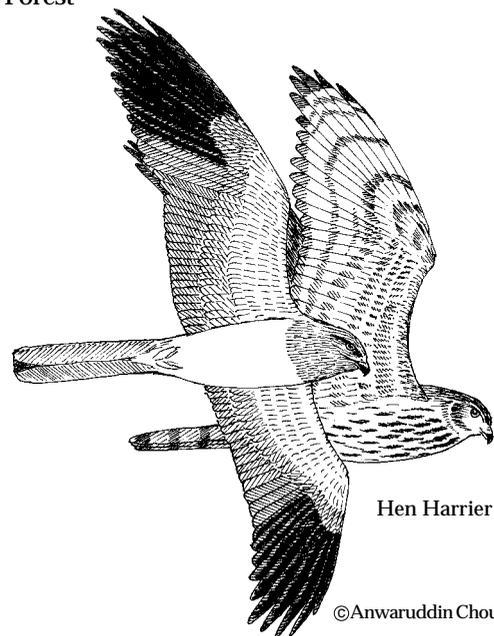
KP = Kyakankwin Pyauk Reserve Forest

BR = Bogalay Royal Lake

LK = Let Khoke Kone Beach

TT = Thante

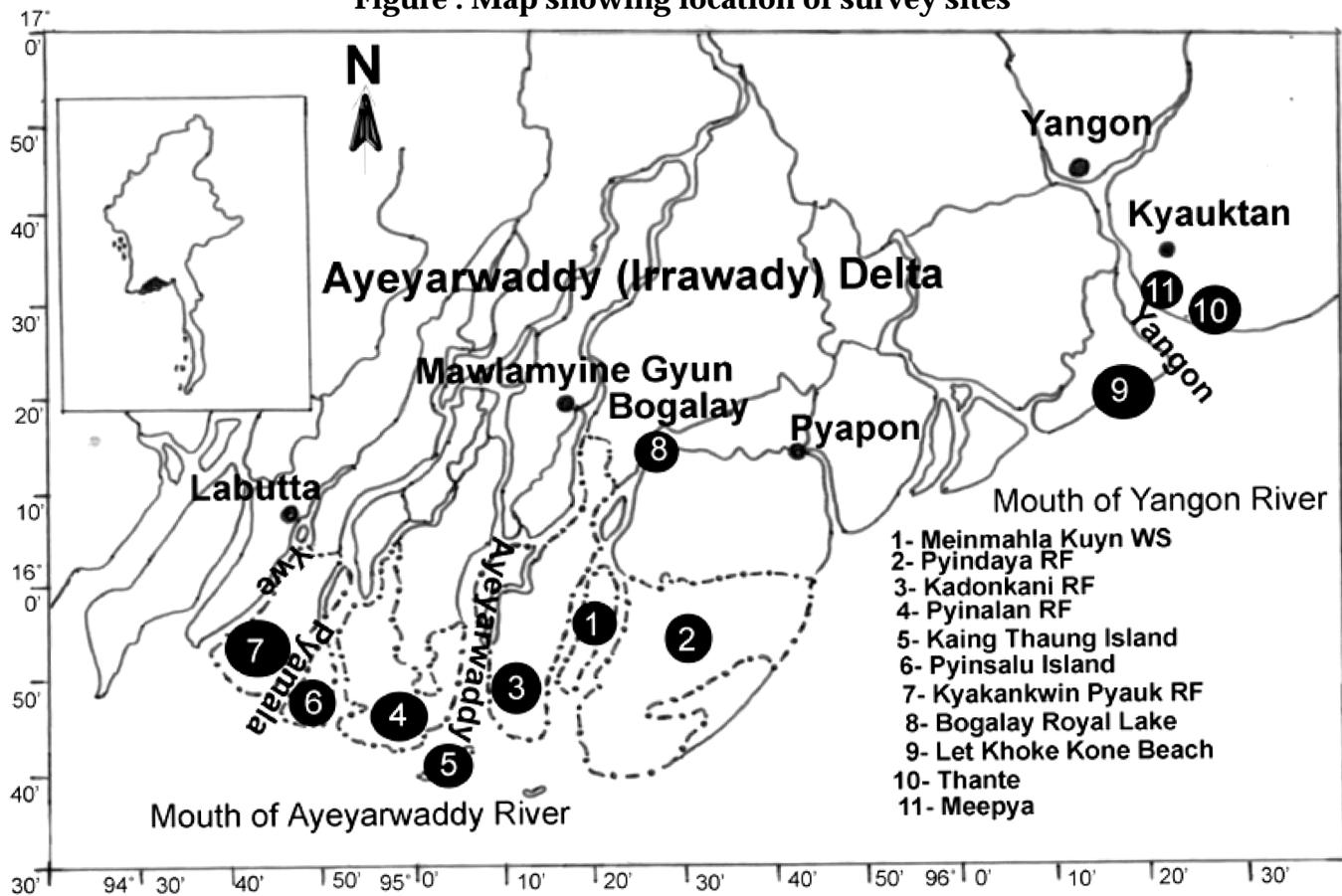
MP = Meepya



Hen Harrier

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Figure : Map showing location of survey sites



Annotated checklist of the birds of Sariska Tiger Reserve, Rajasthan, India

Ghazala Shahabuddin, Raman Kumar & Ashok Verma

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Introduction

Sariska Tiger Reserve is one of the important areas for biodiversity conservation in the state of Rajasthan, located in the Aravalli Hills (27°30'N 76°22'E). It covers an area of 866 km² and is composed of Sariska Wildlife Sanctuary, covering 492 km² and stretches of adjoining reserved and protected forests which together cover 374 km².

Sariska is located in the semi-arid zone of north-western India delineated as biogeographic province 4A (semi-arid Gujarat-Rajputana) in the classification of Rodgers & Panwar (1988). Sariska

forests represent the tropical dry forest ecosystem that exists in this part of India. Low hills and slopes are covered by deciduous forests dominated by *Anogeissus pendula*, mixed with *Boswellia serrata*, *Lannea coromandelica* and *Wrightia tinctoria*. The ridges, hill-tops and drier strata are dominated by *B. serrata*. Floors of valleys that have seasonal streams or perennial springs, harbour much more diverse semi-deciduous riparian forests of *Mitragyna parvifolia*, *Ficus glomerata*, *Phoenix sylvestris*, *Syzygium cumini*, *Diospyros melanoxylon*, *Mangifera indica* and *Terminalia bellerica*, along with bamboo

clumps *Dendrocalamus strictus*. In narrow rocky valleys with perennial water sources, *Phoenix sylvestris* is commoner than the other associate species of riparian forest. In drier and flatter terrain, tropical scrub forest dominates, consisting of *Ziziphus mauritiana*, *Acacia leucophloea*, *Butea monosperma*, *Balanites aegyptiaca*, *Acacia catechu* and *Aegle marmelos*. The understorey of scrub forests consists of shrubs such as *Capparis sepiaria*, *C. decidua*, *Ziziphus nummularia* and *Adhatoda vasica*. Grasses such as *Cenchrus ciliaris*, *Dicanthium annulatum* and *Heteropogon contortus* occur in the scrub forest and other flatter

terrain.

Prior to this study, avifauna in Sariska Tiger Reserve was documented once, more than ten years ago (Sankar et al. 1993). The present paper describes the bird community of Sariska Tiger Reserve based on studies during the period March 2003 to June 2005. The avifauna of Sariska Tiger Reserve was studied through systematic large-scale surveys utilizing point counts as well as opportunistic observations throughout the study period. Birds were identified using field guides by Grimmett et al. (1998) and Kazmierczak (2000).

Additions to earlier study

During the current study, a total of 183 avian species were recorded. Twenty-seven bird species have been added to the earlier checklist for Sariska (Sankar et al. 1993). Interesting sightings in this category include Isabelline Wheatear *Oenanthe isabellina*, Bar-headed Goose *Anser indicus*, Eurasian Wryneck *Jynx torquilla*, and the Common Cuckoo *Cuculus canorus*. The attached table (Table 1) lists the bird species recorded by us in Sariska, along with notes on habitat preferences and date and place of rare / solitary sightings. Bird nomenclature and taxonomy follow Manakadan & Pittie (2004).

Possible changes in bird fauna since 1993

53 species recorded by Sankar et al (1993) were not recorded by us. However, Sankar et al (1993) had visited several more sites inside the Reserve than we did, during the course of their surveys. But importantly, several species recorded as being common by Sankar et al (1993) were not seen by us, including Cotton Teal *Nettapus coromandelianus*, Chestnut-bellied Sandgrouse *Pterocles exustus*, Painted Sandgrouse *P. indicus* and Spanish Sparrow *Passer hispaniolensis*. There is possibly a decline in sandgrouse populations in Sariska due to recent changes in vegetation following various water conservation measures, such as check-damming of streams and increased protection of habitat from grazing by domestic cattle. Red Spurfowl *Galloperdix spadicea*, previously reported from the rocky tracts of Pandupol and Salopka, was another species that we did not record. Another striking absence from our list is that of

Grey Hornbill *Ocyrceros birostris*, a frugivorous species, otherwise moderately common in deciduous forests of north-western India. This species, recorded as rare by Sankar et al (1993), was never seen by us inside the Reserve despite the abundance of fruiting *Ficus glomerata* and tall trees along the streams suitable for nesting. It is possible that patches of suitable riparian habitat in Sariska are now too fragmented to support a population of hornbills.

Role of Sariska Tiger Reserve in conservation of regional bird diversity

The list of birds in Table 1 indicates that Sariska is extremely rich in avifauna.

Sariska plays an important role in providing a stopover point for numerous passage migrants such as the Common Rosefinch *Carpodacus erythrinus* that occurs in large flocks during March and October. Other passage migrants include Rosy Starling *Sturnus roseus* and rarely, the Verditer Flycatcher *Eumyias thalassina*. Sariska also provides wintering grounds for many species such as Hume's Warbler *Phylloscopus humei*, Black Redstart *Phoenicurus ochruros*, Eurasian Griffon *Gyps fulvus* and Grey-headed Flycatcher *Culicicapa ceylonensis*. From our observations during summer and monsoon, it appears likely that several insectivorous taxa such as Indian Pitta *Pitta brachyura*, Asian Paradise-Flycatcher *Terpsiphone paradisi*, Eurasian Golden Oriole *Oriolus oriolus* and Pied Crested Cuckoo *Clamator jacobinus* are summer migrants to Sariska.

An important reason for high bird diversity in Sariska may be the existence of a varied topography coupled with a mosaic of forest types including scrub forest, tall riparian forest (gallery forest), hilltop forest and dry deciduous *Anogeissus* forest. For instance, a number of species such as the Crested Serpent-Eagle *Spilornis cheela*, Brown Fish-Owl *Ketupa zeylonensis* and Tickell's Blue-Flycatcher *Cyornis tickelliae* have been found restricted to the few patches of tall riparian forest in Sariska. Riparian forest is also important in providing cover and water for numerous bird species during the harsh summer, such as Indian Treepie *Dendrocitta vagabunda*, Oriental Magpie-Robin *Copsychus saularis* and Oriental White-eye *Zosterops palpebrosus*. Bird communities of each

forest type were found to be rather distinct.

Importance of Sariska for bird conservation

Sariska has justifiably been identified as one of the Important Bird Areas (IBA) in the state of Rajasthan by BirdLife International (Jhunjunwala et al. 2001) due to the fact that it supports seven globally threatened species (see below) and has 30 species out of the 60 that are restricted by habitat to the Indo-Malayan Tropical Dry Zone (Jhunjunwala et al. 2001). Important species in the latter category include Painted Spurfowl *Galloperdix lunulata*, Red-headed Vulture *Aegypius calvus*, Jungle Bush-Quail *Perdicula asiatica* and White-bellied Drongo *Dicrurus caeruleus*.

Species of conservation interest

Two Critically Endangered species and five Near-threatened species occur in Sariska (BirdLife International 2001). Among the Critically Endangered species, the Indian White-backed Vulture *Gyps bengalensis* occurs in Sariska in a small resident population possibly numbering less than ten. Presence of open scrub woodlands, patches of tall forest and high inaccessible cliffs, along with presence of considerable livestock populations, makes Sariska an ideal habitat for this vulture. The Long-billed Vulture *G. indicus*, another Critically Endangered species, also occurs here in a sizeable resident population, often seen soaring, near cliffs. Sariska offers relatively unpolluted habitat and tall cliffs for the nesting of this species.

Most of the Near-threatened species are uncommonly seen in Sariska. Only the Darter *Anhinga melanogaster* was seen frequently in the Reserve at reservoirs such as Kankwari lake and Karnakawas reservoir. There are just a few individuals in the entire Reserve. Painted Stork *Mycteria leucocephala* has been observed feeding in Kankwari lake and at Karnakawas but is not very common in the Reserve. The Oriental White Ibis *Threskiornis melanocephalus* is not very common in Sariska, having been seen only twice so far. It was seen in swampy fallow fields close to Mansarovar Lake and at Karnakawas reservoir. The Greater Grey-headed Fish-Eagle *Ichthyophaga ichthyaetus*,

possibly a resident, was spotted twice in secluded riparian forest abutting a perennial stream at Bandipul. However, the Red-headed Vulture is quite frequently seen in Sariska, soaring near cliffs and once at a kill in scrub forest at Karnakawas.

Local threats to bird communities

Studies on vegetation have revealed that intensive biomass extraction (mainly through grazing and fuelwood collection) is leading to changes in vegetation structure and composition of the forest (Kumar & Shahabuddin 2005). These changes in forest structure are leading to changes in bird species composition (Shahabuddin & Kumar 2005). Several insectivorous bird species such as the Plain Prinia *Prinia inornata*, Red-throated Flycatcher *Ficedula parva*, Tickell's Blue-Flycatcher, Great Tit *Parus major*, Grey-headed Flycatcher, Oriental White-eye, and Painted Spurfowl are adversely affected by changes in forest structure caused by cutting and lopping activities. Some species such as Indian Robin *Saxicoloides fulicata*, Black Redstart, Eurasian Collared Dove *Streptopelia decaocto* and Grey Francolin *Francolinus pondicerianus* are encouraged and are benefiting by habitat degradation. Apart from extractive activities, escalating

tourism is also likely to adversely impact bird communities in Sariska, as tourism is concentrated around permanent springs such as Pandupol, which are critical to landscape-level diversity in the Reserve.

The forest habitat mosaic found in Sariska comprising dry deciduous, scrub and evergreen riparian forest, along with secluded streams and jheels, is now mainly restricted to protected areas in the Aravalli Hills of Rajasthan. In this context, the protection of Sariska Tiger Reserve as a refuge for avian diversity of Indian tropical dry forest in north-western India is of crucial importance (see also Rodgers & Panwar 1988).

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Table 1. Checklist of bird species found in Sariska (March 2003—June 2005)
(R: Resident, W: Winter migratory, S: Summer migratory, P: Passage migrant)

S. No.	Systematic list	Seasonal status	Comments on habitat preferences; dates for raresightings
1	LITTLE GREBE <i>Tachybaptus ruficollis</i>	R	Seen at jheels and waterholes
2	GREAT WHITE PELICAN <i>Pelecanus onocrotalus</i>	W	Occasionally at Karnakawas and Kankwari
3	LITTLE CORMORANT <i>Phalacrocorax niger</i>	R	Seen at jheels and waterholes
4	INDIAN SHAG <i>P. fuscicollis</i>	R	Seen at streams, jheels and waterholes
5	GREAT CORMORANT <i>P. carbo</i>	R	Seen at jheels
6	DARTER <i>Anhinga melanogaster</i>	R	Frequently seen at jheels and waterbodies
7	LITTLE EGRET <i>Egretta garzetta</i>	R	Seen at streams, jheels and waterholes
8	GREY HERON <i>Ardea cinerea</i>	R	Seen at jheels
9	LARGE EGRET <i>Casmerodius albus</i>	R	Seen at jheels
10	MEDIAN EGRET <i>Mesophoyx intermedia</i>	R	Seen at jheels
11	CATTLE EGRET <i>Bubulcus ibis</i>	R	Near water and cultivation
12	INDIAN POND-HERON <i>Ardeola grayii</i>	R	Seen at streams, jheels and waterholes
13	BLACK-CROWNED NIGHT-HERON <i>Nycticorax nycticorax</i>	R?	Karnakawas, 25.x.2003
14	LITTLE BITTERN <i>Ixobrychus minutus</i>	?	A few times in secluded riparian zone
15	PAINTED STORK <i>Mycteria leucocephala</i>	R	Seen regularly at Karnakawas / Kankwari, Mar-Apr 2005
16	BLACK STORK <i>Ciconia nigra</i>	W	Throughout winter at Karnakawas, also streams
17	WHITE-NECKED STORK <i>Ciconia episcopus</i>	R	At jheels and reservoirs
18	GLOSSY IBIS <i>Plegadis falcinellus</i>	V	Seen once at Kankwari, 9.ii.2006
19	WHITE IBIS <i>Threskiornis melanocephalus</i>	R	Seen in fields, at jheels
20	EURASIAN SPOONBILL <i>Platalea leucorodia</i>	R	A few times at jheels
21	GREYLAG GOOSE <i>Anser anser</i>	W	Karnakawas. 24.i.2004
22	BAR-HEADED GOOSE <i>A. indicus</i>	W	Open stretches near wetland, close to village

S. No.	Systematic list	Seasonal status	Comments on habitat preferences; dates for resightings
23	BRAHMINY SHELDUCK <i>Tadorna ferruginea</i>	W	Jheels and reservoirs
24	GADWALL <i>Anas strepera</i>	W	Karnakawas, 29.i.2004
25	MALLARD <i>A. platyrhynchos</i>	W	Karnakawas, 16.xii.2003
26	SPOT-BILLED DUCK <i>A. poecilorhyncha</i>	R	Common at waterholes and reservoirs
27	NORTHERN SHOVELER <i>A. clypeata</i>	W	Common at jheels and reservoirs
28	NORTHERN PINTAIL <i>A. acuta</i>	W	Common at jheels and reservoirs
29	GARGANEY <i>A. querquedula</i>	W	Karnakawas, 12.xi.2003
30	COMMON TEAL <i>A. crecca</i>	W	Infrequent at jheels and reservoirs
31	COMMON POCHARD <i>Aythya ferina</i>	W	Karnakawas, 12.xii.2003
32	ORIENTAL HONEY-BUZZARD <i>Pernis ptilorhynchus</i>	R	Occasional sightings in all habitats
33	BLACK-SHOULDERED KITE <i>Elanus caeruleus</i>	R	Fairly common in scrub forest
34	GREATER GREY-HEADED FISH-EAGLE <i>Ichthyophaga ichthyaetus</i>	R	Seen in riparian forest only
35	EGYPTIAN VULTURE <i>Neophron percnopterus</i>	R	All habitats, commonly near Kankwari village
36	INDIAN WHITE-BACKED VULTURE <i>Gyps bengalensis</i>	R	Soaring near cliffs occasionally
37	LONG-BILLED VULTURE <i>G. indicus</i>	R	Commonly seen soaring and at kills
38	EURASIAN GRIFFON <i>G. fulvus</i>	W	Occasionally seen soaring
39	RED-HEADED VULTURE <i>Aegyptius calvus</i> ¹	R	Often seen soaring and at kills
40	CRESTED SERPENT-EAGLE <i>Spilornis cheela</i>	R	Restricted to dense riparian forest
41	WESTERN MARSH-HARRIER <i>Circus aeruginosus</i>	W	Seen a few times near jheels and reservoirs
42	SHIKRA <i>Accipiter badius</i>	R	Seen in all habitats
43	EURASIAN SPARROWHAWK <i>A. nisus</i>	W	Seen a few times in all habitats
44	WHITE-EYED BUZZARD <i>Butastur teesa</i>	R	Seen a few times in all habitats, more in degraded scrub
45	BONELLI'S EAGLE <i>Hieraetus fasciatus</i>	R	Seen a few times in all habitats
46	BOOTED EAGLE <i>H. pennatus</i>	W	Governor Route, 12.xi.2003
47	OSPREY <i>Pandion haliaetus</i>	W	A few times at jheels
48	COMMON KESTREL <i>Falco tinnunculus</i>	W	Seen a few times in open, rocky habitat
49	LAGGAR FALCON <i>F. jugger</i>	R	16 Dec 03 at Bhaironghati
50	PEREGRINE FALCON <i>F. peregrinus</i>	W	A few times at jheels and scrub forest
51	BLACK FRANCOLIN <i>Francolinus francolinus</i>	R	A few times near jheel in thicket
52	GREY FRANCOLIN <i>F. pondicerianus</i>	R	Mostly degraded scrub forest
53	RAIN QUAIL <i>Coturnix coromandelica</i>	R	Bhaironghati, 9.xii.2003
54	JUNGLE BUSH QUAIL <i>Perdica asiatica</i>	R	Occasionally in scrub forest
55	PAINTED SPURFOWL <i>Galloperdix lunulata</i>	R	Restricted to undisturbed riparian forest
56	INDIAN PEA FOWL <i>Pavo cristatus</i>	R	Common in all habitats
57	WHITE-BREASTED WATERHEN <i>Amaurornis phoenicurus</i>	R	Near jheels and ditches
58	COMMON MOORHEN <i>Gallinula chloropus</i>	R	Near jheels and ditches
59	COMMON COOT <i>Fulica atra</i>	W	Only in jheels and reservoirs
60	LITTLE RINGED PLOVER <i>Charadrius dubius</i>	W	Jheels and reservoirs
61	RED-WATTLED LAPWING <i>Vanellus indicus</i>	R	Jheels, streams and waterholes, open land
62	WHITE-TAILED LAPWING <i>V. leucurus</i>	W	Karnakawas. i.2005
63	BLACK-TAILED GODWIT <i>Limosa limosa</i>	W	Regularly seen at Karnakawas, in Nov 2003 & Mar 2005
64	COMMON REDSHANK <i>Tringa totanus</i>	W	Near jheels and reservoirs
65	COMMON GREENSHANK <i>T. nebularia</i>	W	Near jheels and reservoirs
66	GREEN SANDPIPER <i>T. ochropus</i>	W	Near streams, waterholes and jheels
67	WOOD SANDPIPER <i>T. glareola</i>	W	Near streams, waterholes and jheels
68	COMMON SANDPIPER <i>Actitis hypoleucos</i>	W	Near streams, waterholes and jheels
69	LITTLE STINT <i>Calidris minuta</i>	W	Karnakawas, 4.v.2005
70	BLACK-WINGED STILT <i>Himantopus himantopus</i>	R	Jheels and waterholes
71	STONE-CURLEW <i>Burhinus oedicephalus</i>	P?	Degraded scrub forest
72	RIVER TERN <i>Sterna aurantia</i>	R	Jheels and reservoirs
73	WHISKERED TERN <i>Chlidonias hybridus</i>	W	Jheels and reservoirs
74	WHITE-WINGED BLACK TERN <i>C. leucopterus</i>	W	Kankwari, 27.iv.2005
75	BLUE ROCK PIGEON <i>Columba livia</i>	R	In all habitats, mainly undisturbed
76	LITTLE BROWN DOVE <i>Streptopelia senegalensis</i>	R	Mostly in disturbed habitats
77	SPOTTED DOVE <i>S. chinensis</i>	R	Seen in all habitats apart from Anogeissus
78	RED COLLARED-DOVE <i>S. tranquebarica</i>	R	Mostly in disturbed habitats
79	EURASIAN COLLARED-DOVE <i>S. decaocto</i>	R	Only in disturbed habitats
80	YELLOW-LEGGED GREEN-PIGEON <i>Treron phoenicoptera</i>	R	Mostly in riparian habitat, occasionally in scrub forest
81	ROSE-RINGED PARAKEET <i>Psittacula krameri</i>	R	Mostly in riparian habitat, occasionally in others
82	PLUM-HEADED PARAKEET <i>P. cyanocephala</i>	R	In all habitats
83	PIED CRESTED CUCKOO <i>Clamator jacobinus</i>	R	A few times in scrub forest
84	BRAINFEVER BIRD <i>Hierococcyx varius</i>	R	A few times in scrub forest
85	COMMON CUCKOO <i>Cuculus canorus</i>	P?	A few times in scrub forest

S. No.	Systematic list	Seasonal status	Comments on habitat preferences; dates for resightings
86	ASIAN KOEL <i>Eudynamis scolopacea</i>	R	Mostly in riparian habitat, occasionally in others
87	GREATER COUCAL <i>Centropus sinensis</i>	R	Mostly in scrub, also in riparian habitat
88	COLLARED SCOPS-OWL <i>Otus bakkamoena</i>	R	A few times in scrub forest
89	BROWN FISH-OWL <i>Ketupa zeylonensis</i>	R	Restricted to undisturbed riparian forest
90	SPOTTED OWLET <i>Athene brama</i>	R	In all habitats
91	INDIAN JUNGLE NIGHTJAR <i>Caprimulgus indicus</i>	R	Frequently seen/heard during Mar-May 2005
92	HOUSE SWIFT <i>Apus affinis</i>	R	Near waterbodies
93	SMALL BLUE KINGFISHER <i>Alcedo atthis</i>	R	Only in riparian habitat
94	WHITE-BREASTED KINGFISHER <i>Halcyon smyrnensis</i>	R	Mostly near streams and jheels, also near habitation
95	LESSER PIED KINGFISHER <i>Ceryle rudis</i>	R	A few times at jheels and streams
96	SMALL BEE-EATER <i>Merops orientalis</i>	S	Everywhere in open habitats
97	BLUE-TAILED BEE-EATER <i>M. philippinus</i>	R	Ghandka, ii.2004
98	INDIAN ROLLER <i>Coracias benghalensis</i>	R	Degraded scrub and cultivation
99	COMMON HOOPOE <i>Upupa epops</i>	R	Mostly in degraded habitat
100	COPPERSMITH BARBET <i>Megalaima haemacephala</i>	R	Mostly in scrub forest
101	EURASIAN WRYNECK <i>Jynx torquilla</i>	W	Degraded open habitats
102	BROWN-CAPPED PYGMY WOODPECKER <i>Dendrocopos nanus</i>	R	In all habitats, more in tall forest
103	YELLOW-FRONTED PIED WOODPECKER <i>D. mahrattensis</i>	R	In all habitats
104	LESSER GOLDEN-BACKED WOODPECKER <i>Dinopium benghalense</i>	R	Seen in all habitats
105	INDIAN PITTA <i>Pitta brachyura</i>	P?	Kalighati, 21.vii.2003
106	RED-WINGED BUSH-LARK <i>Mirafra erythroptera</i>	R	Seen in winter in rocky, open areas like Kankwari/Kirashka
107	ASHY-CROWNED SPARROW-LARK <i>Eremopterix griseus</i> ¹	R	Common in rocky, open areas like Kankwari
108	RUFIOUS-TAILED FINCH-LARK <i>Ammomanes phoenicura</i> ¹	R	A few times in degraded open scrub and rocky sites
109	GREATER SHORT-TOED LARK <i>Calandrella brachydactyla</i>	W	Kankwari, 18.xii.2003
110	DUSKY CRAG-MARTIN <i>Ptyonoprogne concolor</i> ¹	R	Near jheels, reservoirs and rocky slopes
111	WIRE-TAILED SWALLOW <i>Hirundo smithii</i>	R	Near jheels and reservoirs
112	RED-RUMPED SWALLOW <i>H. daurica</i>	R	In open areas near ditches and rocky slopes
113	WHITE WAGTAIL <i>Motacilla alba</i>	W	Near streams and jheels
114	LARGE PIED WAGTAIL <i>M. maderaspatensis</i>	R	Near streams and jheels
115	CITRINE WAGTAIL <i>M. citreola</i>	W	Infrequently near jheels
116	GREY WAGTAIL <i>M. cinerea</i>	W	Near streams and jheels
117	EURASIAN TREE PIPIT <i>Anthus trivialis</i>	W	Mainly in undisturbed habitat
118	LARGE CUCKOO-SHRIKE <i>Coracina macei</i>	R	Seen a few times in degraded scrub forest
119	BLACK-HEADED CUCKOO-SHRIKE <i>C. melanoptera</i>	R	Kalighati, 2.x.2003
120	SMALL MINIVET <i>Pericrocotus cinnamomeus</i>	R	Seen mainly in scrub and riparian
121	COMMON WOODSHRIKE <i>Tephrodornis pondicerianus</i>	R	Seen in all habitats
122	RED-VENTED BULBUL <i>Pycnonotus cafer</i>	R	Seen in all kinds of habitats
123	RUFIOUS-TAILED SHRIKE <i>Lanius isabellinus</i>	R	Sariska, 4.iii.2005
124	BAY-BACKED SHRIKE <i>L. vittatus</i>	R	Seen in all habitats
125	RUFIOUS-BACKED SHRIKE <i>L. schach</i>	R	Seen in all habitats
126	SOUTHERN GREY SHRIKE <i>L. meridionalis</i>	R	Several times throughout winter in degraded scrub
127	TICKELL'S THRUSH <i>Turdus unicolor</i>	W	Few times in scrub forest
128	EURASIAN BLACKBIRD <i>T. merula</i>	W	Seen often during Mar-Apr 2005
129	BLUETHROAT <i>Luscinia svecica</i>	W	Near jheels and waterholes
130	ORIENTAL MAGPIE-ROBIN <i>Copsychus saularis</i>	R	Mainly in undisturbed riparian and scrub forest
131	INDIAN ROBIN <i>Saxicoloides fulicata</i>	R	Common in disturbed habitats everywhere
132	BLACK REDSTART <i>Phoenicurus ochruros</i>	W	Seen in all habitats, more common in open habitats
133	COMMON STONECHAT <i>Saxicola torquata</i>	W	Seen occasionally in open scrub habitat
134	PIED BUSHCHAT <i>S. caprata</i>	R	Seen occasionally in degraded scrub
135	GREY BUSHCHAT <i>S. ferrea</i>	W	Twice in scrub forest
136	DESERT WHEATEAR <i>Oenanthe deserti</i>	W	Kankwari, 18.xii.2003
137	ISABELLINE WHEATEAR <i>O. isabellina</i>	W	A few times in rocky degraded areas
138	INDIAN CHAT <i>Cercomela fusca</i>	R	Mostly in rocky riparian habitat
139	YELLOW-EYED BABBLER <i>Chrysomma sinense</i>	R	Occasional sightings in open scrub forest
140	COMMON BABBLER <i>Turdoides caudata</i> ¹	R	Restricted to degraded scrub forest
141	LARGE GREY BABBLER <i>T. malcolmi</i>	R	Restricted to degraded scrub forest
142	JUNGLE BABBLER <i>T. striata</i> ¹	R	Seen in all habitats, more in dense vegetation
143	FRANKLIN'S PRINIA <i>Prinia hodgsonii</i>	R	Mostly in undisturbed habitats
144	JUNGLE PRINIA <i>P. sylvatica</i>	R	Mostly in scrub forest
145	ASHY PRINIA <i>P. socialis</i>	R	Mostly in scrub forest, particularly disturbed
146	PLAIN PRINIA <i>P. inornata</i>	R	Mostly in disturbed habitats
147	COMMON TAILORBIRD <i>Orthotomus sutorius</i>	R	Seen in all habitats, esp. riparian
148	COMMON CHIFFCHAFF <i>Phylloscopus collybita</i>	W	A few times in scrub, near jheels

S. No.	Systematic list	Seasonal status	Comments on habitat preferences; dates for resightings
149	OLIVACEOUS LEAF-WARBLER <i>P. griseolus</i>	W	Seen mainly in rocky streambeds in dense forest
150	HUME'S WARBLER <i>P. humei</i>	W	Seen mainly in undisturbed and riparian habitats
151	GREENISH LEAF-WARBLER <i>P. trochiloides</i>	W	Near Kirashka, 3.x.2003
152	COMMON LESSER WHITETHROAT <i>Sylvia curruca</i>	W	Mainly in disturbed habitats everywhere
153	RUSTY-TAILED FLYCATCHER <i>Muscicapa ruficauda</i>	P?	A few times in undisturbed riparian forest, waterholes
154	RED-THROATED FLYCATCHER <i>Ficedula parva</i>	W	Mostly in riparian also undisturbed scrub
155	VERDITER FLYCATCHER <i>Eumyias thalassina</i>	P?	Seen occasionally in riparian forest
156	TICKELL'S BLUE FLYCATCHER <i>Cyornis tickelliae</i>	R	Mainly in undisturbed riparian forest
157	GREY-HEADED FLYCATCHER <i>Culicicapa ceylonensis</i>	W	Mainly in undisturbed riparian forest
158	ASIAN PARADISE-FLYCATCHER <i>Terpsiphone paradisi</i>	S	Only in undisturbed scrub and riparian
159	WHITE-BROWED FANTAIL-FLYCATCHER <i>Rhipidura aureola</i>	R	Seen mainly in undisturbed habitats
160	GREAT TIT <i>Parus major</i>	R	Mainly in undisturbed habitats esp. riparian
161	PURPLE SUNBIRD <i>Nectarinia asiatica</i>	R	Seen in all habitats, more in open, disturbed areas
162	ORIENTAL WHITE-EYE <i>Zosterops palpebrosus</i>	R	Mostly in undisturbed habitats, particularly riparian
163	CRESTED BUNTING <i>Melophus lathami</i>	R	Mostly in disturbed habitats and scrub forest
164	WHITE-CAPPED BUNTING <i>Emberiza stewarti</i>	W	Seen in all habitats, more in undisturbed habitats
165	RED-HEADED BUNTING <i>E. bruniceps</i>	W	Dec 05 in Kalighati area
166	COMMON ROSEFINCH <i>Carpodacus erythrinus</i>	P	Mostly in degraded scrub forest
167	WHITE-THROATED MUNIA <i>Lonchura malabarica</i>	R	Disturbed scrub and riparian sites
168	SPOTTED MUNIA <i>L. punctulata</i>	R	Near Indauk village, x.2003
169	HOUSE SPARROW <i>Passer domesticus</i>	R	Few times in scrub forest
170	YELLOW-THROATED SPARROW <i>Petronia xanthocollis</i>	R	Seen in all habitats, but more in disturbed forests
171	BAYA WEAVER <i>Ploceus philippinus</i>	R	Open scrub forest near water
172	GREY-HEADED STARLING <i>Sturnus malabaricus</i>	W	Near Haripura, x.2003
173	BRAHMINY STARLING <i>S. pagodarum</i>	R	Seen mainly in disturbed habitats
174	ROSY STARLING <i>S. roseus</i>	P	Seen in flocks in degraded scrub
175	COMMON STARLING <i>S. vulgaris</i>	W	Kankwari, 3.xi.2003
176	ASIAN PIED STARLING <i>S. contra</i>	R	Seen occasionally in scrub forest
177	COMMON MYNA <i>Acridotheres tristis</i>	R	Seen mainly in riparian and scrub habitat
178	BANK MYNA <i>A. ginginianus</i>	R	Seen a few times near villages
179	EURASIAN GOLDEN ORIOLE <i>Oriolus oriolus</i>	S	Seen in all habitats, commonly in undisturbed sites
180	BLACK DRONGO <i>Dicrurus macrocercus</i>	R	Seen in all habitats
181	WHITE-BELLIED DRONGO <i>D. caeruleus</i>	R	Mostly in undisturbed habitats
182	JUNGLE CROW <i>Corvus macrorhynchos</i>	R	Karnakawas, 30.xi.2003
183	INDIAN TREEPIE <i>Dendrocitta vagabunda</i>	R	Abundant in all habitats

¹Based on nomenclature used in Rasmussen & Anderton (2005).

Recoveries from the Newsletter for Birdwatchers (1966)—11

Zafar Futehally

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At our Annual Meeting on 15.i.1967, giving "vital statistics" for the year's performance, I reported that 46 persons had sent articles, 16 of whom were Englishmen and women, and these have proved to be our keenest supporters. The number of subscribers in December 1966 was 375.

There are some splendid articles in the 1966 Newsletter, of the type which could be models for current contributors—pleasant reading based on careful observation. So I thought I would quote extensively from some of these writers,

K.K. Neelakantan, Stewart Melluish, T.J. Roberts, etc. The wealth of material makes it necessary to spread this over more than one issue of *Indian Birds*, and in this one I confine myself to dealing only with 'KKN'.

Writing about the strange choice of roosts by crows, KKN [*NLBW* 6 (1): 1-2] said,

"That crows, mynas, house sparrows, and parakeets roost in larger numbers in trees standing in the middle of crowded bazaars is well known, but I used to think that this was due to the absence of more suitable roosts near by. A recent experience makes me wonder whether these birds

deliberately choose trees in the heart of the town.

"Towards the end of the third week of November I was passing through Shoranur (central Kerala) at 11 p.m. It was a dark night. The spot where we had stopped was at the very centre of this small town, not far from the Railway Station and close to a hotel which is open all night. It is also the town bus stand, and till about 10 p.m. is full of bustle. Throughout the night lorries and buses stop there and small, noisy crowds of people are never absent. The place is also brilliantly lit from dusk to dawn. Yet a clump of *Pongamia* trees standing under a street lamp and in the glare of the fluorescent lights of the hotel sign was full of crows. Those I

saw clearly were all House Crows. They sat without any attempt at concealment, and could easily be seen by people. There were innumerable trees, much taller and larger than the *Pongamia*-s everywhere in the town, but the crows had chosen to roost in the 'lime light'.

"I was surprised to find that some of the crows were calling, some moving from twig to twig, and a few every now and then flying up 50 to 60 ft. into the darkness overhead. Few of these last were seen returning to their perches. One crow sat across an electric wire, calmly preening!

"It was evident from the large and extensive patches of droppings under the trees and the white coating most of the leaves had received that the roost had been in regular use for a long time.

"I believe that many kinds of birds prefer to roost in trees close to man's dwellings. I have found Tree Pies, Blackheaded Orioles, Tailor Birds, Ioras, Whitebrowed Bulbuls, Paradise Flycatchers, Crow-pheasants and Whitebreasted Kingfishers preferring roosts close to the roof. In the Thekkady Game Sanctuary I found large numbers of Grey Wagtails coming from the surrounding forest to a tree near the rest house to roost. Also the trees near Aranya Nivas were extremely popular as roosts. Obviously the proximity of human beings affords some security to the birds from certain kinds of predators. Though I should think that this would be more than set off by the danger from domestic cats. Perhaps the crows of Shoranur were also impelled by this instinct to roost where the constant presence of human beings gave them a feeling of security.

"But those crows which occupied branches close to the road must have spent very disturbed night[s]. Some of them were behaving as though the sun had risen! Did these crows deliberately occupy perches where sleep would be impossible, or were they the late-comers who could not find better accommodation?

"Do crows habitually prefer a grove of spreading trees—such as mango, banyan, etc.—or, do they quite often spend the night scattered about over a larger area in coconut and other trees? In Trivandrum there are still very well-wooded patches with large spreading trees. But I find that at one place crows seem to sleep in small numbers on various coconut trees. This roost is not at all a spectacular one, and I discovered that quite a few crows were spending the night here only because on a number of occasions I happened to hear crows calling from various trees well before sunrise and when crows had not begun to fly about. It should be mentioned that these crows were heard during the non-breeding season, and so such a large number could not have been

occupying nests in that area."

Reporting on his visit to the local zoo, KKN was struck by the antics of a captive Great Hornbill [*NLBW6* (2): 8].

"On 16.1.1996 I paid a visit to the local zoo hoping to spend a couple of hours watching 'wild' birds, particularly some unfamiliar migrants which I expected to find in the bushes and trees which give the zoo its special charm. But, though I did find a Blacknaped Oriole, I found myself spending more time observing the antics of the lone male Great Hornbill that was acquired by the Zoo some time last year.

"The bird was in a cage some 8 ft. x 10 ft. and had been provided with a rusty iron bar to perch upon. The floor was covered with coarse sand mixed with some gravel. I found the bird repeatedly jumping down from the perch to the sandy floor two feet below it, keeping its wings open and laid flat on the ground, running its open bill through the sand. It took in a mouthful of sand, raised its head and let almost all the sand dribble away. Then raising its body, it took hold of one of the flight-feathers of a wing and swiftly combed it with the bill. Then it leaped back to the perch, spent a few seconds there and again jumped to the floor to run through the whole routine. I watched the bird for more than ten minutes, and during this period it must have repeated the performance at least ten times. Some times the bird scooped up the sand, let it fall and 'wiped' its wing feathers with the bill three or four times before returning to the perch. On a few occasions it kept the wing closed while pretending to eat the sand. Once a large stone, about the size of a lemon, got between the mandibles and the bird at once raised its head, opened the bill wider and let the stone fall off.

"I wonder whether the bird was indulging in a form of 'anting', for its behaviour suggested the sort of nervous excitement associated with this phenomenon. If it was a form of 'anting', it must be a habit acquired by the bird in captivity as it is not at all likely that a wild Great Hornbill will come down to the ground for such a purpose. It would be interesting to know whether William, the Great Hornbill who lived in the Bombay Natural History Society's office for nearly 30 years ever showed a tendency to 'ant'."

In the May 1966 *Newsletter*, KKN responded to an article by S.V. Nilakanta, written earlier, on 'bird quarrels'. SVN wrote "For the purpose of these observations two types of quarrels are omitted. They are 1) Quarrels between predators and prey. This being a serious matter of life and death is outside the scope of mere quarrels, and is also a completely one sided affair 2) Quarrels between birds

of the same species. This fascinating study involves social relationships like, pecking order, selection of mates, nesting sites, and such. Observations here are of such a wide scope that they (also) have to be omitted, "This leaves us with quarrels between different species and between the birds and other creatures. Strangely enough, these quarrels seem to be very few, because birds are not given to logical reasoning or revengeful action". KKN gives his own observations about these quarrels [*NLBW6* (5): 5-6].

"On reading Sri Nilakanta's article on bird quarrels, I was reminded of certain squabbles for which peevishness and nervousness rather than competition for food, nest-sites or perches appeared to have been the cause.

"Many years ago I used to pass a *Morinda* (a sort of wild fig with rasp-like leaves and abundance of sulphur-yellow fruits) every day. When the tree was full of fruits a male koel used to spend hours on the tree. Though the branches were laden with ripe fruit and I seldom saw the koel eating anything there, the koel would not allow any other bird to go near this tree. Whenever other koels or smaller birds like the bulbuls attempted to land on a branch, the koel would at once drive them away. He had more of the Man of Property about him than even the owner of a nesting territory.

"The *Chloropsis* (at any rate Jerdon's) also behaves like a dog in the manger though its desire to keep others off has something to do with the food ration. Once a *Chloropsis* arrives on a twig bearing berries or flowers, it spends more time driving other birds away than in feeding.

Once I witnessed a prolonged quarrel between a Spotted Dove and a Pied Crested Cuckoo. They were in a low bush in scrub country (the compound of the Christian College, Tambaram) and spent more than half an hour scrapping. The cuckoo's insistence on coming back to the bush from which the dove always drove it away seemed to be as illogical as was the dove's determination to shoo it off. I did not find any nest anywhere in the neighbourhood.

"Common Mynas have a curious habit of picking a quarrel with one of themselves who becomes the object of a combined assault by five or six of his (or her) kinsfolk. This starts late in the evening when the mynas are presumably on their way to the roost. A small group may be seen on top of a palmyra tree just resting and making the usual noises. Suddenly, before one knows what started it, pandemonium breaks out and all one sees is a couple of mynas tumbling 50 feet to the ground and then rolling about and pecking one another. Meanwhile the others would also have

flown down and would first form a circle of vociferous spectators and then they too would, one by one, join the fray. The whole thing would end as abruptly as it had started and the flock would disperse or move off together as though nothing unusual had happened. This sort of thing seems to be more frequent during the summer months.

“Having strayed from the topic of quarrels between birds of different species, let me conclude with the accounts of quarrels between birds and other animals, and birds and insects. The best example of the former is the quarrel between a squirrel and a shikra which I witnessed some 22

years ago. One would have thought that no self-respecting shikra would let a squeaking palm squirrel disturb its rest, but I found the shikra deserting its perch on being asked ‘to get a move on’ by the squirrel. The shikra sat on a wall up the side of which the squirrel ran. The squirrel’s tactics consisted in making sudden rushes from one side of the wall towards the shikra. I do not remember now whether the squirrel uttered its usual ear-splitting alarm calls, but it had no difficulty in persuading the shikra to seek some other perch.

“On many evenings some months ago I used to enjoy the sight of a dispute between

a Loten’s Sunbird and a dragonfly for the bare twig at the top of a tamarind tree. The twig was probably used more regularly by the dragonfly. Whenever the sunbird occupied this perch, the dragonfly would come and, by merely flying in a determined fashion towards the bird, force it to fly off. But the sunbird would return at once and take possession only to be driven off again by the insect. As the sunbird seldom spent much time on this perch the technical victory may be said to have gone to the dragonfly. “Watching such incidents and trying to find the reasons for them can be an absorbing pastime.”

Correspondence

Comments

“We most certainly have come far since the get together in Zafarbai’s delightful garden in Andheri, Mumbai (then Bombay) to agree on bringing out a *Newsletter for Birdwatchers*. Earlier in the morning, at breakfast, Zafar and I were nonplussed at the call of a bird in the tree branches shading the house. It was the bemused look on the face of Zafar’s teenage son that made me realize we were making fools of ourselves. The “strange” bird was a Five-striped Palm Squirrel *Funambulus pennanti*! While I could be excused for my ignorance since I was till then familiar with the Three-striped Palm Squirrel *F. palmarum*, but that Zafar who probably heard the “chirrup” every day of his Bombay life should be confused would seem inexcusable by any standards. Much, much later, after getting to know legions of birdwatchers, I am now not surprised that the then Honorary Secretary of BNHS and today’s Editor Emeritus of *Indian Birds* could not tell a common rodent from a bird! Most of the birding fraternity does bird watching, literally. Sound just does not play any significant part in their appreciation of birds! Evaluating our progress since that delightful, very properly “old fashioned” breakfast, I can caution my large numbers of young birdwatcher friends that they do not need to be too concerned about being recognized as great birdwatchers or ornithologists. If they regularly enjoy their birds and the world they live in long enough, they will, as a matter of course become “recognized”. They should however also enjoy writing.

“While I was a precocious birdwatcher having had the good fortune to have been a boy in times when birds were common and everywhere and was growing up in a privileged environment dominated by the likes of Dharmakumarsinhji, Salim Ali, Horace Alexander, General Williams—my greatest regret has been that I got intimate with the incomparable Humayun Abdulali rather late in life, Zafarbai just could not escape getting some avian “flu” infection from his already acclaimed relatives. I think he and I both have gained immensely in our desire to see more and more people infected. The *Newsletter for Birdwatchers* will remain a tremendous tribute to my friend and now this *Indian Birds*! Look at your Trustee Board! Taej and Santharam, both of whom I knew as boys! Good friends like “Subu” and Rishad! Suhel I do not know of. I also like the way you do not prefix names with “Dr”. “Dr” Taej Mundkur would make me imagine he has started carrying a stethoscope round his neck instead of a pair of binoculars!

“The talk of prefixes and suffixes reminds me of how long it took me to get rid of the “KS” to my name. It was quite irritating at first, though amusing in later years, to have myself addressed “Mr. K.S. Lavkumar”. There was a period when I almost agreed to try for a Ph.D.—my very good friend, Professor R.M. Naik Ph.D., was adamant that I acquire the suffix and he took me to the Vice Chancellor of the Saurashtra University to have me registered for Ph.D. on the Vice Chancellor’s quota. The whole thing came to an end when the VC instead

suggested I regularly lecture the M.Sc. students! Thinking back, would there have been a period with myself being labeled Dr. K.S. Lavkumar? Taej will remember the day I literally set him afloat in the Gulf of Kachchh to produce a report that still keeps popping up in learned seminars on the Gulf of Kachchh to think of what Taej wrote as an enthusiastic student being included in the environmentalists’ arsenal against the Reliance refinery coming up at Jamnagar, is quite mind boggling—the pen is more powerful than the sword and all that?

“Well this garrulous piece has become quite long. Let me conclude on a more serious note. Anand Prasad’s description is indeed that of a female Gold-naped Finch *Pyrrhoplectes epauletta*. I have seen a flock years ago in Ladakh, beside the track beyond Sissoo. This was long, long before motor vehicles had arrived at Rahla on the Kullu side of the Rohtang Pass. The males are very distinct. The birds I observed were gleaned seeds among sparse grass absolutely in the open and were extremely confiding. Just a word of caution though, the Plum-headed Parakeets *Psittacula cyanocephala* could have been the Slaty-headed Parakeet *P. himalayana*.

“In the “Correspondence” section, Nirmala Chathoth refers to me and the grandala she saw. Last Sunday—16th April—I happened to visit Surat and there, at a nearby lake, this time, I had to disappoint her and a large group of keen birdwatchers by identifying a flock of duck far out on the water as being Lesser Whistling-Duck *Dendrocygna javanica*

and not Large Whistling-Duck *D. bicolor*. I was almost tempted to make them all feel happy by adding a new bird to the Gujarat list! I did precisely comment how indeed we all would have had a new record had I not taken a harder look to decide the dark markings on the neck were shadows and not plumage colour—the next edition of ‘Grimmett et al.’ would have shown Surat as in the range of the Large Whistling-Duck!”

Lavkumar Khacher

14, Jayant Society, Rajkot 360004,
Gujarat, India.
20.iv.2006

More birding news from Puttur

“This season—December to March—has been very good for me as I have had the good fortune to see species that I have never seen before near my house. It is all a matter of being at the right place at the right time and for all I know, these birds

might be regularly visiting and I have been totally unaware of it.

“One Sunday in December, I saw a pair of Heart-spotted Woodpeckers *Hemicircus canente* for the first time near my house. This is my only sighting of them here...I was so thrilled to see them high up in the *Carea arborea* tree. Then, one Sunday in January, I reached my favourite bird watching spot—a log in front of the *Carea arborea* and *Terminalia paniculata* trees—rather late in the morning. It was nearly eight and I did not have any hope of seeing anything. Just then, a grey blur flew over my head from behind and disappeared into the shrubbery on my left. I just got a glimpse of something grey. Then I began to hear the most weird laughing cackles, not like the flameback woodpecker but rather like a child mocking another. The prancing movements of a female Black-naped Monarch-Flycatcher *Hypothymis azurea* for a while distracted me. It would puff out its chest and fan its tail comically as it searched in the foliage for insects. What a strange looking bird it is—like a dull coloured thing which has dipped its head in blue dye! Then suddenly I

saw a large grey bird just in front of me some distance away and it just took my breath away! It was a Malabar Grey Hornbill *Ocyrceros griseus*! Though I have seen this bird before in Nagarhole, this is the first time I saw it in Puttur. The weird laughing sounds were made by this bird.

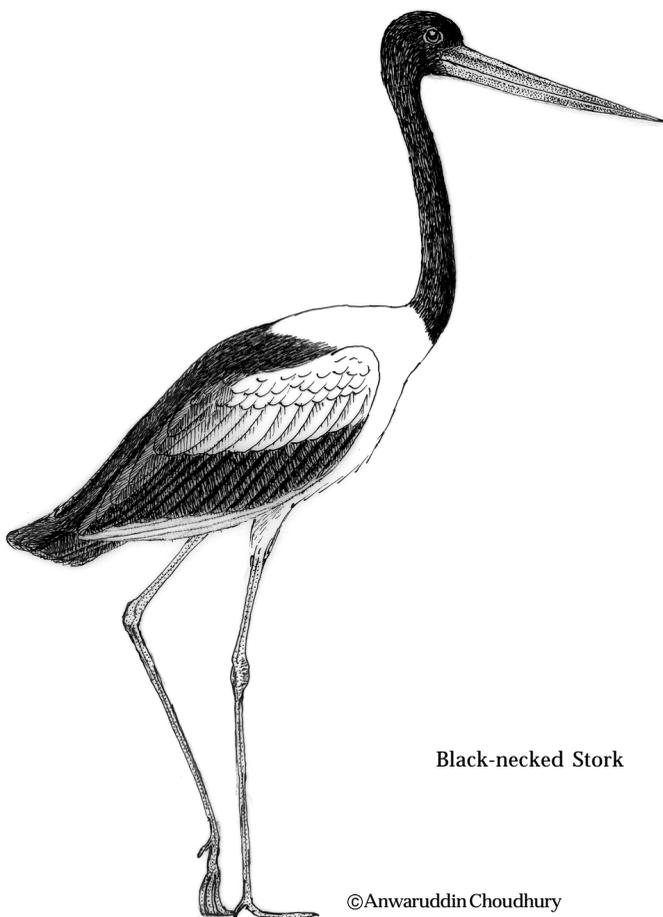
“Then in February, I watched a small active bird outside my bedroom window and identified it as the Franklin’s Prinia *Prinia hodgsonii*. There are many birds here, which I have a lot of difficulty in identifying as they do not keep still at all. I was pleased to be able to identify this one. It’s quite common here but I was never able to pay much attention to it due to its habit of not sitting still for even a single nanosecond. While I was busy watching the prinia, I was aware of a largish bird in the foreground. Watching it from the tail of my eye, I thought it was a drongo and so paid no attention to it. When I finally looked at it properly, I saw that it was a different shape—more like an oriole or myna and I trained my binoculars on it. You could have knocked me down with a feather when I realized what it was—an Asian Fairy-Bluebird *Irena puella*! The red eyes and the blue sheen on the head and wings were unmistakable. When I was on a forest trek with my family last year in Periyar Tiger Reserve, Kerala, we had heard this bird but it had remained hidden in the foliage and we could not see it and now here it was, right in front of me, sitting quietly, without uttering a sound! It found me, as they say. I have noticed Yellow-browed Bulbuls *Iole indica* also doing this—they sing from a hidden place and when they are in view, they remain silent. It seems to be a survival tactic.

“Next Sunday, I watched a pair of Pied Flycatcher-Shrikes *Hemipus picatus* for the first time. I had to search in my field guide to identify it, as I had never seen these birds before.

“So I have had a lot of fun seeing ‘new’ birds this season...”

Pragati Nayak

Aashirwad, Sampe, P.O. Aryapu, DK
574210



Black-necked Stork

©Anwaruddin Choudhury

Editorial

“Taxonomy (the science of classification) is often undervalued as a glorified form of filing—with each species in its prescribed place in an album; but taxonomy is a fundamental and dynamic science, dedicated to exploring the causes of relationships and similarities among organisms. Classifications are theories about the basis of natural order, not dull catalogues compiled only to avoid chaos.” Stephen Jay Gould (1990; *Wonderful life: The Burgess shale and the nature of history*. Hutchinson Radius.)

There is an old adage that states, “Wisdom begins by calling things by their right names.” That is what taxonomy aims to do—name all life without confusion or ambiguity. At least that was what Carl von Linne set out to do almost 250 years ago. His classifications were based on basic morphology; today, additional criteria including song and DNA are used. The rules of the game are these days known as the *International Code of Zoological Nomenclature* and are framed by the International Commission on Zoological Nomenclature, based in London.

Although taxonomy is a science for the professional (and perhaps the serious amateur), taxonomic decisions have two important consequences that affect all of us, birdwatchers and scientists alike.

One consequence is a direct result of the order that nomenclature brings into a world that humans perceive as confusing. Scientific nomenclature (i.e.,

naming) isolates each taxon (genus, species, subspecies, etc.) so precisely that confusion with another does not arise. However, this is not the case with the common names of birds. Names within a language, say English, have changed over the years and are a source of constant disagreement between birdwatchers as they are not bound by rules as is scientific nomenclature. Different languages call the house crow by different names. But its scientific binomen is the same throughout the world - *Corvus splendens*. So, nomenclature is a precision tool for naming a taxon.

Another use of taxonomy is indirect, but of serious impact. With the ongoing evolution of taxonomic methodology, the status of taxa is in flux. A more flexible tool bag than in Linnaean times allows contemporary taxonomists to achieve greater accuracy in establishing a taxon. This might result in species

being split, races being promoted to species level, and so on. Such changes might lead to the recognition of a taxon that requires conservation action—perhaps because of its endemism, rarity or threatened survival. So, nomenclature becomes an engine for conservation action.

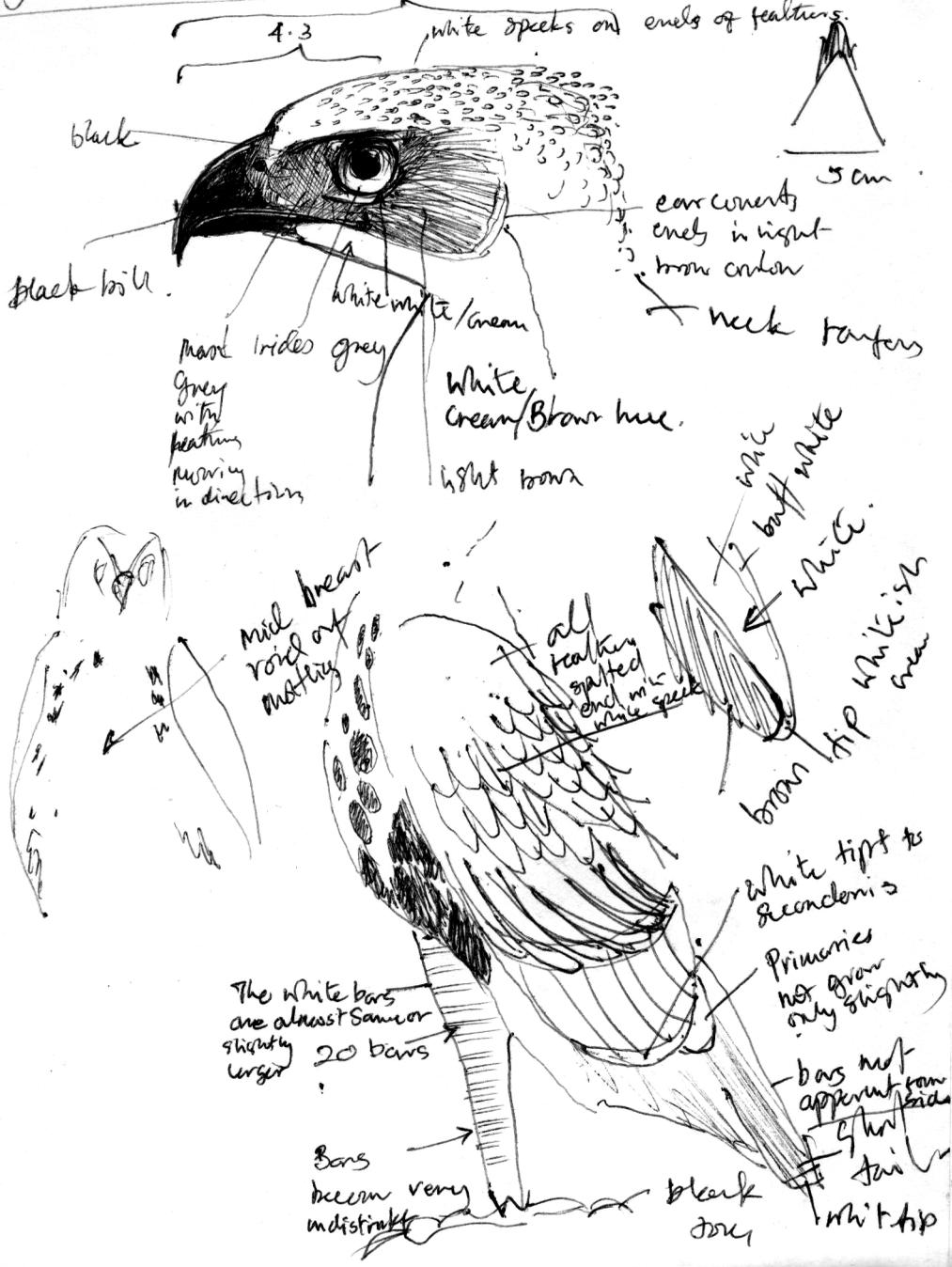
Given its importance, we hope that the paper on taxonomy in this issue of *Indian Birds* will be of great interest to you, our readers, and help you unravel the intricacies of this evolving science. We are grateful to the authors and the editor of *British Birds* for allowing us to reprint the paper in *Indian Birds*.

All this notwithstanding, the subjects of this science go about their lives, blissfully ignorant of our esoteric labours, yet dependent on us for their continued survival.

-Aasheesh Pittie

25/7/95 Unagame

Quercite Black Eagle 9 cm





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