

species for our life lists faster than we are losing them because of taxonomic changes at the species level.

However, the phylogenetic species concept is challenging the biological species concept for supremacy. It argues that species should be based on the differences among populations and does not consider the issue of reproductive compatibility to be relevant, as such. A species is defined as the smallest diagnosable units (this is a population that has a character that distinguishes from other populations) with a parental pattern of ancestry and descent (this ensures that males, females, and juveniles of one species are not considered different species, and neither are plumage aberrations such as albinos or dark morph hawks). Most practicing taxonomists use some form of this species concept now, although it is still undergoing revision and has not completely displaced the biological species concept. However, I rather suspect that it will over the next 30 years or so. When it does, the number of species of birds recognized in North America will probably about double, and in the world will go from the current about 9,700 to somewhere between 18,000 and 25,000. Although, it is not officially in use for the AOU checklist committee, I think it has influenced the treatment of isolated populations. The split of the Scrub Jay into three species, for example, has its roots in the phylogenetic species concept.

The role of technology

Two technological features of modern life have had a huge effect on bird taxonomy that is only just beginning to be reflected in compilations such as the AOU checklist. These are the computer, which has allowed the development of much more sophisticated analyses, and increasing knowledge of genetics, especially DNA studies. Computers are essential to modern taxonomic studies because they enable researchers to analyze

vast amounts of data and to perform complicated analyses. It is no accident that the phenetic and phylogenetic approaches have arisen in the last 30 years. Both rely heavily on the ability of computers to analyze large amounts of data, and do many analyses in a short period of time.

Biochemical studies have revolutionized taxonomic studies in many groups of organisms, including birds. The first studies were in the 1960s when Charles Sibley analyzed egg-white proteins to look at relationships among families. This was rapidly superseded by work using proteins gathered from body tissues and blood. In the late 1970s, Sibley was back on the scene with his DNA hybridization studies. The technique of DNA hybridization is a little complex, but basically goes like this. DNA is a molecule with two strands of a sugar with molecules called nucleotides sticking out from these strands. There are four different kinds of nucleotides: adenine, guanine, thymine, and cytosine (A, G, T, and C from now on). A and T, and C and G can form moderately strong chemical bonds, which join the two strands of DNA together in the form of a helix, basically a twisted ladder. Genetic changes between species primarily result from changes in the order of the nucleotides along a strand of DNA. The order of the nucleotides determines the order of amino acids in proteins, and this is the heart of the system of heredity in all life. In DNA hybridization, scientists attempt to measure how different the nucleotide order is in the DNA of one species compared to another. To do this, first a DNA sample of species 1 is heated. This causes the chemical bonds between the nucleotides joining the two strands to break, giving single strands of DNA. This DNA is then radioactively marked. It is then joined with a much larger sample of unmarked DNA from species 2. This mixture is cooled, which allows the DNA to reform the chemical bonds and again

you have double stranded DNA. Because the mixture is dominated by the unmarked DNA of species 2, the radioactive strands of species 1 join not with the DNA of their own species, but with the DNA of species 2. So the mixture now contains, unmarked DNA of species 2, and marked DNA that is hybrid; one strand is radioactively marked and comes from species 1, the other strand is unmarked and comes from species 2. Now when this hybrid DNA is heated, the two strands will dissociate and become single strands. The temperature at which the dissociation occurs will be higher if the two strands match up well and progressively lower as the match between strands is poorer. So, by measuring the temperature at which the dissociation occurs one can estimate how different the DNA of two species is. Two species whose DNA dissociates at higher temperature have more similar DNA and are more closely related than those whose DNA dissociates at lower temperature and which have less similar DNA.

Sibley used DNA hybridization to look at relationships among all birds down to the subfamily level and in some groups much lower (Sibley and Ahlquist 1985, 1990). This work has been very influential, although there are some problems with Sibley's analyses, and he tended to over-interpret his data. Over the past decade, other DNA techniques have become important, including DNA restriction mapping and DNA fingerprinting. These techniques rely on enzymes that chop the DNA in certain places based on the nucleotide sequence. They provide somewhat finer resolution than DNA hybridization. Finally, DNA sequencing, where the scientist actually gets the complete order of the nucleotides on a piece of DNA, and so can compare exactly the differences among species or even individuals within a species has become an important tool within the last five years. So far, it