The Past, Present and Future of Biological Taxonomy

An Honors Thesis (HONRS 499)

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Abstract

This honors thesis examines the history, present applications and the current issues of biological taxonomy, the study of classifying, identifying and naming organisms. The history portion examines the development of taxonomy through the works of many naturalists and biologists. One biologist in particular, Carl Linnaeus, established guidelines and the framework for nomenclature of all organisms. The present applications of taxonomy focus on the developments of taxonomy when it is integrated with evolutionary theory. This integration, named systematics, focuses on determining ancestor-descendent relationships among organisms. The present portion also examines what characteristics a taxonomist might use to determine an organism’s classification. Finally the future portion of this thesis focuses on current issues that might affect taxonomy in future years. This includes taxonomy’s role in species conservation, DNA taxonomy, taxonomic databases and an alternative system of nomenclature called the PhyloCode.
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The Past: Early Taxonomy

Introduction

Taxonomy is defined as the science of identifying and classifying organisms. This science began as early as the 3rd century B.C. with the philosopher Aristotle and has flourished ever since. Through the hard work and dedication of biologists from the 16th century to the present, taxonomy has become an effort to determine, name, and describe every species on this planet. Even the early years of taxonomy still impact our lives today. Carl Linnaeus, named the father of taxonomy, developed the rules and guidelines of naming any new species, and his rules are still used today. Early biologists also established the five main division of all life—animal, plants, fungi, protists and bacteria—that have led to a more thorough study of every type of organism on this planet.

Pre-Linnaeus

The first person to come up with a system to classify and identify organisms was the philosopher Aristotle. Aristotle made observations and discoveries in multiple areas of biology including comparative anatomy, reproduction/embryology, and his detailed studies of invertebrates, fishes, birds, and other organism (Coonen 1977). His attention to detail and observation made his work *Historia animalium* significant in the 3rd century, B.C. (Mayr 1982). Focusing on the animal species, Aristotle first divided all known animals at that time between the “blood” and the “bloodless,” referring to vertebrates and invertebrates, a division that is still used in taxonomic ranks to this day (Mayr 1982). He also separated fish, birds, reptiles and amphibians based on thermoregulation (warm-blooded or cold-blooded) and form of birth (live birth or egg-laying), much as is done today (Mayr 1982).
Aristotle’s method of classification is called downward classification. Simply put, the biggest group, called the *summum genus*, is divided into two subordinate groups based on specific characteristics. The subdivisions continue to be made until there is only one item in the subordinate group, similar to how a dichotomous key is used (Mayr 1982). Another aspect of Aristotle’s classification was called essentialism, where the name of an organism is its essence or the distinguishing character that sets it apart from other organism (Mayr 1982, Coonen 1977). Both downward classification and essentialism were applied to the biological taxonomy guidelines that were used by Linnaeus.

After Aristotle, most development in classification and biological taxonomy came from naturalists studying plants. There are a couple reasons why botany was the field of choice over zoology. First, plant specimens were easier to keep than animal specimens (Mayr 1982). Methods to collect and store plant specimens were available well before the sixteenth century, while methods to create and keep an animal specimen that would not be destroyed by insects were not developed until the 18th century (Mayr 1982). Another reason was that the interest in plants came from their medicinal properties that were often used by doctors (Mayr 1982). For this reason, many notable botanists were also physicians.

The first person to study botany extensively was Aristotle’s own pupil named Theophrastus (Green 1927, Gundersen 1918, Mayr 1982). His famous work “History of Plants” was written in the 1st century A.D. and is considered the oldest botanical book (Green 1927, Gundersen 1918). His book recognized over 500 species of plants as well as descriptions for each (Green 1927, Gundersen 1918). His main division for classification purposes was the plant’s growth form (herb, shrub, tree, etc.) as well as whether it was cultivated for agricultural purposes. (Gundersen 1918, Mayr 1982). As for nomenclature, Theophrastus used the common
Greek names to give identity to the plants he described whose names we still use today (Green 1927). The notable thing about Theophrastus’s work was that his descriptions of flowers, leaf arrangements, floral anatomy, fruits, seeds and other features read much as a modern botanist would describe a plant, just with different terminology (Green 1927). Theophrastus also recognized certain features that are unique to modern plant families (Green 1927). Because of his achievements, he is considered to be the “Father of Botany” and his work was the chief authority on botany for the next three centuries (Green 1927, Gundersen 1918).

The next notable botanist was the Greek physician Dioscorides. During the first century A.D., Dioscorides traveled the Mediterranean with the army of the Roman Empire and explored the wide variety of flora found there (Mayr 1982). His main work, *Materia medica*, included over 600 species, most of which had practical uses such as medicine, perfumes, spices, etc. (Green 1927, Mayr 1982). *Materia medica* became another authoritative work in botany for the next millennium, alongside Theophrastus’s work (Green 1927, Gundersen 1918, Mayr 1982).

The next advancement in botany nomenclature did not come until the sixteenth century with the three German naturalists known as the “German fathers of botany” (Green 1927, Gundersen 1918, Mayr 1982). Their primary contribution was more thorough descriptions of local plants in the central European region and, most importantly, more dependable illustrations and figures to aid identification (Green 1927, Gundersen 1918, Mayr 1982).

One of these German naturalists was Otto Brunfels, a Protestant monk and teacher. His main work was *Herbarum Vivae Icones*, written in 1530 (Green 1927, Gundersen 1918). *Herbarum Vivae Icones* had over 150 illustrations of plants found in the Strasburg region (Gundersen 1918, Mayr 1982). In terms of botanical taxonomy, Brunfels grouped plants based on their medicinal properties even if they were not related (Green 1927). However, Brunfels
only used one word to name each species, instead of multiple words as in today’s nomenclature (Green 1927).

Another German naturalist was Leonard Fuchs, a Bavarian physician. His work was the *Stirpium Historia*, published in 1542 (Green 1927). The book had over 500 species with wood engravings as illustrations, as well as a glossary of botanical terminology (Green 1927, Gundersen 1918). Fuchs arranged the plants alphabetically using both Greek and German names for the genera he discovered and described (Mayr 1982). Fuchs also used two words as the name for the species, reflecting the species and its variety rather than today’s genus and species (Green 1927).

Another well-known German naturalist was Hieronymus Tragus, also called Hieronymus Bock. Bock’s works were similar to Fuchs and Brunfels, except he included additional information such as the habitat where the plant was found as well as its location to give additional information to aid identification (Mayr 1982). Bock’s format was the first example of a true field guide of plants giving way to future field guides with a similar format (Mayr 1982). He also noted other features such as the structure of the male and female parts of the flower that were not included in the other works of naturalists (Green 1927). As far as nomenclature, Bock used a style similar to Fuch, though Bock went so far as to change some of the names Fuch had used (Green 1927).

With more plant species being discovered and described, using multiple names to describe one species became an issue among botanists. In 1623, a botanist named Gaspard Bauhin published *Pinax Theatri Botanici*. His book listed all known plant species, along with every name or synonym of that species (Green 1927, Gundersen 1918). In future publications, Bauhin listed species names that were plurinomial or more than two words (Green 1927).
Another well-known botanist was the British naturalist, John Ray. His great work was the *Historia Planetarum* which had descriptions of all plant species known at the time, similar to Bauhin’s *Pinax* (Goerke 1973, Green 1927, Gundersen 1918, Mayr 1982). Like many other botanists before him, Ray divided plants based on their form of growth, but he was the first to make the division between monocotyledons and dicotyledons, a division used in modern botany (Green 1927, Goerke 1973, Gundersen 1918). Another contribution of Ray is that he classified these organisms based on multiple characteristics such as flower structure, root structure, vegetative characteristics, etc., providing more accurate taxonomic groupings based on multiple characteristics (Goerke 1973, Mayr 1982).

Another important botanist was the French biologist, Joseph Tournefort. In the 1700’s he published the *Institutiones Rei Herbariae* which was a comprehensive list of plant species to be used as a reference (Green 1927, Mayr 1982). Tournefort used visible characteristics from the fruit and flower, particularly the presence and number of petals (Green 1927, Mayr 1982). Two additional contributions to botanical taxonomy from Tournefort were that generic names only consisted of one word, and there were clear divisions at the class, genus, and species level (Green 1927, Mayr 1982).

**Linnaeus**

The father of modern taxonomy was the Swedish botanist, naturalist and physician Carol von Linné, or Carl Linnaeus. Linnaeus’s fame started out when he devised a new system of classification for plants not based on their growth forms but based on the number and arrangements of the male parts—the stamens—and the female parts—the pistils—on the flower (Goerke 1973, Koerner 1999, Mayr 1982). This new system was dubbed “the sexual system”
and it became a popular tool for plant identification. It was published in 1735 in the book *Systema Naturea* with a dichotomous division of all the plant species known at the time using his sexual system (Hagberg 1953). *Systema Naturea* also included a classification scheme of both the animal kingdom and of common rocks and minerals (Goerke 1973). In his classification, the animals were divided as quadrupeds, birds, amphibia (which included reptiles), fishes, insects and worms (this class was a catch-all group for any of the animals that did not fit the descriptions in the previous group) (Hagberg 1953).

Linnaeus's most significant work was the *Species Planatarum* published on May 1, 1753. The significance behind this work was the use of binomial nomenclature to name species (Goerke 1973, Mayr 1982, Whittaker 1969). Binomial nomenclature had been used before (especially in Bauhin's works), but this was the first time it was consistently used throughout the text, setting guidelines and rules for any future nomenclature (Goerke 1973). According to Linnaeus, the first name was the generic name to define the genus and the second name would be the *differentia* or principal point of difference between similar species in the genus (Goerke 1973). The second name was referred to Linnaeus as the *nomina trivialia*, or the epithet as we call it today (Goerke 1973). *Nomina trivialia* means convenient name, and Linnaeus hoped that distinguishing features used for identification would be used as the epithet like color, location or some other common feature (Goerke 1973, Mayr 1982). Linnaeus also included higher taxonomic ranks including kingdom, phylum, class, order, family, and so on to set up the future hierarchy used in taxonomy (Mayr 1982). Then in 1758 the tenth edition of *Systema Naturae* was published issuing the same binomial nomenclature rules for zoological species (Goerke 1973).
The Other Kingdoms

Since the time of Linnaeus, all organisms were classified as an animal or a plant under the two kingdom system (Dodson 1971, Whittaker 1969). The distinction between the two kingdoms appeared simple enough. Animals were defined to be heterotrophic, limited growth in tissues, no cell walls in the cells, and some form of locomotion (Dodson 1971, Hogg 1860, Whittaker 1969). Plants, on the other hand, were autotrophic, limitless growth in their tissues, cell walls present, and all were non-motile (Whittaker 1969, Dodson 1971). However innovations in microscopy and other technologies made classifying other organisms more difficult (Andersen 1998). Further studies of these organisms that included bacteria, fungi, algae, and protozoa made taxonomists feel the necessity to add more kingdoms to the Linnaean classification system (Whittaker 1957, Whittaker 1969).

Traditionally bacteria, as well as cyanobacteria (originally called blue-green algae), were classified as plants because both had cell walls (Whittaker 1969). However closer examination into their cellular structure led to evidence that they were not related to plants. Firstly, not many were photosynthetic, and many had a motile lifestyle (Whittaker 1969). Also many of these bacteria were reducers that used absorption of their external environment as their mode of nutrition (Whittaker 1969). With the advancement of electron microscopy it was also found that bacterial cells did not contain nuclei, mitochondria, plastids and other organelles found in cells of other organisms (Dodson 1971, Whittaker 1969). With this information many scientists agreed that the bacteria compared to other cellular types provided a clear diagnostic characteristic (Dodson 1971, Whittaker 1969). Bacteria were then called prokaryotes (literally meaning before nucleus) while other organisms were labeled as eukaryotes (literally meaning true nucleus).
Since then, bacteria were either classified as a subkingdom or as their own kingdom (Dodson 1971, Whittaker 1969).

Traditionally, fungi were classified as plant because of their non-motile lifestyle (Dodson 1971, Whittaker 1969). However, more research into fungi led to the discovery of characteristics that they lack of chlorophyll, have a different dikaryotic condition (where two nuclei are in the same cell but aren’t fused) than plants, and the possession of hyphae and mycelium (Whittaker 1957, Whittaker 1969). The most defining characteristic of fungi that helped separate them from other groups of organisms was their absorptive mode of nutrition, where digestive enzymes are secreted to the external environment to obtain organic matter (Whittaker 1957, Whittaker 1969). These diagnostic characteristics led fungi to be placed at a higher taxonomic rank in the plant kingdom or their own kingdom (Whittaker 1969).

Protists and other unicellular eukaryotes were controversial back during the 1600’s. With the invention of the microscope, many biologists had the ability to see and observe these small creatures, notably Antony van Leeuwenhoek and his “animalcules” (Rothschild 1989). Not much was known about these microorganisms, except that they displayed mobility—a characteristic of animals (Rothschild 1989, Scamardella 1999). This led to Linnaeus putting most of these microorganisms into the class Vermes and their own order called the Zoophyta (Rothschild 1989). These organisms eventually were called Protozoa, meaning first animals, first used by George Goldfuss in 1820 (Rothschild 1989, Scamardella 1999). This new group included the ciliates (also called the infusoria because they appeared in infusions), the corals, rotifers, the bryozoans, and other types of unicellular organisms (Andersen 1998, Rothschild 1989). Eventually more research on these microorganisms led to different classification schemes.
The first person to suggest and devise a new classification scheme was Sir Richard Owen, a British paleontologist (Hogg 1860, Rothschild 1989, Scamardella 1999). In 1859 Owen defined the terms organism, plant and animal in his essay called “Palaeontology” that first appeared in *Encyclopedia Brittanica* (Dodson 1971, Rothschild 1989). He defined plant as an organism that “is rooted, has neither mouth nor stomach, exhales oxygen, and has tissues composed of cellulose” (Hogg 1860). An animal, according to Owen, was an organism that “can move, when it receives the nutritive matter by a mouth, inhales oxygen and exhales carbonic acid, and develops tissues (Hogg 1860).” Anything else that do not have these characteristics, or “superadditions” as Owen termed them, were labeled as a protozoa (Rothschild 1989, Scamardella 1999). His new kingdom Protozoa contained the sponges, the ciliates, diatoms and other common protists (Rothschild 1989, Scamardella 1999).

In 1860 John Hogg, a British naturalist, suggested another kingdom similar to Kingdom Protozoa. He first kept all the kingdoms suggested by Linnaeus (including the inanimate kingdom of minerals) and added his fourth kingdom: Regnum Primigenenum, or the Primigenal kingdom (Hogg 1860, Rothschild 1989, Scamardella 1999). This kingdom was essentially the same as Owen’s kingdom (Scamardella 1999). Instead of calling them protozoa, Hogg gave them the name Protoctista (literally meaning first created things) because he felt that the name protozoa implied that these creatures were more closely related to animals than plants (Dodson 1971, Hogg 1860, Rothschild 1989, Scamardella 1999). Hogg thought that the protoctista had characteristics both similar to animals and plants and suggested that these organisms were the common ancestors of higher level animals and plants (Hogg 1860, Scamardella 1999).

In 1863, two American ornithologists, Thomas B. Wilson and John Cassin, introduced their kingdom with their presentation “On A Third Kingdom of Organized Beings” (Rothschild
1989). It included Kingdom Animalia, Kingdom Plantae and the new Kingdom Primalia (Rothschild 1989). Their definition for Kingdom Primalia included unicellular organisms or any colony of unicellular creatures that were capable of life (Rothschild 1989). The new kingdom included everything that Hogg and Owen included in their own kingdoms and more. The subkingdoms for Kingdom Primalia were Algae, Lichenes, Fungi, Spongiae and Conjugata (consisting of the rhizopods, ciliates and gregarines), taking many taxonomic groups from the animal and plant groups (Rothschild 1989).

Then, in 1866, a biologist named Ernst Haeckel wrote the book *Generelle Morphologie der Organismen* in response to Darwin’s *Origin of Species* and to create the first classification that clearly showed evolutionary relationships (Rothschild 1989). He named his new kingdom Protista (literally meaning the ones who came first in time) (Rothschild 1989). His first draft of the kingdom included the bacteria but not the cyanobacteria, the slime molds, the sponges and many of the protozoa and algae. He also placed the lichens, fungi and the red, brown and green algae in the plant kingdom. He also placed the ciliates in the animal kingdom (Rothschild 1989).

However, Haeckel published another book, *Das Protistenreich*, in which he revised his classification scheme (Rothschild 1989, Scamardella 1999). He realized that what defined a protist was the absence of sexual reproduction as well as the absence of a larval stage (Rothschild 1989, Scamardella 1999). This new definition led Haeckel to move the sponges and the volvocine algae into the animal kingdom while the ciliates were moved into Kingdom Protista (Rothschild 1989, Scamardella 1999).

Haeckel’s Protista classification scheme was the one that was widely adopted among scientists (Rothschild 1989). However, other scientists still wanted to make revisions. One example was Otto Bütschli, a German biologist. In the 1880’s, Bütschli commented on
Haeckel’s reliance on physiological evidence and his assumption that the protist group was monophyletic, meaning that all the protists descended from one common ancestor (Rothschild 1989, Scamardella 1999). Haeckel tried to make kingdom Protista monophyletic, but even admitted, based on the diversity of the group as well as the limited knowledge on these organisms, that Protista was most likely polyphyletic, or from multiple ancestors (Rothschild 1989). Bütschli suggested instead to classify based on morphological evidence (Rothschild 1989). All the protists with animal-like qualities were placed under Protozoa and all the protists with plant-like qualities were placed under Protophyta (Rothschild 1989, Scamardella 1999). Any protist that were ambiguous in their characteristics were placed under Protista Neutralia (Rothschild 1989).

In 1911 C. Clifford Dobell, a British biologist, brought new perspective to the protist group. Instead of referring to them as unicellular, Dobell called them acellular, referring to the fact that they do not act the same as multicellular organisms (Rothschild 1989). With protists being distinct compared to other organisms, Dobell created the field of protistology with works such as Introduction to the Study of the Protozoa and Handbook of Protozoology (Rothschild 1989, Scamardella 1999). This new field of study made the term protist became well-accepted in the taxonomic field and started deeper investigation into these types of organisms (Rothschild 1989, Scamardella 1999).

In the 1940’s an American biologist named Herbert Copeland proposed his own classification system in many articles leading up to his book The Classification of Lower Organisms, published in 1956 (Dodson 1971, Mayr 1982, Scamardella 1999). His four kingdom system was the first time bacteria were placed as their own kingdom: Kingdom Mychota (Mayr 1982, Scamardella 1999, Whittaker 1969). Bacteria were given the name
Monera in an earlier publication by Haeckel, but Copeland felt it was a misnomer because the name was first given to refer to a fragment of an amoeba that was mistaken for a bacteria by Haeckel (Dodson 1971, Rothschild 1989). Copeland felt that bacteria should be in their own kingdom because of their distinct prokyarotic characteristics (Rothschild 1989, Whittaker 1957). Copeland also resurrected the term Protoctista as it had nomenclatural priority over protist because it was published first (Rothschild 1989, Scamardella 1999). His Kingdom Protoctista included the slime molds, the fungi, the ciliates, the protozoa, and most algae (Dodson 1971, Whittaker 1969). His Kingdom Plantae was for organisms capable of photosynthesis as well as the presence of chlorophyll a and b and xanthophyll which consisted of the land plants and the green algae (Dodson 1971, Scamardella 1999, Whittaker 1969). His Kingdom Animalia was defined by the presence of a blastula and gastrula stage during development (Dodson 1971, Scamardella 1999, Whittaker 1969). Because of his definition, Copeland moved the sponges from the protists to the animals (Dodson 1971).

Another scheme of classification came from the American ecologist, Robert Whittaker. Whittaker saw that there were three common divisions among all the organisms. First was the division between prokaryote and eukaryote (Rothschild 1989). The second division was between unicellular and multicellular organisms (Rothschild 1989, Scamardella 1999). For that reason, the protist kingdom included all the unicellular organisms except the red, green and brown algae that were grouped with plants (Scamardella 1999, Whittaker 1969). Bacteria were placed in Kingdom Monera once again after being classified as a subkingdom in the protist kingdom (Rothschild 1989, Scamardella 1999, Whittaker 1969). The other unique feature of Whittaker’s proposed classification is that the mode of nutrition (photosynthetic, ingestion, absorption) became an important evolutionary characteristic to classify organism (Rothschild 1989,
Scamardella 1999, Whittaker 1969). This made Whittaker take the fungi, which were traditionally classified as either plants or protists, into their own separate kingdom for the first time because of their unique absorptive abilities (Andersen 1998, Scamardella 1999, Whittaker 1969). More revisions had been made during that time, but only Whittaker's 5-kingdom system has been used consistently.

Conclusion

Through the work of Linnaeus, nomenclature of species was established leading to the development of the nomenclature codes for each division of organisms. With the ranks of many organisms well-established, the next focus on taxonomy focused around the evolutionary relationships between organisms. After Charles Darwin's theory of natural selection, a new goal in taxonomy was set: to create a more “natural” classification, or one that displays the correct evolutionary relationships. To help establish this new idea the fields of phenetics, cladistics and molecular taxonomy have been constructed and well integrated with traditional taxonomy to achieve a more “natural” classification.
The Present: Evolutionary Theory and Systematics

Introduction

Before Darwin, scientific literature displayed a creationist view of the world's origins. This perspective produced the fundamental ideas that species do not change and that there would always be a constant number on the planet. However, Charles Darwin and his theory of evolution by natural selection changed that perspective. In his theory, Darwin believed that organisms change all the time via the process of natural selection. Certain organisms would have different adaptations that allowed for better fitness or a better chance of reproduction compared to other organisms of the same species. These adaptations would lead to reproductive and ecological isolation from other organisms creating a new species. As evolution became accepted into the biological community, there was a need to integrate this theory with the taxonomic system already established.

Evolution and Natural Taxons

When Darwin introduced his theory of evolution by natural selection, he would create the central concept of all biology. His famous work *The Origin of Species* proposed that every species has a common ancestor and each species is differentiated through modification specifically in response to natural selection (Mayr 1982). Darwin also mentioned how his new theory would apply to the field of biological taxonomy. In his opinion, classification would reflect the genealogy from the common ancestor to its descendants (Mayr 1982). Smaller modifications would separate into smaller or more inclusive ranks while bigger modifications would separate into larger or less inclusive ranks (Mayr 1982).

Species Concept

How to define a species is a still-ongoing debate. Before Darwinian biology, Linnaeus and many other naturalists used Aristotle’s essentialist philosophy to define species (Mayr 1982). The essentialists’ species concept tried to find an organism’s “essence” or “degree of difference” to make it stand out from other species (Mayr 1982). When the theory of evolution was proposed, Darwin demonstrated mechanisms of speciation specifically through modes of isolation that created distinct groups of populations via evolution (Gornall 1997, Mayr 1982). Any new species concepts proposed focused on reproduction as well as ancestor-descent relationships (C.C. de Pinna 1999, Claridge et al. 1997).

One of the first species concepts to be introduced was the biological species concept introduced by Ernst Mayr in the 1940’s. He defined species as “groups of actually or potentially interbreeding natural populations, which are reproductively isolated from other such groups” (C.C. de Pinna 1999, Claridge et al. 1997, Dobzhansky 1935, Hausdorf 2011, Mayr 1982, Wiley 1981). The biological species concept, or BSC, offered a lot of utility, but there are two problems that it does not address. One issue is that the BSC is specific to biparental organisms,
leaving out many organisms that reproduce asexually (C.C. de Pinna 1999, Claridge et al. 1997, Hausdorf 2011). Another problem with this species concept is that the differentiation between species is determined by the fact that two groups or populations can no longer interbreed. In the biological field it is hard to determine if any and all populations in a species can interbreed and determine the gene flow between two populations accurately (Claridge et al. 1997).

Other species concepts that were later proposed focused more on evolutionary characteristics instead of reproduction isolation mechanisms. Another popular species concept is the phylogenetic species concept. The phylogenetic species concept, or PSC, was defined in 1992, where species are the “smallest diagnosable cluster of individual organisms within which there is a parental pattern of ancestry and debate (Claridge et al. 1997, Hausdorf 2011).” In laymen’s terms, what defines a species is that a species has a unique diagnostic characteristic that sets it apart from other populations (Claridge et al. 1997, Hausdorf 2011). Considering there is much diversity within species especially subspecies in animals and varieties in plants there will be many more populations moving to a species-level rank based on the PSC (C.C. de Pinna 1999, Claridge et al. 1997, Cracraft 1997, Hausdorf 2011). PSC also has much more utility compared to the BSC, as it can apply to organisms with asexual modes of reproduction, and finding a diagnostic characteristic is easier to notice in the field compared to gene flow and interbreeding populations (Claridge et al. 1997, Hausdorf 2011).

There have been other species concept that have been introduced other than the PSC and BSC. The evolutionary species concept has similar principles to the PSC in that it focuses on the evolutionary history of a species (C.C. de Pinna 1999, Wiley 1981). This species concept defines species as “a single lineage of ancestor-descendant populations which maintains its identity from other such lineages and which has its own evolutionary tendencies and historical
Another species concept is the cohesion species concept. The cohesion species concept is defined as "the most inclusive group of organism having the potential for genetic and/or demographic exchangeability (Hausdorf 2011)." This species concept ascertains the degree of exchangeability in the gene pool between two organisms by examining genetic drift between the individuals in their niche or environment (Hausdorf 2011). Another species concept is the genic species concept. The genic species concept is defined as "groups that are differentially adapted and, upon contact, are not able to share genes controlling these adaptive character, by direct exchanges or through intermediate hybrid populations (Hausdorf 2011)."

This species concept is similar to the BSC because it references reproduction isolation mechanisms, but it references reproductive isolating mechanisms that are responsible for adaption and divergence (Hausdorf 2011). The debate still continues to find a universal species concept, but it is clear to see that there are many changes in the phenotype and the genome of a population after speciation occurs.

Characters

Characters are defined as features that arise in evolution by modification of a previous cytogenetic or molecular sequence that previously existed in a parental organisms (Wiley 1981). Characters can be a number of things such as structural features, functional features, ecological habitats, behavior, anatomy and physiology, etc., that a taxonomist uses to separate and classify organisms (Wiley 1981). A taxonomist prefers a homology or an evolutionary-derived characteristic. If one or more taxons share this homology, it is considered a synapomorphic character, meaning that this derived character came from one common ancestor (Wiley 1981, Murrell 2010). Special derived characteristics can appear in two distinct taxons that do not have any relation to each other. For example, birds and many insects have the ability to fly but they
are not closely related. This is caused by co-evolution where unrelated taxons develop the same characteristics even though they are not related. The characteristics by co-evolutions are called homoplasies (Lukhtanov 2010, Wiley 1981). Because homoplasies can be deceptive in determining evolutionary relationships, taxonomists need to be careful on which characteristics to choose.

**Cladistics, Phenetics and Systematics**

One of the first attempts to reconstruct evolutionary relationships was Willi Hennig, a German entomologist, in the 1950’s (Lukhtanov 2010, Schlee 1969). Henning proposed that phylogenies could be constructed into diagrams known as clades based on knowledge of derived characteristics among taxa (Kavanaugh 1978, Lukhtanov 2010, Schlee 1969, Wiley 1981).

Hennig cladistics is based on the concept of monophyletic groups defined as a taxon with a common ancestor and all the descendants of that common ancestor (Kavanaugh 1978, Schlee 1969, Wiley 1981). To determine if a group is monophyletic one would look at the apomorphic characteristics (Kavanaugh 1978, Lukhtanov 2010, Schlee 1969). If one characteristic was shared by only two groups, then the theory would be that those two taxons shared a common ancestor and would be grouped together in the clade. There are some problems with Hennigian cladistics. Along with homoplasises there may be very few apormorphic characteristics to analyze to create an accurate clade (Lukhtanov 2010).

To help combat this problem a new phylogenetic system was proposed called phenetics, or numerical taxonomy. Instead of using very few apormorphic characteristics in the analysis of phylogenetic relationships, all derived characters are included in the analysis (Kavanaugh 1978, Lukhtanov 2010). However there are some clear differences between phenetics and cladistics. Cladisitic studies are based on the age of the derived characteristic (when it first evolved and in
what organism) while phentics studies the difference between the apomorphic characteristics (Kavanaugh 1978, Sokal and Sneath1963). Compared to cladistics, phenetics studies characteristics in a quantitative manner instead of qualitative giving phenetics the name numerical taxonomy (Lukhtanov 2010, Sokal and Sneath1963). The calculations used in phenetics weigh each taxonomic characteristic equally so that there is no bias of any characteristic used to construct the phylogeny (Lukhtanov 2010, Sokal and Sneath1963, Wiley 1981).

There are two typical tests used in phenetics: the method of maximum parsimony and the method of maximum likeness. The method of maximum parsimony is focused mostly on morphological characteristics (Huelsenbeck et al. 2001, Lukhtanov 2010). In this method, the characters are analyzed where an apomorphy evolved in as few evolutionary lineages as possible so that the proposed phylogeny will have the least amount of homoplasies (Felsenstein 1978, Lukhtanov 2010, Sokal and Sneath1963). This method works well with analyzing small number of taxons, but larger phylogenies created by this method might be less parsimonious with the number of characters required to analyze (Sokal and Sneath 1963).

The other kind of test is the method of maximum likeness. This test is used for phylogeny constructions based on molecular data, genotypic data and the distances found in genes to determine genetic variation (Felsenstein 1978, Lukhtanov 2010, Wiley 1981). Because molecular data is easier to calculate and more applicable to algorithms this method tends to have more application than the method of maximum parsimony (Lukhtanov 2010). The method of maximum likeness has similar limitations to the other phonetic method where analyzing multiple taxons is difficult. However this phonetic method relies heavily on Bayesian statistics to help in this specific task (Huelsenbeck et al. 2001). Bayesian analysis takes the maximum likelihood
calculation, along with the prior probability, to create the posterior probability (Huelsenbeck et al. 2001). This posterior probability takes the maximum likelihood analysis and produces faster results on computers and algorithms (Huelsenbeck et al. 2001).

**Current Taxonomy for Taxonomic Groups**

For animal taxonomy, phylogenetic relationships are determined by two major criteria: comparative morphology and developmental biology (Fingerman 1981). One characteristic used by animal taxonomists is the symmetry of animals. Asymmetrical, radial and bilateral symmetry is one of the major homology used to divide animals on the phylum level (Fingerman 1981). Another feature used by taxonomists is whether or not the animal body is divided into segments (Fingerman 1981). In terms of developmental biology a major division between animals are protostomes and deuterostomes. The difference between the two depends on how the embryo forms. During cell division or cleavage in the embryo an indentation called the blastopore forms to become the body cavity of the organism. In protostomes the blastopore develops into the mouth, while in deuterostomes the blastopore develops into the anus (Fingerman 1981). Molecular techniques have also been used in animal taxonomy especially in more inclusive taxonomic ranks (Fingerman 1981).

For plant taxonomy, it is difficult to determine which species concept to use, especially the biological species concept. Many plants form colonies from a single root system, leaving little or no genetic diversity among essentially the clones found within the colony (Gornall 1997). Also, hybridization rates among plants are exceedingly high both in nature as well as cultivated species, whose gene pools have been altered several times for horticultural purposes (Gornall 1997). For this reason there are many cryptic species, different species all named as
one species (Gornall 1997). The best species concept used for plants is the PSC since
distinguishable characteristics can help separate the hybrids and cryptic species as separate
species to avoid confusion among taxonomists (Gornall 1997).

In plant taxonomy a wide array of characteristics are used to determine evolutionary
relationships. One of the more common types is comparative morphology which was used by
the early botanists. Morphological characteristics such as leaf venation, leaf patterns, leaf shape,
woody or not, stem characteristics and more are used to distinguish plant taxa (Murrell 2010,
Sivarajan 1991). An important part of the morphology that was especially emphasized by
Linnaeus was the arrangement and number of the male part of the flower, the androecium, as
well as the female part of the flower, the gynoecium (Mayr 1982, Murrell 2010). Naturalists in
the past used these characteristics to create keys and ranks, which were closer to a natural
classification despite the lack of technology and information we have today (Mayr 1982, Murrell
2010). Another important part of plant taxonomy is in the genetics, specifically the
chromosomes. Plants tend to have different ploidy states where plants can be diploid (2 sets of
chromosomes per cell), polyploid (more than 2 sets of chromosomes per cell) and sometimes
even haploid (1 set of chromosome per cell) (Sivarajan 1991). The number of chromosomes can
help determine differences between plant taxa (Sivarajan 1991).

Current taxonomy for bacterial species tends to be more difficult compared to other
eukaryotic organisms. First off many species concepts are specific to sexual organisms and the
 genetic exchange between parents, but many bacteria tend to be asexual (Cohan 2001,
Goodfellow et al. 1997). Bacteria can exchange genes with other organisms with processes such
as conjugation or recombination, but those tend to be very rare (Cohan 2001, Goodfellow et al.
1997). If genetic exchange does occur, bacteria do not exchange enough genetic to lead to
speciation (Cohan 2001, Goodfellow et al. 1997). Many bacteriologists instead look at another factor known as the ecological niche. Each organism requires certain environmental requirements to help it survive and reproduce. Bacteria that have specific niche requirements are called ecotypes (Cohan 2001). If mutations occur within an ecotype, and that mutation is favorable in that niche compared to the other bacteria, then divergence will occur through the process of natural selection (Cohan 2001, Goodfellow et al. 1997). Eventually these mutations separating the ecotypes will lead to different strains and then different species (Cohan 2001). This type of divergence fits well with the cohesion species concept (Cohan 2001).

As for taxonomic methods, bacteriologists before used phenotypic characteristics such as cell structure and biochemical reactions, but there is more emphasis on molecular systematics today (Cohan 2001, Goodfellow et al. 1997). One current technique is DNA composition to compare the ratio between the nucleotides in the genome specifically the percentage of guanine and cytosine present. Usually every genera has their unique cytosine-guanine percentage, while species within a genera do not differ among each other above 10% of their cytosine-guanine ratio (Goodfellow et al. 1997). Another technique is DNA-DNA hybridization, where strands of DNA from different individuals are paired together to see if they complement each other (Goodfellow et al. 1997, Stackebrandt and Goebel 1994). If the two strands pair up with very few errors in the sequence, then that indicates they are closely related (Goodfellow et al. 1997, Stackebrandt and Goebel 1994). Typically the same species will have 70% DNA-DNA relatedness during hybridization at a specific temperature (Goodfellow et al. 1997, Stackebrandt and Goebel 1994). Another popular taxonomic method is examining the 16S ribosomal RNA sequences. The reason why these sequences are interesting is because there is not much gene exchange with these sequences and that these sequences are highly conserved, meaning over evolutionary time
the sequences do not change very much (Goodfellow et al. 1997, Stackebrandt and Goebel 1994).

Studies involving ribosomal RNA sequences has led to many discoveries in the microbiological world including the discovery of the domain system. A molecular biologist named Carl Woese examined the ribosomal RNA in bacteria, specifically in a group of bacteria called the archaebacteria known for being extremophiles or living in extreme environments (Woese et al. 1990). Woese found that there was a significant difference between the archaebacteria and the other bacteria in terms of the structure of the rRNA, as well as patterns found in the RNA polymerase enzyme (Woese et al. 1990). Woese considered elevating the archaebacteria to a rank above kingdom called domain. Woese's proposal included three domains: Archaebacteria, Eubacteria (consisting of all the other bacteria) and Eucarya or Eukarya (all the eukaryotic organisms) (Woese et al. 1990). Woese's proposal has been accepted and is featured in many biology textbooks today. The domain rank is being considered the first rank to be in conjunction with systematics and evolutionary theory (Woese et al. 1990).

Fungal taxonomy is also a challenge similar to bacterial taxonomy. The fungal kingdom includes many different kinds of organisms, from mushrooms to yeast and some protists. The diversity in the fungal kingdom is vast, as most of these organisms don't have similarity in terms of structure or genetics (Brasier 1997). To identify fungal species, the most common approach is to isolate them in a nutrition media so that fruiting structures that come from the fungus can be analyzed (Brasier 1997). Because fruiting structures and sexual processes can be so easily studied in labs the biological species concept is applied to fungal specimens (Brasier 1997). However this method is usually for only more studied taxa in the fungal kingdom, and fruiting structures can't apply to asexually reproducing species (Brasier 1997). Because of this, more
emphasis has been placed on molecular methods similar to bacteria (Brasier 1997, Bruns et al. 1991). Methods like DNA-DNA hybridization and sequence analysis have shown great success to delineate fungal species similar to the methods used in bacteriology (Brasier 1997, Bruns et al. 1991).

Conclusion

The theory of evolution revolutionized the field of taxonomy. With the aspiration of creating a more natural classification, the new fields of phenetics and cladistics were established. New technology in molecular taxonomy also gave taxonomists new characteristics to use in delineating taxa. However, mixing the Linnaean taxonomic system with new taxonomic methods has created controversial issues among taxonomists, such as whether using molecular or DNA techniques is suitable for taxonomic needs. Other issues address the effect of the species concept on conservation efforts and biodiversity studies. There even exist some proposals to change the entire Linnaean system.
The Future: Current Issues

Introduction

There are many controversial issues facing the field of taxonomy today. Four of those issues include species conservation, DNA barcoding, the invention of the PhyloCode, and taxonomic databases. The species concept debate determines where we delineate organisms at the species level, and that can greatly impact the conservation efforts for that species. DNA barcoding is becoming a new popular technique in taxonomy, though some taxonomists are apprehensive of its accomplishments. Finally, naming species, genera and other ranks have been becoming a greater concern in taxonomy today. One concern is that the names for every species known so far hasn’t been organized properly prompting the creation of a taxonomic database. Another concern is that naming ranks does not fit well with evolutionary theory, leading to the invention of an alternative nomenclature system called the PhyloCode.

Taxonomy and Species Conservation

In the 1960’s and 1970’s, the declining biodiversity of the world became an issue among many countries. To protect its natural resources, the United States passed many laws regarding the issue including the Endangered Species Act or the ESA in 1973 (National Research Council 1995). The ESA’s goal was to protect the endangered and threatened species of animals and plants found in the U.S. The federal government would be responsible to protect these species by protecting the habitat of the endangered species, as well as preventing any obstacle or event that might increase the risk of extinction on the animal. The ESA does not only protect species but also specific subspecies and varieties of animals and plants that are endangered or threatened (National Research Council 1995). Another important part of the ESA is that recovery of critical
habitat features for endangered species needs to be an essential part to the protection of endangered species (National Research Council 1995).

Species conservation is solely based on how species are defined and classified (Mace 2004, Marris 2007, Morrison III 2009, National Research Council 1995). The problem is that species are constantly being redefined based on which species concept is being applied. The two most common species concepts used to delineate species are the biological species concept and the phylogenetic species concept. As stated before the biological species concept defines species as a group of organisms that interbreed and are reproductively isolated from other populations (C.C. de Pinna 1999, Cracraft 1997, Dobzhansky 1935, Hausdorf 2011, National Research Council 1995). The phylogenetic species concept defines species as the smallest group of organisms with a distinguishable evolutionary characteristic (C.C. de Pinna 1999, Cracraft 1997, Hausdorf 2011, National Research Council 1995). The difference between the use of either species concept is how many species are there. Typically there will be more species under the PSC than the BSC (Cracraft 1997, Mace 2004, Morrison III 2009, National Research Council 1995, Peterson 2006). The reason for this is because under the PSC, many subspecies, varieties, and distinct populations formally grouped as one species with the BSC will be elevated to species status (Cracraft 1997, National Research Council 1995). In fact, scientists estimate that there could be up to 48% increase in the number of species if the PSC was solely used (Cracraft 1997, Morrison III 2009). Many biologists feel that the number of species is not important and that conservation should be focused on protecting the ecosystem instead (Marris 2007).

Another concern is that if the taxonomy of a species changes it might be irrelevant in terms of species conservation. One example would be organisms with economic value that are going to be protected because of human demand (Morrison III 2009). Another case would be
when conservation efforts are already in place for a species regardless of its taxonomic ranking. Recent evidence has shown that polar bears and brown bears are more genetically related than previously thought, meaning that polar bears are a subspecies of brown bear (Marris 2007, Morrison III 2009). The USFWS nonetheless still considers the polar bear a distinct species that is threatened and conservation efforts are focusing more on the polar bear, especially now because of climate change (Morrison III 2009). Another example is the endangered green sea turtle, where recent evidence has shown that it is not genetically different than the non-endangered black sea turtle (Karl and Bowen 1998, Morrison III 2009). However conservation efforts still continue for the green sea turtle despite its taxonomic invalidity (Karl and Bowen 1998, Morrison III 2009).

DNA Barcoding

DNA barcoding is the newest taxonomic method that is getting increased support by scientists because of its many achievements. Many recent studies have shown that various types of organisms including plants, insects, fish, mammals, etc., have been successfully delineated or identified using the method of DNA taxonomy (Dasmahapatra and Mallet 2006, DeSalle et al. 2005, Miller 2007, Tautz et al. 2003). Because of this technology many scientists have discovered cryptic species which are different species grouped as the same species because of similar morphological or ecological data (Dasmahapatra and Mallet 2006, DeSalle et al. 2005). Many scientists have stated the concern that DNA taxonomy would be too expensive to be used in the taxonomic field. However new technology is allowing DNA barcoding to be less expensive and better storage facilities are being developed for DNA samples (Dayrat 2005, Miller 2007, Tautz et al. 2003). With this new technology scientists believe that DNA sequences
should be used in museums, herbariums and educational institutions to be the reference for each individual species along with its specimen (Dasmahapatra and Mallet 2006, Dayrat 2005, Tautz et al. 2003).

There are still issues that scientists find in the field of DNA barcoding. The first concern the variation found in the DNA sequence itself. The basis of DNA sequencing is that there would be enough variation in the sequence to distinguish between two species (Dasmahapatra and Mallet 2006, Mallet and Willmott 2003). However, every individual has their own DNA variation; if there are not enough specimens collected for a study then the variation found between the individuals would be mistaken as the variation found between species (Dasmahapatra and Mallet 2006, DeSalle et al. 2005). Also there is the concern that DNA barcoding focus solely on one gene or a small portion of an organism’s genome (Dasmahapatra and Mallet 2006, DeSalle et al. 2005, Mallet and Willmott 2003, Moritz and Cicero 2004). Multiple genes should used as the diagnostic variation to delineate species, just as multiple morphological characters should be used (DeSalle et al. 2005, Mallet and Willmott 2003). Also, each gene is different, meaning that some may not mutate very much over the course of many generations or they mutate too much, skewing how much variance there is between species (DeSalle et al. 2005, Mallet and Willmott 2003). The biggest concern from scientists is that the DNA barcoding will replace older taxonomic methods, but many advocates for DNA taxonomy are saying that DNA taxonomy will be used side by side with other current taxonomic methods (Dasmahapatra and Mallet 2006, Dayrat 2005, Mallet and Willmott 2003, Miller 2007, Moritz and Cicero 2004).
PhyloCode

When Linnaeus created his system of taxonomy, he had a creationist view of the world and thought there was a constant number of species on Earth, approximately 10,000 (Mayr 1982, Pennisi 2001). His system of binomial nomenclature, along with his ranks of kingdom, phylum, class, etc., became quickly adopted into the three nomenclature codes: the International Code of Zoological Nomenclature (ICZN), the International code of Bacteria (ICNB) and the Internal Code of Nomenclature for algae, fungi and plants (ICN) (Adl et al. 2007, Murrell 2010). Each of these codes created an extensive list of rules for each major division of organism based off Linnaean taxonomy. However, with the theory of evolution and the study of systematics, many taxonomists found problems with Linnaeus's rank-based nomenclature.

One main concern with rank-based nomenclature is the accuracy of depicting evolutionary relationships among ranks. Many taxonomists feel that many of the ranks in Linnaean taxonomy are arbitrary and do not relate to systematics (Cantino 1998, Cantino 2004, Pennisi 2001, Withgott 2000). William Hennig, a German entomologist, suggested that groups should be classified based on shared derived characteristics and that group should derive from one common ancestor also known as a monophyletic group (Cavalier-Smith 1998, Withgott 2000). To try to meet this standard that all ranks should be monophyletic, there is always new shifting, grouping and splitting in taxonomic ranks to correlate to the current evolutionary data. However, that does not solve the whole problem. There are only seven ranks in the Linnaean system to hold all the species and their appropriate classification. For this reason, taxonomists had to create other taxonomic rankings, such as subfamily, superorder, tribe, etc., just to create the appropriate hierarchy (Cantino 2004, Moore 1998). Also common names are still kept even
though they are not monophyletic such as Class Reptilia, which consists of organisms that come from multiple common ancestors or a polyphyletic group (Forey 2002, Moore 1998).

The other big issue is that changes in the taxonomic name of a species is very difficult. If a taxonomist wants to split up a genus into several genera or a family into several families, then that taxonomist would have to think of new names for all those new groups that would follow the code of that organism. Additionally, the taxonomist would have to designate a type for all those new groups. A type is a representative (usually a specimen) of that whole taxonomic group whether it be family, genus or species (Moore 1998, Murrell 2010). If a taxonomist wants to group a specimen into a specific rank, it must compare it to the type to see if it matches its characteristics (Forey 2002, Moore 1998, Murrell 2010, Pennisi 2001). However naming all the ranks and obtaining all type specimens involves a great deal of effort. Grouping ranks together may be a hassle as well. For example, if the genus Ajuga was added to the family Teurcrioidae, the family would have to be renamed Ajugoideae (Pennisi 2001). The reason for the name change is because the name Ajugoideae was published first, and the principle of nomenclatural priority makes the first name published the official name of the whole rank (Cantino 2004, Murrell 2010, Pennisi 2001).

To help correct these problems Kevin de Queiroz, a herpetologist from the University of California, Berkeley, and his colleague Jacques Gauthier, a paleontologist from Yale, devised a new classification system for reptiles using only clades (Pennisi 2001, Withgott 2000). They named their new system the PhyloCode. They shared their discovery at an AIBS (American Institute of Biological Sciences) workshop at Harvard where Phillip Cantino, a plant taxonomist from Ohio State University, became a strong advocate (Pennisi 2001). With his help, de Quieroz
and Gauthier presented the draft of their new system online at www.ohio.edu/phylocode to receive feedback from other biologists (Pennisi 2001, Withgott 2000).

The idea behind the PhyloCode is the use of clades and naming them. In terms of clades there are three kinds of definitions that could be applied to the clade. Let us say there are 4 taxons or general taxonomic groupings, D, E, F and G with an outgroup taxon C (Figure 1). The taxon that contains all these taxons would be taxon X. If one used a node-based definition that would define Taxon X be the least inclusive clade containing the taxons D,E,F and G (Forey 2002, Lee 1999, Withgott 2000). If one used a stem-based definition that would define Taxon X as all the taxons that would be closely related to taxon F but not taxon C (Figure 1, Forey 2002, Lee 1999, Withgott 2000). Stem-based definitions are typically used if there is not much evidence about the relationships between taxons D,E,F and G but there is enough support to say that taxon C is an outgroup (Figure 1, Forey 2002). For stem-based and node-based definitions there is the minimum of at least 2 specifiers or 2 reference taxa to define the taxon C (Forey 2002, Lee 1999, Withgott 2000). The last definition is apomorphy-based clades and that would define taxon X as all the taxons with one specific derived evolutionary characteristic C (Forey 2002, Lee 1999, Withgott 2000).
After the draft of the PhyloCode came out, many biologists had concerns about this new nomenclature. The first one was the concern of the reference taxa used to define a taxon. There is no common reference taxon used, so any taxon can be used. Without a reference taxon the names of the clades can be less informative without a visual phylogeny present (Lee 1999). Another concern is if phylogenies change. New scientific studies will keep changing how scientists view evolutionary relationships between taxons. Granted, if there are changes in PhyloCode, the taxon just would be redefined by different reference taxa, but that does not mean it is more stable than Linnaean ranks (Pennisi 2001). The biggest concern with the PhyloCode is how to name species. The most current draft of the PhyloCode has no current method to name species (Berry 2002, Cantino 1998, Cantino 2004, Forey 2002, Lee 2002, Pennisi 2001). Despite the instability in Linnaean taxonomy, species are still critically important for conservation purposes as well as biodiversity studies (Berry 2002, Cantino 1998, Pennisi 2001). There have been several suggestions to remedy this situation. One is to use uninomials or to reduce the species name to its specific epithet (Cantino 1998). However the specific epithet was originally designed by Linnaeus to be the *nomina trivialia*, or the trivial name, to describe a common
feature about the specimen like its color, for example nigrum, or its location, canadensis (Goerke 1973). Many species share the same epithets, meaning many species could have the same name (Cantino 1998). Another suggestion is hyphenation so that the white oak, Quercus alba, would be Quercus-alba, so species would still have the same name. However there is concern that the name of the genus would keep changing thus changing the name of the hyphenated uninomial (Cantino 1998, Lee 2002). Other biologists suggest using a system of numbers where each number describes a specific characteristic (Lee 2002, Moore 1998).

The PhyloCode is still gaining support from many scientists, and the hope is it that someday it will replace or be parallel to the International Code of Botanical Nomenclature, which is now currently the ICN (Berry 2002, Moore 1998, Withgott 2000). However, many scientists do not believe that the Linnaean system of taxonomy will ever disappear. Because of its familiarity among all scientists and its longevity, it would be hard to simply get rid of it (Moore 1998, Withgott 2000). Many scientists are suggesting that the two systems be used side by side with the name designated by [P], for the PhyloCode or [L], for Linnaean taxonomy, to indicate which system is being used (Cantino 2004, Forey 2002, Pennisi 2001). Whether the Linnaean system stays or goes, it is pretty clear that the PhyloCode will be an important part in the future of biology.

Taxonomic Databases

A new move in taxonomy is to publish taxonomic data on electronic databases (Shanmughavel 2007). The move away from print journals is to help scientists have more accessible information compared to before (Dayrat 2005, Shanmughavel 2007). To get a taxonomic species formally recognized with a name, description and recognition in the scientific
community one must go through a peer-reviewed journal and get published (Dayrat 2005, Shanmughavel 2007). However, there are over 25,000 proposed new species every year and in many different journals (Shanmughavel 2007). To keep up with any taxonomic changes electronic databases would be good mostly to avoid taxonomic synonyms or different names for the same species (Dayrat 2005). Some of these databases include the CATE project, ZooBank, MycoBank, GenBank, Global Biodiversity Information Facility, International Plant Names Index, and many more (Huang and Qiao 2011, Shanmughavel 2007). The controversy for many scientists behind these new databases is that anyone can publish a taxonomic name without the peer-review process (Borrell 2007). To help change that many scientists are that these new databases rely on peer-reviewed journals in order to help any taxonomist to make sure that their new proposed new species hasn’t been already named and described (Borrell 2007).

Conclusion

There are many current and controversial issues in taxonomy demonstrating that this field is always changing with the new scientific discoveries. Because biology is dependent on taxonomy, new changes in biology will keep changing taxonomy to suit its needs. Taxonomy will keep being a dynamic subject and who knows what changes will happen in the next five, ten or twenty years. However the goal of classifying and identifying all species on the planet will still be an everlasting ambition.
Work Cited


