KAS BULLETIN

NEWSLETTER OF THE KANSAS ACADEMY OF SCIENCE

VOL. 43 NO 2 www.KansasAcademyScience.org August, 2018

150th Kansas Academy of Science Annual Meeting

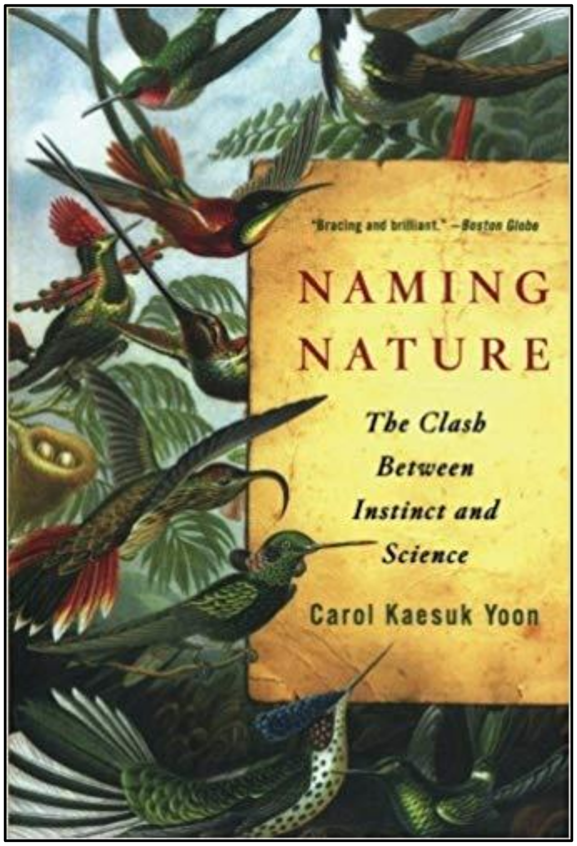
The 150th annual meeting of the Kansas Academy of Science was held on April 6th & 7th, 2018, at Washburn University. The meeting began Friday, with a field trip to the Kansas Bureau of Investigation Forensics Labs. The building has specific areas reserved for each department of the lab including biology, DNA, toxicology, chemistry, firearm/tool marks, latent prints, trace evidence, digital forensics, vehicle processing, and evidence storage. Friday evening, KAS Transactions editor Mike Everhart gave a talk commemorating 150 years of science in Kansas, followed by a sumptuous banquet. Keynote speaker, Dr. Scott Hawley gave an enlightening talk on the latest advances in cellular meiosis. For years scholars have held the concept of chromosomal unzipping and subsequent replication, however, the actual process of unzipping remained obscure. Dr. Hawley's research shed light upon the actual molecular processes behind this unzipping and their pertinent applications to cancer research. The somewhat unexpected cold snowy conditions prevented the Crane Observatory visit that evening.

The following day offered concurrent oral presentations on topics ranging from the annual Paleontological Symposium, animal behavior, ecology and organismal biology, entomology, geology, and molecular biology to science education. During the luncheon, the keynote speaker was Dr. Rebecca Schmidt-Jeffris, an expert in the arthropod predators of agricultural crops such as those feeding on strawberries and corn. During coffee breaks posters could be examined the in the lobby. An account of the annual meeting can be found online and in the Transactions Spring 2018 issue.

KBI Forensic Science Center, Topeka, KS

Book Review: “Naming Nature” by Carol Kaesuk Yoon. 2009. 341 p.

By Hank Guarisco, editor



This delightful book belongs on the shelf of every biologist of whatever persuasion. Besides being trained as a research population geneticist, the author has a commanding dexterity with the written word, resulting in a profound and beautifully written book. She does not limit her research to evolutionary biology, but garners pertinent information from other disciplines, including anthropology and medicine.

The discussion involves naming the natural world around us, and the clash between our instinct and science in this process. During the time of Carl Linnaeus, the father of taxonomy, most people were very interested in nature and often kept various plant and animal parts in a “cabinet of curiosities” in their homes. Linnaeus was extremely adept at ordering plants and animals into natural groups, and developed the system of binomial nomenclature, ie. genus and species, to give scientific names to each organism. The first edition of his work, *Systema Naturae*, was published in 1735 when he was 28 years of age. In his day, species were immutable, since Darwin’s *On the Origin of Species* did not appear on the scene until 1859.

Darwin’s research made him realize that species were ever evolving due to the process of natural selection, and he created a rudimentary tree of life with a trunk and limbs, to illustrate groups that had diverged over time. The time of Linnaeus and Darwin was also the time of great explorations of unknown parts of the world. Soon, new forms of life arrived in Europe that did not conveniently fit into the accepted system of classification, and much taxonomic work was done in museums to sort it out.

The rediscovery of Gregor Mendel’s work on genetics in 1900 and the simultaneous improvements in medical laboratory research of diseases began a new era in biology. Experimentation and advances in genetics quickly dominated the field, while taxonomists continued their work in the traditional manner. The science of naming life became the exclusive domain of a dwindling number of experts, and amateurs became fewer and fewer.

Complaints mounted against taxonomists. If taxonomy was a science, what was it testing? Experts that were intimately familiar with a particular group of plants or animals had an innate feeling as to how it should be classified. They “knew” which characters were more important in determining its place in nature. This relatively unscientific view was challenged by a University of Kansas graduate student named Robert Sokal. He believed all of the specimens’ characters should be measured, then run through a computer program which would determine their relations to one another. He collaborated with Charles Michener, a recognized expert on bees of the world, to develop a classification of a group of bees by numbers alone. This was the birth of numerical taxonomy.

But even numerical taxonomy had its limits. Some characters **are** more important than others, so treating them equally was sometimes misleading. Behind the morphological characters used to distinguish species was their DNA. Molecular biologists began examining and comparing the DNA of species and constructing evolutionary trees of their own. In many cases, they agreed with the prevailing classification based on morphology. However, there were instances where major changes had to be made. In 1976, a microbiologist named Carl Woese who studied methane-producing bacteria in swamps and in the intestines of animals discovered that their RNA was so different from any other bacteria, that they actually comprised a new kingdom, the Archaebacteria. It was older than all other forms of life, which included two other kingdoms: the regular bacteria and the Eukaryotes (all plants and animals). His ideas were not well received since they were so radically different from the prevailing views.

The next advance in the science of evolutionary taxonomy (systematics) began in 1950 when Willi Hennig proposed the classification system now known as cladistics. He recognized that only some similarities were important to determine evolutionary relationships. Quoting the author: "He realized that to identify groups that were similar because they were close relatives – that is, the common descendants of a particular species – he needed to identify the similarities that were shared uniquely by those descendants and no other groups." Although this seems to be a small but significant change, havoc was created when cladists following Hennig's system insisted that only "real groups" be named. This led to some startling consequences: the group called "fish" no longer existed! An evolutionary tree based on cladistics revealed that lung fish and mammals were the last to split from one another. They are more closely related to each other than to the other fish. This becomes very disturbing to taxonomists, not to mention everyday people, who have become more and more estranged from nature and its naming than ever before.

The author then proceeds to explore how people around the globe name animals. The prominent ornithologist, Ernst Mayer, discovered that natives of New Guinea recognized 136 different species of birds of paradise while he recognized 137 species. The difference was explained by the presence of a pair of cryptic species that looked identical. Other primitive societies and humans through the ages have all named the plants and animals in their immediate environs. This recognizing and naming has been going on for such a long time that there is actually a small part of the brain that is responsible for recognizing living organisms. Studies of individuals with brain injury due to trauma or the Herpes virus have revealed this amazing fact. These people cannot distinguish a carrot from a cat, leaving them in a very confused state of mind.

Because of the human propensity to name life forms, it comes as no surprise that taxonomists would resist the recent changes that have been made. Although genetic analysis and cladistics have resulted in a better scientific understanding of the ordering of earth's life, it goes against our innate methods of grouping organisms. We still believe in fish.

In this age of declining biodiversity, it is imperative that more people become interested in the natural world which we are destroying. Most taxonomy has shifted from the describing of new species to the ordering and rearranging what has already been described. More work is needed in simply naming and describing newly discovered species.

Being a scientist, the author had assumed that the only correct way to order life was the scientific way. But she came to realize that: "…science was neither the best nor the only valid way to order and name the living world." "I eventually came to see that science itself might be undermining the very thing it sought to perfect: humanity's understanding of life. I also realized that those many apparently incorrect names and categorizations – the orderings created by people across the world and throughout history as they reveled in the life around them – actually were not wrong."

In conclusion, I recommend this fascinating book to scientist and layperson alike. It is a good treatment of the history of systematics as well an insightful human perspective of naming the living world around us.

Genetically Engineered Fungus Is A Mosquito-Killing Machine

Fungi Volume 11, No.2 Summer 2018

If you're wild about wild mushrooms, you know - and loathe - mosquitoes. But for many in the world, mosquitoes are more than a summertime irritation. Malaria kills nearly half a million people every year, according to the World Health Organization (WHO). In some of the hardest-hit areas in sub-Saharan Africa, the mosquitoes that carry the malaria parasite have become resistant to traditional chemical insecticides, complicating efforts to fight the disease. A new study by **Bilgo et al.** (*Nature Scientific Reports* 7[1]:3433) suggests that a mosquito-killing fungus genetically engineered to produce spider and scorpion toxins could serve as a highly effective biological control mechanism to fight malaria-carrying mosquitoes.

The researchers used the fungus *Metarhizium pingshaensei*, which is a natural killer of mosquitoes. The fungus was originally isolated from a mosquito and previous evidence suggests that the fungus is specific to disease-carrying mosquito species, including *Anopheles gambiae* and *Aedes aegypti*. When spores of the fungus come into contact with a mosquito's body, the spores germinate and penetrate the insect's exoskeleton, eventually killing the insect host from the inside out. In nature, the fungus requires fairly high doses of spores, and a large amount of time to have lethal effects. To boost the fungus' deadly power, researchers engineered the fungus with several genes that express neurotoxins from spider and scorpion venom. The toxins act by blocking the calcium, potassium and/or sodium channels required for the transmission of nerve impulses. Both, spider and scorpion, toxins have already been approved by the U.S. Environmental Protection Agency for insecticidal use. Their most potent fungal strains, engineered to express multiple toxins, are able to kill mosquitoes with a single spore. Further, their fungal strains were capable of preventing transmission of disease by more than 90% of mosquitoes after just five days. The fungus is specific to mosquitoes and does not pose a risk to humans. Further, the study results suggest that the fungus is also safe for honey bees and other insects. How so? When the international team of researchers inserted the toxin genes into the *Metarhizium* fungus, they included an additional failsafe: a highly specific promoter sequence, or genetic "switch," which ensures that the toxin genes can only be activated in the blood of insects. As a result, the fungus will not release the toxin into the environment. To further ensure the safety of non-target insect species, the researchers also tested the engineered fungal strains on honey bees. The team deliberately infected local bees using both passive methods (exposing the bees to spore-coated fabric) and direct methods (spraying the bees with spores suspended in liquid). After two weeks, no bees had died as a result of the toxin-boosted fungus. Besides malaria, a number of other mosquito-borne diseases such as dengue, yellow fever, viral encephalitis and filariasis may also be combated using this new mold.

Some Amphibians Bouncing Back After Chytrid Fungus Pandemic

Fungi Volume 11, No.2 Summer 2018

Regular readers of FUNGI have seen the news go from bad to worse with regards to a global die-off of amphibians due, in part, to a pandemic of chytridiomycosis (a deadly skin disease caused by a group of primitive fungi called chytrids). The problem has been seen pretty much in every corner of the planet; numerous species have already gone extinct and more are sure to follow. Finally, some good news. It seems that after decades of affliction, some species of amphibians seem to be recovering. An investigation into both the pathogen and its hosts, published by **Voyles et al.** (*Science* 359[6383]:1517-1519) reveals that while the fungus remains as virulent as ever, natural evolutionary processes are at work and the surviving host species are less susceptible.

In the 1970s and '80s, many scientists studying amphibians in relatively pristine areas of Australia, Central and South America, and North America witnessed massive die-offs of their study populations. Some were unable to find any individuals in areas where abundant populations had been present only a year earlier. Finally, in 1998 researchers identified the pathogen responsible for these declines, a chytrid fungus they named *Batracholchytrium dendrobatidis*. By this time, the pathogen had swept through most of Central America and Australia and caused the extinction of as many as 200 species of amphibians. The fungus infects the skin of amphibians, and so perturbs the animals' osmotic regulation. The resulting imbalance of body fluids leads to organ failure and death.

Scientists have detected the fungus that causes chytridiomycosis on all continents except Antarctica. As a result, conservation efforts have mostly shifted from stopping the pathogen's spread to preserving remnant populations in captive colonies. In some areas, especially low-elevation, warm areas in the tropics, amphibian populations appear to be able to persist with the fungus, while high-elevation populations of several species, such as those in the mountains of Central and South America or the Sierra Nevadas in California, are extirpated. The chytrids may have been spread between continents by the trade in amphibians, including *Xenopus* frogs, which were used for pregnancy testing in the early 20th century, and American bullfrogs, which are still shipped to many regions of the world where people have an appetite for frog legs. Researchers are currently studying drivers of transmission, including landscape, climate, and host community ecology, in hopes of identifying ways to reduce the impacts of this disease. Unfortunately, because these diseases do not directly affect human populations, resources for managing threats to wildlife are relatively sparse.

Xenopus Frog

In 2004, Voyles led a team to Panama to see firsthand the decimation caused to frogs and salamanders there; the fungus was believed to have been introduced there, accidentally, by humans several years before. More recently, when Voyles and her team returned to Panama to monitor the sites of the outbreak, they found that some of the amphibian species were recovering, despite samples from the animals revealing the fungus was still present. How were the amphibians doing it? When Voyles and colleagues compared contemporary samples of *B. dendrobatidis* collected from Panamanian amphibians with samples collected at the time of the outbreak they were, by all measures, practically unchanged. The team examined the pathogen’s growth rate, ability to produce infectious zoospores, pathogenicity in live animals, and whole genome sequences, finding no significant differences between the historical and current samples, to their great surprise. She and her colleagues then turned their attention to the amphibians themselves. Skin secretion samples - which contains antimicrobial peptides - collected from the frogs and salamanders before the disease outbreak and since the recovery exhibited differences in their abilities to block the growth of *B. dendrobatidis*. Although the pathogen-inhibiting ability of the secretions varied considerably from species to species, in all cases those samples taken from before the disease outbreak were less effective than those taken after. It is not yet clear how the secretions have changed. In the words of the researchers, the results suggest the host amphibians have evolved and that it's likely that the more-resistant amphibian communities also have genetic, behavioral, and other adaptations that help them stave off the pathogens. Evolution in action! But amphibians are far from being out of the woods yet, so to speak. Voyles team estimates that only approximately 20% of the local species initially affected by the disease have since recovered. As for the rest, it's not yet known how many have been lost for good, or how many may still recover.

KANSAS ACADEMY OF SCIENCE
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MAIL TO:

The 151st KAS Annual Meeting will be held jointly with the
94th Kansas Entomologic Society Annual Meeting
on March 29th & 30th, 2018
at Johnson County Community College, Overland Park, KS