So, You Discovered a New Species?*
How Do You Know, and What Are You Going to Name It?

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Against a backdrop of the biodiversity crisis that we are facing currently, the question of how many species inhabit our planet now and how many have been discovered so far needs to be addressed. Most conservative estimates give 10 million for the total number of species and 2 million for those discovered so far. That means nearly 80% of our planet’s biodiversity remains to be discovered and named. Traditional taxonomists rely largely on morphological features to identify and delineate species, but in recent years, molecular methods have gained enthusiastic acceptance by taxonomists worldwide. Molecular taxonomists use genetic divergences in a chosen segment of a mitochondrial DNA for species delineation and generate a molecular barcode unique to each species. The International Barcode Of Life (iBOL) data system (BOLD), holding >10 million barcodes, is an open-access repository serving taxonomists worldwide. Naming new species is a fascinating and exciting component of taxonomy. International nomenclatural guidelines notwithstanding, discoverers enjoy a certain degree of freedom in naming their discoveries.

1. Introduction

In 2011 the late theoretical ecologist Sir Robert May lamented, “We know how many books the Library of Congress has but cannot tell you how many distinct species of plants and animals we share our world with” [1]. Ironically, the situation is not very different even today; estimates of total biodiversity on Earth vary widely. Based on rigorous logic, Mora et al. (2011) [2] put the

*Vol.27, No.6, DOI: https://doi.org/10.1007/s12045-022-1389-z

Keywords
Biodiversity, undiscovered species, taxonomy, morphotaxonomy, cryptic species, species concepts, DNA taxonomy, barcode, International Barcode of Life (iBOL), Barcode Of Life Database (BOLD), naming new species.
total number of species at 8.7±1.3 million, a figure generally accepted by many biodiversity experts. However, a more recent estimate, based on a comprehensive study by Larsen et al. (2017) [3], places our planet’s biodiversity at a mind-boggling one billion at least! An unbelievable 100-fold jump from the 2011 estimate! The authors based their estimate on two observations: (1) noneukaryotic diversity, which earlier estimates ignored or grossly underestimated, may account for 70 to 90% of the total diversity, and (2) a high degree of cryptic species diversity among arthropods, which may be revealed only by molecular methods, and therefore, missed by classical taxonomists. If the estimate by Larsen et al. is anywhere near the truth, one wonders if we will ever be able to discover, even using the relatively faster DNA methods, millions of the undiscovered species and catalog them. Ironically, many species are disappearing forever from the planet even before being discovered due to anthropogenic activities (the so-called ‘sixth extinction’ [4, 5]). For example, it is estimated that in the world’s rain forests alone, 37 species on an average are lost forever every day! It seems like a race we may never be able to win!

While estimates of the total biodiversity are uncertain, available figures of the total number of species recorded so far are in constant flux because new species are being discovered and documented almost every day, and databases are not updated regularly. In 2020, nearly 407 new species of animals were discovered and described in India alone [6]. Further, taxonomic inventories are plagued by synonymy (two taxonomists giving two different names to the same species). Also adding to the uncertainty of inventories are the ‘splitters’ (taxonomists splitting one genus or species into two or more) and ‘lumpers’ (those combine two or more species into one). Nevertheless, according to the latest edition of the Catalogue of Life [7], the total number of species discovered and cataloged so far is nearly 2.3 million. (<20% of the estimated total biodiversity). This leaves well over 6 million species to be discovered and named (Figure 1)!

Equally uncertain is the total number of species recorded so far because new species are being discovered every day, and databases are not updated regularly.
2. Discovering New Species

"On taking it out of my net and opening the glorious wings, my heart began to beat violently, the blood rushed to my head, and I felt much more like fainting than I have done in apprehension of immediate death. I had a headache the rest of the day, so great was the excitement produced by what will appear to most people a very inadequate cause."

(Alfred Russel Wallace (1869), upon capturing a never-seen-before birdwing butterfly on Bucan Island, Malay Archipelago) [8]

Who will unravel this monumental hidden treasury of biodiversity and give names? Do we have adequate taxonomic expertise for different taxa? Classical taxonomy as a discipline has become endangered as a disproportionate number of biologists of the present generation are choosing cell and molecular biology areas for their specialization. How many universities are there now in the world that offer a taxonomy course? The average molecular biologist works most likely on problems being faced by humans—disease, aging, and nutrition, and his/her interest in biodiversity may not extend beyond a handful of model species (Viruses, Escherichia coli, Streptomyces, Arabidopsis, Caenorhabditis, Drosophila, ze-
brafish, and mouse).

Modern molecular taxonomic methods might expedite biodiversity inventories, but they alone cannot ‘discover’ new species unless somebody brings a specimen or a tissue of a putative species for identification. Who will do that? Field biologists, obviously! Regrettably, it is not only classical taxonomy that is suffering from benign neglect but also field biology. A Young taxonomist going out into the field in search of new species gets to observe not only what is there but also what is happening there. He or she will also develop a sense of wonder about nature around him and an awareness of the importance of its conservation for human wellbeing. One who eschews field observations in favor of a laboratory study misses fascinating sights and sounds that nature offers—colorful butterflies flitting around a plant in full bloom, a spider trapping an unwary fly in its web, chemically disciplined army ants marching by, symphonic frog croaks in a recently flooded pond, and many more. One of my ecology professors teaching freshman biology classes used to say that the most effective way to develop, not mere interest in, but passion for biology in students is to take them out on a field trip for a few days to a nearby rainforest, a desert, or a wetland, and let them observe and learn from nature (He actually used to do that, subject to resource availability). Marine ecologist Paul Dayton drives home this point more forcefully, “There is simply no substitute for actually experiencing nature, to see, to smell, and listen to the integrated pattern that nature offers an open mind” [9]. Fleishner et al. [10] explain the benefits and methods of field-based pedagogy in biology. Field biology courses are a rarity in our undergraduate biology curricula. I strongly believe that all our incoming students choosing biology specialization should be required to take a course in field biology before they are drawn irretrievably to the relatively more secure laboratory studies.

Which taxonomic groups have the maximum number of ‘discoverable’ species? Species diversity, in general, is known to increase with decreasing organismal body size. Chances of you stumbling onto a new species are, therefore, significantly higher.
if you are studying small body-sized taxa (insects, mites, fungi, internal parasites, and nematodes, for instance).

What kinds of habitats should biodiversity specialists be exploring to find new species? Relatively inaccessible and hence hardly explored ecosystems, experts say.

While talking about biodiversity in my ecology classes my sales pitch used to be something like this:

“Don’t sit in the laboratory glued to your analyzer, sequencer, or the confocal microscope. Go out, nature beckons you. Be a Darwinian naturalist and explore the fascinating diversity of life everywhere, particularly in less explored ecosystems—uncharted tropical jungles, dark and damp caves, mysteriously deep oceans, and the netherworld of speciose groundwaters. Chances are that you might stumble upon a species new to science and experience the excitement, if not at a Wallacean level, of unraveling a hidden secret of mother nature. Besides bringing to light a hither-to-unknown species, you will also have the privilege of naming it—just imagine the possibilities, you could name your discovery after your research mentor, your beloved, or even your favorite movie actor!”

When you, as a young taxonomist, find in your explorations a plant or animal which appears to be a new species belonging to the taxon in which you are a specialist, you must be fully confident about its identity before you announce your discovery to the world in the form of a publication in a journal dedicated to taxonomy. It is common for young taxonomists to seek validation of their identification by sending a specimen or its detailed documentation to a recognized authority on the taxonomy of the taxon.

How could you be positive about a discovery being new to science? Could it not be an ecotype or subspecies of a species already known and well represented elsewhere? How do taxonomists distinguish a hither-to-unknown species from the already known? What criteria are used to delineate a species? How are the classical methods different from the more recent molecu-
lar methods of taxonomy? Let us first look at some basic concepts and ideas about species.

3. Species Identification and Delineation

"No one definition has satisfied all the naturalists; yet every naturalist knows vaguely what he means when he speaks of a species."


The traditional naturalist's concept of species that Darwin refers to was prevalent even earlier during the early 18th century when Carl Linnaeus systematized naming species by introducing binomial nomenclature, a system that continues even to this day.

A more formal concept of species, and perhaps more relevant in evolutionary and ecological investigations, is the 'biological species concept' [12]. Originally conceived by Alfred Wallace but articulated and championed much later by Ernst Mayr, it emphasizes reproductive isolation as the hallmark of a species. Species, according to this concept, are "groups of interbreeding natural populations that are reproductively isolated from other such groups." The problem with this definition is that it is nearly impossible to demonstrate that any two related, putative species do not interbreed in nature. It is also known that two species, although interfertile, in nature do not interbreed because their niches are different. How about hybrids (mule, for instance)? Where do they belong? Why are Neanderthal humans given a separate species status (Homo neanderthalensis) although they are supposed to have interbred with the extant humans (Homo sapiens), as evidenced by the presence of Neanderthal genes in H. sapiens genome? These are some uneasy questions that adherents of the biological species concept are confronted with.

Traditional taxonomy ('morphotaxonomy') has been relying largely on differences in morphological features (color, color patterns, appendages, and other visible body features) for species delineation. (Morphological characters, unlike any species-specific behavioral attributes, can be identified and quantified using even museum-preserved specimens). Taxonomists identify species us-
ing available dichotomous keys for selected morphological characters, which is not an easy task unless one has a certain level of expertise in the taxonomic group being studied. The assumption underlying the delineation of species here is that significant differences in morphological attributes between two related species are the result of reproductive isolation. Critics of classical taxonomy point out that the following species attributes render reliance on morphological differences alone ineffective for species identification or their delineation [13]:

- **Sexual dimorphism**: Males and females belong to the same species but differ markedly in so many morphological attributes.

- **Life history stages**: In some taxa (notably moths and butterflies), the adult stages of related species appear so similar in morphological features (‘cryptic species’), but their larval (caterpillar) stages differ significantly in their microhabitats and their food plants. Such cryptic species are easily missed by traditional taxonomists.

- **Phenotypic plasticity**: (The same species exhibiting a different morphology in response to a variable factor in their habitat) could also cause confusion.

- **Homoplasy**: Two related species living in a similar environment and facing similar environmental pressures tend to evolve similar morphology and behaviors.

Another crisis that traditional taxonomy has been facing presently for documenting biodiversity is what is called a ‘taxonomic impediment’, an acute shortage of trained taxonomists for some taxa in many geographical regions, notably the tropics. It is not uncommon for Indian taxonomists to send collected specimens of uncertain species identity to the British Museum or other global taxonomic repositories for confirmation of their identification. This persistent taxonomic impediment has apparently hastened the acceptance of molecular taxonomic methods by traditional taxonomists.
Figure 2. Barcodes are ubiquitous! A sample of consumer products (livestock also in some cities) bearing barcodes that digitally store relevant information about the product.

In India, two apex governmental organizations, the Zoological Survey of India and Botanical Survey of India are mandated to collect and document the rich biodiversity of India, and their taxonomists offer their taxonomic expertise to young taxonomists.

4. Barcoding Life: Molecular Methods for Identification and Delineation of Species

There is hardly anybody these days who is not familiar with barcodes. They are ubiquitous and hard to miss on any product you buy (apples, wheat flour, shampoos, mobile phones, laptops...) from your neighborhood store or online from Amazon. (In the town where I teach currently, even cattle have barcode tags clipped onto their ears) (Figure 2). It is amazing how a tiny rectangle filled with lines of different thicknesses and a set of numbers (the Universal Product Code (UPC)) can reveal so much information about the product when read by a barcode reader at the checkout counter in the store.

Now, imagine having a unique barcode for every living species on this planet. This is the thought that must have flashed in his mind when in 2003, Paul Hebert, the pioneer molecular taxonomist, published his first paper on DNA taxonomy [14]. In that seminal paper that laid the foundation for DNA taxonomy, Hebert et al. proposed that the mitochondrial DNA gene cytochrome C oxidase subunit 1 (CO1), present in all animal species, would be an
ideal molecular taxonomic tool since the amino acid sequence of CO1 is unique to a species. To test the ability of the CO1 amino acid profile to correctly identify species, the authors selected 150 species of Lepidopterans1 already well-delineated through traditional taxonomic methods and collected the CO1 sequences for each to check how closely the two methods matched. The match between the two was nearly perfect! Further, they showed that the same method could also be used to delineate species. Soon DNA taxonomy started gaining worldwide support as an alternative to traditional taxonomy. An important advantage that the new taxonomic tool had over morphology-based taxonomy was brought to light when Daniel Janzen submitted for barcoding a suspected cryptic species, the skipper butterfly (Astraptes fulgerator) collected from the tropical forests of Costa Rica. What was till then thought to be a single species turned out to be a complex of >10 distinct but cryptic (in adult stage only) species that had been evading detection by traditional morphology-based taxonomic methods [15] (Figure 3). In this context, it is germane to note Larsen et al.’s. [3] claim that there could be 2 to 6 cryptic species for every arthropod morphospecies. Lending further support to DNA taxonomy, Schmidt et al. (2015) [16], studying the taxonomy of Central European bees, claimed that “DNA barcoding largely supports 250 years of classical taxonomy”. Köhler [17] and Hubert and Hamer [18] give a brief account of the history and basic principles of DNA taxonomy. (Methods of generating DNA barcodes and delineation of species using them are given in Box 1.)

Figure 3. DNA Bar-codes of two cryptic species of skipper butterfly (A-straptes flugerator). These two species could not be distinguished from one another by traditional taxonomic methods. (Image source: IDT “Barcode of Life”, idtdna.com)

1The insect family that includes butterflies and moths.

There could be 2 to 6 cryptic species for every arthropod morphospecies.
Box 1. DNA barcodes: How they are generated and used as a taxonomic tool

**Generation of barcodes**
1. A piece of tissue is taken from the specimen, the species status of which is to be established.
2. DNA is extracted from the tissue following standard procedures.
3. Selected region of the DNA (CO1 for most animals, ITS (internal transcribed spacer) for fungi, and rbcL and matK for plants) is amplified using PCR primers.
4. The amplified PCR products are sequenced, to generate a barcode of nucleotide sequences.
5. The barcode along with other required information is submitted to the Barcode of life database (BOLD) library.
6. Barcodes in the BOLD library are algorithmically clustered according to similarity, and these clusters are individually assigned a unique Barcode Index Number (BIN) and given separate web page (BINs are proxies to species).

**Figure A.** A typical datasheet from the Barcode Of Life Database (BOLD) system for a beetle species from South Australia. Information provided includes amino acid and nucleotide sequences of the chosen DNA segment and the correspondingly colored barcode and details of geography and the depositor (Source: BOLD.org).

Contd.
Box 1. Contd.

Identification and delineation of species
1. The system compares the barcode sequence of the unknown species with related BINs in the library and statistically tests the level of concordance or discordance between the two, which helps in establishing the species status of the unknown sample.
2. Delineation of species is based on the basic criterion that barcodes at a higher taxonomic level should show significantly higher sequence divergence than within a species. Special analytical tools like Automatic barcode Gap Discovery (ABGD) evaluate barcode gaps that satisfy this criterion, and flag them as potential new species. In such a case, morphological and any other characters of the taxon are used for confirmation of their new-species status.

The Handbook published by BOLD System [27] gives all the information a novice taxonomist needs to pursue DNA taxonomy and utilize BOLD System services.

How does the molecular method work to delineate species?Basically, it looks at the extent of divergence (genetic distance) in CO1-650 nucleotide sequences among related species and the unknown. Although very complex and sophisticated statistics are used for delineation, the statistical principle behind them is not very different from that of an ANOVA F-test or a Student’s t-test-divergence among groups should be significantly higher than within groups. Among North American birds, the mean genetic distance between closely related species was found to be 18 times higher than that within species [19]. For Indian spiders, the mean genetic distances within a species and between species of a genus were found to be 1.04% and 9.32%, respectively [20]. While using this criterion for species delineation, it is assumed that the observed molecular divergences are manifested as species-specific morphological and behavioral attributes that ensure reproductive isolation in nature. Does this mean that a CO1 sequence significantly different from other such sequences in a cluster could be considered a distinct species in the sense of classical taxonomy? In how many cases does the observed divergence translate to a physiological function or a behavioral attribute of ‘fitness’ value? How does this molecular delineation fare on the touchstone of biological species definition? Practitioners of molecular taxonomy

For Indian spiders, the mean genetic divergence between species is 8.6% higher than the mean genetic divergence within a species.
are cautious and prefer to call them molecular operational taxonomic units (MOTU), a unit already in vogue in bacterial taxonomy, and contend that MOTUs are pragmatic proxies to species.

DNA taxonomy is not without its critics, who point out its deficiencies [21]. Even in the early stages of its meteoric rise, some taxonomists were cautioning about “abandoning the benefits of morphological studies in favor of a limited molecular identification system” [22]. Over the years, molecular taxonomists brought to light certain vexatious problems with this method. I list a few here:

- Intraspecific and interspecific sequences in large populations might be so similar as to render the establishment of divergence thresholds problematic.

- Intraspecific genetic divergences in some insect families are unacceptably high (up to 13%).

- Presence of genetic introgression, incomplete lineage sorting, horizontal gene transfer, and uneven rates of evolution across taxa may lead to incorrect identification.

- Presence of nuclear mitochondrial pseudogenes (NUMT) might also cause incorrect identification of species.

- Some taxa like corals are recalcitrant to DNA taxonomic methods.

For plant species identification, mtDNA (CO1) is found to be an unsuitable candidate because nucleotide substitution rates in plants are much less than in animals. A 2-locus combination of \( \textit{rbcL} \) and \( \textit{matK} \) (\textit{Maturase K}, a plastid gene) has been found to be a reliable plant barcode. More recently, ITS2 (The internal transcribed spacer 2 (ITS2) region of nuclear ribosomal DNA) is being used for barcoding plants and fungi.

With the growing realization that DNA taxonomy is not a panacea for all taxonomic ills, modern taxonomists have been advocating and adopting an ‘integrative’ approach, in which both traditional
and molecular methods of taxonomy work in tandem towards a definitive identification and delineation of species [23, 24].

Its shortcomings notwithstanding, DNA taxonomy has been receiving increasing acceptance worldwide. About this molecular tool, Janzen says, “It will do for biodiversity what the printing press did for literacy.” Experts believe that DNA marker tools can be applied to address and answer questions relating to ecology and evolution [25]. The generation of DNA barcodes for any species requires no prior knowledge of its taxonomic position. Another plus point is that taxonomists can verify their past records and speed up the definitive identification of new records by applying molecular taxonomic methods to museum-preserved specimens. Under the aegis of the International Barcode of Life (iBOL), organization taxonomists of many countries are currently using barcoding tools for inventorying the biodiversity of their countries (see Box 2). In India, the Zoological Survey of India (ZSI) and Botanical Survey of India (BSI), the premier organizations with a mandate to collect and document our country’s biodiversity, have been barcoding thousands of their museum collections preserved for the last one hundred years. More recently, ZSI scientists have barcoded >100 morphospecies of Indian spiders [20].

5. Naming New Species

What is in a name? “A lot” says Ohl [26] in his delightful book The Art of Naming. He considers scientific naming a joyful and creative art and that taxonomy “displays both wisdom and wit of the artful scientists who practice it.”
Box 2. International Barcode of Life

Concerned about the presently alarming rate of Earth's biodiversity losses and convinced that molecular barcoding is a reliable tool for quick species identification and delineation and the right and expeditious way forward to document the biodiversity of our planet, an international consortium (International Barcode of Life (iBOL)) was established in 2008 to document our planet's biodiversity using DNA barcoding technology.

The international organization, the brainchild of DNA taxonomy pioneer Paul Hebert (hailed as the 'Father of Barcode Taxonomy') was set up in 2008 with an ambitious and grandiose mission to generate DNA barcodes for every species on Earth and to establish a repository for them. With 26 nations participating and more than 1000 biodiversity experts collaborating, iBOL has been able to generate nearly 10.3 million barcodes (as of February 2022) representing >760,000 Barcode Index Numbers (BIN) (proxies to species).

The repository maintained by iBOL is called the Barcode of Life Database (BOLD) System (https://boldsystems.org). It is an international cloud-based, open-access informatics platform for barcoding system. Any taxonomist from anywhere can access it to generate barcodes for the documented and putative new species and deposit them with the BOLD System. A typical entry in the BOLD database for a given species includes, in addition to the nucleotide and amino acid sequences and the corresponding barcode, other useful information on its geography and ecology (Figure A in Box 1). Scientists worldwide can freely access this mega library of barcodes.

iBOL’s proximate goal is to generate barcode coverage for 2.5 million species by 2026. With the advent of the high throughput next generation sequencing (NGS) technology, DNA taxonomists believe that the stage is set for embarking on ‘metabarcoding’ where, in addition to speeding up barcode generation, an entire environmental sample (of lake bottom mud, for example) can be sequenced simultaneously to unravel species composition and their ecosystem-level interactions (It is not clear how ecological interactions like competition and predation could be deduced from the analysis!).

DNA barcode system is also helping in the detection of illegal wildlife trade and invasive species. Experts say that the day is not too far off when by inserting a small piece of tissue of the plant or animal that you found into a handheld device (like a smartphone), you will know the identity of the species instantly if already recorded, and a lot more information about it. A futuristic tagline on iBOL’s website (https://ibol.org) says, “Imagine world’s biodiversity at your fingertips...”
While you are free to give your discovery a species name of your choice, the international community of taxonomists expects that you follow certain time-honored rules and norms while naming a new species. A comprehensive compendium of the rules is given in the International Code of Zoological Nomenclature (ICZN) for animals and the International Code of Nomenclature for Algae, Fungi, and Plants (ICN) for plants. For instance, adherence to Latin grammar is recommended for naming a new species (e.g., the species name for mango is *indica*—not *M. indicus*). Gender also is important if a species is named after a person. A new species of aloe from South Africa was originally named *Aloe thompsonii* but later changed to *A. thompsoniae* when it became known that Thompson was a female. Many taxonomists around the world generally, but not always, follow the widely accepted nomenclatural code. The prevailing convention for naming a new species is that it should highlight its unique, species-specific attribute. Following are a few examples:

- Country or a defined geographical region: (mango (*Mangifera indica*), barbet (*Megalaima asiatica*), Indian roller bird (*Coracias benghalensis*), Brazilian brown bat (*Eptesicus brasiliensis*).

- Morphological attributes: A prominent beak – Darwin’s finch (*Geospiza magnirostris*); a long snout: the Western Ghats frog (*Nasikabatrachus* (the prefix *Nasika* means nose or snout in Sanskrit).

- Color: Golden oak (*Quercus aureum*); blue passionflower (*Passiflora caerulea*); Coral reef fish the yellow tang (*Zebrasoma flavescens*)

- Pattern: Spots—six-spotted mite (*Eotetranychus sexmaculatus*); stripes—Eastern chipmunk (*Tamias striatus*).

Another tradition that taxonomists are encouraged to follow when naming a species is to choose preferentially its local or indigenous name if already known and in vogue. The Indian mackerel *Rastrelliger kanagurta* is an example of such a tradition. *Kanagurta*
is the vernacular (Telugu) name that fishermen along the Andhra and Odisha coasts use to refer to Indian mackerel.

Linnaeus named us humans as *Homo sapiens* (The ‘wise’ Homo). For a species that alone usurps 25% of Earth’s primary productivity, degrades pristine ecosystems with impunity, and has been responsible for the extinction of thousands of species, what an irony to be named ‘sapiens’!

Naming new species after celebrities has become popular in recent years (see Box 3). One wonders if eponymy is going to be a tradition in the future among taxonomists discovering new species. Is it an honor coveted by biologists? When the genus of a newly discovered fish was named *Dawkinsia* as a tribute to him, the famous Darwinian biologist Richard Dawkins apparently felt that he achieved immortality of sorts! How about buying such honors? Can a wealthy person expect you to name after him or his beloved wife any new species you might discover in your exploration into a hitherto unexplored tropical forest on a remote island if he financed that exploratory expedition? I leave you to ponder over a scenario of the direction species naming might take in the future. Assume that sometime in the future, our national animal, the Bengal tiger (*Panthera tigris bengalensis*), is brought to the brink of extinction by anthropogenic activities and bad conservation strategies. To save the tiger from extinction, conservationists have come up with a comprehensive strategy that entails a budget of a whopping 5 billion dollars. That is a lot of money for a country like India to invest on saving one species! Assume then that an Ambani or Adani comes forward and offers to bear the entire cost of the project with the proviso that the tiger’s scientific name should be renamed after him. What would you do? Decline his offer outright? Or would you gratefully accept the offer and muse rather philosophically, “After all, what is in a name? A tiger by any other name would be just as majestic and just as ferocious and will keep burning bright in the forest of the night.”
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**Box 3. Eponymy (naming things after famous people)**

You must be already familiar with eponymous terms like Darwinism, Wallace Line, Linnean nomenclature, Ramachandran Plot, and Krebs cycle in life sciences, and terms like Boltzmann constant, Bosons, and Raman spectra in physical sciences, all named after famous scientists. Eponymy in plant and animal species is common. Here are some samples:

- Madagascan wooly lemur (*Avahi cleesei*): Actor and comedian John Cleese.
- Rain forest treefrog (*Hyloclisis princecharlesi*): Prince Charles of U.K.
- A newly discovered velvet spider from Iran (*Louredia phoenixi*): American rock singer Lou Reed and Hollywood actor Joaquin Phoenix.
- Himalayan forest thrush (*Zootera salimali*): Famous ornithologist Salim Ali.
- Marine ostracod (*Bisopina mozarti*): Austrian composer Amadeus Mozart.
- Endemic Greek fish (*Silurus aristotelis*): Greek polymath Aristotle.
- Green pit viper from Arunachal Pradesh (*Trimeresurus salazar*): Salazar, a character from J. K. Rowling’s *Harry Potter* Series.
- Slime mold beetle (*Agathidium bushi*): U.S. President George Bush.
- Fern (*Gaga Germanotta*): Pop star Lady Gaga.
- A plant endemic to Kerala (*Humboldita sanjappae*): Genus name after the explorer naturalist Alexander Humboldt and species name after the Indian plant taxonomist M. Sanjappa.

Some taxonomists honor their mentors by naming their new discovery after them. A new internal trematode parasite from an anchovy fish was named *Thrysotrema hanumantharaoi* by its discoverer in honor of her mentor. How about taxonomists naming the new species they had discovered after themselves? Such an immodest and egotistical practice is, fortunately, a rarity in biological nomenclature.

*Contd.*
Box 3. Contd.

Are there any interesting trends in the etymology of new species named after scientists? A most recent study [28] finds a consistent gender bias in the etymology of new parasitic species. Among the 596 new species of parasitic worms discovered during the last two decades, the authors observed that “male scientists were immortalized (by the new species being named after them) disproportionately more frequently (81%) than female scientists (19%).” I wonder if a similar bias exists in the case of other taxa also.

Suggested Reading


[15] P. D. N. Hebert, et al., Ten species in one: DNA barcoding reveals cryptic species in the neotropical skipper butterfly Astraptes fulgerator,


