LETTERS

Edited by **Jennifer Sills**

Federal barriers to Cannabis *research*

ALTHOUGH THE MAJORITY of the general public (*1*) and the professional medical community (*2*) in the United States support the therapeutic use of *Cannabis sativa* as a pharmacological agent, the U.S. federal government's *Cannabis* research policies have blocked externally valid, randomized clinical trials on the effects of *Cannabis*. To conduct research on *Cannabis*, scientists must submit to a lengthy and arduous application process, often lasting for years. The research requires permission from multiple governmental agencies, including some with expressly stated opposition to any therapeutic uses, such as the Drug Enforcement Agency (*3*).

However, the application process is a mere nuisance compared with the biggest obstacle presented by the federal government: All *Cannabis* used for research purposes must be purchased through the National Institute on Drug Abuse (NIDA) (*4*). The tetrahydrocannabinol (THC) potency levels in the *Cannabis* available through NIDA are much lower than those in *Cannabis* products used by medical patients. The highest THC level available to researchers is 12.4% (*5*). The only two clinical studies funded by NIH in 2015 used products with potency levels between 3.5 and 7.0% THC (*6*, *7*). In contrast, the *Cannabis* sold in Colorado now averages 18.7% THC, with some strains registering as high as 35% THC (*8*), and no potency limits exist for the concentrates and ingestible products sold in most states where medical *Cannabis* is legal at the state level.

The scarce research the U.S. government has approved thus offers little insight into the effects actually experienced by patients and recreational users. As long as clinical research on *Cannabis* is controlled by regulators expressly opposed to any increase in its consumption, health care cost reductions may be missed, and intoxication and long-term effects will remain unknown. Most important, many severely ill patients may suffer unnecessarily because no one knows the true risks and benefits of consuming *Cannabis sativa*.

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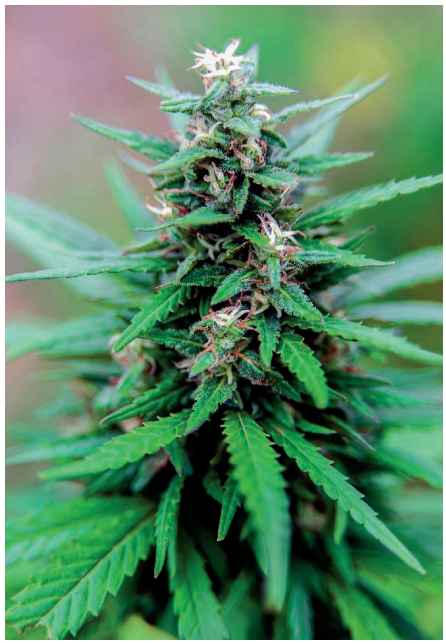

***Cannabis sativa*.**

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No surprise that comb jellies poop

AS ONE OF the organizers of the recent meeting on comb jellies (ctenophores), I feel obliged to comment on the News In Depth story "Comb jelly 'anus' guts ideas on origin of through-gut" (A. Maxmen, 25 March, p. 1378), published online on 23 March with the title, "Why watching comb jellies poop has stunned evolutionary biologists." I was stunned that videos showing defecation of waste through the anal pores of ctenophores astonished anyone. Those who have looked closely at comb jellies have seen and reported this process for well over a century.

In 1850, Louis Agassiz found that waste products were expelled from comb jellies through sphincter-like anal pores, which open and close during bouts of defecation (*1*). Thirty years later, the German zoologist Carl Chun used injected dyes and tracking of waste particles to expand on Agassiz's results in great detail (*2*). Since then, scientists have amply confirmed Agassiz's and Chun's findings and studied how the process of defecation works (*3*). Nearly every invertebrate textbook in the 20th century shows the anal pores of ctenophores. This literature was omitted or grossly misrepresented in the News story to erroneously claim a novel discovery of a through-gut in comb jellies.

It is now recognized that ctenophores expel waste from both ends. They eject bulky indigestible food fragments, which do not enter the stomach or food canal system, through the mouth. Meanwhile, unused or small waste particles in the food canals are periodically shunted into the stomach and anal canals, where they are expelled through the anal pores (*3*). In contrast to the implication of the News story, the two exit methods of waste products are not contradictory or mutually exclusive. It should not surprise anyone that comb jellies poop and have a through-gut.

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Digital identifiers for fungal species

SPECIES-LEVEL CLASSIFICATION OF life has been a cornerstone of biology for centuries. Most macro-organisms are described soon after discovery, but species of prokaryotes, micro-eukaryotes, and fungi often lag far behind in formal description because they are small, extremely diverse, and difficult to cultivate and often lack discriminatory morphological characteristics.

D. Hibbett ("The invisible dimension of

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fungal diversity," Perspectives, 11 March, p. 1150) recently argued that missing species names (Latin binomials) in the kingdom Fungi hamper communication about formally undescribed species derived from molecular surveys of the environment. He pleaded for changes in the International Code of Nomenclature for Algae, Fungi, and Plants (*1*). We argue that Latin binomials are not urgently needed for precise communication and delimitation of environmental species known only from DNA barcode sequences.

In the UNITE database for molecular identification of fungi, we have adopted the species hypotheses concept to provide unique digital object identifiers (DOIs) for all fungal species known from sequence data (*2*, *3*). We have, for example, used this concept to analyze the Archaeorhizomycetes species (*4*) examined by Hibbett. The species hypotheses concept accounts for taxonomic uncertainty through multiple alternative cut-off levels for species delimitation. As in the Linnaean tradition, it relies on molecular keys, reference sequences, and voucher material specified by taxonomists.

Several major microbial identification pipelines, notably QIIME (*5*), use the species hypotheses identifiers as a community standardization measure. The Barcode of Life Data System similarly assigns barcode index numbers to animal taxa (*6*). Both systems enable straightforward communication of machine-readable but formally undescribed species across scientific studies. Both serve to facilitate future descriptions of those taxa by aggregating data on, for example, geographical distribution and substrate of collection. When voucher material or cultures become available, a formal species description can draw on the molecular and other data amalgamated in the above databases.

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Response

SPECIES CLASSIFICATION PLATFORMS based on DNA sequences, including the UNITE system, allow ecologists and evolutionary biologists to conduct sophisticated research programs without reference to Latin binomials. However, the entities that they catalog—such as species hypotheses (described by Kõljalg *et al.*), virtual taxa (*1*), or barcode index numbers (*2*)—are obscure concepts. Although useful to specialists, these concepts are unfamiliar to the general public. In contrast, the notion of species is deeply ingrained in human culture, even if evolutionary biologists understand that there is no universal, objective criterion for defining a species (*3*). Species names in the form of Latin binomials are useful for communicating knowledge of biodiversity not only to nontechnical audiences such as legislators, educators, and members of the media, but also to the vast majority of biologists, who are not microbial ecologists.

Kõljalg *et al.* assert that species classification is a cornerstone of biology and lament the lag between discovery and description of fungal species and other microorganisms. This lag time would be greatly diminished if species could be formally defined based on molecular sequences. However, this is not possible under the International Code of Nomenclature for Algae, Fungi and Plants (*4*), which requires physical type specimens regardless of their quality or scientific utility. The Code can only be modified once every 7 years by a vote of the Nomenclature Section of the International Botanical Congress. The next opportunity to change the Code will be in 2017. Adoption of sequence-based species description would promote the integration of molecular ecology and traditional taxonomy, which would be facilitated by resources such as UNITE.

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