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How to conserve wild plants? Give the world the power to read them.

If you are illiterate, a library is at best a tempting storehouse of thin sheets of firewood. If you are bioilliterate, that great green mass is simply something in the way, something to be replaced, turned to compost, or fed to the inanimate and animate extensions of the human genome.

K & K have herded a fine batch of botanical cats into a collective review of where the plant priesthood stands on the natural history of plant conservation. I would like to hope that every graduate student and practitioner of wild plant biology invests a weekend in reading it from cover to cover. But my non-botanist lifetime of enjoying, using and relying on many thousands of species of tropical plants leaves me feeling that this book, and all this book's antecedents and parallels, constitute a massive body of priceless information that realizes only a very small portion of its potential. It is as though we had the Library of Congress and all the world's other massive repositories of the written word forlornly dotted across a firmly illiterate society.

I am standing in a Costa Rican rainforest, magnificent subjects of this book in all directions and underfoot. There are a thousand species of plants within a long stone's throw. Nearly every one of them is a described species with a proper scientific name, a handle that you can plug into Google and come up with something. Nearly all of these species or their near relatives have been studied, sampled, thought about and are in "the literature". And I cannot identify a single species.

Oh yes, I can collect a branch, press and dry that branch, take it to INBio or the Missouri Botanical Garden or the U. S. National Herbarium or Kew or the many other dead plant depositories. I can take that branch to a botanical library and slog my way through keys and descriptions with a vocabulary of abaxial, tomentose, spicate, cespitose, and cornifoliar stipules. I can seduce a world-level authority into spending a day in the forest and peering at the branch. I can wait 2.3 years until the branch flowers, put a digital image on the web, and plead for someone to give me the name - which they will from some far distant country. Now multiply all that by 1000. Stalemate.

I am a user. I use plants. They mean something to me. They are the food for the caterpillars that I inventory. They are the fruits for the birds that feed my caterpillars to their nestlings. They are the puzzling sources for amazing lead molecules such as the caffeine you had for breakfast. They are the personal bank account and investment portfolio of the ocean of landowners that surrounds the conserved wildlands I and many others struggle to facilitate into survival through non-damaging biodiversity development. We need to be able to read them - now, on the spot, in real time - but we cannot. They are to me as the bright colors on the walls of an art museum are with no guide, no brochure, no labels. And you cannot see the morphine, caffeine, turpentine, lignins and genes that change from book to book. It's all green. Small surprise that their destiny is that of firewood and biomass shoveled into the craw of the great consumer.

So we have in one hand a great, burgeoning and decaying body of academic - with some practical flavors - knowledge and experience about wild plants, encapsulated in the world's herbaria, botanical gardens, libraries, URLs and plant biologists' brains. We have on the other hand, still, fortunately, some substantial amounts of wild plant diversity, especially, but certainly not exclusively, in the tropics. And standing between the two, 99.999% bioilliterate, we have 5 billion people. And when any one of those people wants to do something with one of those plant species, now for real purposes - with the potential of leading that person or some greater part of society to want to see that plant species survive - that person quite simply cannot now, in real time, get the name for that plant. The name, the unique identifier. Why the name? Because without a name it is just another green blob. Without a name there is no way into the collective knowledge of specific plants. Try using Google without a name. Type in green and brown, 3 m tall, sawtoothed leaf margins, growing on wet soil, at 10 degrees north, 85 degrees west, and see what you get. Or try to look that up in Index Kewensis.

It is time for a zoological observation. It is fascinating to now know, through the agility and miracle of sequencing, that hippos are the ancestors of whales. But what I want to know is how to tell apart all the species of whales when I am standing in a supermarket looking at a whale steak, or standing on a hot tropical beach wondering whether to call the vultures or the Smithsonian to the newly stranded whale. Sequencing has another function besides revealing phylogeny.

Imagine what it would do to any and all aspects of human interactions with wild plants if you - any of you - could walk up to any plant anywhere - seedling, sapling, 40 m tree, grass, root, pressed leaf, or fallen log - and know in a few seconds its scientific name. I need not describe how today's technology would then let you use that name to get into the warehouse of collective botanical knowledge. That capacity would transform far more than the science of plant biology, the conservation of plants, and the superficial ways we currently make

use of the incredible diversity of form, physiology, genetics and chemistry of plants. It would be to plants what the printing press was to stories, education, science, law, medicine and communication.

Science fiction? Yes, it has been for many decades if not centuries. Step out of the space ship and point the gadget, and it says - friendly, unfriendly, poisonous, curative, edible, spit it out. But no more. Today we have the capacity to essentially barcode animals with a 650 base pair sequence of the CO1 mitochondrial gene, build libraries of those sequences, and miniaturize the sequencing process into a cheap, fast and hand-held gadget. One for the belt or backpack of anyone on the planet. 30 million sequences in a chip the size of your thumbnail. 30 million pieces of collateral information in another chip. And the cell-phone uplink for a dialogue with Google and its equivalents. The emergence of this process is now in motion, in its nascent germination through initiatives bubbling up in the free-standing museums and pilot projects spearheaded by Paul Hebert at the University of Guelph (e.g., Godfray 2002, Hebert et al 2003a, b, Stoekle 2003, Janzen 2004, and see <http://phe.rockefeller.edu/BarcodeConference/index.html>) and the marine biodiversity inventory initiative (http://phe.rockefeller.edu/PDF_FILES/DNAbarcode.pdf).

Unfortunately, the CO1 mitochondrial gene sequence that works so well with animals does not appear to be a good species-level unique identifier for plants. Additionally all those neat secondary compounds long evolutionarily designed to gum up the inner workings of herbivores - be they fungi, bacteria or animals - are quite unpleasant for sequencing engineering. However, my plea is single-minded. It should take only a minute fraction of the energy that has been invested in plant phylogenies and within-population variation to locate the "right" gene sequence to serve as a species-level unique identifier for plants, so that the engineering process can get on with creating a hand-held barcorder for plants as one and the same as the hand-held barcorder for animals and fungi. Perhaps it is already known - the usable CO1 gene sequence for animals was not a new discovery, to say the least, but rather the novelty was Hebert's decision to use it as a species-level identifier.

Yes, we can still spend tomes arguing as to whether *Sweitenia macrophylla* is one or ten species, or whether the rainforest population of *Cordia alliodora* is the same species as is the dry forest population of *Cordia alliodora*. But with a barcorder, I - and the farmer, forester, conservation biologist, ecologist, taxonomist, biodiversity prospector, ecotourist - can know that this sapling of *S. macrophylla* is not one of its ten sympatric look-alikes, and that it is indeed *C. alliodora* rather than any one of the other 15 species of sympatric *Cordia*. And since I probably know where I am, my barcorder does not have to tell the *Cordia*

in front of me from the 100+species growing in other countries. Now multiply all that by the 13,000 species of plants in Costa Rica. Or the 400,000 in the world.

I - a hard core field biologist and biodiversity developer dependent on being able to identify wild living plants on the spot - have always viewed, and used, herbaria and their constructors as incredible libraries of plant biodiversity. But the need for a barcorder serendipitously multiplies their value enormously. What if you could snip a square cm piece of paper out of each book in the world's libraries and instantly have a hand-held index to all books (and if properly linked, the readable contents of those books)? In my not so humble opinion, the vastly greatest contribution to plant conservation - and all the rest of wild plant science - that could be made by the botanical community at this time would be to figure out the right gene (or two, if absolutely necessary), determine the methodological tricks to get its sequence quickly and cheaply out of most herbarium specimens, and join that proactively to the above-mentioned initiative to create and arm the barcorder. It is a no-brainer that every subsequent sequence from a plant at the time of collection, and from all the users who are motivated enough to allow the georeferenced sequences they obtain with their barcorder to be included, will rapidly expand the geographic coverage and functionality of such a plant sequence library.

Put your head back and imagine. You step into that great green living mass, on your way home from school, as you file your chainsaw, as you taste your samples. A chip of tissue into the gadget in your hand tells you its name, now. You ask first those plants that to you have some salient trait. Soon many are old friends with names, the basis for communication. And when/if your chip of collaterals is large, or you have Google or whatever access through your cell phone, you can let your fingers do the walking.

What is missing from this scenario? The hardest part. Think on the example of bioprospecting for rainforest drugs to support conservation. Old wine. If you could put a penny tax on every cup of coffee - we make three trillion a year - you could pay all conservation and taxonomic costs for all of the world forever. Caffeine is *the* number one rainforest drug. The trick is not finding *Coffea arabica* or the technology of the cup of coffee, or even its medical ramifications. The trick is getting the penny tax and having it go to conservation and the taxonomy behind it. At this late stage, impossible.

Yes, there will be huge gains in bioliteracy and all that entails from creating the hand-held barcorder. But once again we are on the brink of producing something extremely useful to global society – like a cup of coffee - while leaving the profession - botanists, other biologists, taxonomists, conservationists and all the other pro bono users - without a budget to gather and maintain the information the user links to once the plant is identified, and to massage that information into

more digestible formats. Somehow the barcorder *must* have built into it a system whereby everytime you ask it for a name, a penny drops into a bucket, the bucket that supports conservation and taxonomy. Many millions of user events, many millions of pennies. More users, more pennies. More bioliteratcy, more pennies. We buy a postage stamp without a blink, we pay our phone calls with only the mildest of grumping, we do not begrudge our highway taxes. The emergence of the barcorder demands a three-member team - the science of plant sequencing, the microengineering of miniaturization of a currently laboratory process, and the emergence of an entrepreneurial force aimed at delivery of a self-supporting social good.

Do we want to conserve wild plant diversity? Yes. The answer does not lie in better keys, more keys, more images on the web, more web sites, more species pages, more descriptions, more phylogenies, more specimens, more maps, more anythings. Those are necessary collaterals, but not sufficient. The answer lies in a process that will for the first time connect the collective species-level biodiversity knowledge of the world to any and all users, on the spot, now. Fast, cheap and on-site single (or very few) gene sequencing – developed for the purpose of identification - has the potential to deliver the species-specific linkage between the species and its human-known collaterals. There is a huge opportunity for the botanical community to thrust itself into a position of friendly social global prominence – just as have education, agriculture, medicine and communication. Now is the time.

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