Citizen Scientists Key to Halting Sudden Oak Death (Op-Ed)

Matteo Garbelotto, University of California,
Berkeley

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EXPERT VOICES OP-ED & INSIGHTS

Shown above are lesions on the tree, which is one of the signs that the fungus is spreading. This fungus infests several species of oak trees. Infected trees develop bleeding or oozing cankers on the lower trunk. There is no treatment available once trees develop cankers. Shortly afterwards, the fungus is spread by spores, and usually begins to spreads in other nursery material. This fungus causes mortality in a short period of time.

CREDIT: Joseph O`Brien USDA Forest Service

Matteo Garbelotto is an extension specialist and adjunct professor in the Department of Environmental Science, Policy and Management at the University of California, Berkeley. An expert in forest pathology and emergent infectious disease, he contributed this article t LiveScience's Expert Voices: Op-Ed & Insights.

The notable achievements that can result from engaging citizens in researc are well known, and the practice of working with so called "citizen scientists", aka volunteers, has been established since these individuals started playing a pivotal role in the counting of birds in the early 1900s.

Nonetheless, there is still a prevalent belief that volunteers can only participate in research programs basically as unpaid field technicians, playing a role that is strictly limited by the supervision of "professional" scientists. Despite statements on the need to move citizen science forward published as early as 2008, currently, the will of leading scientists and major funding agencies to trust citizen scientists' data and financially support large projects heavily relying on volunteers is simply wanting.

The educational role of any activity involving the public is not in discussion here, but I would like to present some insights based on my personal experience (now backed by results of recent peer-reviewed publications) and supported by newly announced citizen science projects.

After spending over 50 percent of my time since 2006 working with volunteers on large projects, it is my opinion that in a funding-limited world, one of the best ways to move basic science forward is to work closely with the invaluable resource volunteers provide. We should not only employ them to report or count organisms, but also treat them as peers and build strong cooperative efforts in which task are properly shared between professional and volunteer researchers.

I am a forest pathologist and part-time mycologist working on, among other projects, Sudden Oak Death (SOD), an exotic forest disease that is forever changing the composition of coastal forests in Northern California and Southern Oregon. In 2006, I decided to enlist volunteers to understand the fine-scale distribution of the disease. At that time, the cost of the operation was approximately $100,000, and I was able to fund it mostly because funding agencies and their grant reviewers recognized that the activity, called SOD blitzes, had a strong educational component — but, there was no belief the program could generate valid data.

We started by enlisting grass-roots environmental leaders in several communities and developed compulsory training sessions for each of them that guided hundreds of participants in properly identifying and collecting samples. We then used the bulk of the funding to process all collected plant material using laboratory tests that properly diagnose SOD.

In six years, we went from fewer than 100 to more than 600 fully trained participants, and we expect collections to be more than 25,000 samples in 2013. Last year, over one million people accessed the results through the Web and newspapers. The cost of the blitzes has almost doubled in six years, but $200,000 would have only supported three or four technicians to do the fieldwork without the volunteers.

The quality of the collected material, the willingness of volunteers to share information about their own private property (by providing samples), the intimate knowledge that locals have of their own neighborhoods, and the validation of all samples through the lab work have generated the most extensive fine-scale map of the distribution of a forest disease in the world. The data covers tens of thousand of hectares throughout California. Since last year, the data that volunteers generated has become the backbone of the most comprehensive distribution map of SOD, called SODmap, where volunteer, government and academic data are all combined.

The knowledge of the fine-scale distribution of the disease is essential for predicting (and preventing) oak infections, as the pathogen will infect oaks only if they are within a couple of hundred meters of infected trees. Those results would be unimaginable from simply hiring three or four technicians per year.

Volunteers have definitely stepped up with the SOD blitzes, but it is another project that truly highlights how volunteers can be scientific peers to their academic counterparts. With recent estimates of fungi diversity ranging from approximately 720,000 to over 5.1 million species — of which only approximately 99,000 (or about 10 percent) have been described — the status of this group of organisms as poorly known is well-established and frequently discussed in the scientific literature. By contrast, 90 percent of plants have been described worldwide, according to estimates.

Identifying specimens by tracking a species-specific DNA component ("barcode") is an invaluable technique for tracking organisms like fungi that spend most (or all) of their life cycles in a microbial stage. Yet researchers have selected DNA barcodes for only a small fraction of described fungal species. While everybody agrees that DNA barcodes must be associated with well-preserved, and accurately described, vouchered specimens (possibly types or holotypes), there is a deep schism in the scientific community about which specimens qualify as being "good enough" to provide a DNA barcode.

One side is pushing for DNA barcodes to be provided only by academic experts in the field, while the other side, which I represent, supports a larger-scale effort through which reasonably well-curated collections may provide the vouchers for DNA barcodes. With an estimated 600,000 undescribed species, and assuming 5,000 taxonomists (a huge overestimate of mycologists with some training in taxonomy worldwide), bridging the gap in knowledge within 40 years would require everyone to classify 120 species during their career. That relies on a ridiculously hopeful estimate of 15,000 new descriptions per year. Between 1980 and 2000, "only" 1,100 species were described per year, as reported by Bruce Barcott in The New York Times in September 2004.

In a recently published paper, my colleagues and I describe an alternative approach that would help fill the gap in knowledge. We sampled every one of the 6,000 taxa present in a fungal collection, extracted DNA from them, and attempted to generate a DNA barcode for each. The collection, housed in the Museum of Natural History in Venice, has a peculiarity: amateur mycologists collected 95 percent of the specimens, and the collection is entirely curated by non-academic volunteers.

In the end, we submitted over 1,100 internal transcribed spacer (ITS) DNA barcode sequences to the National Institutes of Health's (NIH) GenBank, and are still analyzing about 400 more. With the help of two leading taxonomy institutions (Centraalbureau voor Schimmelcultures in the Netherlands and NIH's National Center for Biotechnology Information), we analyzed the quality of the data with an approach that we describe in detail in our paper.

Results showed that less than 5 percent of the samples were grossly misidentified, and another 5 percent had minor potential misclassification issues. Therefore, out of a total of 1,500 samples, 1,350 barcodes could be generated with good quality for vouchered specimens. This was done by a single mycologist working part-time on a project over about six years, using traditional (not next-generation) sequencing techniques.

The method we described further allows us to pinpoint problems and has already triggered a revision of the most problematic groups housed in the Venice collection. Granted, Italy has one of the most solid traditions in the world for macrofungal (i.e. mushroom) classification, and the collection is the official outlet of the largest amateur mycological association in the world (Associazione Micologica Bresadola), which includes over 13,000 current members. However, many other countries have comparable "amateur" expertise.

It is time we as academicians, and the agencies that fund us, leave our ivory towers and generate true synergy with peers whose knowledge is, not unlike ours, a true calling. Error rates by specialists currently involved in submitting sequences have been estimated to be around 20 percent. So, actually, working with amateur mycologists may reduce that error rate by half and allow for an order of magnitude increase in the speed at which we bridge the gap in knowledge on fungal taxonomy. It is time for "citizen basic science" to be embraced.

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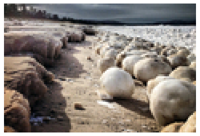
- 

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