

# COMMENT



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The International Center for Tropical Agriculture in Colombia holds 65,000 crop samples from 141 countries.

## Feeding the future

We must mine the biodiversity in seed banks to help to overcome food shortages, urge **Susan McCouch** and colleagues.

Humanity depends on fewer than a dozen of the approximately 300,000 species of flowering plants for 80% of its caloric intake. And we capitalize on only a fraction of the genetic diversity that resides within each of these species. This is not enough to support our food system in the future. Food availability must double in the next 25 years to keep pace with population and income growth around the world. Already, food-production systems are precarious in the face of intensifying demand, climate change, soil degradation and water and land shortages.

Farmers have saved the seeds of hundreds of crop species and hundreds of thousands of 'primitive' varieties (local domesticates called

landraces), as well as the wild relatives of crop species and modern varieties no longer in use. These are stored in more than 1,700 gene banks worldwide. Maintaining the 11 international gene-bank collections alone costs about US\$18 million a year.

The biodiversity stored in gene banks fuels advances in plant breeding, generates billions of dollars in profits, and saves many lives. For example, crossbreeding a single wild species of rice, *Oryza nivara*, which was found after screening more than 6,000 seed-bank accessions, has provided protection against grassy stunt virus disease in almost all tropical rice varieties in Asia for the past 36 years<sup>1</sup>. During the green revolution, high-yielding rice and wheat varieties turned India into a net

food exporter. By 1997, the world economy had accrued annual benefits of approximately \$115 billion from the use of crop wild relatives<sup>2</sup> as sources of environmental resilience and resistance to pests and diseases.

The time is ripe for an effort to harness the full power of biodiversity to feed the world. Plant scientists must efficiently and systematically domesticate new crops and increase the productivity and sustainability of current crop-production systems.

Why does plant breeding need a boost? Because new, high-yielding seeds that are adapted for future conditions are a cornerstone of sustainable, intensified food production<sup>3</sup>. Since the mid-1990s, progress in conventional plant breeding has ►

► slowed, despite the phenomenal yield gains of the past. Part of the reason is that only the tip of the biodiversity iceberg has been explored and used<sup>4</sup>.

Crop wild relatives, landrace varieties and previously undomesticated wild species represent sources of new variation for agriculture. Such plants have survived repeated and extreme environmental challenges, yet their resilience and adaptive capacity remain largely untapped and poorly understood. A wealth of genetic information has been left behind throughout the history of plant domestication and scientific crop improvement. It must now be deployed.

Plant breeders often worry that using wild species or landrace varieties is too risky, scientifically and economically. It took 20 years and 34,000 attempts to cross a domesticated rice variety with a distantly related, highly salt-tolerant wild relative from India before fertile offspring were obtained<sup>5</sup>. It will now take at least 4–5 years of breeding to eliminate unwanted wild characters to generate a new high-yielding, salt-tolerant rice variety (see [go.nature.com/knzt15](http://go.nature.com/knzt15)). That is too long for most plant-breeding programmes, especially in the private sector.

Insufficient genetic and phenotypic information about most of the holdings in gene banks makes plant breeders even more reluctant. Politics has also created obstacles. The Convention on Biological Diversity (see [go.nature.com/njhon](http://go.nature.com/njhon)) is an international treaty that, although vital for consolidating efforts to conserve the diversity of life on Earth, has created significant barriers to the sharing of genetic material, including of domesticated plants and their wild relatives<sup>6</sup>.

Happily, things are changing. The International Treaty on Plant Genetic Resources for Food and Agriculture<sup>6</sup> (ITPGRFA), negotiated in 2004, now governs access to crop diversity. It mandates that a portion of any monetary benefits derived from the commercialization of products from gene-bank materials is put into a fund that supports conservation and sustainable use of crop genetic resources.

On the technical front, we are now able use a plant's genetic make-up to predict its agronomic potential and traits. Plant breeders commonly use genetic markers to identify individual plants carrying specific genes for disease and pest resistance or stress tolerance, without ever exposing the plants to the relevant agents. Breeders can use genome-wide approaches to eliminate 70–80% of individuals in any generation without having to invest in laborious multi-environment field testing.

### THREE STEPS

How should we begin to mine biodiversity for food security? A logical first step is to obtain a sample of sequence information from the genomes of all non-duplicate plant

samples in the world's gene banks that are available under the terms and conditions of the ITPGRFA — perhaps up to 2 million. This 'fingerprint' for each plant will serve as the basis for assessing genetic relationships, and will make it possible to systematically select subsets of material for in-depth investigations. Sequencing costs are plummeting, making such an effort feasible.

Sequence data provide a genomic 'parts list' that can help to decipher mechanisms that enable plants to adapt to myriad environments, and can guide our remodelling of cropping systems for the future. Linking sequence data with conventional 'passport information' about collection locality and original environment should call attention to the genetic potential of many hidden crop resources.

Second, we must analyse the phenotypes of gene-bank accessions to evaluate their traits and overall performance. This is the most intellectually challenging, complex, costly and time-consuming stage. We cannot hope to evaluate all gene-bank accessions in all relevant environments, even with the advent of high-throughput phenotyping technologies. Using sequence data in combination with phenotypic, geographical and ecological information will enable researchers to target field experiments strategically and to develop models that can predict plant performance. This will make plant breeding faster, more efficient and cheaper.

Assessing the breeding potential of unfamiliar plant materials typically requires them to be crossed with modern, 'elite' varieties. Their offspring are then evaluated in environments of interest to farmers and breeders, over several years. Often, the genetics of high-performing offspring can be traced back to DNA inherited from wild or landrace donors that are agriculturally less productive. For example, the wild tomato species *Solanum pennellii* was used to double commercial tomato yields under a wide range of growing conditions<sup>7</sup>, and the wild rice species *Oryza rufipogon* increased yields of elite varieties of rice by more than 25% (ref. 8). Thus, useful genetic traits are moved across the breeding barrier, expanding the genetic diversity of domesticated plants and opening up new opportunities for environmental resilience and future gains in quality and yield<sup>4</sup>.

A third key step is to create an internationally accessible informatics infrastructure to catalogue the diversity in the world's seed collections. This would link seeds and genetic stocks directly to passport, genomic and phenotypic information<sup>9</sup>, thereby engaging the creativity of geneticists and breeders

and fuelling plant improvement for years to come. This requires an unprecedented effort in data management and sharing. Today, seed data are typically recorded and managed by different people, such as gene-bank curators, agronomists and breeders, often in different institutions and in different database systems.

But it is doable. The Global Biodiversity Information Facility (GBIF) — an online network that facilitates open access to "information about the occurrence of organisms" — provides a good example of such an infrastructure and has changed how biodiversity is studied. But the GBIF does not currently handle the complex genomic data necessary for our efforts.

Most importantly, results from genomics and agronomic research must be connected to the communities that are creating new varieties of crops. An international network of scientists in both the public and the private sectors must work together to provide seeds and plants to farmers and commercial plant breeders for further crossing and testing in different environments. The research community must pay specific attention to the development of locally adapted varieties that meet the needs of the world's poorest farmers.

How much would such a systematic, concerted, collaborative global effort to feed the future cost? We estimate around \$200 million annually. This seems like great value, given that as a society we have spent \$3 billion on sequencing the human genome, \$9 billion on constructing CERN's Large Hadron Collider near Geneva in Switzerland (plus about \$1 billion a year in running costs) and can spend up to \$180 million on a single fighter jet.

After all, as the ecologist Charles Godfray put it: "If we fail on food, we fail on everything". ■

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On behalf of attendees and organizers of the Crop Wild Relative Genomics meeting held in Asilomar, California, in December 2012. See [go.nature.com/nrpoe3](http://go.nature.com/nrpoe3) for full author list.

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