nature genetics

Growing quality

Brazil's success in applying a systems approach to agricultural productivity has been rapidly followed by an expansion in postgraduate training with particular strength in agronomy, plant molecular biology and biotechnology. Research publications with international impact will be a key to sustaining and exporting these successes.

The sixtieth Brazilian Congress on Genetics, which took place 26–29 August in Guarujá, wove together a brilliant assortment of all strands of the discipline. Topics ranged from the origins of the tripartite Indigenous-African-European mixtures of the Brazilian population (*PLoS Genet.* **4**, e1000037, 2008 and *Nature* **488**, 370–374, 2012) to models of gene flow in the hybridization zones of wild species of butterflies and bromeliads. The genetic knowledge and unifying genomics perspective of the participants opened the complexity of South America's biota in interesting ways. For example, the spectacular winter-flowering *Tabebuia* trees provoked discussion of the respective roles of color and karyotype, as there are yellow-flowering species with high ploidy and pink and white trumpet-shaped blossoms in many species with smaller genomes.

The productivity of Brazilian biologists cannot be faulted, but many we talked with complained that they are incentivized to quantity and diversity of publications, making it difficult for their work to have an impact on journals and readers overseas. Although small publishable units are good for rapid communication and exploration of the research landscape, we find that high-impact publications usually arise from international collaborations bringing multifaceted approaches to bear and from sustained, deep investigation of major problems by dedicated teams. As we already recommend in other countries, we encourage those responsible for evaluating and rewarding researchers in Brazil to assess the increasing value of Brazilian publications to the international community and the added value of collaborative research so that we can learn from your scientists and work better together. This might mean fewer publications, but these will have more readers and users.

In genomics, we have recently seen Brazilian researchers make major contributions to collaborative publications such as the global survey of honeybee diversity published in this issue on page 1081. In this report, the genomes of Africanized bees with their greater disease resistance, reproductive advantages and vigorous stinging response in defense of their colony will be of particular interest to researchers and apiculturalists in the Americas. The recent publication of *Eucalyptus* genomes (*Nature* **510**, 356–362, 2014) provides an excellent model for the importance of genomic tools to the basic biology and agricultural development of this fast-growing crop tree.

Brazil has become a major agricultural exporter thanks to its research institution EMBRAPA implementing a comprehensive approach to farming the previously unproductive central cerrado region (http://www.economist.com/node/16886442). Within a systems approach to agricultural productivity, one problem can be overcome by planting a mixture of species, another problem by crop rotation, yet another by a transgenic variety and another by introgression of a naturally occurring trait monitored by molecular markers. No one solution will work as needs and conditions evolve, so the good news for biologists is that there are unlimited research problems in commercial agriculture and a corresponding set of solutions in the historical ancestors of today's crops as well as the wild species that surround them. For example, the boll weevil is not deterred by cotton engineered to express *Bacillus thuringiensis* toxins, but several other plants do contain inhibitors that might be employed as future deterrents.

A good example of an agricultural application offering research in fundamental genomic problems is sugarcane, a newly valuable prospect for sustainable tropical fuel bioethanol production. Sugarcane has been somatically propagated by humans for about a thousand years by the somewhat laborious practice of planting and regularly replanting slices of stem with buds. This practice probably came about because of the difficulty of making crosses in an aneuploid segregating allopolyploid with ten genomes from one recent ancestor and eight genomes from another. Rhizome traits have not been selected and retained, markers were scarce and, were a linkage map to be made, it would resemble a hammock. However, given appropriate SNP markers, sustainability might be achieved via breeding for roots and rhizomes (for example, see *Trop. Plant Biol.* **4**, 22–30, 2011 and *Genome* **47**, 988–993, 2004).

Next year, Brazil aptly hosts both the International Congress of Plant Molecular Biology (IPMB; http://www.plantsci.org.uk/events/11th-international-congress-plant-molecular-biology) for the first time in Latin America and Evolution (http://sbg.org.br/Evolution2015/) with growing confidence that the world has a lot to learn from the experience and enthusiasm of its researchers in the biological sciences. ■