Guest Editorial

OMICS-Related Research in South America

THIS SPECIAL ISSUE of *OMICS* is devoted to the omics-related research in South America. Most of the papers come from Brazil, which was the first (and so far the only) South American country to undertake genome sequencing and remains a leader in genomics-oriented research. The genome sequencing of the plant pathogen *Xylella fastidiosa* by a consortium of ~50 labs from the Brazilian state of São Paulo took several years, but this project provided the scientists with invaluable experience that allowed them to accomplish complete genome sequencing of several other important genomes, such as plant parasites *Xanthomonas axonopodis*, *Xanthomonas campestris*, and *Leifsonia xyli*, and the causal agent of leptospirosis, *Leptospira interrogans*. Importantly, the genome sequencing was followed by a variety of post-genomics projects, including development of improved growth media for *Xylella* and detailed comparative analysis of various plant pathogens. In the past years, researchers throughout Brazil have moved far beyond microbial genomics, as evidenced by the mini-review on the non-coding RNA in the human genome, a metagenomics study of cyanobacterial biofilms, and the study of *Trypanosoma vivax* ESTs included in this volume, as well as the existence of a number of more ambitious projects on the much larger genomes of crop plants.

While other South American countries have not participated in genome sequencing efforts so far, their scientists have, like other Brazilian groups, exploited the complete and unfinished genome sequences available in GenBank. The ever-reducing cost of computing power has made post-genomic bioinformatics an increasingly accessible area of research. Bioinformatics may stimulate complementary experimental work, as exemplified by the work reported here by a group from the University of Chile who characterized each of the eight rhodanese-like sulfurtransferases encoded in the genome of *Acidithiobacillus ferrooxidans*, a bacterium that is widely used in biomining. Such detailed biochemical analysis of the genome-derived sequences is a very valuable contribution to the annotation of future microbial genomes. The last two papers in this issue represent more theoretical approaches—an analysis of the “alternate” ORFs that can affect gene calling and genome annotation, and a comparative analysis of the promoter areas of the ionotropic receptor of glutamate genes in human, rat, and mouse. Having had first-hand experience of the research work in the region, we hope that this selection of quality papers will provide the readers of *OMICS* with a better understanding of South American omics research and encourage further scientific collaboration.

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