

PLANT GENETICS

Uncommon or garden genomics

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With the increased sophistication and capacity of DNA sequencing technologies, we have become used to seeing reports of evermore ambitious genome sequencing projects. It no longer seems impossible that there will be a time when genome sequences are available for all the plants in one's garden. For Huan Liu of the Beijing Genomics Institute (BGI), China, and colleagues, that time is now — well, almost. The BGI team have taken samples of all the plants in the Ruili Botanical Garden in southwest China, close to the border with Myanmar, and attempted to sequence them.

There are 1,093 species growing in the Ruili Botanical Garden, and young leaves were taken from all of them, put on ice, and shipped to the BGI headquarters in Shenzhen, a distance of well over 1,000 km. There, using a machine that utilizes DNA nanoball and combinatorial probe–anchor synthesis technologies, the researchers generated short reads from which genomes for 761 of the samples were produced. These represent 689 species from 137 families and 49 orders; 54 terabytes of sequence data with an average sequencing depth of 60× per species. Analysis of this huge dataset is still ongoing, but so far genome and chloroplast sequence data have enabled the molecular identification of 257 plants at the species level and 504 at the family level.

Despite its size, this project's primary goal was to test the feasibility of the approach for even larger-scale genome sequencing. The lessons learned from sequencing an entire garden will be invaluable for global scale sequencing projects, such as the 10,000 Plant Genomes Project (<https://db.cngb.org/10kp/>), or the even more ambitious Earth BioGenome Project (<https://www.earthbiogenome.org/>). Nevertheless, this research provides a valuable resource for botanists worldwide as, along with the sequence data, digitized images of all the specimens are being made available.

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