

Crop genomes and beyond

Increasing amounts of crop genomic resources, along with new technical achievements in genome analysis, can facilitate basic and translational research in agriculture, and expand the ability to meet the global challenge of food production and security.

Agricultural genomics has been one of the essential areas in *Nature Genetics*. In the wake of the growing number of reference genomes or resequencing studies of major crops published in recent years, single reference genomes appear to be inadequate in representing the genomic diversity of each species. Pan-genomes have become important resources for agricultural genomics research. Currently, pan-genomes have been assembled for a wide range of species including bacteria, humans and plants. In particular, crop genomics has expanded rapidly in this pan-genome era, with the publication of pan-genome assemblies for various plant species, such as rice (Q. Zhao et al. *Nat. Genet.* **50**, 278–284; 2018) and tomato (M. Alonge et al. *Cell* **182**, 145–161.e23 and L. Gao et al. *Nat. Genet.* **51**, 1044–1051; 2019). The available sequences of crop genomes and pan-genomes have dramatically accelerated agricultural research. Pan-genomes provide new genetic information that is absent in some of the single reference genomes, and thus these assemblies are able to capture more genetic variations within a species. However, to better catalog and interpret crop pan-genome data, new analytical approaches will need to be developed.

Continual efforts are being made to expand the assemblies of reference genomes to multiple lines of a particular crop. In this issue of *Nature Genetics*, Haberer et al. report *de novo genome assemblies* of four European flint maize lines and a comparison with two US Corn Belt genomes, providing insights into the dynamics of intraspecies variation in repeat and gene content in maize genomes. This work makes an important contribution to the maize genome collection, including both dent and

flint corns. Earlier this year, two studies contributed to major progress in cotton genomics. Huang et al. (*Nat. Genet.* **52**, 516–524; 2020) reported the assembly of the first *Gossypium herbaceum* genome and improved assemblies of *Gossypium arboreum* and *Gossypium hirsutum* genomes, followed by analyses of the phylogenetic relationships and origin history of cotton A genomes. Chen et al. (*Nat. Genet.* **52**, 525–533; 2020) performed sequencing and analysis of the genomic diversification of five allopolyploid cotton species, providing insights into polyploidy genome evolution and epigenetic landscapes for cotton improvement. These high-quality reference genomes will enable further studies on genomic diversity, genome evolution and adaptation, or the genetic basis of agricultural traits.

The current age of big data presents analytical challenges that require the development of new technologies. Advances and innovations in experimental and computational approaches have facilitated basic research in crop genomics. For example, Voichek and Weigel (*Nat. Genet.* **52**, 534–540; 2020) have developed a new *k*-mer-based genome-wide association approach and applied the method to 2,000 phenotypes in *Arabidopsis thaliana*, tomato and maize, detecting new associations with structural variants and with regions missing from reference genomes. Continued development and optimization of computational methods will be necessary to increase the accuracy and efficiency with which genomic or phenotypic data can be analyzed and interpreted.

New genomic resources and analytical approaches can provide fundamental and translational potential for crop improvement, would will help address

some of the global challenges currently faced by society. Under the pressures of population growth and climate change, the question of how to sustainably feed the world has become a priority. The rapid growth of genomic data has led to major discoveries regarding the genetic basis of plant physiological traits, including flowering, yield increase, fruit quality or disease resistance. The development of improved crops will continually contribute to food production and security, and expand the ability to meet the global food demand. In a better future for all, there should be zero hunger—one of the *Sustainable Development Goals* set by the United Nations.

We are in an exciting time for crop genomics, with increasing diversity and innovation in study design and approach. New technologies have been developed for assembling haplotype-resolved sequences from polyploid genomes. Genome-editing tools have been utilized in crop species to target desired genes and improve agricultural traits. Crop pan-genomes have improved the understanding of genome structural variations within the genus and will potentially revolutionize the future directions of crop genomic studies. Science built on genomic resources and technological innovations requires smooth exchange of data and research participation from the global scientific community. We look forward to seeing the different ways in which pan-genome data can be used for promoting better agriculture, food security and healthy environments. □

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