Technologies to boost breeding

Breeding crops with a high yield and superior adaptability is vital to maintaining global food security. New technologies on multiple scales are re-engineering traditional plant breeding to meet these challenges.

Although practised for thousands of years, crop breeding remains a demanding and time-consuming task. A major problem is the long generation time of crops, as breeding needs frequent crossing and selfing. This issue of *Nature Plants* reports a powerful method to accelerate breeding¹. The technical rationale is to shorten the generation cycle by extending the photoperiod using supplemental LED lighting. This represents an intriguing step forwards, but is only one of many technological breakthroughs that promise to boost modern breeding.

Breeding is nothing more nor less than directed evolution under artificial selection. Significant progress has been made in conventional breeding methods by utilizing desirable genetic variations. Semi-dwarfness was bred into modern rice and wheat varieties, leading to high-yield and lodging-resistant varieties; maize was biofortified with increased beta-carotene; the non-ripening tomato was developed with extended shelf-life. These agronomically desirable traits revolutionized our food production but the alleles underlying them were identified later.

Most agronomic traits have a complex genetic nature; what may seem to be simple traits rely on the combination of multiple genes. Worse still, most genes display pleiotropic effects so improving one trait can adversely affect others. A breeder's main task is labour-intensively seeking the optimal combination of genes for particular conditions.

The development of molecular and quantitative genetics offers a good opportunity to accelerate breeding by selecting either for known genes or quantitative trait loci using genetic markers, rather than effects on phenotypes. Last year Zeng et al. reported the development of super rice varieties based on known elite alleles that are associated with grain quality and yield by crossing three parental lines in five years². This was a demonstration of the development of elite crop varieties through well-designed marker-assisted selection (MAS), the availability of high-throughput genotyping making the MAS simpler to implement.

Another route is to harness heterosis. Hybrid breeding revolutionized agriculture in the twentieth century. In 1974 the first hybrid rice variety was released in China, leading to a yield gain of 20–30%. The use of heterosis in maize breeding is even older. In the early 1900s, maize hybrids were already commercialized due to their superior performance. No single gene or subset of genes can explain heterosis in all systems. As Xuehui Huang and colleagues showed in 2016, different rice hybrid breeding systems used different loci³.

Despite the success of conventional and hybrid breeding, yield increases may have plateaued for staple crops (see for example <http://go.nature.com/2ASJeK> or <http://go.nature.com/2CzBtff>). This is surprising given that scientists have uncovered many genes that are claimed to increase yield. Desirable alleles may be lacking or existing gene pools underexplored; alleles found by functional studies to affect phenotypes may be disappointing when bred into commercialized varieties; polyploid crops can be resistant to breeding gain and efficient methods of selection may be lacking. Looking forwards, genome editing and genomic selection may boost breeding.

Traditional mutagenesis methods produce random mutations across genomes, but these mutant alleles are rarely agronomically meaningful. Etienne Bucher and colleagues recently proposed a method for stress-controlled mobilization of retrotransposons⁴, representing a semi-targeted approach for generating new mutations. Targeted mutagenesis technologies are now widely used in plants, especially the CRISPR technologies, which can generate desirable mutations in a swift and convenient manner. For example, Caixia Gao and Jinlong Qiu showed that genome editing can engineer three homoalleles simultaneously in hexaploid wheat to confer resistance to powdery mildew⁵. By using single guide RNAs (sgRNAs) targeting virus DNA, CRISPR can also engineer plant resistance against viruses^{6,7}.

For more complex traits, if the regulatory genes or sequences have been characterized CRISPR can be used in combination with

genetic design to generate a series of alleles with a continuous range of phenotypes for screening, as demonstrated recently by Zachary Lippmann's group⁸. They showed rapid generation of *cis*-regulatory alleles in tomato that confer a continuum of phenotypic variation for yield-related traits. The growing toolbox of genome editing will allow the generation of more variations, providing even greater potential for producing desirable agronomic traits.

Genomic selection (GS), is theoretically similar to MAS but it uses high-density genome-wide markers. GS employs predictive computational models that are developed from a training population to make genome-wide predictions of phenotypes in a breeding population. Published GS examples often use biparental or multiparental populations.

Another typical application of GS is to turbocharge underexploited genebanks. In 2016, Jianming Yu's group showed that high-accuracy models can be developed to predict the traits of sorghum accessions in gene banks, demonstrating a strategy to assess and utilize valuable but poorly explored germplasms⁹. The same year saw genomic predictions of wheat landraces, and soybean accessions although with comparatively lower accuracies. High-throughput phenotyping platforms provide an opportunity to develop accurate prediction models at a lower cost.

This is an exciting time with new technologies to accelerate breeding, and innovations continuing to be made. Let us hope that it will not be long before these developments create a new revolution in agriculture. □

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References

1. Watson, A. et al. *Nat. Plants* <https://doi.org/10.1038/s41477-017-0083-8> (2018).
2. Zeng, D. et al. *Nat. Plants* **3**, 17031 (2017).
3. Huang, X. et al. *Nature* **537**, 629–633 (2016).
4. Thieme, M. et al. *Genome Biol.* **18**, 134 (2017).
5. Wang, Y. et al. *Nat. Biotechnol.* **32**, 947–951 (2014).
6. Ji, X. et al. *Nat. Plants* **1**, 15144 (2015).
7. Baltes, N. J. et al. *Nat. Plants* **1**, 15145 (2015).
8. Rodríguez-Leal, D. et al. *Cell* **171**, 470–480 (2017).
9. Yu, X. et al. *Nat. Plants* **2**, 16150 (2016).