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# Editorial overview: 21st Century solutions for crop improvement

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After receiving the invitation to co-edit this special issue, we both thought that over two decades in would be a good timepoint to provide an 'on the fly' assessment of 21st century plant biotechnology. We were as one in believing that Clustered Regularly Interspersed Short Palindromic Repeats (CRISPR)/CRISPR-associated system technology was a dominant force here, but equally that a number of other technologies facilitating *de novo* domestication [1], including both the intellectual paradigm shift this engendered as well as the near-mandatory need to expand our capacity of transformation and the need to embrace artificial intelligence in order to accelerate breeding in the hope of meeting what are likely the greatest societal challenges of our generation(s). In this brief editorial, we intend not only to highlight what is covered in this issue but simultaneously to address why it is essential to meeting these challenges.

As stated above, CRISPR-based technologies dominate current high-profile works in plant biotechnology, hence, our choice to include five articles addressing this. While the acceptability, or otherwise, of gene editing is not universal worldwide, a considerable number of companies have already established regulatory procedures for the growth of gene-edited crops [2]. Given the high number of articles in this area, we felt it appropriate to kickoff the issue with the cornerstone review of Capdeville et al. [3], which provides a wonderful state-of-the-art overview of current possibilities providing a 2023 catalog of what is possible alongside an infectiously upbeat outlook for future possibilities of this game-changing tool. Following on from this fundamental review are a series of reviews focusing on the application of CRISPR technologies. In the first of these, Liu et al. detail the use of genome editing in plants paying particular attention to various aspects concerning the large-scale generation of CRISPR variants. They detail the libraries already created and then focus on the evaluation of spatiotemporal expression and the evolution of protein activities [4]. In a companion review, Pan et al. describe how the use of guide RNA libraries in rice and maize have proven instrumental in recent studies facilitating genetic screening as well as both directed and quantitative trait evolution [5]. Rounding of this series of articles (although CRISPR does reappear later!), is the article of Selma et al., which described the use of CRISPR in plant metabolic engineering. As they state, the plant kingdom represents the greatest natural source of added-value compounds [6]. The possibility, therefore, to sustainably engineer this for human needs is therefore vast. In their review, Selma et al. provide a broad review of the use of CRISPR to improve both metabolic and agronomic traits both reviewing past successes and presenting a perspective for their future application.

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*De novo* domestication has received considerable interest — particularly due to the expanding human population and the adverse impact of climate change with respect to crop yield [7]. The review by Ahn et al. provides comprehensive insight into areas that should be considered for ideotype selection in soybean [8]. In it, they detail the complex intellectual process that is necessary to correctly identify the important domestication traits that should be introduced using soybean as a case study. Having acquired such ideas from a technical perspective, the major hurdle remains transformation, unless the introgression of domestication genes is attempted [1]. In their review, Lee and Wang explain how morphogenic transcription factors, including BABY BOOM, WUSCHEL, and GROWTH- REGULATING and INTERACTING FACTORS, greatly enhance plant transformation efficiency [9]. They both provide a detailed review of how this is achieved as well as listing the species recalcitrant to transformation that this approach has aided. While the use of the transcription factors described by Lee and Wang is clearly expanding the number of transformable species, this has not yet been universally shown to be possible, let alone widely adopted. For this reason, the use of other methods for confirming gene function, including transient expression systems, has proven highly useful for up- or downregulation of protein expression. For more subtle-based level changes, Alamillo et al. define CRISPR/Cas9 of hairy root cultures as a highly powerful strategy. They review this approach focusing on the transformation-recalcitrant legumes and describe for this strategy could inform future crop improvement strategies [10].

A massive current challenge is feeding more people on less land and this will require a dramatic acceleration of our breeding programs. Great promise in this direction comes from machine learning that should obviate the need to test all breeding outcomes in practice and rather to focus on the best-case scenarios. Here, we have assembled three papers that cover this area. In the first of these, Hu et al. describe how genomics and deep machine learning are highly complementary in that both are data-driven fields [11]. They highlight the use of the latter in regulatory genomics, that is, functional noncoding DNA-regulated gene expression. For this purpose, they focus on two emerging trends: the modeling of very long input sequences and the balance of model predictability and interpretability, given the latter exhibits greater capability to meet biological demands. The second, that of Guo and Li, details progress in phenotype prediction via machine learning categorizing such predictions as those relying on genotypic information, those on environmental information, and those using both types of information. In doing so, they review both the potential of the approach and highlighting the perspective of this nascently developing field [12]. Finally, the review of Ferrao et al., which reviews the emergent use of machine learning in applications to improve the flavor and nutritional content of horticultural crops [13]. This is partially driven by increased consumer demand for quality foodstuffs resulting in a paradigm shift for breeders who had previously focused largely on yield. The problem with breeding for flavor and nutrition is that experimental methods of testing for these characteristics are costly and time-consuming. Ferrao et al. discuss how machine learning approaches can complement such methods and indeed even reduce their scope to more manageable levels rendering breeding for quality far more tractable.

A field recently emerging in the microbial sciences is systems metabolic engineering wherein traditional metabolic engineering is complemented with systems biology, synthetic biology, and evolutionary engineering. In

their review, Li et al. discuss how this approach can be used for high-oil maize breeding [14]. In doing so, they both provide a historical overview of both the need for high-oil maize and the relative success of achieving it to date before suggesting strategies based on systems metabolic engineering by which understanding achieved in other traditional oil crops can be harnessed in the improvement of the world's number-one crop. Another tool to enhance breeding that has undergone a renaissance in recent years is that of apomixis — a process of asexual reproduction that enables us to bypass meiosis and thereby fix any elite genotype. The review by Xiong et al. provides a 21st century update on this long-studied phenomenon [15]. It covers the little that is known concerning its origin and dynamics as well as the limited success of introducing apomixis by introgression breeding before providing a perspective on the evolving strategy of synthetic apomixis covering both the state-of-the-art and future perspectives of this highly important biotechnological tool.

This collection concludes with three stand-alone articles covering plant synthetic biology, single-cell analysis, and gapless-genome sequencing. In the first of these, Rizzo et al. provide a rebuild of the classical microbiological workflow in a manner that renders it appropriate to plants [16]. In addition, they review several recent examples of this approach as well as documenting a clear perspective as to how such approaches should best develop in the future. A further currently greatly expanding aspect of plant biotechnology is that afforded by single-cell analysis. This emerging field has obtained massive recent research interest across the biological sciences and a number of papers have demonstrated that it provides considerable clues to developmental progression in plants [17,18]. However, in their forward-looking review, Xu and Jackson argue compellingly that functional analysis alongside single-cell analysis is a must as without such analyses, the biological relevance of changes observed within expression atlases is questionable [19]. This challenge also likely needs to be addressed by *de novo* domestication that would allow development of crops to better fit their current or future environments. The review of Zhang et al. [20] provides a clear overview of this approach, including their own work in domesticating wild rice [21]. Importantly, they also provide a forward-looking perspective for this emergent field, which provides useful guidelines as to how it can be best utilized.

Finally, we come to gapless-genome sequencing. An obvious prerequisite for gene-editing-based *de novo* domestication is a genome sequence for the wild or partially cultivated species. Next-generation sequencing

has dramatically advanced our portfolio of sequenced species with over 1000 species being documented as having high-quality genome sequences [22,23]. While the breadth of sequencing as well as the utility of pan-genomes have been very frequently reviewed, the recent optimization of genome sequencing, namely the gapless- or telomere-to-telomere sequence, has not. In their review, Gladman et al. detail the development of such approaches as well as providing a forward-looking perspective as to how this field is likely to develop [24].

## Declaration of Competing Interest

The authors declare no competing interests.

## References

1. Fernie AR, Yan J: **De novo domestication: an alternative route toward new crops for the future.** *Mol Plant* 2019, **12**:615-631.
2. Buchholzer M, Frommer WB: **An increasing number of countries regulate genome editing in crops.** *New Phytol.* (1) 2023, **237**:12-15.
3. Capdeville N, Schindele P, Puchta H: **Getting better all the time — recent progress in the development of CRISPR/Cas-based tools for plant genome engineering.** *Curr Opin Biotechnol* 2022, **79**:102854.
4. Liu T, Zhang X, Li K, Zhing D, Deng Q, Lu Y: **Large-scale genome-editing in plants: approaches, applications and future perspectives.** *Curr Opin Biotechnol* 2023.
5. Pan C, Li G, Bandyopadhyay A, Qi Y: **Guid RNA library based CRISPR screens in plants: opportunities and challenges.** *Curr Opin Biotechnol* 2023.
6. Selma S, Ceulemans E, Goossens A, Lacchini E: **CRISPR tools for plant metabolic engineering: achievements and perspectives.** *Curr Opin Biotechnol* 2023.
7. Zsögön A, Peres LEP, Xiao Y, Yan J, Fernie AR: **Enhancing crop diversity for food security in the face of climate uncertainty.** *Plant J* 2022, **109**:402-414.
8. Ahn E, Botkin J, Curtin SJ, Zsögön A: **Ideotype breeding and genome engineering for legume crop improvement.** *Curr Opin Biotechnol* 2023.
9. Lee K, Wang K: **Strategies for genotype-flexible plant transformation.** *Curr Opin Biotechnol* 2023.
10. Alamillo JM, Lopez CM, Martinez Rivas FJ, Torralbo F, Bulut M, Alseekh S: **CRISPR/Cas9 and hairy roots: a perfect match for gene functional analysis and crop improvement.** *Curr Opin Biotechnol* 2023.
11. Hu X, Fernie AR, Yan J: **Deep learning in regulatory genomics: from identification to design.** *Curr Opin Biotechnol* 2023, **79**:102887.
12. Guo T, Li X: **Machine learning for predicting phenotype from genotype and environment.** *Curr Opin Biotechnol* 2023, in press.
13. Ferrao LFF, Dhakal R, Dias R, Tieman D, Whitaker V, Gore MA, Messina C, Resende M: **Machine learning applications to improve flavor and nutritional content of horticultural crops through breeding and genetics.** *Curr Opin Biotechnol* 2023, in press.
14. Li H, Fernie AR, Yang X: **Using systems metabolic engineering strategies for high-oil maize breeding.** *Curr Opin Biotechnol* 2023.

15. Xiong J, Hu F, Ren J, Huang Y, Chaolei L, Wang K: **Synthetic apomixis: clonal seeds to fix heterosis.** *Curr Opin Biotechnol* 2023.
16. Rizzo P, Chavez BG, Dias SL, D'Auria JC: **Plant synthetic biology: from inspiration to augmentation.** *Curr Opin Biotechnol* 2023.
17. Thieme CJ, Rojas-Triana M, Stecyk E, Schudoma C, Zhang W, Yang L, Miñambres M, Walther D, Schulze WX, Paz-Ares J, *et al.*: **Endogenous Arabidopsis messenger RNAs transported to distant tissues.** *Nat Plants* 2015, **1**:15025.
18. Otero S, Gildea I, Roszak P, Lu Y, Di Vittori V, Bourdon M, Kalmbach L, Blob B, Heo JO, Peruzzo F, *et al.*: **A root phloem pole cell atlas reveals common transcriptional states in protophloem-adjacent cells.** *Nat Plants* 2022, **8**:954-970.
19. Xu X, Jackson D: **Single-cell analysis opens a goldmine for plant functional studies.** *Curr Opin Biotechnol* 2023.
20. Zhang J, Yu H, Li J: **De novo domestication: retrace the history of agriculture to design future crops.** *Curr Opin Biotechnol* 2023, in press.
21. Yu H, Lin T, Meng X, Du H, Zhang J, Liu G, Chen M, Jing Y, Kou L, Li X, *et al.*: **A route to de novo domestication of wild allotetraploid rice.** *Cell* 2021, **184**:1156-1170 e1114.
22. Purugganan MD, Jackson SA: **Advancing crop genomics from lab to field.** *Nat Genet* 2021, **53**:595-601.
23. Gui S, Martinez-Rivas FJ, Wen WW, Meng M, Yan J, Usadel B, Fernie AR: **Going broad and deep: sequencing driven insights into plant physiology, evolution and crop domestication.** *Plant J* (3) 2023, **113**:446-459.
24. Gladman N, Goodwin S, Chougule K, McCombie WR, Ware D: **Era of gapless plant genomes: Innovations in sequencing and mapping technologies revolutionize genomics and breeding.** *Curr Opin Biotechnol* 2023.