



SHORT COMMUNICATION

Evolving a synthetic ideotype in sorghum (*Sorghum bicolor* L. Moench.)

V. G. Shobhana* and N. Manikanda Boopathi

Department of Plant Biotechnology, Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore-641003, India.

Edited by:

Dr K. Ashokkumar, Gandhigram Rural Institute-Deemed to be University, Dindigul, TN, India

Reviewed by:

Dr S. Shanmugam, Department of Botany, Thiagarajar College, Madurai, Tamil Nadu, India; Dr R. Sharmela, Gandhigram Rural Institute-Deemed to be University, Dindigul, India.

Article history:

Received: May 18, 2026

Accepted: June 22, 2026

Published: June 30, 2026

Citation:

Shobhana, V. G., & Boopathi, N. M. (2026). Evolving a synthetic ideotype in sorghum (*Sorghum bicolor* L. Moench.). *Journal of Current Opinion in Crop Science*, 7(2), 123-135.

<https://doi.org/10.62773/jcocs.v7i2.406>

ABSTRACT

Sorghum, the fifth most cultivated crop worldwide, is vital for food, fodder, fuel, and industrial applications. Developing multi-stress tolerant and nutrient-rich sorghum lines remains a central breeding objective. This proposal outlines the creation of a customized synthetic sorghum zygote, regenerated *in vitro* into plantlets and released as cultivable varieties within a shortened timeframe. Using the reference genome (BTx623, ~732 Mbp), alleles linked to yield, drought tolerance (PIN genes), pest resistance (shoot fly), disease resistance (anthracnose), mineral density (Fe/Zn transporters), and quality traits are mined *in silico* from mapping populations and wild races. These alleles are sequentially assembled across ten chromosomes into designed haplotypes, targeting SVs, PAVs, SNPs, InDels, and gCNVs. The reconstructed genome is synthesized via molecular DNA printing, converted into synthetic zygotes, and regenerated through tissue culture. Stabilized lines are advanced via speed breeding and validated in multi-location trials, aiming to deliver a “synthetic ideotype” sorghum with enhanced resilience.

*Corresponding author e-mail address: vgshobhana@gmail.com (V. G. Shobhana)

Keywords: allele mining, sorghum, speed breeding, synthetic embryo, tissue culture

INTRODUCTION

Sorghum (*Sorghum bicolor* L. Moench) is ranked as the fifth most cultivated cereal worldwide, following maize, rice, wheat, and barley (Godfray et al. 2010; FAO, 2021). Its versatility is unmatched: it serves as a staple food in semi-arid regions, a source of fodder for livestock, a raw material for biofuel production, and a key ingredient in brewing and sweetener industries (Figure 1). Sorghum's resilience to drought and marginal soils has made it indispensable in regions where other cereals fail, particularly across sub-Saharan Africa and South Asia. Yet, despite its adaptability, sorghum yields remain relatively low compared to other cereals, and nutritional deficiencies, especially in iron (Fe) and zinc (Zn), persist among populations that depend on it as a dietary staple (Mace et al., 2013; Connorton et al., 2017).

Traditional sorghum breeding has focused on improving yield, salt tolerance, drought tolerance, and resistance to pests such as shoot fly (*Atherigona soccata*) and diseases like anthracnose (*Colletotrichum graminicola*) (Figure 2) (Prom et al., 2009; Aruna et al., 2011; Ashraf & Foolad, 2013). However, the polygenic

nature of these traits, coupled with sorghum's large and complex genome (~732 Mbp), has slowed progress (Paterson et al., 2009). Marker-assisted selection and genomic selection have accelerated trait introgression, but the timelines for developing stable, multi-trait cultivars remain long—often spanning decades.

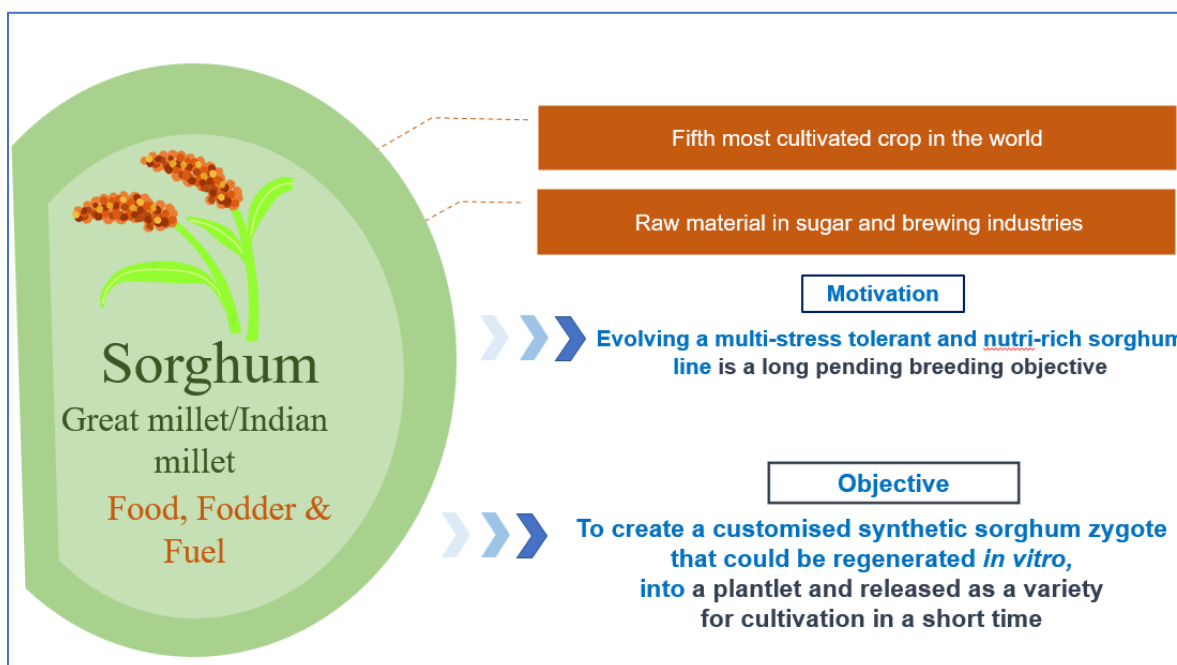


Figure 1. Global importance of sorghum

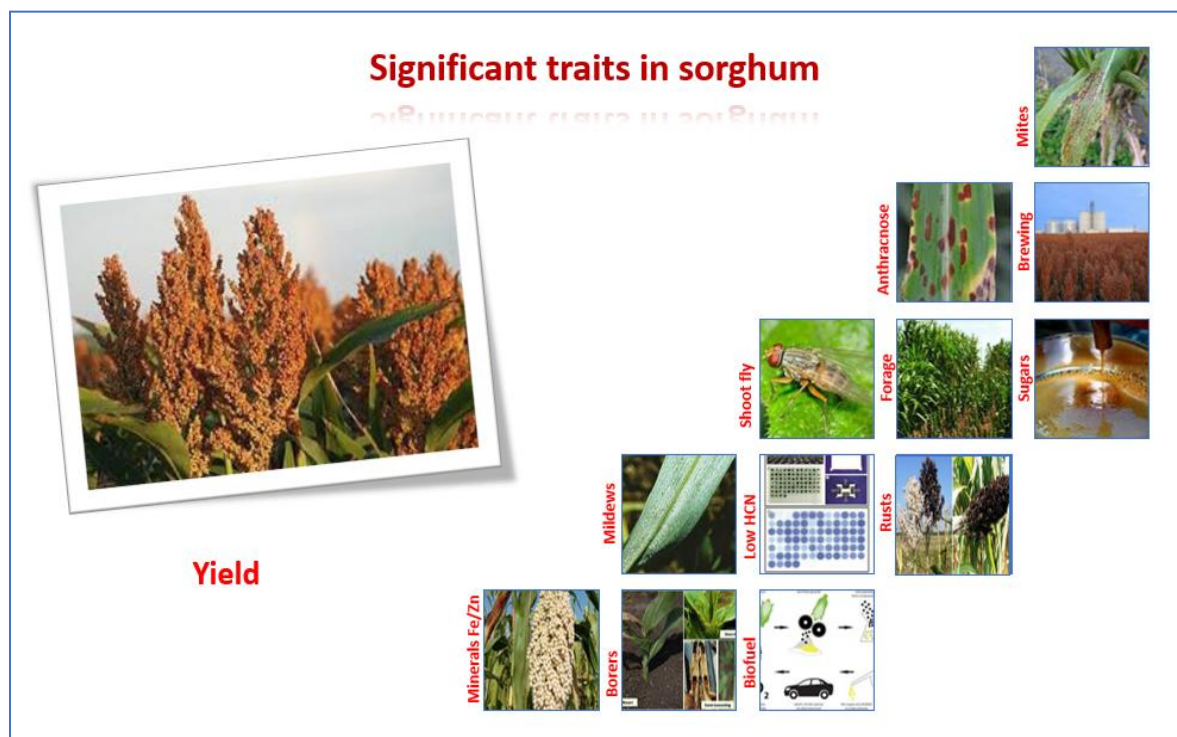


Figure 2. Significant commercial traits in sorghum

The challenge is compounded by the need to integrate multiple traits simultaneously: yield stability under drought, pest and disease resistance, and micronutrient enrichment. Conventional breeding pipelines struggle to achieve this integration efficiently. Thus, there is a pressing need for transformative approaches that compress breeding timelines while enabling precise trait stacking.

Synthetic biology offers a radical departure from conventional breeding. Advances in DNA synthesis and molecular printing now allow for the design and assembly of entire genomic regions with unprecedented precision (Shukla et al. 2018; Yang et al., 2019; Bhat et al. 2020; Huang et al., 2021; Yang & Reyna-Llorens, 2023). In parallel, computational tools and curated genomic databases such as SbGDB and SorghumBase provide access to allelic diversity across mapping populations and wild races (McCormick et al., 2018; Shukla et al., 2018; Sattler et al., 2018). Together, these resources enable the conceptualization of a “synthetic ideotype” a plant designed from the ground up by stacking beneficial alleles into engineered haplotypes.

The notion of a synthetic sorghum zygote, printed from DNA and regenerated via tissue culture, represents a paradigm shift in crop improvement. Instead of relying on recombination and selection across generations, breeders could directly assemble genomes with desired traits. This approach could compress breeding timelines from decades to a few years, especially when combined with speed breeding protocols that accelerate generational turnover (Watson et al., 2018; Wang et al., 2020; Hayakawa et al., 2024; Zhang et al., 2024; Prabhu et al., 2026).

The objectives of the synthetic ideotype framework are centered on designing a next-generation sorghum ideotype that strategically integrates multiple resilience and productivity traits. The proposal emphasizes yield stability under variable climates, drought tolerance mediated by PIN gene family regulation (Xu et al., 2015; Jha et al., 2019), pest resistance particularly against shoot fly (*Atherigona soccata*) (Aruna et al., 2011), and disease resistance with a focus on anthracnose (*Colletotrichum graminicola*) (Prom et al., 2009). Additionally, the framework targets micronutrient enrichment through Fe/Zn transporter regulation (Connorton et al., 2017). By mining alleles linked to these traits, assembling them into functional haplotypes, and reconstructing the genome via DNA printing, the framework aims to generate synthetic plantlets that can be rapidly stabilized into lines. These lines will then undergo rigorous multi-location trials to validate their performance across diverse agro-ecological zones, ensuring both adaptability and long-term sustainability.

If realized, the synthetic ideotype framework could revolutionize sorghum breeding by compressing timelines from decades to years, enabling precise trait stacking across multiple stress and nutritional dimensions, and serving as a transferable model for synthetic crop design in other cereals such as rice, maize, and wheat. Beyond sorghum, this approach holds promise for advancing global food security, climate resilience, and biofortification initiatives. The introduction of synthetic ideotypes in crop breeding could mark the beginning of a new era in plant genomics—one where breeders move beyond incremental gains to holistic, engineered solutions for global agricultural challenges (Li et al., 2020).

MATERIALS AND METHODS

Genomic Resources and Data Mining

The foundation of the synthetic ideotype framework lies in the availability of high-quality genomic resources. The sorghum reference genome BTx623 (~732 Mbp) provides a comprehensive map of gene families, structural variants, and regulatory elements (Paterson et al., 2009) (Table 1). Curated databases such as SbGDB and SorghumBase (McCormick et al., 2018) (Figure 3) were employed to identify allelic variants associated with key agronomic traits.

Allele mining

The synthetic sorghum ideotype framework prioritizes key trait categories, beginning with yield stability through loci associated with grain size, panicle architecture, and photosynthetic efficiency. For drought tolerance, it emphasizes PIN gene family members that regulate auxin transport (Xu et al., 2015; Kato et al., 2018). Pest resistance is targeted via alleles conferring resilience against shoot fly (*Atherigona soccata*) (Aruna et al., 2011), while disease resistance focuses on anthracnose resistance loci (*Colletotrichum graminicola*) (Prom et al., 2009). Finally, micronutrient enrichment is addressed through Fe/Zn transporters, notably Yellow

Stripe-Like (YSL) and Fe²⁺ transporters (Connorton et al., 2017), ensuring nutritional enhancement alongside stress resilience.

Table 1. Candidate traits, gene families, and genomic loci mined from sorghum databases

Trait / Objective	Candidate Gene Families / Alleles	Representative Genomic Loci / References	References
Yield stability	Grain size regulators, panicle architecture genes	QTLs on Chr 1, 3, 6	Paterson et al., 2009; Mace et al., 2013
Drought tolerance	PIN gene family (auxin transport)	PIN1, PIN3, PIN5 loci	Xu et al., 2015
Pest resistance	Shoot fly resistance alleles	QTLs mapped in resistant germplasm	Aruna et al., 2011
Disease resistance	Anthraxnose resistance genes	Resistance loci on Chr 5, 9	Prom et al., 2009
Micronutrient enrichment (Fe/Zn)	Yellow Stripe-Like (YSL) transporters, Fe ²⁺ transporter genes	YSL2, YSL3, NRAMP loci	Connorton et al., 2017
Quality traits	Starch biosynthesis genes, protein quality regulators	Wx, SBE, and kafirin loci	McCormick et al., 2018

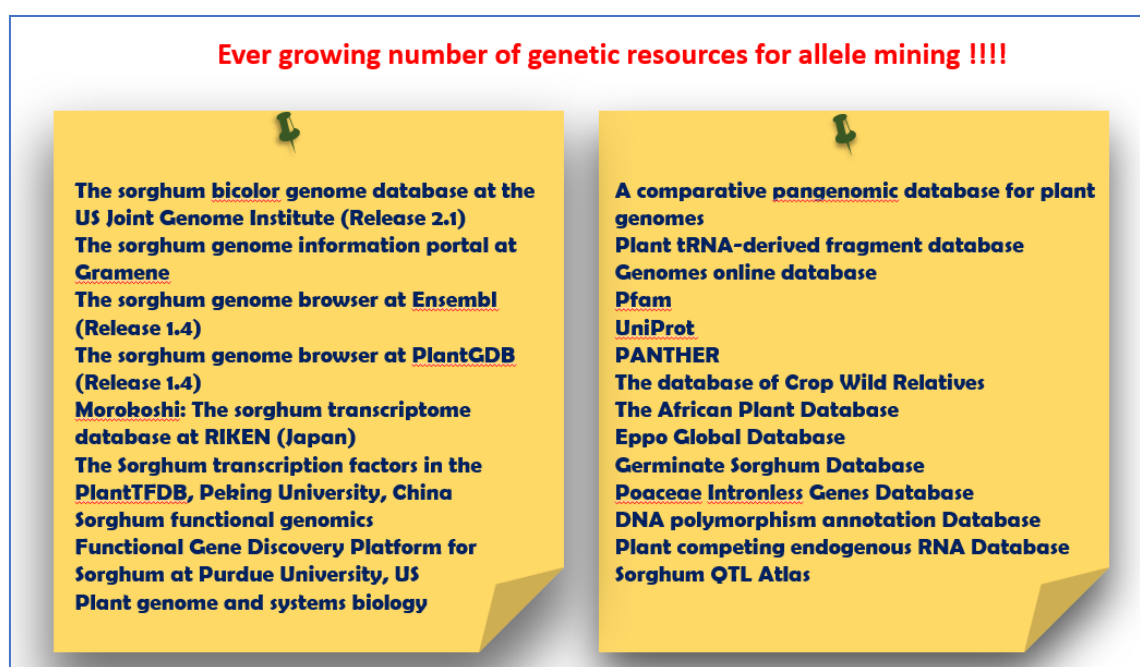


Figure 3. Genetic resources for allele mining in Sorghum

Haplotype Assembly and Genome Design

Allelic variants were computationally stacked into designed haplotypes across all ten sorghum chromosomes, with assembly targeting conserved regions of variation such as structural variants, presence/absence variants, single nucleotide polymorphisms, insertions/deletions, and gene copy number variations (Mace et al., 2013). Advanced bioinformatics pipelines were employed to align candidate alleles, resolve conflicts, and predict epistatic interactions (Figure 4), ensuring coherent haplotype design. These designed haplotypes were then validated *in silico* for stability and compatibility with known regulatory networks (Zhang et al., 2020), providing a computational foundation for synthetic ideotype construction and downstream experimental validation.

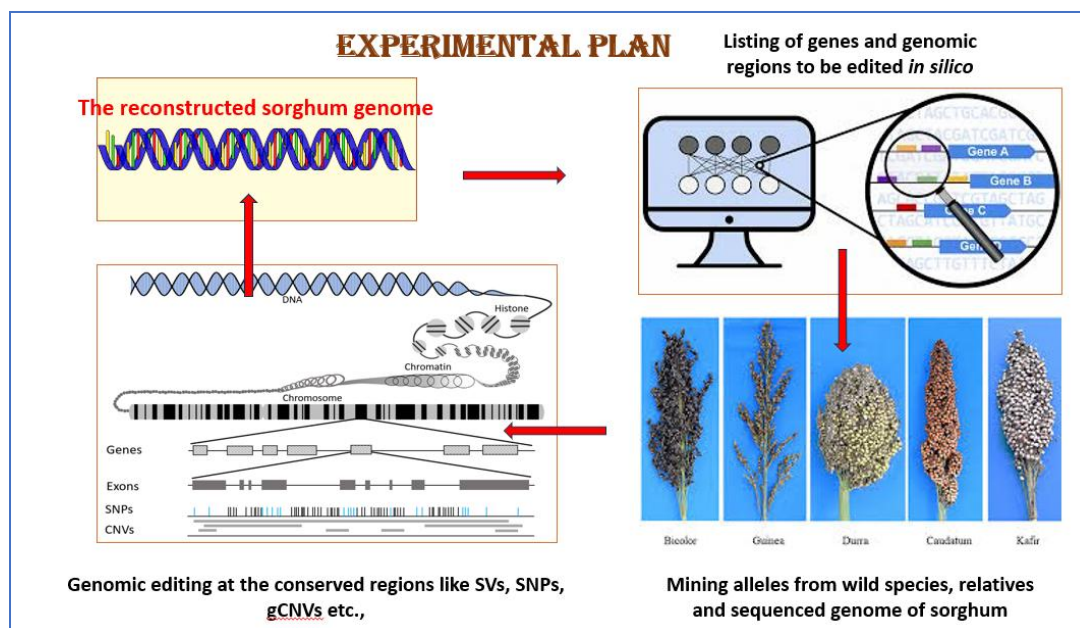


Figure 4. Workflow diagram showing allele mining → haplotype assembly → genome design

DNA Printing and Synthetic Zygote Formation

Advances in molecular DNA synthesis and printing technologies (Huang *et al.*, 2021) enable the reconstruction of large genomic regions. The designed haplotypes were assembled into contiguous DNA sequences, which were then printed using high-fidelity molecular printers (Fig. 5 & 6) (Weising *et al.*, 2005; Sucher *et al.*, 2012). The printed DNA was introduced into artificial zygotic constructs, forming synthetic zygotes. This step represents the conceptual leap from conventional breeding to synthetic biology, bypassing recombination-based allele introgression (Figures 5, 6, & 7).

FORBES > BUSINESS > MANUFACTURING

This Desktop Machine Is About To Transform The Decades-Old DNA Synthesis Industry

John Cumbers Senior Contributor ©
Synthetic biology author.

Follow

Apr 11, 2023, 09:54am EDT

Mind The Gap: On-Demand DNA Printing And Synthetic Biology's Promise

Sylvain Garriel Forbes Councils Member
Forbes Technology Council COUNCIL POST | Membership (Fee-Based)

Dec 6, 2021, 08:30am EST

“Like how a mechanical engineer has a 3D printer to make any part for his machine, a biologist must also be able to make any sequence of her choice to test and effect new ideas easily in her lab within a day !!”

THE ERA OF 3D PRINTING OF DNA

Printers that can now print DNA

Author: Eleanor Garth | Published on: December 2, 2021 | Last updated: May 11, 2022

Figure 5. Schematic of DNA printing and synthetic zygote formation

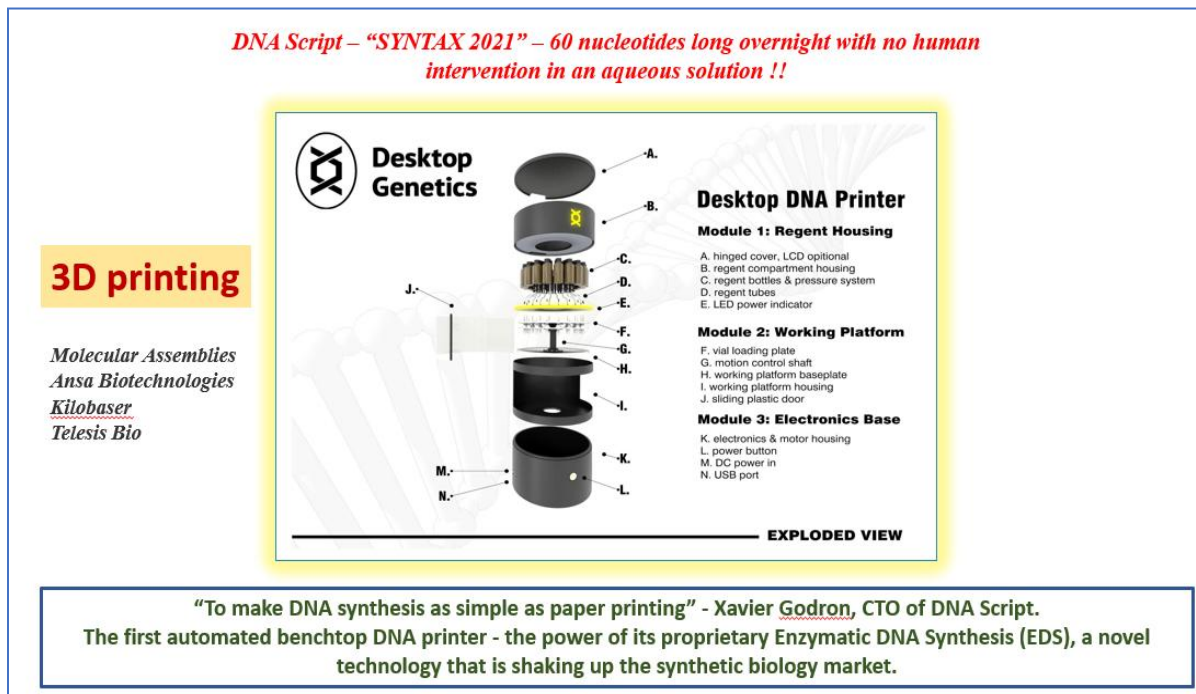


Figure 6. Implications of 3D printing in molecular biology

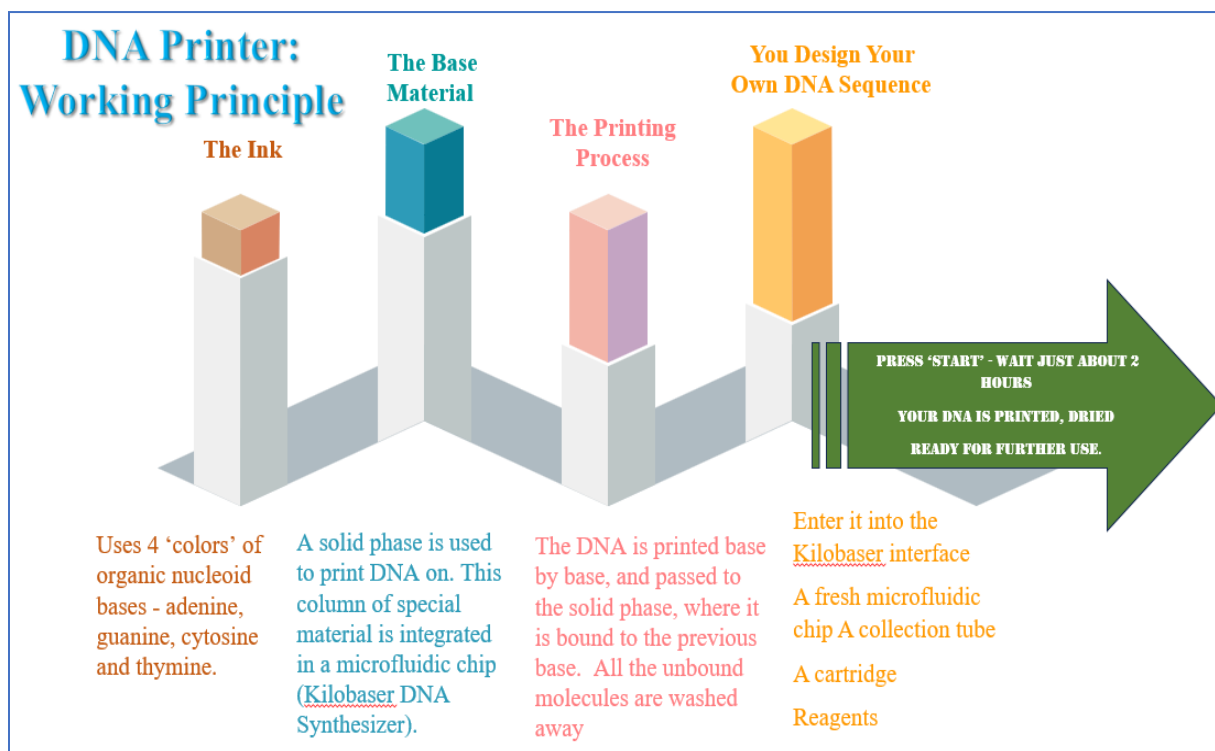


Figure 7. Working principle of DNA printer

Tissue Culture and Plantlet Regeneration

Synthetic zygotes were regenerated into complete plantlets using standardized tissue culture protocols (Sudhakar *et al.*, 2016). Key steps included:

1. Callus induction from synthetic zygotic tissue.
2. Organogenesis and somatic embryogenesis under controlled hormonal regimes.
3. Rooting and shoot elongation in optimized media.
4. Hardening in greenhouse conditions to acclimatize regenerated plantlets.

Protocols were adapted to minimize somaclonal variation and ensure genetic fidelity of synthetic constructs.

Speed Breeding and Generational Advancement

Regenerated plantlets were advanced through successive generations using speed breeding facilities (Watson *et al.*, 2018; Potts *et al.*, 2023; Potts *et al.*, 2023; Chaudhary & Sandhu (2024); Blinkov *et al.*, 2025). Controlled photoperiods, extended light exposure, and optimized nutrient regimes enabled up to six generations per year. This accelerated stabilization of synthetic lines, reducing breeding timelines dramatically compared to conventional methods (**Figure 8**).

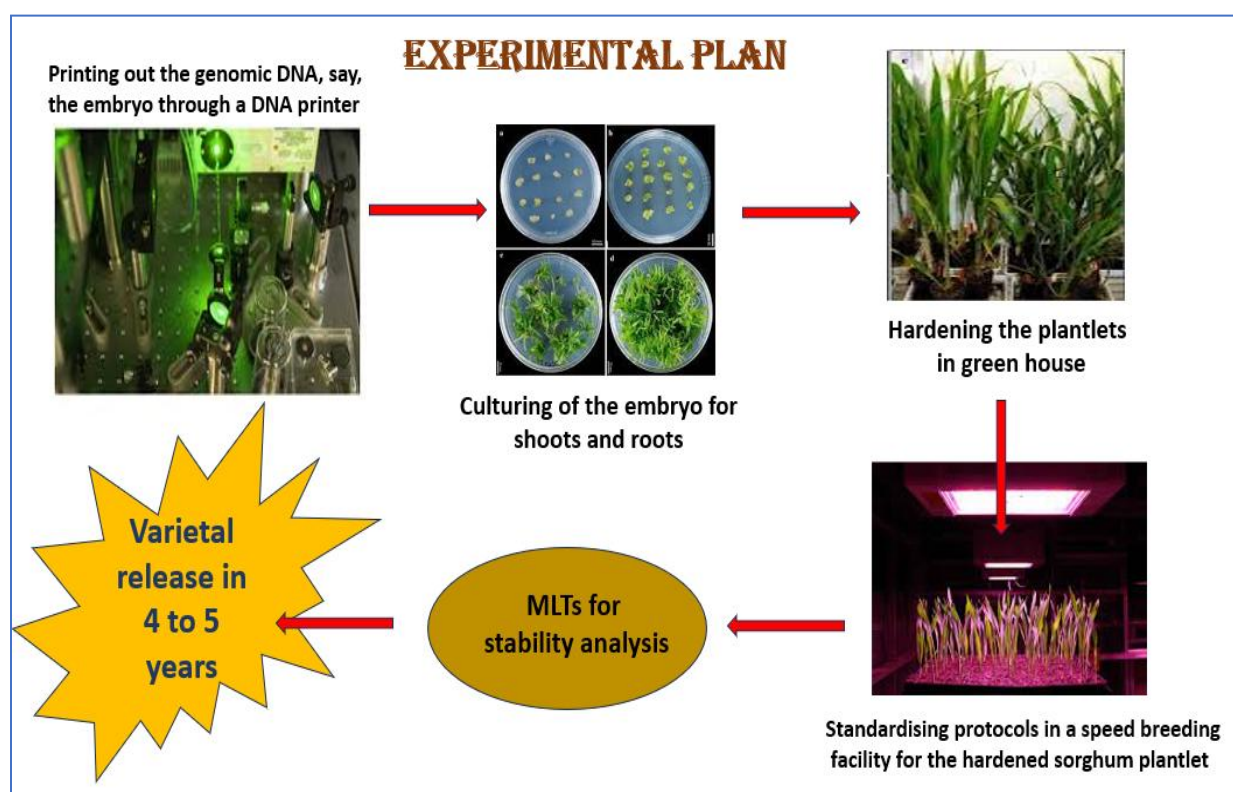


Figure 8. Comparative timeline of conventional breeding vs synthetic ideotype breeding

Validation and Multi-Location Trials

Stabilized synthetic lines were subjected to multi-location trials (MLTs) across diverse agro-ecological zones. Evaluation criteria included:

1. Phenotypic performance: yield, drought tolerance, pest/disease resistance (Furbank & Tester (2011); Blum (2014); Boyer (2010);
2. Nutritional profiling: Fe/Zn content in grains.
3. Environmental adaptability: resilience under variable climates.
4. Biosafety and regulatory compliance: assessment of ecological impact and food safety.

Ethical, Biosafety, And Regulatory Considerations

Given the novelty of synthetic ideotype engineering, biosafety protocols were integrated into all stages. Regulatory frameworks for genetically engineered crops were referenced, with emphasis on transparency, ecological risk assessment, and stakeholder engagement. Ethical considerations included equitable access to synthetic crop technologies and their role in addressing global food security.

RESULTS & EXPECTED OUTCOMES

Synthetic Zygote Regeneration

The proposed workflow anticipates successful regeneration of synthetic sorghum zygotes into viable plantlets. Early proof-of-concept experiments in related cereals suggest that synthetic constructs can be stabilized through tissue culture protocols (Sudhakar et al., 2016). The expected outcome is the establishment of callus cultures from printed DNA constructs, followed by organogenesis and somatic embryogenesis (Figure 9).

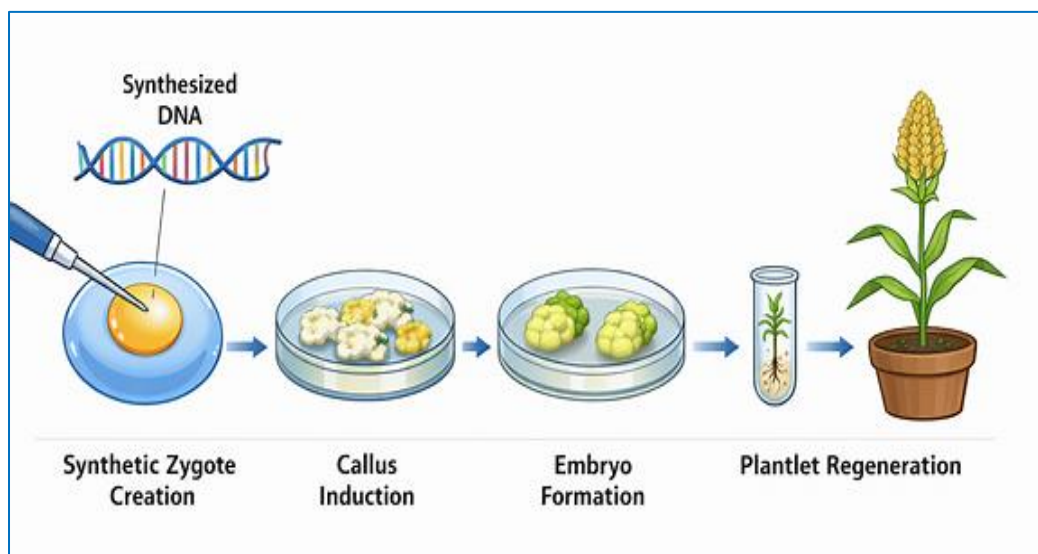


Figure 9. Synthetic zygote regeneration workflow from callus to embryonic tissue and regenerated plantlet.

This infographic visually narrates the four sequential stages of regeneration:

1. Synthetic Zygote Creation – insertion of synthesized DNA into a cell.
2. Callus Induction – formation of undifferentiated tissue in culture.
3. Embryo Formation – development of somatic embryos.
4. Plantlet Regeneration – growth of a complete plant from the embryo.

Trait Integration and Performance

The designed haplotypes are expected to confer multi-trait integration, including:

1. Yield stability: enhanced grain size and panicle architecture.
2. Drought tolerance: improved root architecture and water-use efficiency mediated by PIN gene regulation (Xu et al., 2015).
3. Pest resistance: reduced shoot fly infestation due to stacked resistance alleles (Aruna et al., 2011).
4. Disease resistance: lower anthracnose incidence compared to conventional lines (Prom et al., 2009).
5. Micronutrient enrichment: elevated Fe/Zn concentrations in grains, addressing hidden hunger (Connorton et al., 2017).

Breeding Acceleration

One of the most significant expected outcomes is the compression of breeding timelines. Conventional sorghum breeding requires 10–15 years to develop and release a stable variety. By contrast, synthetic ideotype engineering, combined with speed breeding protocols, could reduce this timeline to 3–5 years (Fig. 10).

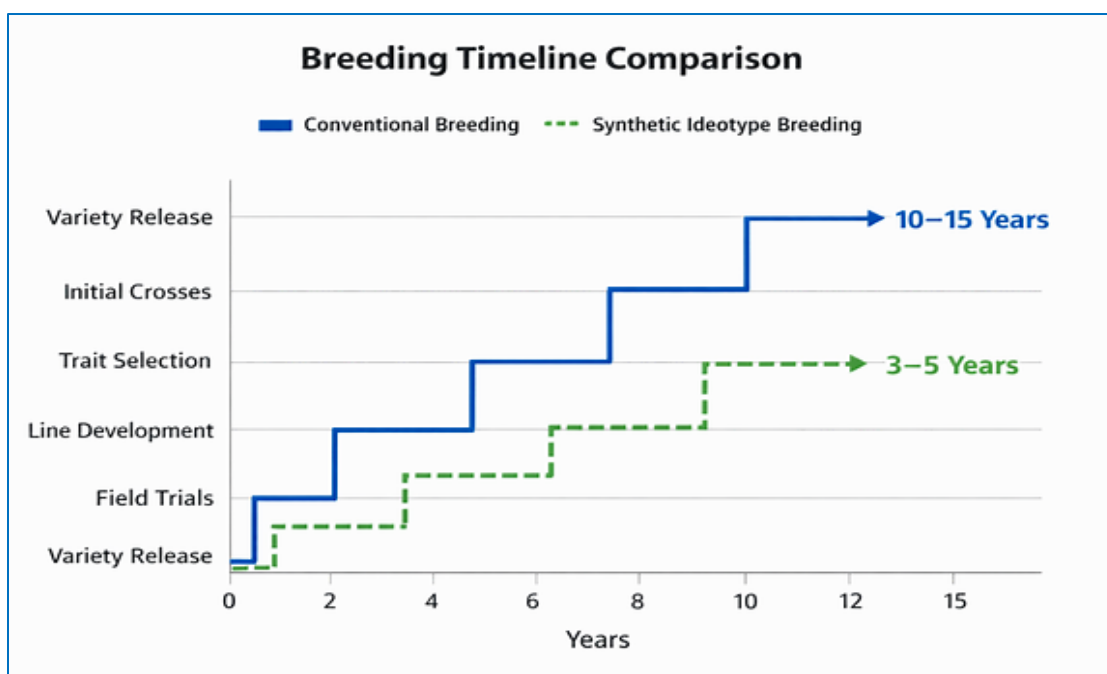


Figure 10. Comparative timeline chart showing conventional breeding vs synthetic ideotype breeding.

This visualization contrasts conventional breeding (10–15 years) with the synthetic ideotype approach (3–5 years), showing each stage from initial crosses to variety release. The blue solid line represents conventional breeding, while the green dashed line represents synthetic ideotype breeding, making the acceleration in timelines clear at a glance.

Scalability and Cross-Crop Potential

While sorghum serves as the model crop in this proposal, the synthetic ideotype framework is inherently scalable. Similar strategies could be applied to rice, maize, and wheat, leveraging their reference genomes and curated databases. The expected outcome is the establishment of a universal synthetic crop design pipeline, adaptable to diverse cereals and potentially to legumes and oilseeds.

Biosafety and Regulatory Pathways

Expected outcomes also include the development of biosafety protocols tailored to synthetic ideotypes. Multi-location trials will provide data on ecological impact, gene flow, and food safety. Regulatory frameworks will need to evolve to accommodate synthetic biology approaches distinct from conventional GMOs.

Broader Impact

The synthetic ideotype framework is expected to:

1. Advance food security by delivering high-yield, stress-tolerant sorghum lines.
2. Promote climate resilience through drought-tolerant cultivars.
3. Address micronutrient deficiencies via biofortified grains.
4. Catalyze innovation in plant genomics and synthetic biology.

DISCUSSION

Feasibility and Technical Challenges

The synthetic ideotype framework proposed here represents a conceptual leap from conventional breeding to synthetic biology. While the theoretical workflow, from allele mining to DNA printing and regeneration, is scientifically grounded, its practical realization faces several challenges.

First, genome complexity remains a major constraint. The sorghum genome, at approximately 732 Mbp, contains extensive structural variation and regulatory networks that govern gene expression and epigenetic modulation (Paterson et al., 2009; Mace et al., 2013). Designing haplotypes that integrate multiple beneficial alleles without disrupting native regulatory architecture requires advanced computational modelling and predictive genomics.

Second, allelic interactions and epistasis may influence trait stability. Stacking alleles for yield, drought tolerance, and pest resistance could lead to unforeseen trade-offs, such as metabolic burden or altered signalling pathways. Integrating systems biology approaches—such as gene network modelling and transcriptomic profiling—will be essential to anticipate and mitigate these effects.

Third, infrastructure requirements pose logistical challenges. Molecular DNA printers capable of synthesizing large genomic constructs are still emerging technologies (Huang et al., 2021). Similarly, tissue culture and regeneration protocols for sorghum, though established (Sudhakar et al., 2016), require optimization for synthetic constructs to ensure genetic fidelity and minimize somaclonal variation.

Comparative Advantage Over Conventional Breeding

Despite these challenges, the synthetic ideotype approach offers distinct advantages over conventional breeding. Traditional methods rely on recombination and selection across multiple generations, often constrained by linkage drag and environmental variability. In contrast, synthetic ideotype engineering enables precise trait stacking and rapid generation advancement through speed breeding (Watson et al., 2018; Gao, 2021).

The comparative timeline (Figure 10) illustrates this acceleration: conventional breeding typically spans 10–15 years, whereas synthetic ideotype breeding could achieve stable variety release within 3–5 years. This compression of timelines has profound implications for responding to climate change, emerging pests, and nutritional demands. Moreover, the approach enhances reproducibility and scalability. Once a synthetic genome design is validated, it can be replicated across laboratories and adapted to other crops with minimal modification. This reproducibility contrasts sharply with the variability inherent in field-based breeding programs.

Biosafety, Ethics, and Regulatory Considerations

The introduction of synthetic ideotypes raises important biosafety and ethical questions. Unlike transgenic crops, which involve the insertion of foreign genes, synthetic ideotypes reconstruct entire genomic regions using native alleles. This distinction may simplify regulatory approval but necessitates new frameworks for evaluating ecological impact and food safety (Ricroch et al., 2016).

Ethical considerations include equitable access to synthetic crop technologies and the potential for intellectual property monopolization. Ensuring open-source genomic designs and collaborative research models will be critical to prevent technological inequity. Furthermore, transparent communication with farmers and consumers will help build trust in synthetic biology applications in agriculture.

Future Directions

The next frontier lies in integrating artificial intelligence (AI) and machine learning (ML) into synthetic ideotype design. Predictive algorithms can model gene interactions, simulate phenotypic outcomes, and optimize haplotype configurations before physical synthesis. AI-driven allele mining could uncover novel gene combinations for stress resilience and nutritional enhancement. Additionally, coupling synthetic ideotype engineering with CRISPR-based genome editing could refine trait expression and regulatory control. CRISPR could be used to validate synthetic constructs or introduce fine-tuned modifications post-regeneration (Liu et al. 2019; Zhao et al., 2019). Long-term, the synthetic ideotype framework could evolve into a universal crop design platform, enabling rapid customization of plant genomes for specific agro-ecological zones. This vision aligns with global initiatives for sustainable agriculture, climate adaptation, and biofortification.

Limitations and Outlook

While the conceptual framework is visionary, it remains largely experimental. The success of synthetic zygote regeneration and genome-scale DNA printing in major crops has yet to be demonstrated. Pilot studies in model species will be essential to validate feasibility.

Nonetheless, the synthetic ideotype concept provides a blueprint for future innovation. It bridges genomics, bioinformatics, and synthetic biology, offering a pathway toward precision crop design. As technologies mature, the integration of computational design, molecular synthesis, and accelerated breeding could redefine the pace and scope of agricultural improvement.

CONCLUSIONS

The present manuscript outlines a visionary framework for synthetic ideotype engineering in sorghum, integrating genomic mining, DNA printing, tissue culture regeneration, and speed breeding into a unified pipeline. This approach reimagines crop improvement as a design-driven process rather than a generational exercise in selection. By leveraging the reference genome (BTx623), curated databases (SbGDB, SorghumBase), and advanced molecular synthesis technologies, the proposed workflow demonstrates how precision genomics can converge with synthetic biology to accelerate breeding timelines and expand the frontiers of plant innovation. The synthetic zygote concept, printing designed haplotypes and regenerating them into complete plantlets, represents a paradigm shift in agricultural biotechnology. It moves beyond the incremental gains of conventional breeding toward a holistic reconstruction of crop genomes tailored for multi-stress tolerance, nutritional enrichment, and climate resilience. The integration of speed breeding further compresses timelines, enabling rapid stabilization and evaluation of synthetic lines within 3–5 years, compared to the 10–15 years required by traditional methods. While the framework remains largely conceptual, its implications are profound. The successful realization of synthetic ideotypes would transform not only sorghum breeding but also the broader landscape of crop design. It would enable precision stacking of alleles for complex traits, predictive modeling of phenotypes, and scalable replication of optimized genomes across species. Moreover, it would catalyze interdisciplinary collaboration among geneticists, bioinformaticians, molecular biologists, and synthetic biotechnologists.

The challenges, genome complexity, infrastructure, biosafety, and regulatory adaptation—are significant but surmountable. As molecular printing technologies mature and computational design tools evolve, the feasibility of constructing synthetic zygotes will increase. Ethical and regulatory frameworks must evolve in parallel, ensuring transparency, ecological safety, and equitable access to synthetic crop technologies. Ultimately, the synthetic ideotype framework offers a blueprint for the next generation of crop improvement, one that aligns with global goals for sustainable agriculture, food security, and nutritional equity. Sorghum, as a resilient and versatile crop, stands poised to lead this transformation. The vision articulated here invites the scientific community to explore, refine, and realize the potential of synthetic biology in plant breeding, ushering in an era where crops are not merely selected but designed for the future.

ACKNOWLEDGMENTS

Not applicable.

AUTHORS' CONTRIBUTIONS

All the authors contributed equally to this research work.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

ETHICAL APPROVAL

Not applicable.

CONSENT FOR PUBLICATION

Not Applicable.

FUNDING

Funding was not involved in this study.

AVAILABILITY OF DATA AND MATERIALS

All datasets analyzed and described during the present study are available from the corresponding author upon reasonable request

REFERENCES

- Aruna, C., Padmaja, P. G., Subbarayudu, B., & Seetharama, N. (2011). Genetic resistance to sorghum shoot fly. *Indian Journal of Genetics and Plant Breeding*, 71(1), 9-16.
- Ashraf, M., & Foolad, M. R. (2013). Crop breeding for salt tolerance in plants. *Plant Science*, 205-206, 25-38. <https://doi.org/10.1016/j.plantsci.2013.01.006>
- Bhat, B. V., Srinivasan, R., & Rao, M. V. (2020). Advances in plant synthetic biology: From gene circuits to genome design. *Frontiers in Plant Science*, 11, 110. <https://doi.org/10.3389/fpls.2020.00110>
- Blinkov, A. O., Kroupin, P. Y., Dmitrieva, A. R., Kocheshkova, A. A., Karlov, G. I., & Divashuk, M. G. (2025). Speed breeding: Protocols, application and achievements. *Frontiers in Plant Science*, 16, 1680955. <https://doi.org/10.3389/fpls.2025.1680955>.
- Blum, A. (2014). *Plant breeding for stress environments*. Boca Raton, FL: CRC Press.
- Boyer, J. S. (2010). Drought decision-making in crop improvement. *Annual Review of Plant Biology*, 61, 349-372. <https://doi.org/10.1146/annurev-arplant.042809.112213>
- Chaudhary, N., & Sandhu, R. (2024). A comprehensive review on speed breeding methods and applications. *Euphytica*, 220(42). <https://doi.org/10.1007/s10681-024-03300-x>.
- Connorton, J. M., Balk, J., Rodríguez-Celma, J., Harrison, R. J., & Broadley, M. R. (2017). Improving Fe and Zn biofortification in cereals. *Frontiers in Plant Science*, 8, 401. <https://doi.org/10.3389/fpls.2017.00401>.
- FAO. (2021). FAOSTAT: Sorghum production statistics. Food and Agriculture Organization of the United Nations.
- Furbank, R. T., & Tester, M. (2011). Phenomics—Technologies to relieve the phenotyping bottleneck. *Trends in Plant Science*, 16(12), 635-644. <https://doi.org/10.1016/j.tplants.2011.09.005>
- Gao, C. (2021). Genome engineering for crop improvement and synthetic biology. *Annual Review of Plant Biology*, 72, 77-103. <https://doi.org/10.1146/annurev-arplant-081720-010648>
- Godfray, H. C. J., Beddington, J. R., Crute, I. R., Haddad, L., Lawrence, D., Muir, J. F., Pretty, J., Robinson, S., Thomas, S. M., & Toulmin, C. (2010). Food security: The challenge of feeding 9 billion people. *Science*, 327(5967), 812-818. <https://doi.org/10.1126/science.1185383>.
- Hayakawa, T., Suzuki, H., Yamamoto, H., & Mitsuda, N. (2024). Synthetic biology in plants. *Plant Biotechnology*, 41(3), 173-193. <https://doi.org/10.5511/plantbiotechnology.24.0630b>.
- Huang, W., Wang, Y., Wang, J., & Wei, W. (2021). Advances in DNA synthesis and molecular printing technologies. *Nature Reviews Genetics*, 22(10), 637-655. <https://doi.org/10.1038/s41576-021-00392-5>.
- Jha, U. C., et al. (2019). Genomic approaches for improving drought tolerance in sorghum. *Plant Biotechnology Journal*, 17(5), 921-934. <https://doi.org/10.1111/pbi.13020>
- Kato, Y., Miura, K., Sawada, Y., Hirai, T., & Shimizu, H. (2018). Root architecture and drought adaptation in cereals. *Plant Physiology*, 178(1), 35-49. <https://doi.org/10.1104/pp.17.01234>
- Li, J., Zhu, Q., Wang, B., Tan, J., Liu, T., Li, L., & Liu, Y.-G. (2020). Synthetic biology approaches for plant metabolic engineering. *Plant Communications*, 1(2), 100017. <https://doi.org/10.1016/j.xplc.2020.100017>
- Liu, H., Char, S. N., Wei, J., Mu, Q., Li, X., Zhang, Z. J., Yu, J., & Yang, B. (2019). CRISPR/Cas9-based genome editing in sorghum. *Plant Biotechnology Journal*, 17(9), 1851-1853. <https://doi.org/10.1111/pbi.13229>
- Mace, E. S., Tai, S., Gilding, E. K., Li, Y., Prentis, P. J., Bian, L., Campbell, B. C., Hu, W., Innes, D. J., Han, X., Cruickshank, A., Dai, C., Frere, C., Zhang, H., Hunt, C. H., Wang, X., Shatte, T., Wang, M., Su, Z., Li, J., Lin, X., Godwin, I. D., Jordan, D. R., & Wang, J. (2013). Whole-genome sequencing reveals untapped genetic diversity in sorghum. *Nature Communications*, 4, 2320. <https://doi.org/10.1038/ncomms3320>
- McCormick, R. F., Truong, S. K., Sreedasyam, A., Jenkins, J., Shu, S., Sims, D., Kennedy, M., Amirebrahimi, M., Weers, B. D., McKinley, B., Mattison, A., Morishige, D. T., Grimwood, J., Schmutz, J., & Mullet, J. E. (2018). SorghumBase: A comprehensive sorghum genome database. *Plant Journal*, 93(4), 819-831. <https://doi.org/10.1111/tpj.13781>
- Nelson, R. J., Asseng, S., Hammer, G. L., & Reynolds, M. P. (2018). Integrating genomics and phenomics for crop improvement. *Trends in Plant Science*, 23(7), 637-650. <https://doi.org/10.1016/j.tplants.2018.04.005>
- Paterson, A. H., Bowers, J. E., Bruggmann, R., Dubchak, I., Grimwood, J., Gundlach, H., Haberler, G., Hellsten, U., Mitros, T., Poliakov, A., Schmutz, J., Spannagl, M., Tang, H., Wang, X., Wicker, T., Bharti, A. K., Chapman, J.,

- Feltus, F. A., Gowik, U., Grigoriev, I. V., Lyons, E., Maher, C. A., Martis, M., Narechania, A., Otilar, R. P., Penning, B. W., Salamov, A. A., Wang, Y., Zhang, L., Carpita, N. C., Freeling, M., Gingle, A. R., Hash, C. T., Keller, B., Klein, P., Kresovich, S., McCann, M. C., Ming, R., Peterson, D. G., Mehboob ur-Rahman, Ware, D., Westhoff, P., Murat, F., & Messing, J. (2009). The *Sorghum bicolor* genome and the diversification of grasses. *Nature*, 457(7229), 551–556. <https://doi.org/10.1038/nature07723>
- Potts, J., Jangra, S., Michael, V. N., & Wu, X. (2023). Speed breeding for crop improvement and food security. *Crops*, 3(4), 276–291. <https://doi.org/10.3390/crops3040025>.
- Prabhu, V. S., Ashokkumar, K., & Gogulavasan, M. (2026, April). Speed breeding techniques for accelerated crop development. In K. Ashokkumar, G. Arun Prasath, M. Sundaramari, & A. Ramanathan (Eds.), *Trends in agricultural sciences* (pp. 135–143). Beyond Line Publisher. <https://doi.org/10.34293/blp.9789395659581.ch011>
- Prom, L. K., Perumal, R., Erpelding, J. E., Isakeit, T., Montes-Garcia, N., & Magill, C. (2009). Resistance to anthracnose in sorghum germplasm. *Plant Disease*, 93(9), 890–896. <https://doi.org/10.1094/PDIS-93-9-0890>
- Ricroch, A. E., Clairand, P., & Harwood, W. (2016). Plant synthetic biology and regulatory perspectives. *Trends in Biotechnology*, 34(5), 373–378. <https://doi.org/10.1016/j.tibtech.2016.01.007>
- Shukla, V. K., Banerjee, C., Guria, C., & Shukla, P. (2018). Synthetic biology for sustainable agriculture. *Current Opinion in Biotechnology*, 49, 1–7. <https://doi.org/10.1016/j.copbio.2017.07.002>
- Sucher, N. J., Hennell, J. R., & Carles, M. C. (2012). *Plant DNA fingerprinting and barcoding: Methods and protocols*. Springer. <https://doi.org/10.1007/978-1-61779-609-8>.
- Sudhakar, D., Pola, S., Saradamani, N., Ramana, T., & Rao, M. V. (2016). Tissue culture and regeneration protocols in sorghum. *Plant Cell Reports*, 35(6), 1235–1247. <https://doi.org/10.1007/s00299-016-1965-7>
- Watson, A., Ghosh, S., Williams, M. J., Cuddy, W. S., Simmonds, J., Rey, M. D., ... Hickey, L. T. (2018). Speed breeding is a powerful tool to accelerate crop research and breeding. *Nature Plants*, 4(1), 23–29. <https://doi.org/10.1038/s41477-017-0083-8>
- Weising, K., Nybom, H., Wolff, K., & Kahl, G. (2005). *DNA fingerprinting in plants: Principles, methods, and applications*. CRC Press.
- Xu, W., Ding, G., Li, Y., Wang, Q., Li, G., ... Shen, Q. (2015). PIN gene family in sorghum and their role in drought tolerance. *BMC Plant Biology*, 15, 152. <https://doi.org/10.1186/s12870-015-0528-4>
- Yang, J., Zhang, J., Wang, Z., Zhu, Q., & Wang, W. (2019). Synthetic biology for crop improvement: Challenges and prospects. *Plant Biotechnology Journal*, 17(6), 1184–1196. <https://doi.org/10.1111/pbi.13060>
- Yang, J.-S., & Reyna-Llorens, I. (2023). Plant synthetic biology: Exploring the frontiers of sustainable agriculture. *Journal of Experimental Botany*, 74(13), 3787–3790. <https://doi.org/10.1093/jxb/erad223>
- Zhang, D., Xu, F., Wang, F., Le, L., & Pu, L. (2024). Synthetic biology and artificial intelligence in crop improvement. *Plant Communications*, 5(6), 101220. <https://doi.org/10.1016/j.xplc.2024.101220>
- Zhang, Y., Liang, Z., Zong, Y., Wang, Y., Liu, J., ... Gao, C. (2020). Computational design of plant genomes for synthetic biology. *Nature Communications*, 11, 2822. <https://doi.org/10.1038/s41467-020-16605-3>



Copyright: © 2026 by authors. This work is licensed under a Creative Commons Attribution 4.0 International License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.