



Recent Advances in Genomics-Assisted Breeding in Bitter Gourd

*Riya A. Patel¹, Vaishnavi R. Gadge¹, Naresh R. Makwana¹, Rajesh R. Acharya² and Mausami Y. Tandel³

¹Department of Genetics and Plant Breeding, B. A. College of Agriculture, Anand Agricultural University, Anand, Gujarat, India

²Research Scientist (Vegetable), Main Vegetable Research Station, Anand Agricultural University, Anand, Gujarat, India

³Department of Genetics and Plant Breeding, College of Agriculture, Bharuch, Navsari Agricultural University, Gujarat, India

*Corresponding Author's email: riyapatel8419@gmail.com

Bitter gourd (*Momordica charantia* L.) is an economically important cucurbit valued for its nutritional, medicinal and therapeutic attributes. However, genetic improvement through conventional breeding has been constrained by a narrow genetic base, complex inheritance of quantitative traits and significant genotype x environment interactions. Recent advances in genomics-assisted breeding have revolutionized bitter gourd improvement by enabling precise identification and utilization of genomic variation. High-quality reference genomes, including telomere-to-telomere assemblies, together with genome-wide association studies (GWAS), quantitative trait loci (QTL) mapping and functional genomics, have facilitated the discovery of genes governing yield, fruit quality, disease resistance and abiotic stress tolerance. Emerging approaches such as marker-assisted selection, genomic selection, targeted genome editing, speed breeding and high-throughput phenotyping are accelerating cultivar development and improving selection efficiency. Nevertheless, limited transformation efficiency, genotype-dependent regeneration and insufficient integration of multi-omics datasets remain major constraints to the widespread application of these technologies. Future integration of pangenomics, multi-omics, artificial intelligence-assisted breeding and precision genome editing is expected to enhance genetic gain and expedite the development of climate-resilient, high-yielding and nutritionally enriched bitter gourd cultivars.

Keywords: Bitter gourd, GWAS, QTL Mapping, Functional Genomics, CRISPR/Cas9, Speed Breeding

Introduction

Bitter gourd is an important commercial cucurbit of the family *Cucurbitaceae* and Genus *Momordica*. In India, its area and production during 2023-24 was 135 (000' Ha) and 1728 (000' m tonnes) respectively (Anon., 2024). Bitter gourd also known as balsam pear or bitter melon, has long been valued in tropical and subtropical regions for its unique culinary profile and potent medicinal properties. It is an essential component in traditional medicine for treating oxidative stress and diabetes because it is rich in bioactive compounds like vicine, polypeptide-p and charantin. Its breeding has historically been slow, depending on traditional phenotypic selection that was unable to keep up with changing disease pressures and climatic change, despite the gourd's economic and nutritional significance. The area of bitter gourd study has experienced a major transformation in the last few years. Bitter gourd has evolved from an orphan crop to a model for cucurbit genomics thanks to the combination of high-throughput sequencing, accurate genome assembly and sophisticated functional genomics.



Importance

Develops climate-resilient cultivars that are more able to withstand abiotic challenges like heat, drought and salinity. Uses genome editing, genomic selection and marker-assisted selection to increase breeding efficiency. Identifies genes linked to bioactive substances like momordicin and charantin, improving the quality of nutrition and medicine. Promotes sustainable agriculture by creating cultivars that are both ecologically friendly and high-yielding. Aids in the understanding of the interactions between genotype and environment, resulting in the creation of cultivars that perform consistently in a variety of settings and seasons. Provides the basis for upcoming precision breeding techniques including multi-omics-based crop improvement and CRISPR-Cas9 genome editing.

High-Quality Genomic Resources: The T2T Era

A high-resolution reference genome is an essential component of modern genomics-assisted breeding (GAB). Though they frequently had gaps in intricate areas like centromeres and telomeres, early drafts of the bitter melon genome offered preliminary insights. A Telomere-to-Telomere (T2T), gap-free genome assembly for elite cultivars like Y52 was delivered by researchers in 2026, marking a significant milestone. PacBio HiFi and Oxford Nanopore ultra-long sequencing are used in this assembly, which covers 11 chromosomes and is roughly 298.0 Mb in size.

Why T2T Matters

Traditional assemblies often missed repetitive genomic regions in the genome-highly repetitive sequences that actually house critical regulatory elements. The T2T assembly allows for:

- Centromere Mapping: Precise annotation of centromeric regions, which is vital for understanding chromosome segregation and evolution.
- Structural Variant Discovery: Identification of large-scale inversions and deletions that often control complex traits like fruit shape and disease resistance.
- Comprehensive Databases: The establishment of platforms like Bittergourd DB integrates this genomic data with transcriptomic and metabolomic maps.

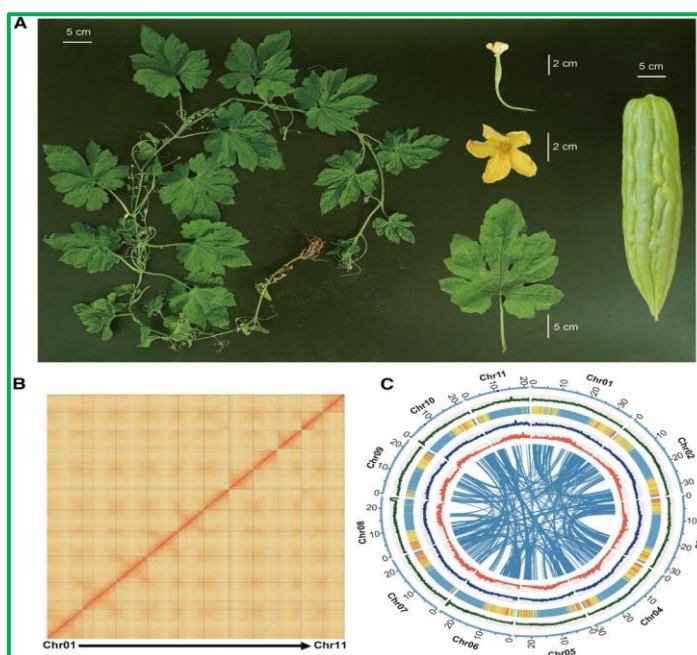


Fig 1: Overview of the gap-free reference genome of bitter melon Y52 (Zhang et al. 2026)

Advanced Trait Discovery through GWAS and QTL Mapping

Limitations in breeding program

- Limited availability of diverse germplasm and large mapping populations
- Low marker density and incomplete genomic resources compared with major crops
- Population-specific QTLs with poor reproducibility across environments
- Strong genotype x environment (G x E) interactions affecting QTL stability
- Limited functional validation of candidate genes identified through GWAS/QTL mapping
- Lack of breeder-friendly, diagnostic molecular markers for routine marker-assisted selection
- Insufficient high-throughput phenotyping for complex quantitative traits

Current Breeding Challenges in Bittergourd

- Narrow genetic diversity in cultivated bitter gourd germplasm
- Complex inheritance of yield, fruit quality and abiotic stress tolerance traits
- Difficulty in pyramiding multiple desirable traits into elite cultivars
- Limited genomic information for economically important traits such as nutritional quality and medicinal compounds (charantin and cucurbitacins)
- Poor integration of genomics with conventional breeding programmes
- Limited multi-location and multi-season validation of marker–trait associations
- Inadequate genomic resources for wild relatives and exotic germplasm

The initial step in GAB is to comprehend the genetic architecture of agronomic characteristics. Researchers have used Quantitative Trait Loci (QTL) mapping and Genome-Wide Association Studies (GWAS) to analyze polygenic traits, going beyond basic Mendelian features. In bitter gourd, several trait-specific genomic regions have been identified through biparental mapping populations, bulked segregant analysis (BSA/BSR-seq) and GWAS. QTLs associated with **fruit length, fruit diameter, fruit tubercle development, rind colour, sex expression, flowering behaviour and yield-related traits** have been reported. Fine mapping of genomic regions governing **gynoecy and sex determination** has been particularly significant because gynoecious lines serve as valuable female parents for hybrid seed production. Recent studies have also identified candidate genes and genomic regions associated with resistance to **Papaya ringspot virus (PRSV)**, powdery mildew and other important diseases, while transcriptome-based analyses have provided insights into genes regulating **charantin biosynthesis, cucurbitacin metabolism and stress-responsive pathways**.

Key loci for the following have been effectively discovered in recent studies:

- **Fruit Morphology:** Using bulked segregant RNA sequencing, genomic areas linked to fruit length and the development of fruit tubercles have been identified.
- **Nutrient Uptake:** Similar multi-omics techniques in bitter gourd are finding regulatory networks for the uptake of Fe, Zn and N in an effort to improve the crop's potential for biofortification, in keeping with more general cereal research.

Functional Genomics: EMS Mutation Libraries

While sequencing tells us *what* is there, functional genomics tells us *what it does*. A major breakthrough in 2026 was the creation of large-scale Ethyl Methanesulfonate (EMS)-induced mutant libraries. One such library consists of over 3,000 M1 plants, with whole-genome resequencing identifying over 76,000 mutations across nearly 14,000 genes. By using a MutMap-based approach, scientists rapidly identified the causal gene *McEGY1*, which is responsible for chlorotic (yellowing) phenotypes in leaves and fruit. This platform allows researchers to "knock out" specific genes to observe their effects on plant health and yield.

Precision Breeding: CRISPR/Cas9 and Genome Editing

The CRISPR/Cas9 system in particular has evolved from a theoretical tool to a useful breeding application. CRISPR enables precise targeted genome editing to the plant's own

DNA without adding foreign genetic material, in contrast to conventional transgenic (GMO) techniques.

CRISPR is being used in bitter melon to target:

Manipulating the biosynthesis of bitterness-related compounds (cucurbitacins) to produce mild cultivars for wider market appeal is one of the consumer traits.

Fruit set and production are directly impacted by yield optimization, which involves modifying hormonal pathways to increase female flower ratios.

Abiotic Stress: Increasing resistance to salinity and drought by focusing on genes related to osmotic control.

Climate Resilience and Nutrient Efficiency

Bitter melon breeding has moved toward resistance since extreme weather events become more frequent due to climate change. The bitter melon is especially vulnerable to water scarcity, which restricts its ability to develop and store nutrients.

Mineral Synergy and Drought Mitigation

Genomic selection aids in the identification of naturally resilient lines, but it functions best when combined with physiological interventions, according to recent research. For example, it has been discovered that applying potassium (K), zinc (Zn), calcium (Ca) and silicon (Si) topically can lessen drought stress by lowering ion leakage and preserving relative water content. The precise transporters and signaling genes that enable some bitter melon cultivars to use these minerals more efficiently under stress are now being identified using genomics methods.

Speed Breeding and High-Throughput Phenotyping

A new variety is released after 8–12 years of traditional breeding. Generation time can be shortened by 2.5 to 5 times with the use of speed breeding, which manipulates temperature and light in controlled conditions.

The procedure is significantly more effective when genomics is added (Genomics-Assisted Speed Breeding or GASB):

1. High-Throughput Phenotyping (HTP): This method quickly evaluates root structure and plant health in real-time using X-ray CT scans and UAV-based multispectral imagery.
2. Early Selection: Breeders employ molecular markers to determine a seedling's "breeding value" within days of germination, rather than waiting for a plant to mature and produce fruit

Future Directions: Super-Pangenome and Multi-omics Integration

The future of genomics-assisted breeding in bitter melon lies in the integration of super-pangenomics with multi-omics approaches. Unlike a single reference genome, a super-pangenome captures the complete genetic diversity of cultivated varieties, landraces and wild *Momordica* species by identifying rare and desired genes, structural variants and novel alleles associated with important agronomic traits. This approach facilitates the discovery of valuable alleles for disease resistance, abiotic stress tolerance, fruit quality and nutritional traits that were lost during domestication.

Complementing pangenomics, **multi-omics integration** combines genomics, transcriptomics, proteomics, metabolomics, epigenomics and phenomics to provide a comprehensive understanding of complex biological processes. In bitter melon, integrated multi-omics can accelerate the identification of candidate genes and regulatory networks controlling economically important traits such as **gynoecy, fruit morphology, cucurbitacin and charantin biosynthesis, disease resistance and tolerance to drought, salinity and heat stress**. The integration of transcriptomic and metabolomic datasets will further enable the elucidation of pathways governing the synthesis of medicinal compounds, while phenomic platforms will improve the accuracy of trait evaluation under field conditions.

Future breeding strategies will increasingly integrate **super-pangenomics, multi-omics datasets, artificial intelligence (AI), machine learning and genomic prediction** to enhance selection accuracy and accelerate cultivar development. Such data-driven precision

breeding approaches are expected to facilitate the development of **high-yielding, climate-resilient, nutritionally enriched and disease-resistant bitter gourd cultivars**, thereby supporting sustainable vegetable production under changing climatic conditions. Bitter gourd breeding will become more digital, accurate and sustainable in the future by combining these varied genetic libraries with AI-driven predictive modeling.

Conclusion

The potential of bitter gourd has been completely redefined by the latest developments in genomics-assisted breeding. The tools that researchers today have are unparalleled, from the completion of T2T gap-free genomes to the use of CRISPR/Cas9 and speed breeding. Besides simply increasing yields, these technologies offer the door for a more sustainable agricultural system in which crops are inherently pest-resistant, water and nutrient-efficient, and health-optimized. Bitter gourd is positioned to take the lead in the worldwide market for medicinal vegetables as these genomic resources continue to develop.

References

1. Anonymous (2024). Department of Agriculture & Farmers Welfare. <https://agriwelfare.gov.in/en/StatHortEst>
2. Bayer, P. E., Golicz, A. A., Scheben, A., Batley, J., & Edwards, D. (2020). Plant pan-genomes are the new reference. *Nature plants*, 6(8), 914-920.
3. Chen, K., Wang, Y., Zhang, R., Zhang, H., & Gao, C. (2019). CRISPR/Cas genome editing and precision plant breeding in agriculture. *Annual review of plant biology*, 70(1), 667-697.
4. Cui, J., Yang, Y., Luo, S., Wang, L., Huang, R., Wen, Q., ... & Hu, K. (2020). Whole-genome sequencing provides insights into the genetic diversity and domestication of bitter gourd (*Momordica* spp.). *Horticulture research*, 7.
5. Korte, A., & Farlow, A. (2013). The advantages and limitations of trait analysis with GWAS: a review. *Plant methods*, 9(1), 29.
6. Kumar, S., Singh, R. & Patel, M. (2023). Genomics-assisted breeding for disease resistance in cucurbits. *Scientia Horticulturae*, 315, 111023.
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.
8. Zhang, Y., Wang, X., Wang, Y., Niu, Y., Han, X., Tan, J., ... & Yu, R. (2026). Telomere-to-telomere genome assembly and comprehensive mutation library facilitate bitter gourd breeding and functional genomics research. *Plant Communications*, 7(4).