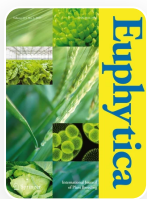


High-resolution QTL mapping of horticultural traits in muskmelon (*Cucumis melo* L.) using genotyping-by-sequencing

Published: 16 April 2026

Volume 222, article number 73 (2026) [Cite this article](#)



Euphytica

[Aims and scope](#) →

[Submit manuscript](#) →

[Anroop Kaur](#), [Megha Sharma](#), [Sukhpreet Kaur Bhatia](#), [Devender Sharma](#), [Sat Pal Sharma](#),
[Ajinder Kaur](#) & [Navraj Kaur Sarao](#)

200 Accesses [Explore all metrics](#) →

Abstract

Muskmelon (*Cucumis melo* L.) is an economically and nutritionally important vegetable crop with significant genetic variability. Fruit traits significantly influence consumer preference and market value, with most quality parameters governed by multiple genes and influenced by environmental factors. High-resolution quantitative trait loci (QTL) mapping can elucidate the genetic basis of these traits, facilitating marker-assisted breeding. In this study, QTL mapping was performed for melon quality traits using an $F_{2:4}$ population of 110 individuals derived from a cross between muskmelon variety Punjab Sunehri and Snap melon accession SM2012-1. The F_4 population was phenotyped during the spring and rainy seasons of 2023. A genetic linkage map was constructed using the Genotyping-by-Sequencing (GBS) approach, comprising 13 linkage groups and 1962 single nucleotide polymorphism (SNP) markers. Nine horticultural traits were evaluated: days to first male flower appearance, fruit maturity, fruit weight, fruit length, fruit width, flesh thickness, fruit cavity length, cavity width and total soluble solids. QTLs were

identified across both seasons on chromosomes 1, 2, 3, 5, 9, 10, and 12, explaining 7–71% of the phenotypic variance (PVE), with logarithm of odds (LOD) scores ranging from 2.6 to 8.7. Notably, overlapping QTLs for fruit weight, fruit length, and fruit maturity were consistently detected at the same positions on chromosomes 3 and 9 in both seasons. These results provide valuable insights for fine-mapping of QTLs and support the integration of marker-assisted selection (MAS) in melon breeding programs.

 This is a preview of subscription content, [log in via an institution](#)  to check access.

Access this article

[Log in via an institution](#)

Subscribe and save

✓ Springer+

from €37.37 /Month

Starting from 10 chapters or articles per month

Access and download chapters and articles from more than 300k books and 2,500 journals

Cancel anytime

[View plans](#) →

Buy Now

Buy article PDF 39,95 €

Price includes VAT (India)

Instant access to the full article PDF.

[Institutional subscriptions](#) →

Explore related subjects

Discover the latest articles, books and news in related subjects, suggested using machine learning.

[Agricultural Genetics](#)

[Genetic mapping](#)

[Plant Genetics](#)

[Plant Breeding](#)

[Quantitative trait](#)

[Quantitative trait loci](#)

Data availability

The datasets presented in this study can be accessed in online repositories. The names of the repository/repositories and accession number(s) can be found below:

[<https://dataview.ncbi.nlm.nih.gov/object/PRJNA1122332?reviewer=sloahbkt5ugh7e41d7pguuspn0>]
(<https://dataview.ncbi.nlm.nih.gov/object/PRJNA1122332?reviewer=sloahbkt5ugh7e41d7pguuspn0>), PRJNA1122332.

References

Amanullah S, Liu S, Gao P, Zhu Z, Zhu Q, Fan C, Laun F (2018) QTL mapping for melon (*Cucumis melo* L.) fruit traits by assembling and utilization of novel SNPs based CAPS markers. *Sci Hortic* 236:18–29. <https://doi.org/10.1016/j.scienta.2018.02.041>

Amanullah S, Osae BA, Yang T, Abbas F, Liu S, Liu H, Wang X, Gao P, Luan F (2022) Mapping of genetic loci controlling fruit linked morphological traits of melon using developed CAPS markers. *Mol Biol Rep* 49:5459–5472. <https://doi.org/10.1007/s11033-022-07263-x>

Amanullah S, Li S, Osae BA, Yang T, Abbas F, Gao M, Wang X, Liu H, Gao P, Luan F (2023) Primary mapping of quantitative trait loci regulating multivariate horticultural phenotypes of watermelon (*Citrullus lanatus* L.). *Front Plant Sci* 13:1034952. <https://doi.org/10.3389/fpls.2022.1034952>

Andrews S (2010) FastQC: a quality control tool for high throughput sequence.data. <http://www.bioinformatics.babraham.ac.uk/projects/fastqc>

Anonymous (2021) Package of practices for cultivation of vegetables: Punjab Agricultural University, Ludhiana. https://www.pau.edu/content/ccil/pf/pp_veg.pdf

Argyris JM, Díaz A, Ruggieri V, Fernández M, Jahrman T, Gibon Y (2017) QTL analyses in multiple populations employed for the fine mapping and identification of candidate genes at a locus affecting sugar accumulation in melon (*Cucumis melo* L.). *Front Plant Sci* 8:1–20. <https://doi.org/10.3389/fpls.2017.01679>

Baloch AM, Baloch AW, Liu S, Gao P, Baloch MJ, Wang X, Davis AR, Ali M, Luan F (2016) Linkage map construction and QTL analysis of fruit traits in melon (*Cucumis melo* L.) based on caps markers. *Pak J Boanyt* 48(4):1579–1584

Behera TK, Dey SS, Sirohi PS (2006) ‘DBGy-201’ and ‘DBGy-202’: two gynoeocious lines in bitter gourd (*Momordica charantia* L.) isolated from indigenous source. *Indian J Geneics Plant Breed* 66:61–62

Bernardo R (2020) Breeding for quantitative traits in plants, 3rd edn. Stemma Press, Woodbury

Castanera R, Ruggieri V, Pujol M, Garcia-Mas J, Casacuberta JM (2020) An improved melon reference genome with single-molecule sequencing uncovers a recent burst of transposable elements with potential impact on genes. *Front Plant Sci* 10:1815.
<https://doi.org/10.3389/fpls.2019.01815>

Chang C, Wang Y, Tung C (2017) Genome-wide single nucleotide polymorphism discovery and the construction of a high-density genetic map for melon (*Cucumis melo* L.) using genotyping-by-sequencing. *Front Plant Sci* 8:1–11.
<https://doi.org/10.3389/fpls.2017.00125>

Collard BCY, Jahufer MZZ, Brouwer JB, Pang ECK (2005) An introduction to markers, quantitative trait loci (QTL) mapping and marker-assisted selection for crop improvement: the basic concepts. *Euphytica* 142(1–2):169–196.
<https://doi.org/10.1007/s10681-005-1681-5>

CEIC Data (2025) India: area of horticulture crops in major states – Fruits: Muskmelon. Retrieved from CEIC Data database

Department of Agriculture & Farmers Welfare (2012–2024) Horticulture statistics: Production of fruits (muskmelon), Punjab. Government of India.

Dhillon NPS, Ranjana R, Singh K, Eduardo I, Monforte AJ, Pitrat M (2006) Diversity among landraces of Indian snapmelon (*Cucumis melo* var. *momordica*). *Genet Resour Crop Evol* 54:1267–1283. <https://doi.org/10.1007/s10722-006-9108-2>

Dhillon NP, Singh H, Pitrat M, Monforte AJ, McCreight JD (2014) Snapmelon (*Cucumis melo* L. *momordica* group), an indigenous cucurbit from India with immense value for melon breeding. In: XXIX international horticultural congress on horticulture: sustaining lives, livelihoods and landscapes (IHC2014), pp 1102:99–108

Diaz A, Fergany M, Formisano G, Ziarsolo P, Blanca J, Fe Z (2011) A consensus linkage map for molecular markers and quantitative trait loci associated with economically important traits in melon (*Cucumis melo* L.). *BMC Plant Biol* 11:111.

<https://doi.org/10.1186/1471-2229-11-111>

Doyle JJ, Doyle JL (1990) Isolation of plant DNA from fresh tissue. *Focus* 12:13–15

Eduardo I, Arus P, Monforte AJ (2007) Estimating the genetic architecture of fruit quality traits in melon using a genomic library of near isogenic lines. *J Am Soc Hortic Sci* 132:80–89. <https://doi.org/10.21273/JASHS.132.1.80>

Esteras C, Nuez F, Picó B (2011) Genetic diversity studies in cucurbits using molecular tools. In: Wang Y, Behera TK, Kole C (eds) *Cucurbits: genetics, genomics and breeding of cucurbits*. Science, New Hampshire, pp 140–198

Galpaz N, Gonda I, Shem-Tov D, Barad O, Tzuri G, Lev S (2018) Deciphering genetic factors that determine melon fruit-quality traits using RNA-Seq based high-resolution QTL and eQTL mapping. *Plant J* 94:169–191. <https://doi.org/10.1111/tpj.13838>

Gao M, Liang X, Liu X, Guo Y, Xu H, Liu J, Gao Y, Yuan C, Luan F (2020) QTL mapping of fruit and seed related traits in watermelon using Genotyping by sequencing based High density linkage mapping. <https://doi.org/10.21203/rs.3.rs-107825/v1>

Garcia-Mas J, Benjak JA, Sanseverino W, Bourgeois M, Mir G, González VM (2012) The genome of melon (*Cucumis melo* L.). *Proc Natl Acad Sci U S A* 109:11872–11877.

<https://doi.org/10.1073/pnas.1205415109>

Garin V, Lehermeier C, Moreau L (2021) The influence of QTL allelic diversity on QTL detection in multiparent populations. *BMC Genomic Data* 22(1):9.

<https://doi.org/10.1186/s12863-021-00960-9>

Gonzalo MJ, Oliver M, Garcia-Mas J, Monfort A, Dolcet-Sanjuan R, Katzir N, Arus P, Monforte AJ (2005) Simple-sequence repeat markers used in merging linkage maps of melon (*Cucumis melo* L.). *Theor Appl Genet* 110:802–811.
<https://doi.org/10.1007/s00122-004-1814-6>

Harel-Beja R, Tzuri G, Portnoy V (2010) A genetic map of melon highly enriched with fruit quality QTLs and EST markers, including sugar and carotenoid metabolism genes. *Theor Appl Genet* 121:511–533. <https://doi.org/10.1007/s00122-010-1327-4>

Hossain MF, Rabbani MG, Hakim MA, Amanullah ASM, Asanullah ASM (2010) Study on variability character association and yield performance of cucumber (*Cucumis sativus* L.). *Bangladesh J Sci Ind Res* 4(3):297–311

Kaur A, Sharma M, Manan J, Bindu (2017) Comparative performance of muskmelon (*Cucumis melo*) hybrids at farmers' field in district kapurthala. *J Krishi Vigyan* 6:24–31.
<https://doi.org/10.5958/2349-4433.2017.00043.5>

Kaur A, Sharama M, Bhatia SK, Sharma S, Gill R, Kaur G, Sarao NK (2025) Quantitative trait loci mapping for Fusarium wilt using genotyping by sequencing based genetic map in melon (*Cucumis melo*). *Sci Hortic* 343:114050

Kirkbride JH (1993) Biosystematic monograph of the genus *Cucumis* (Cucurbitaceae): botanical identification of cucumbers and melons. U.S. Department of Agriculture, Systematic Botany and Mycology Laboratory Beltsville, Maryland 20705–2350. Parkway Publishers Boone, North Carolina, U.S.A

Kumar H, Pal AK (2022) Analysis of variance components for quantitative traits in muskmelon (*Cucumis melo* L.). *Ann Plant Soil Res* 24:288–293.
<https://doi.org/10.47815/apsr.2022.10163>

Lian Q, Fu Q, Xu Y, Hu Z, Zheng J, Zhang A, He Y (2021) QTLs and candidate genes analyses for fruit size under domestication and differentiation in melon (*Cucumis melo* L.) based on high resolution maps. BMC Plant Biol 21:126.

<https://doi.org/10.1186/s12870-021-02904-y>

Liang X, Gao M, Amanullah S, Guo Y, Liu J, Gao Y, Yuan C, Luan F (2022) Identification of QTLs linked with watermelon fruit and seed traits using GBS- based high-resolution genetic mapping. Sci Hortic 303:111237. <https://doi.org/10.1016/j.scienta.2022.111237>

Lorieux M (2012) MapDisto: fast and efficient computation of genetic linkage maps. Mol Breed 30:1231–1235. <https://doi.org/10.1007/s11032-012-9706-y>

Meru G, McGregor CE (2016) Genotyping by sequencing for SNP discovery and genetic mapping of resistance to race 1 of *Fusarium oxysporum* in watermelon. Sci Hortic 209:31–40. <https://doi.org/10.1016/j.scienta.2016.06.005>

Monforte AJ, Oliver M, Gonzalo MJ, Alvarez JM, DolcetSanjuan R, Arus P (2004) Identification of quantitative trait loci involved in fruit quality traits in melon (*Cucumis melo* L.). Theor Appl Genet 108:750–758. <https://doi.org/10.1007/s00122-003-1483-x>

Monforte AJ, Diaz A, Cano-Delgado A, van der Knaap E (2014) The genetic basis of fruit morphology in horticultural crops: lessons from tomato and melon. J Exp Bot 65:4625–4637. <https://doi.org/10.1093/jxb/eru017>

Moreno E, Obando JM, Dos-Santos N, Fernandez-Trujillo JP, Monforte AJ, Garcia-Mas J (2008) Candidate genes and QTLs for fruit ripening and softening in melon. Theor Appl Genet 116:589–602. <https://doi.org/10.1007/s00122-007-0694-y>

Obando-Ulloa J, Moreno E, Garcia-Mas J, Nicolai B, Lammertyn J, Monforte AJ, Fernandez-Trujillo JP (2008) Climacteric or non-climacteric behavior in melon fruit 1.

Aroma volatiles. *Postharvest Biol Technol* 49:27–37.

<https://doi.org/10.1016/j.postharvbio.2007.11.004>

Osae BA, Amanullah S, Liu H, Liu S, Saroj A, Zhang C (2022) CAPS marker–base genetic linkage mapping and QTL analysis for watermelon ovary, fruit and seed–related traits.

Euphytica 218(4):39. <https://doi.org/10.1007/s10681-022-02990-5>

Pereira L, Ruggieri V, Pérez S, Alexiou KG, Fernández M, Jahrman T, Pujol M, Garcia–Mas J (2018) QTL mapping of melon fruit quality traits using a high–density GBS–based genetic map. *BMC Plant Biol* 18:324. <https://doi.org/10.1186/s12870-018-1537-5>

Pitrat M (1991) Linkage groups in *Cucumis melo* L. *J Hered* 82:406–411

Pitrat M (2016) Melon genetic resources: phenotypic diversity and horticultural taxonomy. In: Grumet R, Katzir N, Garcia–Mas J (eds) *Genetics and genomics of Cucurbitaceae*, vol 20. Springer Nature, Cham, pp 25–59.

https://doi.org/10.1007/7397_2016_10

Pitrat M (2008) Melon (*Cucumis melo* L.). In: Prohens J, Nuez F (eds) *Handbook of plant breeding: vegetables I*, vol 1. Springer New York, New York pp 283–315

Poland JA, Rife TW (2012) Genotyping–by–sequencing for plant breeding and genetics. *Plant Genome* 5(3):92–102. <https://doi.org/10.3835/plantgenome2012.05.0005>

Praneetha S, Muthuselvi R (2021) Combining ability studies in snap melon (*Cucumis melo* var. *momordica*). *Pharma Innov J* 10(12):2541–2544

Praneetha S, Muthselvi, Kousalya R (2024) Association studies on yield and yield components in snapmelon (*Cucumis melo*. Var. *Momordica*). *Madras Agric J* 111:1–3. <https://doi.org/10.29321/MAJ.10.00MA02>

Rakhi R, Rajamony L (2005) Variability, heritability and genetic advance in landraces of culinary melon (*Cucumis melo* L.). *J Trop Agric* 43(1–2):79–82

Ren Y, McGregor C, Zhang Y, Gong G, Zhang H, Guo S (2014) An integrated genetic map based on four mapping populations and quantitative trait loci associated with economically important traits in watermelon (*Citrullus lanatus*). *BMC Plant Biol* 14:33. <https://doi.org/10.1186/1471-2229-14-33>

Ren Y, Guo S, Zhang J, He H, Sun H, Tian S (2018) A tonoplast sugar transporter underlies a sugar accumulation QTL in watermelon. *Plant Physiol* 176:836–850. <https://doi.org/10.1104/pp.17.01290>

Robinson RW, Decker-Walters DS (1997) *Cucurbits*. CAB International, Wallingford

Ruggieri V, Alexiou KG, Morata J (2018) An improved assembly and annotation of the melon (*Cucumis melo* L.) reference genome. *Sci Rep* 8:8088. <https://doi.org/10.1038/s41598-018-26416-2>

Sandlin K, Prothro J, Heesacker A, Khalilian N, Okashah R, Xiang W (2012) Comparative mapping in watermelon [*Citrullus lanatus* (Thunb.) matsum. et nakai]. *Theor Appl Genet* 125:1603–1618. <https://doi.org/10.1007/s00122-012-1938-z>

Spindel J, Wright M, Chen C, Cobb J, Gage J, Harrington S (2013) Bridging the genotyping gap: using genotyping-by-sequencing (GBS) to add high-density SNP markers and new value to traditional bi-parental mapping and breeding populations. *Theor Appl Genet* 126:2699–2716. <https://doi.org/10.1007/s00122-013-2166-x>

Srivastava AK, Mukerjee A, Tripathi A (2020) Antidiabetic and antihyperlipidemic activities of var. momordica fruit extract on experimental animals. *Future J Pharm Sci* 6(22):1–9. <https://doi.org/10.1186/s43094-020-00116-z>

Torkamaneh D, Laroche J, Bastien M, Abed A, Belzile F (2017) Fast-GBS: a new pipeline for the efficient and highly accurate calling of SNPs from genotyping-by-sequencing data. *BMC Bioinformatics* 18:1–7. <https://doi.org/10.1186/s12859-016-1431-9>

Venkatesan K, Malleswara RB, Senthil N (2016) Evaluation of muskmelon (*Cucumis melo* L.) genotypes for growth, yield and quality traits. *Electron J Plant Breed* 7:443–447. <https://doi.org/10.5958/0975-928X.2016.00056.9>

Wang YH, Wu DH, Huang JH, Tsao SJ, Hwu KK, Lo HF (2016) Mapping quantitative trait loci for fruit traits and powdery mildew resistance in melon (*Cucumis melo*). *Bot Stud*. <https://doi.org/10.1186/s40529-016-0130-1>

Wang G, Dai D, Wang L, Sheng Y, Wang D, Li D, Tian L, Luan F (2022) QTL analysis of flowering-related traits by specific length amplified fragment sequencing in melon. *Crop Sci* 62(1):203–215. <https://doi.org/10.1002/csc.2.20659>

Wang S, Basten CJ, Zeng ZB (2012) Windows QTL Cartographer 2.5 Department of Statistics, North Carolina State University, Raleigh, NC. <http://statgen.ncsu.edu/qtlcart/WQTLCart.htm>

Yadav JP, Grishina M, Shahbaaz M, Mukerjee A, Singh SK, Pathak (2022) *Cucumis melo* var. momordica as a potent antidiabetic, antioxidant and possible anticovid alternative: investigation through experimental and computational methods. *Chem Biodivers* 19(9):e202200200. <https://doi.org/10.1002/cbdv.202200200>

Zhao H, Zhang T, Meng X, Song J, Zhang C, Gao P (2023) Genetic mapping and QTL analysis of fruit traits in melon (*Cucumis melo* L.). *Curr Issues Mol Biol* 45(4):3419–3433.

<https://doi.org/10.3390/cimb45040224>

Acknowledgements

Not applicable.

Funding

Funds were utilized in house sources of Punjab Agricultural University, Ludhiana, Punjab, India.

Author information

Authors and Affiliations

School of Agricultural Biotechnology, Punjab Agricultural University, Ludhiana, Punjab, India

Anroop Kaur, Megha Sharma, Sukhpreet Kaur Bhatia, Ajinder Kaur & Navraj Kaur Sarao

ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora, India, Uttarakhand

Devender Sharma

Department of Vegetable Science, Punjab Agricultural University, Ludhiana, Punjab, India

Sat Pal Sharma

School of Biosciences, Swami Rama Himalayan University, Dehradun, India, Uttarakhand

Megha Sharma

Contributions

NKS and SS conceived the idea of project and planned the study. AK generated the mapping population; AK and MS recorded the phenotypic data of fruit traits; AK, MS, SKB

performed the GBS data analysis, linkage map construction and QTL analysis. DS run the softwares for statistical analysis. AJK did proofreading and guided for field work. AK and DS wrote the rough draft of manuscript; AK and DS edited the final manuscript.

Corresponding author

Correspondence to [Navraj Kaur Sarao](#).

Ethics declarations

Conflict of interest

The authors declare no competing interests.

Additional information

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Rights and permissions

Springer Nature or its licensor (e.g. a society or other partner) holds exclusive rights to this article under a publishing agreement with the author(s) or other rightsholder(s); author self-archiving of the accepted manuscript version of this article is solely governed by the terms of such publishing agreement and applicable law.

[Reprints and permissions](#)

About this article

Cite this article

Kaur, A., Sharma, M., Bhatia, S.K. *et al.* High-resolution QTL mapping of horticultural traits in muskmelon (*Cucumis melo* L.) using genotyping-by-sequencing. *Euphytica* **222**, 73 (2026). <https://doi.org/10.1007/s10681-026-03709-6>

Received

23 November 2025

Accepted

11 March 2026

Published

16 April 2026

Version of record

16 April 2026

DOI

<https://doi.org/10.1007/s10681-026-03709-6>

Keywords

[Horticultural traits](#)

[Genotyping-by-sequencing](#)

[Linkage map](#)

[Muskmelon](#)

[Snapmelon](#)

[Quantitative trait loci](#)