Volume 4, Issue 6, June - 2026
**ISSN (E):** 2938-3781



Web of Agriculture: Journal of Agriculture and Biological Sciences
webofjournals.com/index.php/8

# ADVANTAGES OF MARKER-ASSISTED SELECTION (MAS) AND GENOTYPING IN THE DEVELOPMENT OF DETERMINATE, OPEN-FIELD-ADAPTED TOMATO HYBRIDS: A REVIEW

Sadriddin Olimovich Esonov
Independent Researcher
ORCID ID: 0009-0007-7993-8656

Murodjon Muqumjonovich Kamilov
PhD in Agricultural Sciences
ORCID ID: 0009-0006-9445-4485

Ismoiljon Ibrahimjonovich Abdullaev
PhD in Agricultural Sciences, Associate Professor
ORCID ID: 0000-0003-0222-0763

Shuhratbek Husanboevich Rahmonov
PhD in Agricultural Sciences
ORCID ID: 0009-0009-9264-4738
Andijan Scientific-Experimental Station,
Research Institute of Vegetable,
Melon Crops and Potato, Uzbekistan

**Abstract**

Open-field tomato (Solanum lycopersicum L.), and in particular the processing and machine-harvested fresh-market crop, is built on the determinate growth habit. Determinate (self-pruning) hybrids form compact bushes that flower and ripen synchronously, allowing a concentrated, once-over harvest that is increasingly mechanised. Breeding a competitive determinate hybrid therefore means combining, in a single F1, a defined plant architecture suited to machine harvest, resistance to the field pathogen spectrum — in which bacterial spot and bacterial speck are prominent alongside the fungal, viral and nematode diseases — tolerance of open-field abiotic stress, and the fruit-quality profile the processing and fresh markets demand, notably high soluble-solids content, firmness, uniform ripening and colour. Assembling these largely unlinked, differently inherited traits by phenotype alone is slow and imprecise. Marker-assisted selection (MAS) and modern genotyping allow breeders to track resistance, architecture and quality alleles directly at the DNA level, at the seedling stage and independent of season or pathogen pressure. This review synthesises the molecular-marker resources relevant to determinate open-field tomato: the diagnostic markers for bacterial spot (Rx-3, Rx-4/Xv3, QTL-11) and speck (Pto), for the fungal, nematode and viral diseases, and for the architecture and quality loci that underpin mechanised production — self-pruning (sp), jointless-2 (j-2), fruit shape 8.1 (fs8.1) and the Brix-raising Lin5/Brix9-2-5 locus. Marker-assisted backcrossing, the pyramiding of linked resistance cassettes,

Volume 4, Issue 6, June - 2026
**ISSN (E):** 2938-3781



and the prospects for genomic selection of quantitative field traits are discussed, and priorities for their adoption in the tomato breeding programme of the Andijan Scientific-Experimental Station are proposed.

**Keywords**: Solanum lycopersicum, determinate hybrid, open-field tomato, processing tomato, marker-assisted selection, SNP genotyping, bacterial spot, self-pruning, jointless, soluble solids, mechanical harvest.

## Introduction

A large share of the world's tomato crop is grown in the open field for processing into paste, juice and canned products, and for machine-harvested fresh-market supply. Unlike the tall, continuously growing hybrids of the greenhouse, the open-field crop is dominated by the determinate growth habit. A determinate hybrid forms a compact, self-terminating bush whose flowering and fruit set are concentrated in time, so that most of the crop ripens together and can be gathered in a single mechanical pass. This synchrony, together with a suitable fruit type, is the foundation of the modern processing-tomato industry and of the mechanisation that has made open-field production economically viable. In Uzbekistan, where field tomato is a major vegetable crop and where the processing sector and labour costs both create strong incentives for mechanisation and for uniform, high-solids fruit, determinate hybrids adapted to local field conditions are of considerable practical importance.

The open field exposes the crop to a pathogen and stress spectrum that differs from that of protected cultivation. Bacterial diseases — bacterial spot caused by Xanthomonas species and bacterial speck caused by Pseudomonas syringae pv. tomato — are among the most damaging and least controllable constraints of field tomato, spreading rapidly under warm, wet conditions and resistant to chemical control. Fungal diseases such as early blight, late blight, gray leaf spot and the wilts, root-knot nematode, and the viruses TSWV, TYLCV and ToMV also cause significant losses, while drought and heat impose additional pressure in continental climates. Genetic resistance built into the hybrid, and tolerance of abiotic stress, are therefore central breeding objectives.

For the open-field determinate crop, however, the breeder must combine these resistances with a second, equally important group of traits: the architecture and fruit characteristics that make mechanised, once-over harvest and industrial processing possible. Determinate habit, a jointless pedicel that lets fruit detach cleanly, crush-resistant fruit, uniform ripening, high soluble-solids content and deep colour are all essential, and all are governed by identifiable genes or QTLs. Conventional phenotypic selection for so many largely independent, differently inherited traits is slow and imprecise. Marker-assisted selection (MAS) and modern genotyping resolve much of this difficulty by allowing each target allele to be tracked directly from DNA. This review examines the application of these tools to determinate, open-field-adapted tomato hybrids and their prospects at the Andijan Scientific-Experimental Station.

## Breeding Targets in Determinate Open-Field Tomato

The breeding objective for an open-field determinate hybrid can be grouped into four categories, each with a characteristic genetic architecture that dictates the marker strategy. First, a plant



Web of Agriculture: Journal of Agriculture and Biological Sciences
webofjournals.com/index.php/8

Volume 4, Issue 6, June - 2026
**ISSN (E):** 2938-3781


architecture suited to mechanised, concentrated harvest: the determinate (self-pruning) habit, synchronous flowering and ripening, and a canopy that protects and presents fruit for machine gathering. Second, resistance to the field pathogen complex, in which bacterial spot and speck join the fungal, viral and nematode diseases; most of these resistances are controlled by major genes and are ideal MAS targets. Third, the fruit and harvest traits demanded by mechanisation and processing: a jointless pedicel, crush-resistant fruit shape, firmness, uniform ripening and colour. Fourth, high and stable yield and, critically for processing, high soluble-solids (Brix) content, together with tolerance of field drought and heat.

As in greenhouse breeding, these traits split into two classes. The determinate habit and most disease resistances, together with the jointless and fruit-shape traits, are qualitative, governed by one or a few genes of large effect, and are addressed by classical marker-tagged MAS. Yield, soluble-solids content and abiotic-stress tolerance are polygenic and quantitative, and are better served by QTL mapping and genomic selection. A practical determinate-hybrid programme therefore uses single-gene MAS to fix habit, harvest traits and resistances, and quantitative approaches to improve the yield and quality background.

**Marker Systems for Field-Tomato Breeding**

The marker toolkit for determinate tomato is the same as for greenhouse material, and has moved decisively towards gene-based and SNP assays. Sequence-characterised amplified region (SCAR) and cleaved-amplified-polymorphic-sequence (CAPS) markers, read as diagnostic bands on an agarose gel, remain the practical workhorses for resistance and architecture selection and require only standard PCR equipment; examples relevant to field tomato include the within-gene Pto marker for bacterial speck and InDel markers for the Rx-4 bacterial-spot gene. Single-nucleotide polymorphisms, scored by Kompetitive Allele-Specific PCR (KASP) or by targeted sequencing, offer higher throughput, lower per-sample cost and automation, and are increasingly used for large-population screening and for the genome-wide datasets that genomic selection requires. Multiplexed diagnostic panels that score many resistance genes in a single run are especially valuable for stacking the several resistances a field hybrid must carry.

**Marker-Assisted Selection for Disease Resistance**

Disease resistance is the clearest application of MAS in field tomato. Table 1 lists the principal resistance genes and diagnostic markers, with the bacterial diseases that are particularly characteristic of open-field production placed first.

Volume 4, Issue 6, June - 2026
**ISSN (E):** 2938-3781



Web of Agriculture: Journal of Agriculture and Biological Sciences
webofjournals.com/index.php/8

Table 1. Disease-resistance genes and diagnostic markers for open-field determinate tomato.

| Disease / pathogen | Resistance gene(s) | Chromosome | Diagnostic marker(s) |
|---|---|---|---|
| Bacterial spot (Xanthomonas spp.) | Rx-3 (race T1), Rx-4 / Xv3 (race T3), QTL-11; rx-1, rx-2 (recessive) | 3/5, 11, 11, 1 | Rx-3-linked SCAR, SL20181, Rx4 InDel (pcc14/pcc17) |
| Bacterial speck (Pseudomonas syringae pv. tomato) | Pto (+ Fen) | 5 | Within-gene Pto marker (no recombination) |
| Gray leaf spot (Stemphylium spp.) | Sm | 11 | Sm-linked SCAR |
| Fusarium wilt (F. oxysporum f. sp. lycopersici) | I-1, I-2, I-3 | 11, 11, 7 | TAO1 (CAPS), gene-linked SCAR |
| Verticillium wilt (V. dahliae race 1) | Ve / Ve2 | 9 | Ve-linked SCAR |
| Late blight (Phytophthora infestans) | Ph-3 | 9 | Ph3-SCAR |
| Root-knot nematode (Meloidogyne spp.) | Mi-1.2 | 6 | Mi-23 (SCAR) |
| Tomato spotted wilt virus (TSWV) | Sw-5b | 9 | Sw-5-2, gene-derived SNP/SCAR |
| Tomato yellow leaf curl virus (TYLCV) | Ty-1/Ty-3, Ty-2 | 6, 11 | P6-25, ACY, InDel/CAPS |
| Tomato mosaic virus (ToMV) | Tm-2² | 9 | CAPS |

Bacterial diseases: the field-specific challenge

Bacterial spot and bacterial speck are the resistances that most distinguish field-tomato from greenhouse breeding, and they illustrate both the power and the limits of MAS. Bacterial spot, caused by several Xanthomonas species and races, is countered by a set of loci of differing race specificity: Rx-3 confers resistance to race T1, the Rx-4/Xv3 locus (derived from Solanum pimpinellifolium accessions such as PI 128216) confers hypersensitive resistance to race T3, the recessive rx-1 and rx-2 genes act against race T1, and a quantitative locus on chromosome 11 (QTL-11) contributes broader resistance. An InDel marker within the candidate NBS-LRR gene distinguishes resistant from susceptible Rx-4 alleles, while a linked marker such as SL20181 lies a few centimorgans from the gene and is therefore an imperfect predictor — a reminder that loosely linked markers can be separated from their target by recombination. Bacterial speck resistance is conferred by the Pto gene on chromosome 5; because a diagnostic marker lies within the Pto gene itself, selection is not eroded by recombination, making Pto an ideal MAS target.

**Fungal, nematode and viral resistances**

Field determinate hybrids must also carry the resistances shared with greenhouse material. Gray leaf spot (Sm) and the Fusarium wilt genes (I-1, I-2, I-3) map to chromosome 11 alongside the

Volume 4, Issue 6, June - 2026
**ISSN (E):** 2938-3781




bacterial-spot and TYLCV loci, which has important consequences for pyramiding (Section 7). Verticillium wilt is controlled by Ve, late blight by Ph-3, and root-knot nematode by Mi-1.2, each with established diagnostic markers. Among the viruses, TSWV resistance is conferred by Sw-5b, TYLCV resistance by the Ty loci (tracked by P6-25 and related markers), and ToMV resistance by Tm-2². Where reliable phenotyping demands controlled inoculation — as for the wilts, nematode and viruses — marker selection is especially advantageous, allowing resistant seedlings to be identified before any field exposure.

**Plant Architecture and Mechanical-Harvest Traits**

What sets determinate open-field breeding apart most sharply is the need to select for the architecture and fruit traits that make mechanised, once-over harvest and industrial processing possible. These traits are governed by well-characterised genes and are readily fixed by MAS. Table 2 summarises them.

Table 2. Architecture, harvest and quality loci central to determinate, machine-harvested and processing tomato.

| Trait | Gene / QTL | Value for open-field & processing tomato |
|---|---|---|
| Determinate growth habit | self-pruning (sp), chr 6 | Compact bush; synchronised flowering and ripening for once-over mechanical harvest |
| Jointless pedicel | jointless-2 (j-2), enhancer ej-2 | Removes pedicel abscission zone so fruit detaches without stem; essential for machine harvest and clean processing loads |
| Fruit shape / crush resistance | fruit shape 8.1 (fs8.1) | Square, blocky fruit that resists crushing during mechanical harvest and bulk transport |
| Soluble-solids (Brix) | Brix9-2-5 linked to Lin5 (cell-wall invertase), chr 9 | Raises fruit sugar/soluble-solids ~20%; the key paste-yield trait in processing tomato |
| Uniform ripening | u / GLK2 | Eliminates green shoulder, giving uniform colour for a concentrated, once-over harvest |
| Fruit colour / lycopene | crimson ($og^c$), high pigment (hp-1, hp-2), Beta (B) | Deep red colour and high lycopene demanded by the paste and fresh-market trade |

The determinate habit itself is conferred by the recessive self-pruning (sp) allele on chromosome 6. SP, a member of the CETS/PEBP florigen gene family, controls the vegetative-to-reproductive switch along the shoot; in the homozygous sp/sp state the shoot terminates after a few inflorescences, producing a compact bush whose flowering and ripening are synchronised for once-over harvest. Selecting reliably for the recessive sp allele in a segregating population is precisely the kind of task at which a diagnostic marker excels, since heterozygous carriers cannot be distinguished by phenotype. The jointless-2 (j-2) gene, with its enhancer ej-2, removes the pedicel abscission zone so that fruit separates cleanly from the stem — indispensable for machine harvest and for clean processing loads free of green stem material — while fruit shape 8.1 (fs8.1) produces the square, blocky fruit that resists crushing during mechanical gathering and bulk

Volume 4, Issue 6, June - 2026
**ISSN (E):** 2938-3781


Web of Agriculture: Journal of Agriculture and Biological Sciences
webofjournals.com/index.php/8

transport. Together, sp, j-2 and fs8.1 form the architectural core of a machine-harvestable processing hybrid, and all three can be tracked with molecular markers and combined by MAS into a single background.

**Fruit Quality, Soluble Solids and Abiotic-Stress Tolerance**

For processing tomato, soluble-solids (Brix) content is the single most valuable quality trait, because paste yield is directly proportional to it: a small increase in Brix translates into a large saving in the energy and volume needed to concentrate the crop. The Brix9-2-5 QTL on chromosome 9, introgressed from the wild species Solanum pennellii and linked to the cell-wall invertase gene Lin5, raises fruit sugar content by around 20% and is a classic example of a wild-derived quality allele that can be moved into elite determinate lines by marker-assisted introgression. Uniform ripening, governed by the u/GLK2 locus, eliminates the green shoulder and gives the even colour a concentrated harvest requires, while colour and lycopene content are enhanced by the crimson ($og^c$), high-pigment (hp-1, hp-2) and Beta (B) alleles. Fruit firmness, essential for machine harvest and long-distance transport, and the many small-effect QTLs governing it, complete the quality picture.

Open-field production in continental climates such as Uzbekistan's also demands tolerance of drought and heat. These are polygenic, quantitatively inherited traits for which QTL mapping has identified marker-trait associations, and for which genomic prediction (Section 8) is increasingly effective. Selecting for improved abiotic-stress tolerance alongside the qualitative habit, harvest and resistance traits is the central integrative challenge of determinate-hybrid breeding, and it is exactly the challenge that combined MAS and genomic approaches are designed to meet.

**Gene Pyramiding and Marker-Assisted Backcrossing**

The value of a field hybrid lies in the durable combination of many alleles, and MAS makes this combination achievable. A striking feature of tomato is that several important resistances — the bacterial-spot locus Xv3/Rx4, the gray-leaf-spot gene Sm, the Fusarium gene I-2 and the TYLCV gene Ty-2 — all lie on chromosome 11. Because they are physically linked, assembling them requires selecting for rare recombination events that bring the favourable alleles into coupling phase, so that they can subsequently be inherited together as a single cassette. This is only feasible with molecular markers, which identify the rare recombinant individuals among thousands that phenotype alone could never distinguish; the approach has been used to build processing-tomato lines carrying linked bacterial-spot and TYLCV resistances.

Marker-assisted backcrossing (MABC) is used to move a resistance or quality allele — often from a wild relative, as with the Brix9-2-5 sugar QTL from S. pennellii or the Rx-4 bacterial-spot gene from S. pimpinellifolium — into an elite determinate recurrent parent while recovering that parent's genome quickly. Foreground selection retains the target gene, recombinant selection with flanking markers trims the linkage drag of donor DNA around it, and background selection with genome-wide markers accelerates recovery of the recurrent parent. For traits carried by wild-species introgressions, which often bring undesirable linked alleles, recombinant and background selection are particularly valuable in restoring the elite, machine-harvestable phenotype in the fewest generations.

Volume 4, Issue 6, June - 2026
**ISSN (E):** 2938-3781


Web of Agriculture: Journal of Agriculture and Biological Sciences
webofjournals.com/index.php/8

**Genomic Selection for Quantitative Field Traits**

For the polygenic traits that MAS handles poorly — yield, soluble-solids content, firmness, and drought and heat tolerance — genomic selection (GS) offers a complementary route. GS uses genome-wide marker data from a genotyped and phenotyped training population to build a model that predicts the breeding value of selection candidates from their marker profiles alone, allowing superior individuals to be chosen early and the breeding cycle to be shortened. In tomato, genomic prediction has achieved useful accuracies for yield and soluble-solids content, including under stress conditions, and its power grows with marker density and training-population size. For a determinate open-field programme, the natural progression is to fix the qualitative habit, harvest and resistance traits by MAS, then apply GS to raise soluble-solids content, firmness and yield in the fixed background — a staged strategy that most stations can adopt as genotyping costs fall and reference data accumulate.

**Prospects for Application at the Andijan Scientific-Experimental Station**

The Andijan Scientific-Experimental Station breeds vegetable crops in the Fergana Valley, a major open-field tomato-producing region with a warm continental climate and an active processing sector. The determinate open-field crop is therefore directly within the station's mandate, and a staged adoption of MAS would strengthen its capacity to develop locally adapted, machine-harvestable and processing-suitable hybrids. A pragmatic sequence of priorities might be:

• Begin with gel-based SCAR/CAPS screening for the highest-value field resistances — Pto for bacterial speck (a within-gene, recombination-proof marker), Rx-3/Rx-4 for bacterial spot, and Sw-5, Ty-3 and Mi-1.2 for the major virus and nematode threats.

• Add marker selection for the architecture and harvest traits — self-pruning (sp) for determinate habit, jointless-2 (j-2) for clean fruit detachment and fruit shape 8.1 (fs8.1) for crush resistance — which together define a machine-harvestable, processing-suitable hybrid.

• Characterise a working germplasm panel of local and introduced determinate lines with these markers, and identify resistant, high-quality donors and elite recurrent parents for MABC.

• Use marker-assisted backcrossing, with foreground, recombinant and background selection, to introgress wild-derived alleles — such as the Brix9-2-5 soluble-solids QTL — into adapted determinate parents while limiting linkage drag.

• Progress to pyramiding the chromosome-11 resistance cassette (bacterial spot, gray leaf spot, Fusarium, TYLCV) and, as resources allow, to KASP or targeted-sequencing services and genomic prediction of soluble solids, firmness and drought tolerance.

Such a programme would let the station combine the resistance, architecture and quality alleles needed for competitive determinate hybrids far more efficiently than phenotypic selection, tailored to the pathogen spectrum, mechanisation needs and processing market of Uzbek open-field production.

**Challenges and Limitations**

The same caveats that apply to greenhouse MAS apply here, with some field-specific emphases. Marker reliability depends on tight linkage to the causal gene: gene-based markers such as the within-gene Pto assay are ideal, whereas loosely linked markers — illustrated by the several-centimorgan distance between some bacterial-spot markers and their genes — can be separated

Volume 4, Issue 6, June - 2026
**ISSN (E):** 2938-3781




from the target by recombination and must be validated in local germplasm. Single major-gene resistances, particularly to bacteria, can be overcome by evolving pathogen races, which argues for pyramiding and for continued phenotypic monitoring; shifts in Xanthomonas race structure in field tomato are a documented example. Wild-species introgressions carrying valuable alleles such as Brix9-2-5 often bring linkage drag that must be removed by recombinant selection. Genomic selection demands substantial training data and analytical capacity. And, as always, markers guide and accelerate selection but do not replace field evaluation: final yield, harvestability, soluble-solids content and adaptation must be confirmed phenotypically under the target open-field conditions.

## Conclusion

Breeding determinate tomato hybrids for open-field and processing use requires the simultaneous assembly of a machine-harvestable architecture, resistance to a field pathogen complex in which bacterial spot and speck are prominent, tolerance of field drought and heat, and the fruit-quality traits — above all high soluble-solids content — that the processing industry demands. Phenotypic selection alone assembles this combination slowly and imprecisely. Marker-assisted selection and modern genotyping transform the task: diagnostic markers allow direct selection for the determinate self-pruning habit, for the jointless and fruit-shape traits that enable mechanisation, and for the major bacterial, fungal, viral and nematode resistances, while marker-assisted backcrossing and the pyramiding of linked resistance cassettes stack these alleles efficiently into elite determinate parents. For the quantitative traits of yield, soluble solids and stress tolerance, QTL-based selection and genomic prediction extend the same DNA-based logic. A staged adoption of these tools offers programmes such as that of the Andijan Scientific-Experimental Station a realistic route to developing competitive, locally adapted determinate hybrids for mechanised open-field production and to strengthening national self-sufficiency in vegetable seed.

## References

1. Yang, W., & Francis, D. M. (2005). Marker-assisted selection for combining resistance to bacterial spot and bacterial speck in tomato. Journal of the American Society for Horticultural Science, 130(5), 716–721.
2. Yang, W., Miller, S. A., Scott, J. W., Jones, J. B., & Francis, D. M. (2005). Mining tomato genome sequence databases for molecular markers: application to bacterial resistance and marker-assisted selection. Acta Horticulturae, 695, 241–250.
3. Pei, C., Wang, H., Zhang, J., Wang, Y., Francis, D. M., & Yang, W. (2012). Fine mapping and analysis of a candidate gene in tomato accession PI128216 conferring hypersensitive resistance to bacterial spot race T3. Theoretical and Applied Genetics, 124, 533–542.
4. Sim, S.-C., et al. (2023). Marker-assisted selection to combine alleles for four disease-resistance genes of tomato collocated on chromosome 11. HortScience, 58(5), 495–503.
5. Martin, G. B., de Vicente, M. C., & Tanksley, S. D. (1993). High-resolution linkage analysis and physical characterization of the Pto bacterial-resistance locus in tomato. Molecular Plant-Microbe Interactions, 6, 26–34.
6. Mahfouze, S. A., et al. (2021). Gene-based markers in marker-assisted selection to screen tomato genotypes resistant to Fusarium wilt, late blight, Verticillium wilt, leaf mold, bacterial spot and

Volume 4, Issue 6, June - 2026
**ISSN (E):** 2938-3781


bacterial speck. International Journal of Phytopathology, 10(2).
7. Pnueli, L., Carmel-Goren, L., Hareven, D., Gutfinger, T., Alvarez, J., Ganal, M., Zamir, D., & Lifschitz, E. (1998). The SELF-PRUNING gene of tomato regulates vegetative to reproductive switching of sympodial meristems. Development, 125(11), 1979–1989.
8. Carmel-Goren, L., Liu, Y. S., Lifschitz, E., & Zamir, D. (2003). The SELF-PRUNING gene family in tomato. Plant Molecular Biology, 52, 1215–1222.
9. Soyk, S., Lemmon, Z. H., Oved, M., Fisher, J., Liberatore, K. L., Park, S. J., et al. (2017). Bypassing negative epistasis on yield in tomato imposed by a domestication gene. Cell, 169, 1142–1155.
10. Fridman, E., Pleban, T., & Zamir, D. (2000). A recombination hotspot delimits a wild-species quantitative trait locus (Brix9-2-5) for tomato sugar content to 484 bp within an invertase gene. Proceedings of the National Academy of Sciences, 97, 4718–4723.
11. Fridman, E., Liu, Y. S., Carmel-Goren, L., Gur, A., Shoresh, M., Pleban, T., Eshed, Y., & Zamir, D. (2002). Two tightly linked QTLs modify tomato sugar content via different physiological pathways. Molecular Genetics and Genomics, 266, 821–826.
12. Powell, A. L. T., et al. (2012). Uniform ripening encodes a Golden 2-like transcription factor regulating tomato fruit chloroplast development. Science, 336, 1711–1715.
13. Du, Y., et al. (2025). Molecular breeding of tomato: advances and challenges. Journal of Integrative Plant Biology, 67.
14. Eshed, Y., & Zamir, D. (1995). An introgression line population of Lycopersicon pennellii in the cultivated tomato enables the identification and fine mapping of yield-associated QTL. Genetics, 141, 1147–1162.
15. Foolad, M. R. (2007). Genome mapping and molecular breeding of tomato. International Journal of Plant Genomics, 2007, 64358.
16. Collard, B. C. Y., & Mackill, D. J. (2008). Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. Philosophical Transactions of the Royal Society B, 363, 557–572.
17. Ariyarathna, H. A. C. K., et al. (2024). KASP: a high-throughput genotyping system and its applications in major crop plants for biotic and abiotic stress tolerance. Molecular Biology Reports.
18. Sim, S.-C., Durstewitz, G., Plieske, J., Wieseke, R., Ganal, M. W., Van Deynze, A., et al. (2012). Development of a large SNP genotyping array and generation of high-density genetic maps in tomato. PLoS ONE, 7(7), e40563.
19. Duangjit, J., Causse, M., & Sauvage, C. (2016). Efficiency of genomic selection for breeding population design and phenotype prediction in tomato. Heredity, 116, 395–408.
20. Rotondo, F., Bernal, E., Ma, X., Lewis Ivey, M. L., Sahin, F., Francis, D. M., & Miller, S. A. (2022). Shifts in Xanthomonas spp. causing bacterial spot in processing tomato in the Midwest of the United States. Canadian Journal of Plant Pathology.

Web of Agriculture: Journal of Agriculture and Biological Sciences
webofjournals.com/index.php/8