

Supplementary Table 3. Summary of pan-genome studies of horticultural crops.

| NO. | Crop type | Species | Number of assembled genomes | Method | Assembled Genome Size | Number of Predicted Genes | Sequencing Platform | Objects/Goals | Year | Pulication |
|-----|--------------------------|--|-----------------------------|------------------------------|-----------------------|--------------------------------|---|--|-------|-----------------------------|
| 1 | | <i>Solanum lycopersicum</i> | 13 | Graph-based pan-genome | 770.0 Mb - 1.2 Gb | 31,613 - 34,375 | PacBio, Bionano Genomics, Hi-C | Exploring genomic diversity and SVs in wild and cultivated tomatoes to identify genes for yield improvement and flavor-related traits | 2023 | Nature Genetics |
| 2 | | <i>Solanum lycopersicum</i> | 32 | Graph-based pan-genome | - | 33,863 - 37,237 | PacBio sequel II, Illumina, Hi-C | This graph pangenome was used for genome-wide association study analyses and heritability estimation. | 2022 | Nature |
| 3 | | <i>Solanum lycopersicum</i> | 14 | Map-to-pan, De novo assembly | 774.5-792.0 Mb | 33819-34186 | Oxford Nanopore Technology (ONT) | Revealing multiple SVs related to fruit flavor, size, and production. | 2020 | Cell |
| 4 | | <i>Solanum lycopersicum</i> | - | Map-to-pan | 1,179 Mb | 40,369 | Illumina | The tomato pan-genome uncovers new genes and a rare allele regulating fruit flavor. | 2019 | Nature Genetics |
| 5 | Vegetables | <i>Solanum tuberosum</i> | 44 | De novo assembly | 835.1 Mb -1.71 Gb | 44,859 - 88,871 | PacBio HiFi | The diploid potato genomes and pan-genome revealed high-confidence structural variants associated with carotenoid content in tubers. | 2023 | Nature |
| 6 | | <i>Solanum section Petota</i> | - | Map-to-pan | ~9.05 Gb | 132,355 | PacBio, Short-read and Long-read assemblies | Investigating the impact of transposable elements and ploidy on potato evolution through pangenome analyses of 296 accessions. | 2023 | PNAS |
| 7 | | <i>Capsicum</i> | 3 | Graph-based pan-genome | 3.02-3.76 Gb | 32830-33398 | PacBio, Illumina, Hi-C | Insights into pepper domestication, population differentiation, and genomic regions underlying natural variations in domesticated Capsicum species. | 2023 | Nature Communications |
| 8 | | <i>Brassica oleracea</i> | 27 | Graph-based pan-genome | 539.87-584.16 Mb | 50,346 to 55,003 | PacBio, Nanopore , BioNano, Hi-C, Illumina | Exploring genetic diversity, evolution and structural variation impacts on gene expression across 704 accessions. | 2024 | Nature Genetics |
| 9 | | <i>Cucumis melo</i> ssp. <i>agrestis</i> | 9 | Map-to-pan | 392 Mb | 21,192 | PacBio HiFi, Hi-C | Melon pan-genome construction to elucidate genetic determinants of fruit sweetness, color, and edibility for breeding improvement. | 2023 | Plant Physiology |
| 10 | | <i>Citrullus</i> | 6 | Map-to-pan | - | 21 676 to 22 764 | PacBio CLR, Illumina | Wild watermelon genome assembly to expand genetic diversity and disease resistance in cultivated varieties | 2023 | Plant Biotechnology Journal |
| 11 | | <i>Vitis</i> | 9 | De novo assembly | 469-557.1 Mb | 57,003–74,142 | PacBio SMRT | Genetic diversity in wild grapes, adaptive traits for crop breeding | 2023 | Genome Biology |
| 12 | Fruits | <i>Malus</i> | 13 | De novo assembly | 661.83-668.75 Mb | 590,746 | PacBio CCS , Hi-C | CNV and SV analysis in apple genomes links genetic variations to fruit coloration and resistance | 2023 | Nature Communications |
| 13 | | <i>Malus</i> | 3 | De novo assembly | 1.31–1.32 Gb | 90,147–90,507 | PacBio HiFi, Illumina | Genetic basis of apple domestication based on three reference Malus genome and pan-genomes | 2020 | Nature Genetics |
| 14 | | <i>Vaccinium</i> | - | Map-to-pan | - | 302 090 | Illumina, Hi-C | Genetic diversity and breeding of Cranberry and Blueberry | 2023 | Horticulture Research |
| 15 | | <i>Trapa</i> spp. | 6 | Graph-based pan-genome | 470.61-477.43 Mb | TnA_NL: 32,457, TiB_HR: 34,940 | PacBio, Illumina, Hi-C | Subgenome divergence in <i>Trapa</i> , pangenome analysis | 2023 | Horticulture Research |
| 16 | | <i>Aurantioidaeae</i> | 12 | Graph-based pan-genome | 217.8 - 419.1 Mb | 22,907 - 31,413 | PacBio HiFi, PacBio CLR, Illumina, Hi-C | Evolution of the orange subfamily, citric acid accumulation in citrus fruits | 2023 | Nature Genetics |
| 17 | Ornamental plants | <i>Prunus mume</i> | 9 | De novo assembly | 208.17-237.17Mb | 24,294-31390 | Illumina HiSeq 2000 | The study explores the genetic basis of floral traits and domestication history in <i>Prunus mume</i> , identifying key genes associated with flower color and structure through GWAS. | 2018 | Nature Communications |
| 18 | | <i>Helianthus</i> | 1 | Map-to-pan | - | 61,205 | Illumina HiSeq 2000 | Sunflower pan-genome analysis reveals hybridization with wild species contributed to gene content and disease resistance. | 2018 | Nature Plants |
| 19 | Forest tree | <i>Populus</i> | 19 | De novo assembly | 408.0Mb-448.7Mb | 37520-40713 | Illumina, Oxford Nanopore, Hi-C | Unveiling the evolutionary trajectories of populus through the integration of pan-genomes with transcriptomes, methylomes and chromatin accessibility. | 2,024 | Molecular Plant |
| 20 | Tea plant | <i>Camellia sinensis</i> | 22 | Graph-based pan-genome | 2.79-3.20 Gb | 50,525-63,643 | PacBio Sequel II, Illumina, Hi-C | Genetic diversity in 22 elite tea cultivars; impacts of repeat bursts on leaf color; key genes for bud timing, flavor linked to tea quality enhancement. | 2023 | Nature Plants |