

From genomes to gardens: Introducing a search engine for horticultural crops

July 9 2024

Taxonomy

Taxonomy ID 4081
Scientific name *Solanum lycopersicum* cv. Heinz 1706
Common name tomato Heinz 1706 (BTI)
Order Solanales
Family Solanaceae
Genus *Solanum*
Species *Lycopersicum*
Subspecies Unknown
Variety Unknown
Cultivar Heinz 1706



Genome assembly and annotation

Ploidy diploid
Haplotype resolved No
Genome seq num 13
Genome size 782.52 Mb
No. protein-coding genes 34688
No. mRNAs 34688
No. CDSs 34688
No. proteins 34688
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Publication

Genome page in HortGenome Search Engine. Screenshot of the genome page containing the genome information and picture of the plant. Credit: *Horticulture Research* (2024). DOI: 10.1093/hr/uhae100

As genomics profoundly reshapes our understanding of horticultural crops, researchers often grapple with dispersed and complex genomic

data. This fragmentation significantly hinders effective analysis and application, presenting a clear demand for more cohesive research tools.

Addressing this need is crucial for unlocking the full potential of genomic insights to enhance [crop quality](#), diversity, and resilience in the face of growing agricultural demands.

Researchers from Beijing University of Agriculture, in collaboration with international scientists, have announced the development of HortGenome Search Engine (HSE), published in *Horticulture Research* on April 8, 2024.

[The study](#) introduces a novel search engine designed to query and analyze [genomic data](#) of over 500 horticultural crops, enhancing our understanding of gene functions and crop improvement.

HSE consolidates genomic data from a diverse array of over 500 horticultural crops into a unified platform, providing easy access and efficient comparison of genetic information. Equipped with advanced tools like Basic Local Alignment Search Tool (BLAST) and Synteny Viewer, HSE streamlines gene querying and functional annotation processes.

Features such as batch query interfaces and enrichment analysis simplify data navigation, boosting research efficiency. The engine's capability to identify crucial gene families, like the TCP transcription factors in tomatoes, highlights its essential role in driving forward genomic research and agricultural innovation.

Dr. Zhangjun Fei, co-developer of HSE, states, "The HortGenome Search Engine is a vital breakthrough in horticultural genomics, providing unparalleled access to extensive genomic data. This tool revolutionizes plant genomic research, significantly speeding up crop

improvement discoveries and applications."

The HSE not only streamlines genomic research but also profoundly impacts crop breeding and genetic conservation. By simplifying genomic data access and analysis, HSE enables researchers to quickly pinpoint [genes](#) associated with desirable traits, thus accelerating the breeding of crop varieties that are more nutritious, resilient, and compatible with sustainable agricultural practices.

More information: Sen Wang et al, HortGenome Search Engine, a universal genomic search engine for horticultural crops, *Horticulture Research* (2024). [DOI: 10.1093/hr/uhae100](https://doi.org/10.1093/hr/uhae100)

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