**HortGenome Search Engine, a universal genomic search engine for horticultural crops**

Sen Wang1,2,#, Shangxiao Wei1,2,#,Yuling Deng1,2, Shaoyuan Wu1,2, Haixu Peng1,2, You Qing1,2, Xuyang Zhai1,2, Shijie Zhou1,2, Jinrong Li1,2, Hui Zhang1,2, YunCong Yao1,\*, Zhangjun Fei3,4,\*, Yi Zheng1,2,\*

1Beijing Key Laboratory for Agricultural Application and New Technique, College of Plant Science and Technology, Beijing University of Agriculture, Beijing, China 102206

2Bioinformatics Center, Beijing University of Agriculture, Beijing, China 102206

3Boyce Thompson Institute, Cornell University, Ithaca, NY 14853

4USDA-ARS, Robert W. Holley Center for Agriculture and Health, Ithaca, NY, 14853

\*Correspondence: yaoyc\_20@126.com, zf25@cornell.edu, yz@moilab.net

Horticultural crops comprising fruit, vegetable, ornamental, beverage, medicinal and aromatic plants play essential roles in food security and human health, as well as landscaping. With the advances of sequencing technologies, genomes for hundreds of horticultural crops have been deciphered in recent years, providing a basis for understanding gene functions and regulatory networks and for the improvement of horticultural crops. Despite the availability of valuable genomic data, the information is dispersed across various data warehouses using diverse storage approaches, making it challenging to access and analyze. Consequently, there has been a growing emphasis on employing search engines to explore functional genes, gene relationships, and enhance our comprehension of plant biology. However, standard search engines only provide limited search results when confronted with vast genetic data, leaving a significant amount of genetic information untapped and buried in raw data. To this end, we have developed a lightweight universal search engine, HortGenome Search Engine (HSE; http://hort.moilab.net), which allows querying genes, functional annotations, protein domains, homologs, and other gene-related functional information of horticultural crops. In addition, four commonly used tools, including ‘BLAST’, ‘Batch Query’, ‘Enrichment analysis’, and ‘Synteny Viewer’, have been developed for efficient mining and analysis of these genomic data.