

Heng Chen ♂

1997-03 | Married and have children | PhD Position |
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Research Interests

Plant Secondary Metabolism

Abiotic Stress

Quantitative Traits

Transcriptome

RNA Secondary Structure

Education

2019-09 ~ Now

Plant genetics and breeding (Master)

University of Chinese Academy of Sciences

- Graduate with honors (Expect)

2014-09 ~ 2018-06

Bioengineering (Bachelor)

Nanchang University

- First class scholarship

2015-09 ~ 2018-06

Finance (Bachelor)

Nanchang University

- Double degree

Skills

Molecular Experiments

Expert

Physiological Experiments

Expert

Data analysis

Expert

Meta-Analysis

Advanced

R

Advanced

Python

Good

Publications

- **Heng Chen**, Xiangwen Pan, Feifei Wang, Changkai Liu, Xue Wang, Yansheng Li, and Qiuying Zhang. 2021. 'Novel QTL and Meta-QTL Mapping for Major Quality Traits in Soybean', *Frontiers in Plant Science*, 12(2773). (<https://dx.doi.org/10.3389/fpls.2021.774270>)
- **Heng Chen**, Xiangwen Pan, Feifei Wang, Changkai Liu, Xue Wang, Yansheng Li, and Qiuying Zhang. 2021. 'Molecular Mechanisms of Isoflavone Biosynthesis and Regulation in Soybean: A Review', *Soils and Crops*, 10(02), 126–142. (In Chinese with English abstract)
- **Heng Chen**, Qiuying Zhang, and Xiaobing Liu. 2021. 'Nutritional and Health Benefits of Soybean to Human Immunity', *Plants for Immunity*, (One chapter of the book, Accepted)

Research Progress

Major Quality Traits

Finished

Novel QTL and Meta-QTL Mapping for Major Quality Traits in Soybean

Isoflavone, protein, and oil are the most important quality traits in soybean. Since these phenotypes are typically quantitative traits, quantitative trait locus (QTL) mapping has been an efficient way to clarify their complex and unclear genetic background. However, the low-density genetic map and the absence of QTL integration limited the accurate and efficient QTL mapping in previous researches. This paper adopted a recombinant inbred lines (RIL) population derived from 'Zhongdou27' and 'Hefeng25' and a high-density linkage map based on whole-genome resequencing to map novel QTL and used meta-analysis methods to integrate the stable and consentaneous QTL. The candidate genes were obtained from gene functional annotation and expression analysis based on the public database. A total of 41 QTL with a high logarithm of odd (LOD) scores were identified through composite interval mapping (CIM), including 38 novel QTL and 2 Stable QTL. A total of 660 candidate genes were predicted according to the results of the gene annotation and public transcriptome data. A total of 212 meta-QTL containing 122 stable and consentaneous QTL were mapped based on 1,034 QTL collected from previous studies. For the first time, 70 meta-QTL associated with isoflavones were mapped in this study. Meanwhile, 69 and 73 meta-QTL, respectively, related to oil and protein were obtained as well. The results promote the understanding of the biosynthesis and regulation of isoflavones, protein, and oil at molecular levels, and facilitate the construction of molecular modular for great quality traits in soybean.

Isoflavones

Ongoing

Developmental Dynamic Transcriptome and Systematic Analysis Revealed the Major Genes Underlying Isoflavone Accumulation in Soybean

Soy isoflavone, a class of polyphenolic compounds exclusively occurred in legumes, is an important bioactive compound for both plants and human beings. The outline of isoflavones biosynthesis pathway has been drawn up basically in the previous researches. However, research on the subject has been mostly restricted to research the variation, biosynthesis and regulation of total isoflavone, rather than its components, especially glucosides, the most mainly storage form in soybean. In this study, by using ten recombinant inbred lines (RIL), the contents of six isoflavone components in the different stages of developing soybean seeds were determined to characterize the dynamic variation of isoflavones and investigate the isoflavones accumulation pattern in physiology level. Meanwhile, the whole genome expression profile of four lines was performed to characterize the isoflavones accumulation and regulation pattern in gene expression level. Additionally, based on the meta-analysis method, a total of 42 transcriptome data were integrated and analyzed in this study, aiming to obtain candidate genes which could be effectively affect isoflavone contents in various cultivars. Then, the major or hub genes associated with isoflavones accumulation were identified with the combination of differential gene expression analysis (DE analysis), weighted gene co-expression network analysis (WGCNA) and time series analysis. These genes were also selected via comparing with the results of gene annotation for the QTL from our preceding study. The results promote the understandings on the biosynthesis and regulation of isoflavones at physiology and molecular level, and facilitate to breed elite soybean cultivars with high isoflavone contents.

Oil and Protein

Ongoing

A serials of Transcriptome data Revealed Several Major Genes Influencing Oil and Protein Contents in Soybean

Since the Oil and Protein are genetically related, the current study integrated them aiming to reveal several genes could influence both oil and protein contents. We firstly characterize the dynamic variation of their contents and investigate the accumulation pattern in physiology level. Then, the whole genome expression profile was performed to characterize these traits accumulation and regulation pattern in gene expression level.