

# YUQIAO TANG

Boston, Massachusetts|tang.yuqi@northeastern.edu |(857)7637493

## EDUCATION

**Master of Bioinformatics, Northeastern University**

Boston, MA

**Bioinformatics Major, GPA: 3.75/4.0**

Expected May 2025

**Coursework:** Bioinformatics programming, Algorithms, Statistics for Bioinformatics

**Bachelor of Science in Plant Science, Southwest University**

Chongqing, China

**Agriculture Major, GPA: 3.42/4.0**

June 2023

**Coursework:** Biotechnology, Cell Biology, Genetics, Linear Algebra

## TECHINICAL SKILLS

**Programming Language:** R, Python, Bash Shell

**Bioinformatics Tools:** HISAT2, STAR, vcftools, SAMtools, DESeq2, KEGG, Seurat, ggplot2, Scanpy, SnpEff

**Wetlab Skills:** Gene Cloning, Vector Construction, Transformation, qPCR, Western Blotting, GUS Staining

**Statistics Tools:** Matlab, SPSS

## PUBLICATION

Mengna Yu, ..., *Yuqiao Tang*, etc. "Quantitative Trait Locus Mapping and Transcriptome Analysis Reveal Candidate Genes for a Stem Bending Mutant in Rapeseed (*Brassica napus*). " *Industrial Crops and Products* (0926-6690). 2022: e177, 114456

Mengqi Li†, *Yuqiao Tang†*, etc. "Systematic Characterization of *Brassica napus* HIR Gene Family Reveals a Positive Role of BnHIR2.7 in *Sclerotinia sclerotiorum* Resistance." *Horticulturae* (2311-7524). 2022: 8(10), 874

## Research Experience

**Genomic analysis in neuromuscular patients, Brigham and Women's Hospital, US**

May. 2024-Aug. 2024

- Developed Variant Filtering Pipeline: Designed and implemented a comprehensive pipeline for variant filtering and annotation, utilizing tools like SnpEff and SnpSift. Enhanced data processing accuracy by integrating advanced filtering criteria and quality control measures.
- Conducted Ancestry Analysis: Analyzed genomic data to determine sample ancestry and removed non-European samples. Leveraged admixture analysis techniques to ensure dataset homogeneity, improving the reliability of subsequent analyses.
- Performed Statistical Disease Testing: Executed statistical disease testing using custom scripts to identify potential associations. Analyzed mutation data to detect significant findings, contributing to the understanding of genetic influences on disease.

**Analysis of Gene Families, Southwest University, China**

May. 2021-Sep.2022

- Key Genes Selection and Verification: Identified genes influencing silique length in *Brassica napus* from fox-hunting database; applied qPCR and gene analytical methods for preliminary function verification
- Comparative Genomic Analysis: Utilized blast for comparing target gene sequences with homologous sequences in *Arabidopsis thaliana* and rapeseed; identified motifs, and visualized gene families' evolutionary relationships through MEGA and phym1 models
- Gene Structure and Expression Analysis: Utilized GSDS for gene structure construction, analyzed promoter elements with PlantCare, and mapped expression and resistance patterns using R Language based on extracted gene location data
- Experimental Infection and Analysis: Infected specific plants with *Sclerotinia sclerotiorum*, conducted RNA extraction for qPCR analysis, and interpreted experimental outcomes utilizing SPSS

**Workflow of Transcriptome Analysis Results , Southwest University, China**

Aug. 2021-Jan. 2022

- Processed and Mapped Data: Utilized Fastp to process raw sequencing data and employed STAR to map the cleaned data against the *Brassica napus* reference genome.
- Generated Gene Counts and Detected DEGs: Used FeatureCounts for generating gene counts data and employed the DESeq2 R package for detecting differentially expressed genes (DEGs). Visualized data analysis results with the ggplot2 R package.
- Integrated Analysis Workflow: Integrated the above analyses into a unique workflow for this study, enhancing reproducibility and convenience for subsequent related research in the laboratory.
- Conducted Experimental Infection and Analysis: Infected specific plants with *Sclerotinia sclerotiorum*, performed RNA extraction for qPCR analysis, and analyzed experimental outcomes with SPSS.

## Project Experience

**Update of qPrimerDB - qPCR Primer Database , Northeastern University, US**

Sep. 2023-Jan.2024

- Expanded qPCR Primer Databases: Integrated information to expand qPCR primer database, such as unanalyzed species, recent sequencing results, pan-genomic data, etc
- Optimized Primer Design: Optimized the primer design process (including plant genome and pan-genome primer design), updated software to improve precision and efficiency of data analysis, and completed all primer analysis from JGI database