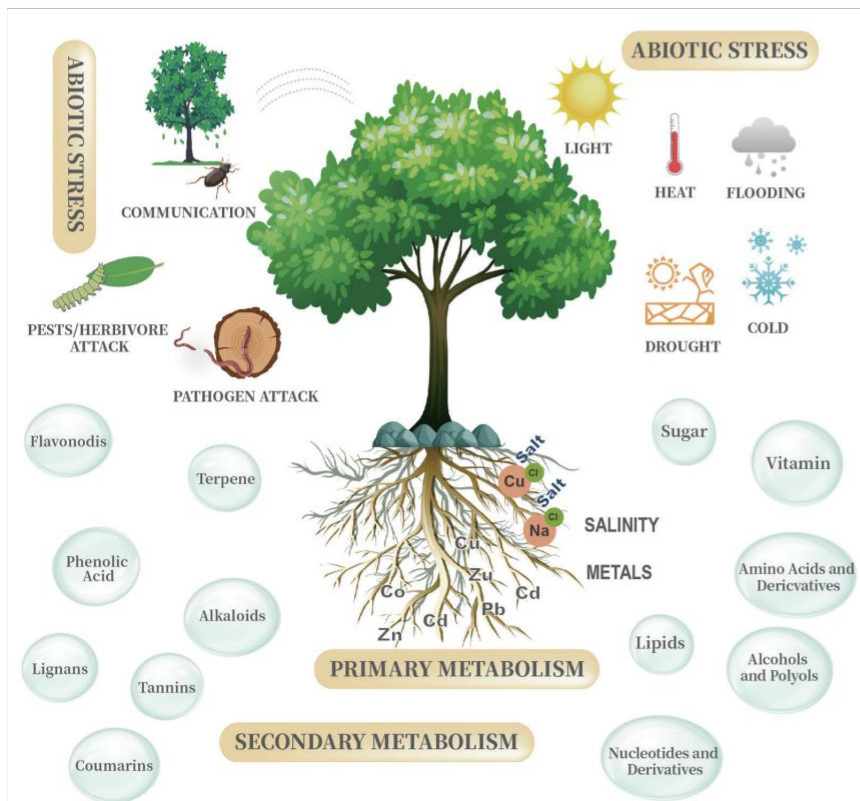


Flavonoids Metabolomics

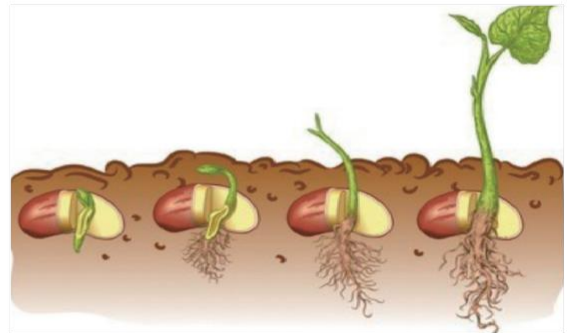


APPLICATIONS

Research In Stress Responed And Environmental Adaptation



Research In Plant Development



Research In Nutrients And Agronomic Traits In Crops



DETECTING PLATFORM



QTOF

Metabolite Identification With MS²



QQQ



Metabolite Quantification With MRM
Gloden Standard

IN-HOUSE DATABASE

Number of metabolites in different classes

Flavone	880	Flavonol	600
Dihydroflavone	270	Dihydroflavonol	50
Anthocyanin	210	Aurone	31
Flavanol	90	Isoflavones	310
Chalcones	230	Biflavone	50
Other flavonoids	800	Total	3700+

PROJECT WORKFLOW



Sending
sample to us



Sample
Extracting



Sample Detecting
On Our Platform



Data
Analysis



Report
Sending

SAMPLE REQUIREMENTS

Sample Type	Recommended Individual sample weight	Minimum Individual sample weight	Recommended Biological duplication
Stem, Bud , Node, Leaf, Root, Flower, Fruit,callus	600mg	300mg	≥3

DETECTING EXPERIENCE



SELECTED PUBLICATIONS

Genomes of the Banyan Tree and Pollinator Provide Insights into Fig-Wasp Coevolution

Graphical Abstract

Highlights

- Genomes of two *Ficus* species and one wasp pollinator revealed by mass resequencing
- Analoid root formation is triggered by an auxin-dependent pathway promoted by light
- A male-specific *YAC12* gene is a candidate gene for sex determination in *F. hispida*
- Genes related to coadaptation contribute to codiversification between fig and wasp

Subfunctionalization of the *Ruby2-Ruby1* gene cluster during the domestication of citrus

Selection of a subspecies-specific diterpene cluster implicated in rice disease resistance

UDP-glucosyltransferase regulates grain size & abiotic stress tolerance associated with metabolite redirection in rice

Carotenoids modulate kernel texture in maize influencing amyloplast envelope integrity

Rowing of the Fruit Metabolome in Tomato Breeding

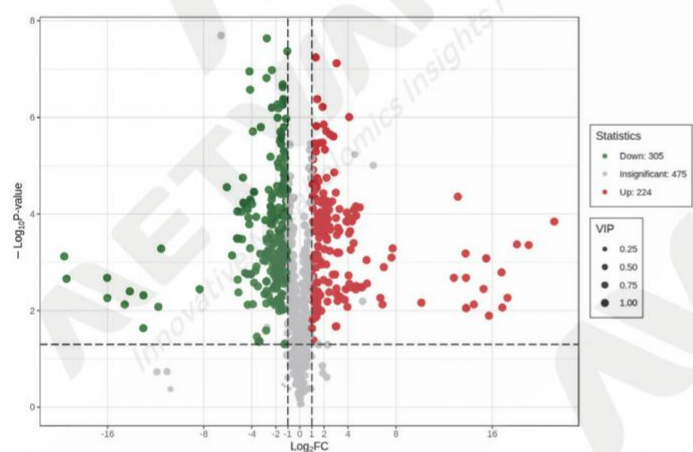
Graphical Abstract

Highlights

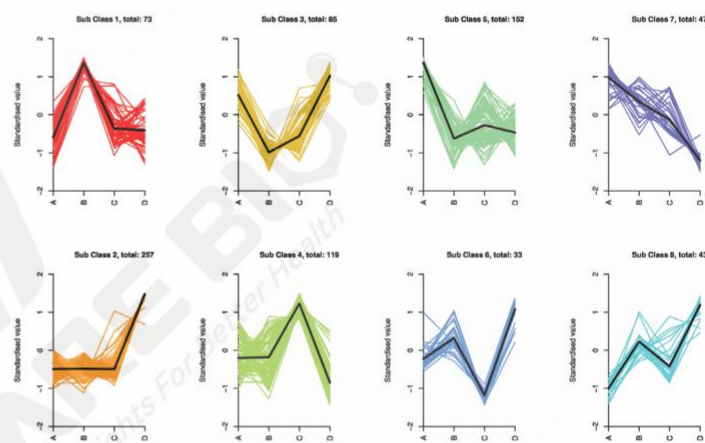
- Multi-omic analysis of tomato bulk revealed new metabolite genes and pathways
- Selection of bulk main gene-allele metabolites altered due to nearby inhibiting genes
- Conventional selection on the major trait that reduced anti-nutritional compounds
- Pink tomato breeding modified hundreds of metabolites, leading to unexpected changes

ANALYSIS LIST

- 01 CV value distribution of all samples
- 02 Principal Component Analysis (PCA)
- 03 Principal component univariate statistical process control
- 04 Hierarchical Cluster Analysis (HCA)
- 05 Sample correlation assessment
- 06 Discriminant Analysis by Orthogonal Partial Least Squares (OPLS-DA)
- 07 Dynamic distribution of metabolite content differences
- 08 Differential metabolite screening
- 09 Volcanic plot of differential metabolites
- 10 Correlation analysis of differential metabolites
- 11 K - Means analysis
- 12 Venn diagram of differential metabolites
- 13 Functional annotation and enrichment analysis of differential metabolites in KEGG database



Volcanic plot of differential metabolites



K-Means analysis



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