Differential metabolic and transcriptomic profiles during different color stages of albino tea plant (*Camellia sinensis*)

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Background

- Tea is one of the most widely consumed non-alcoholic beverages in the world because of great benefits to human health.

- Under certain environmental conditions, such as low temperature or abnormal light intensity, the albino tea cultivars generate yellowish to off-white leaves which are deficient in chlorophyll.

- Compared to normal green cultivars, albino tea cultivar is precious, due to the special flavor, distinct leaf color and scarcity.





Background

‘Anji Baicha’- an albino tea cultivar

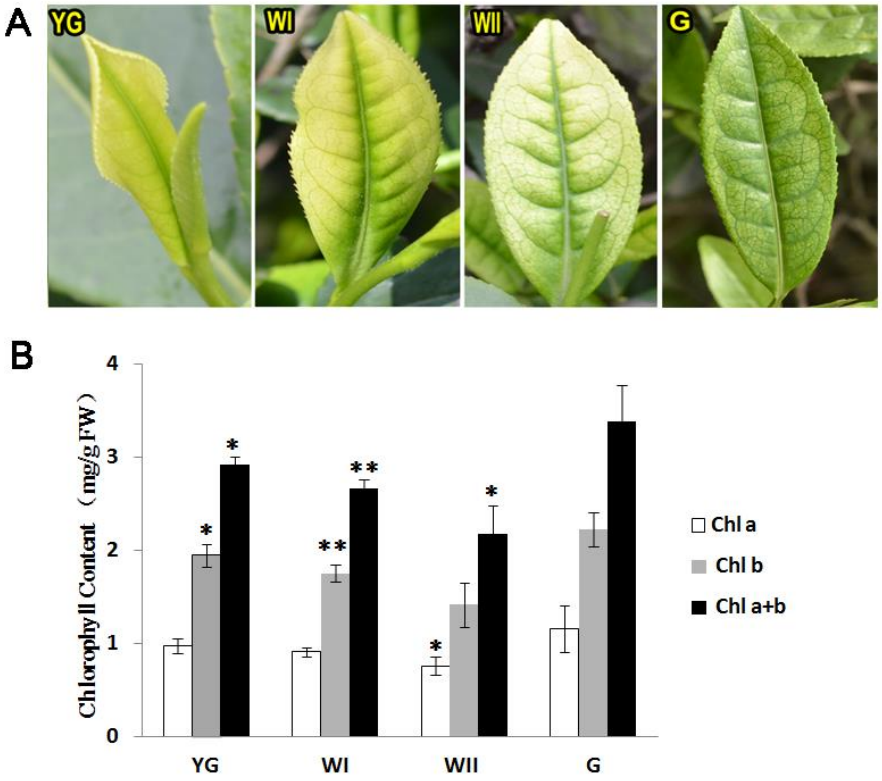
- White shoots at low air temperatures in spring.
- Chlorophyll accumulation is inhibited at low air temperature.
- High free amino acids and low catechins and caffeine concentrations at albino stage.
- Shoots turn green with an increase in air temperature in summer.



Feng et al., Food Chem, 2014, 155:98-104

Results

Reductions in the chlorophyll abundance lead to different colors



‘Anji Baicha’ leaves and chlorophyll concentration at four different stages

Yellow-green (YG) stage, light white (WI) stage, off-white (WII) stage , green (G) stage.

The chlorophyll a + b concentrations in the YG, WI and WII stage leaves were significantly lower than those in the G stage leaves ($p < 0.05$; Student's t test)

Results

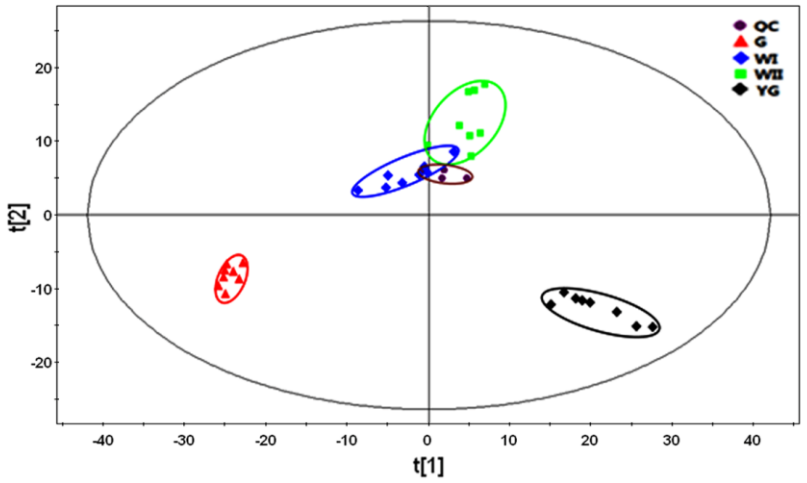
Gas chromatography–mass spectrometry was applied to analyze the metabolite profiles in the different color stages

- GC–MS was applied to detect metabolite profiling during the three albescent stages (YG, WI and WII) and the G stage;
- For each stage, eight independent biological replicates were analyzed;
- After GC–MS analysis, mass spectral deconvolution and removal of the internal standard and pseudo-positive peaks, the number of peaks detected were 1023, 985, 997, and 981 in the YG, WI, WII, and G stages;
- Each peak was originally searched in the NIST and Fiehn databases to identify the metabolites.

Results

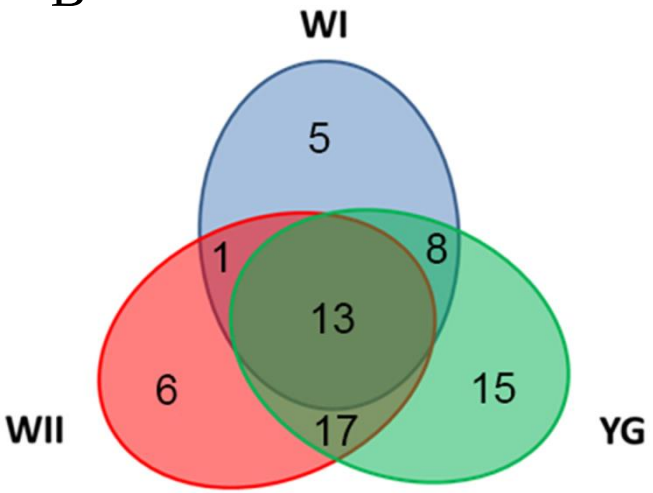
The metabolic profiles of the different color stages were quite different

A



PCA was used to compare the metabolic profiles of the tea plant at three albescent stages (YG, WI and WII) and the G stage.

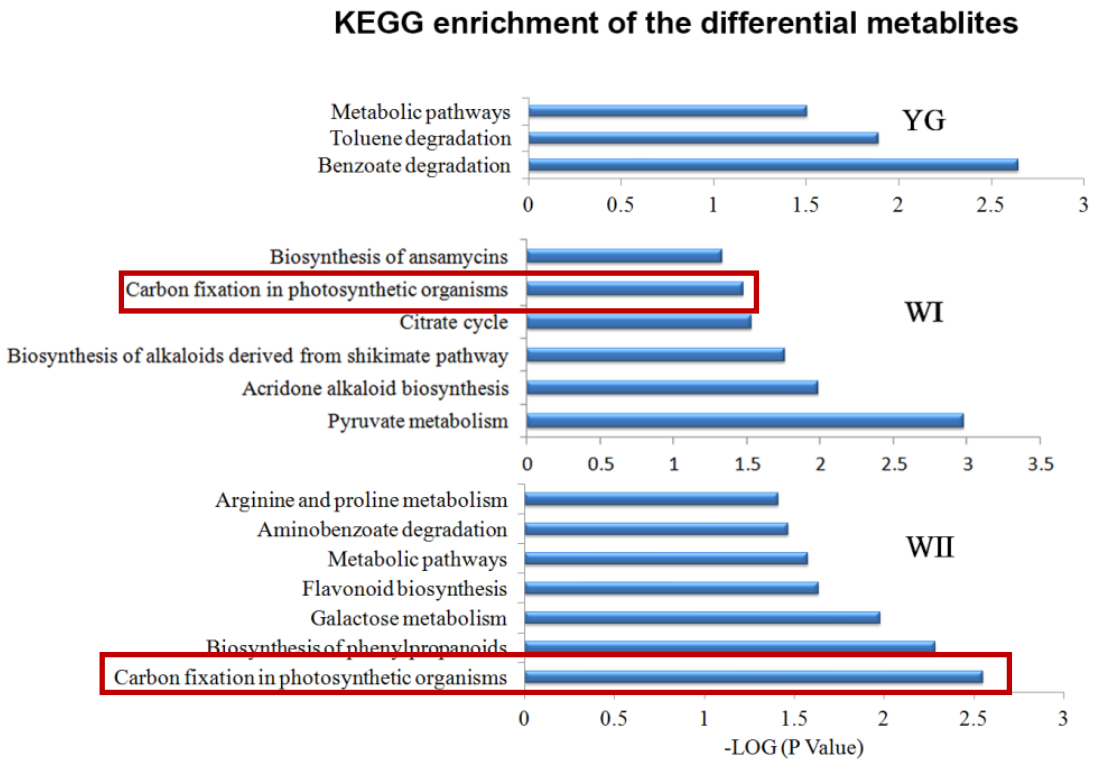
B



Venn diagram of the differential metabolites from the three albescent stages (YG, WI and WII) compared with the G stage

Results

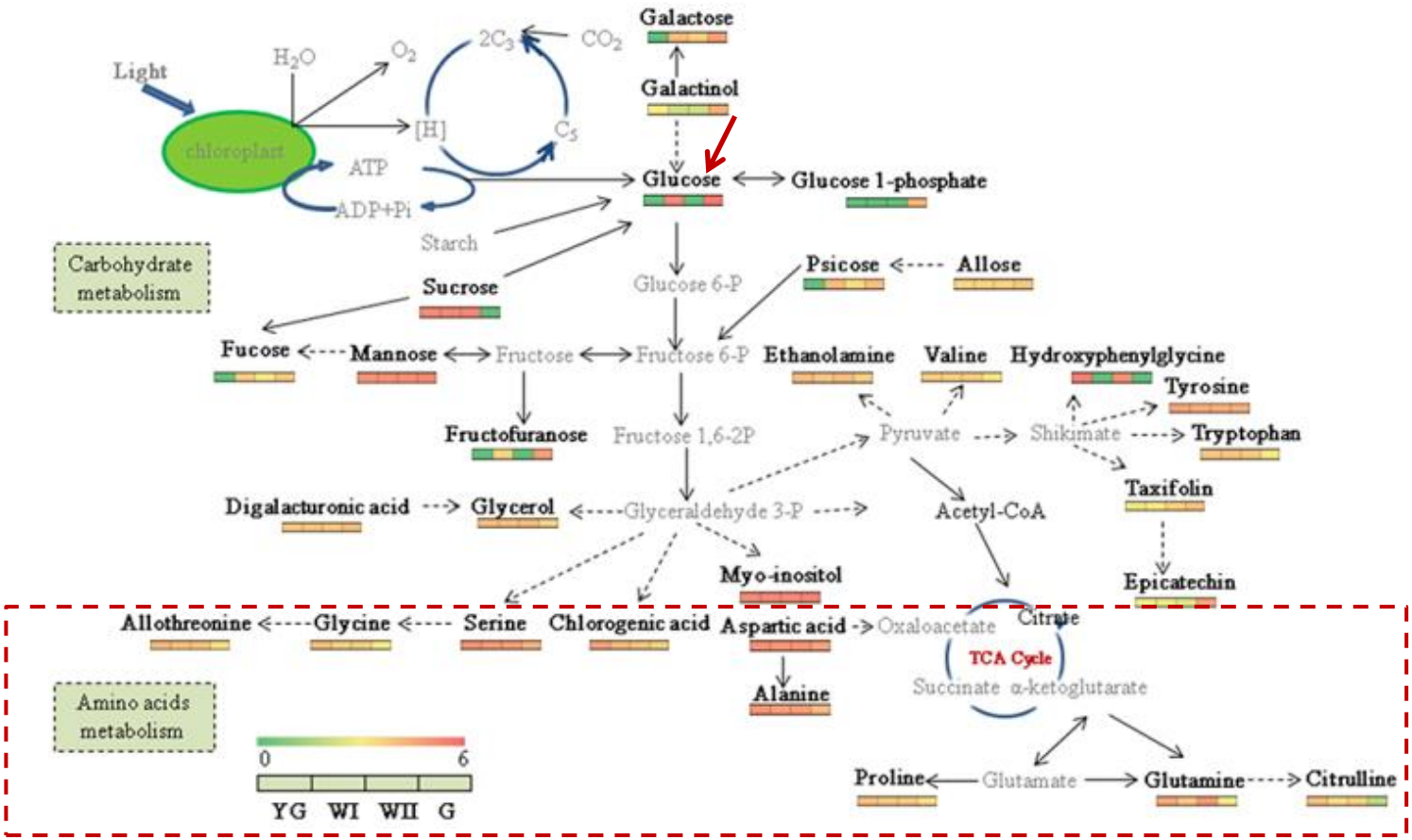
Differential metabolic pathways among the three albescent stages (YG, WI and WII) and the G stage



Differential metabolites in the YG, WI, WII stages compared with those in the G stage were mapped to the distinct metabolic pathways.

Results

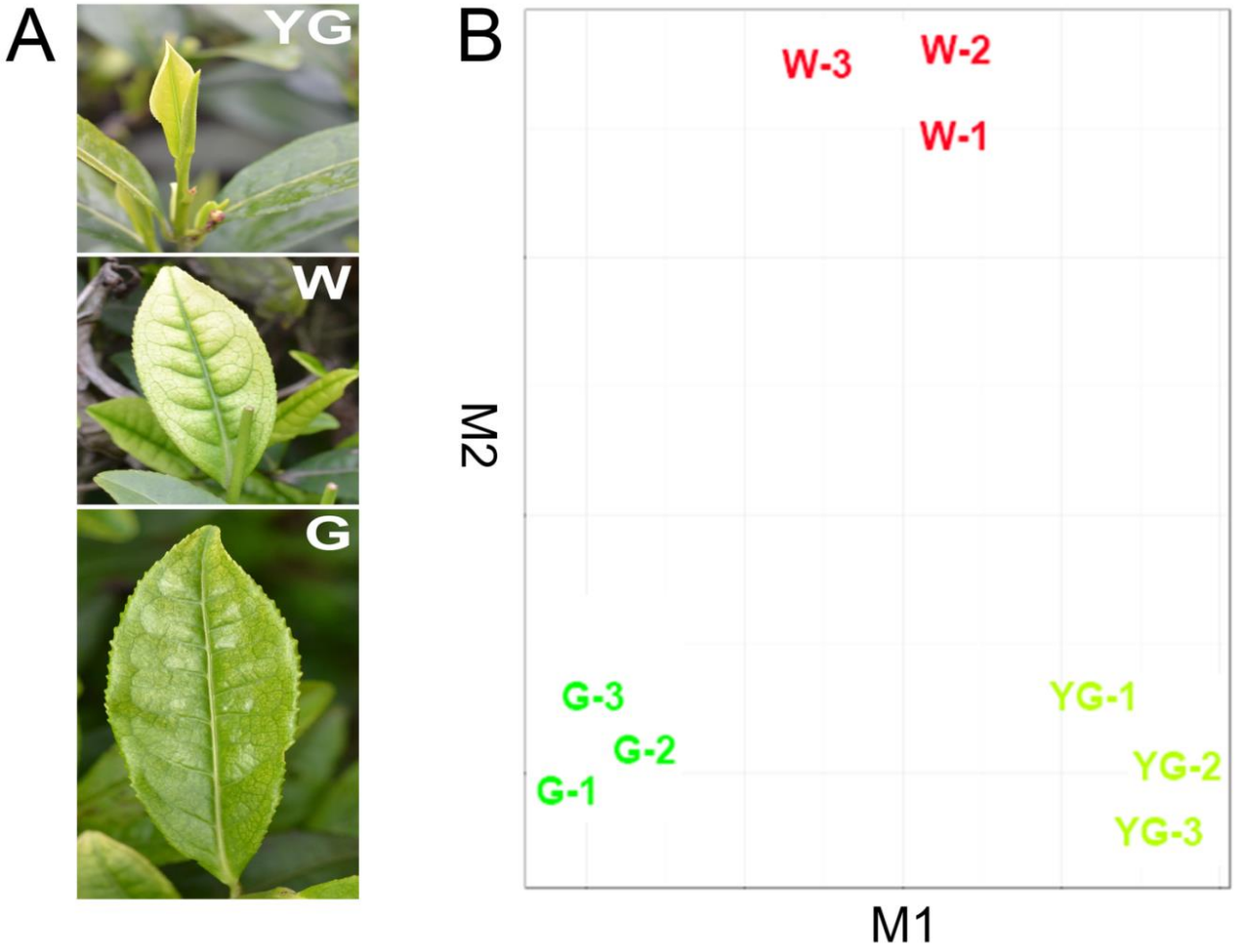
Albescence induces metabolic reprogramming that involves multiple metabolic pathways



Differential metabolites identified in the distinct albescent stages compared with the G stage in this study are shown in bold. Red denotes the highest concentration, and green denotes the lowest concentration.

Results

The transcriptome profiles of the different color stages were quite different



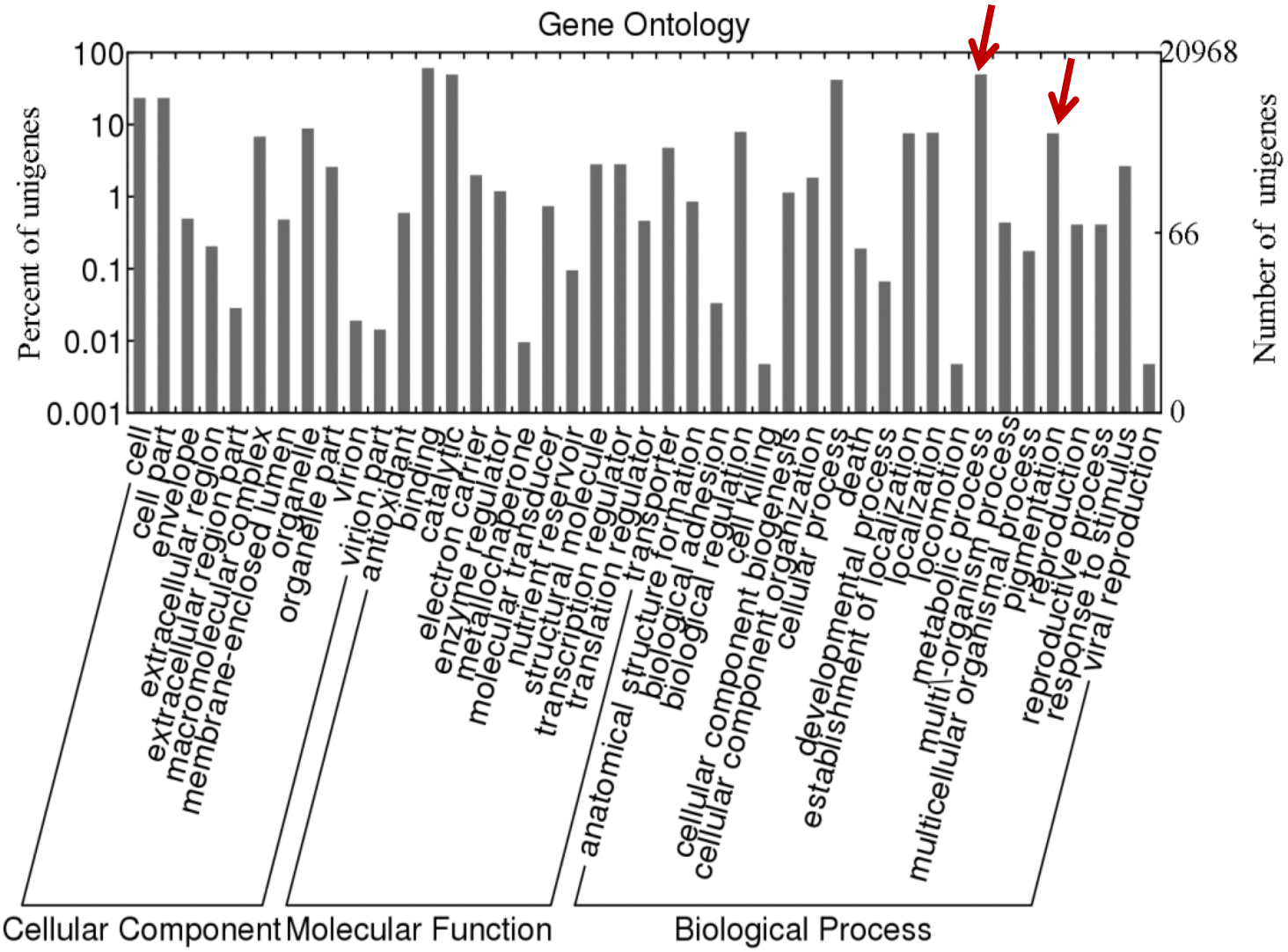
Results

The sequencing and assembly of the 'Anji Baicha' transcriptome

	No. of reads	No. of bases (bp)
Yellow-Green-1	42,522,652	6,314,426,906
Yellow-Green -2	48,556,376	7,183,288,820
Yellow-Green -3	32,069,150	4,767,162,763
White-1	31,243,978	4,652,691,537
White -2	37,897,020	5,632,403,468
White -3	37,230,292	5,571,332,617
Green-1	38,222,704	5,693,731,119
Green-2	29,516,642	4,409,674,597
Green-3	31,963,864	4,665,175,947
Total raw data	329,222,678	48,889,887,774
Total high-quality data	328,386,010	48,553,465,996
Average high-quality read length (bp)	147.9	
Average unigene length (bp)	987.2	
Range of unigene length (bp)	201-28,934	
Unigenes ≥200 bp	**179,951**	**177,648,352**
N50 (bp)	1,648	

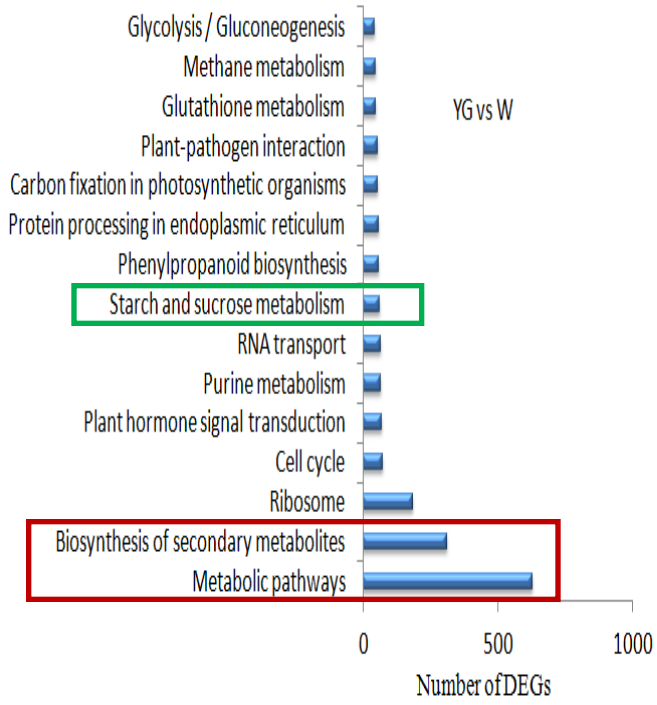
Results

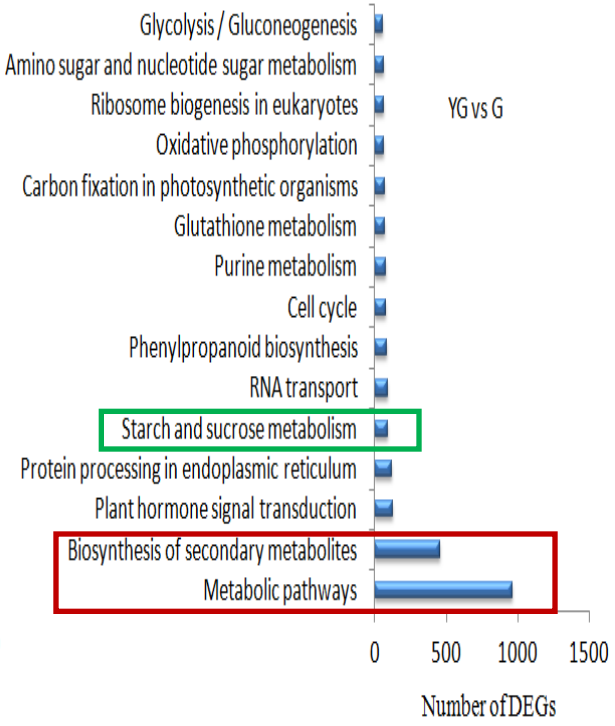
GO classification of all unigenes

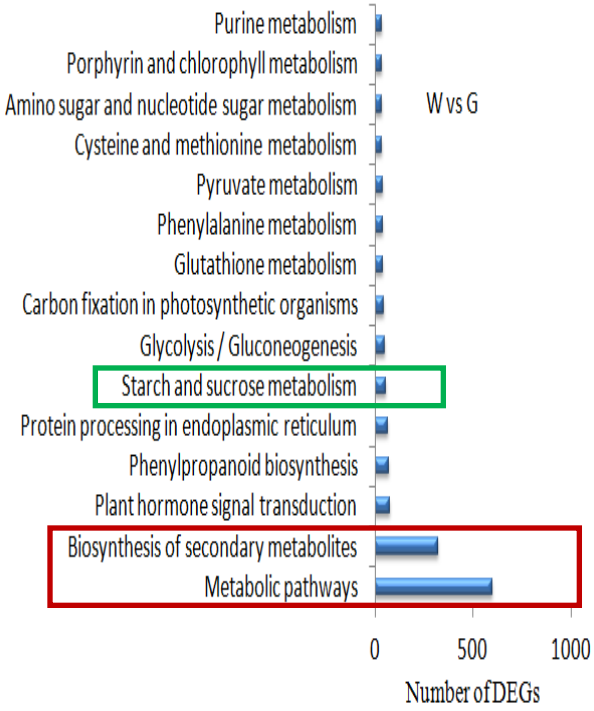


Results

Top 15 KEGG pathway enrichment of all differentially expressed unigenes



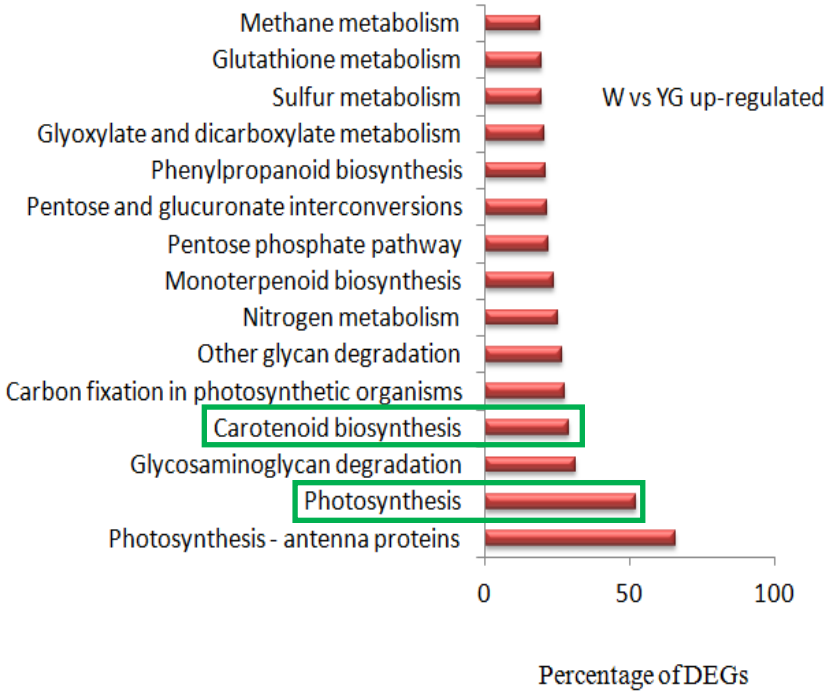


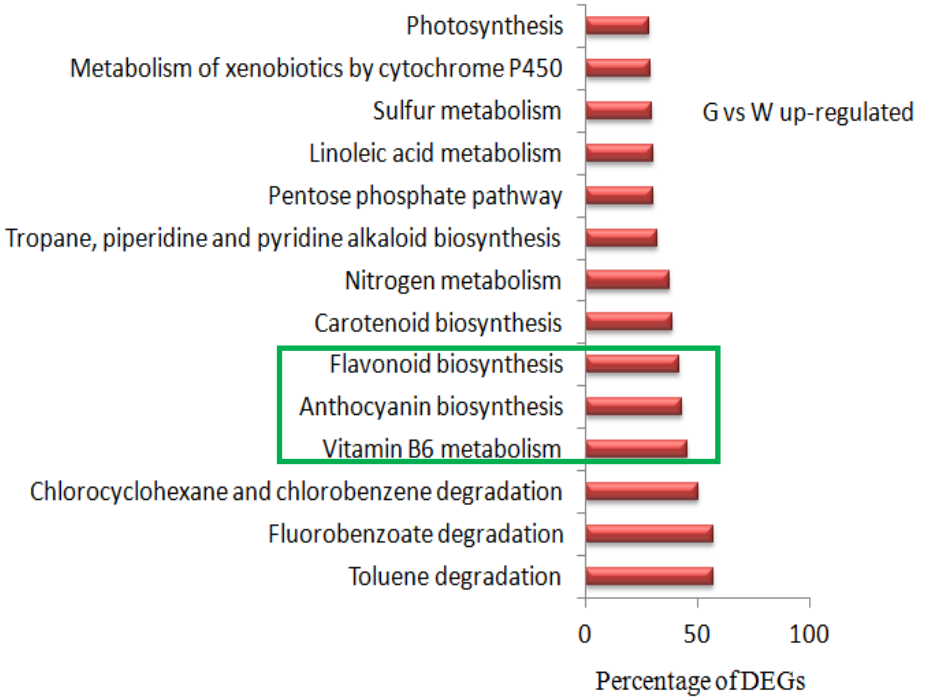


Shared pathway included metabolic pathways, biosynthesis of secondary metabolites, starch and sucrose metabolism, phenylpropanoid biosynthesis, purine metabolism, carbon fixation in photosynthetic organisms, and glycolysis or gluconeogenesis.

Results

Top 15 KEGG pathway enrichment of up-regulated differentially expressed unigenes

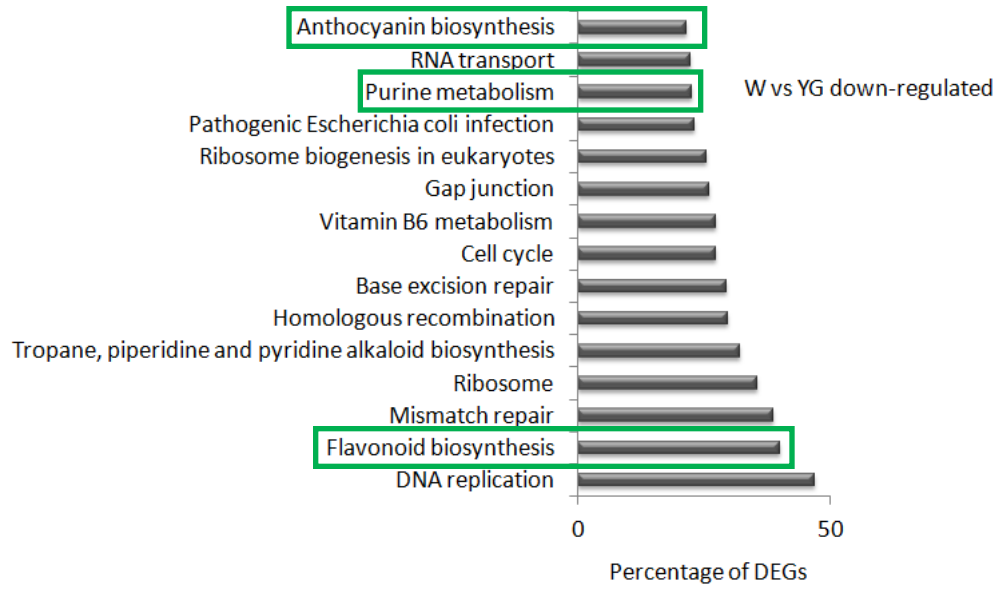


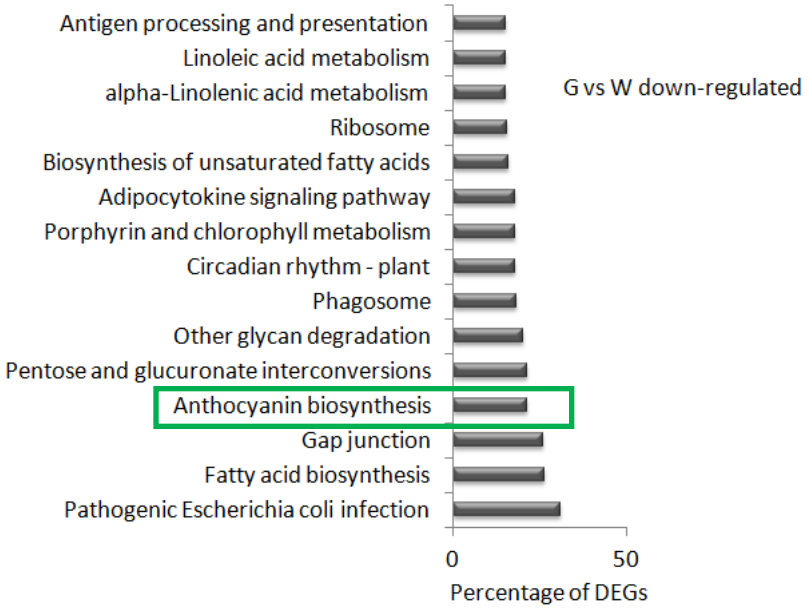


Shared is photosynthesis, carotenoid biosynthesis, nitrogen metabolism, pentose phosphate pathway, and sulfur metabolism.

Results

KEGG pathway enrichment of down-regulated differentially expressed unigenes

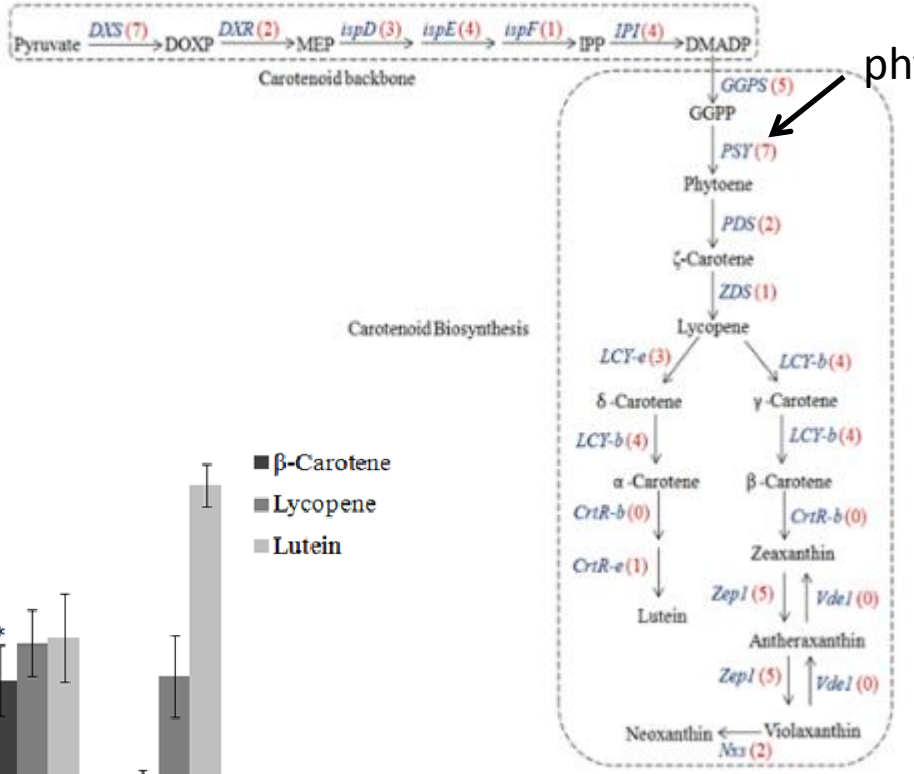




Results

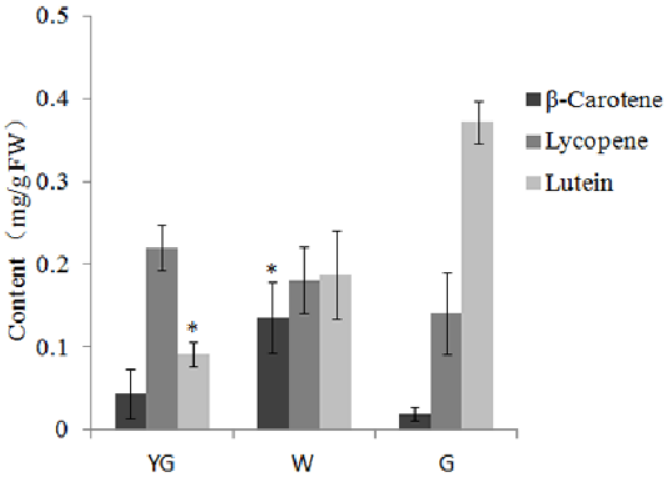
Carotenoid concentrations and the unigenes involved in carotenoid biosynthesis at different stages

B (51)



phytoene synthase (PSY)

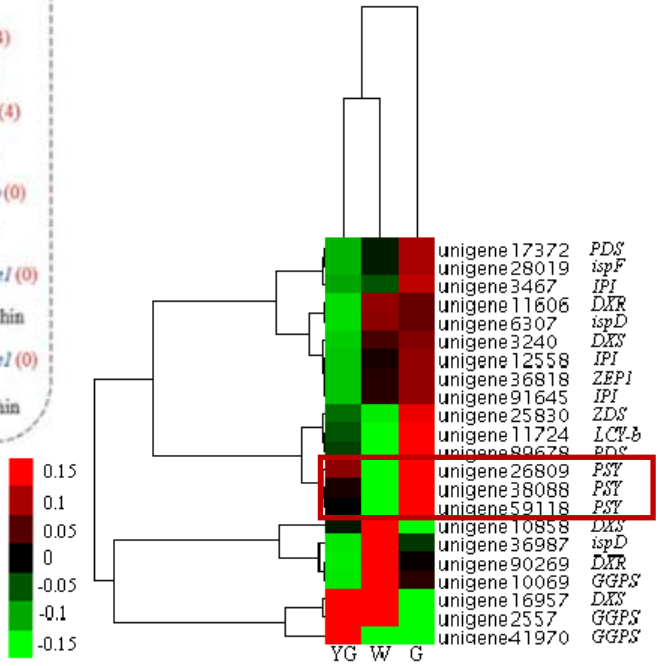
A



The concentrations of β-carotene, lycopene and lutein at different stages

C

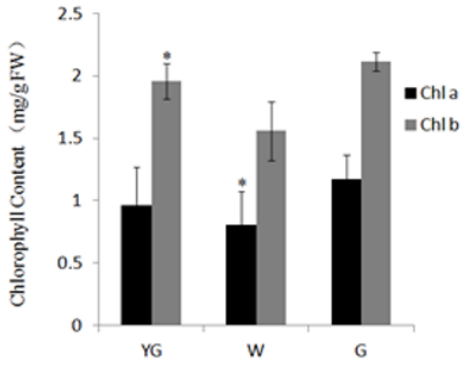
Cluster analysis of all DEGs



Results

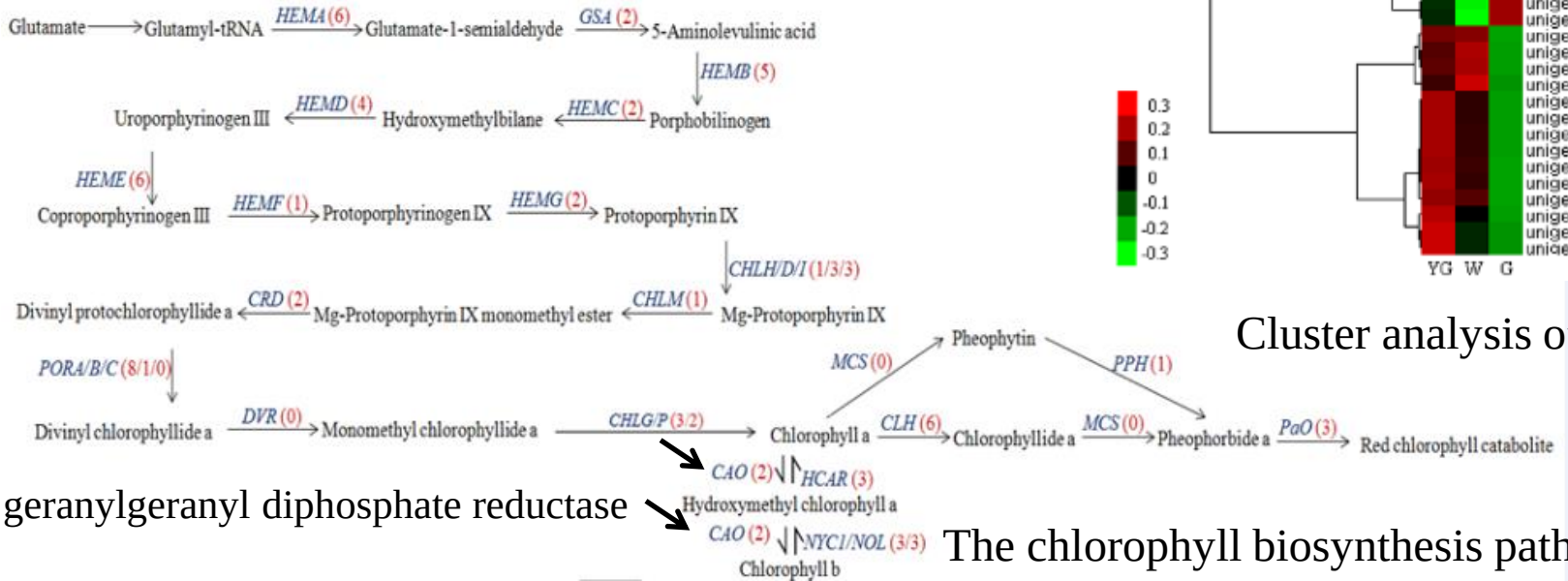
Chlorophyll concentrations and the unigenes involved in chlorophyll biosynthesis at different stages

A



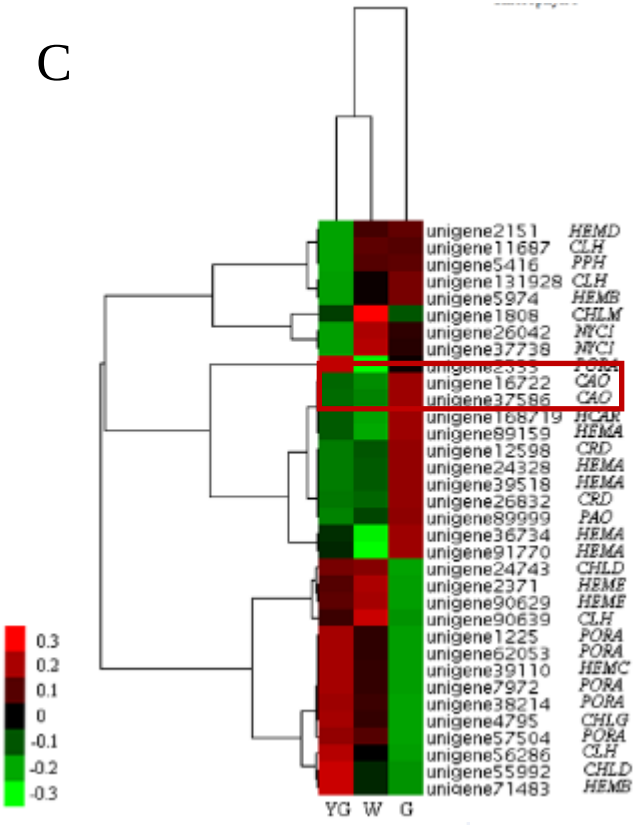
The concentrations of chlorophyll a and chlorophyll b at different stages

B



geranylgeranyl diphosphate reductase

C



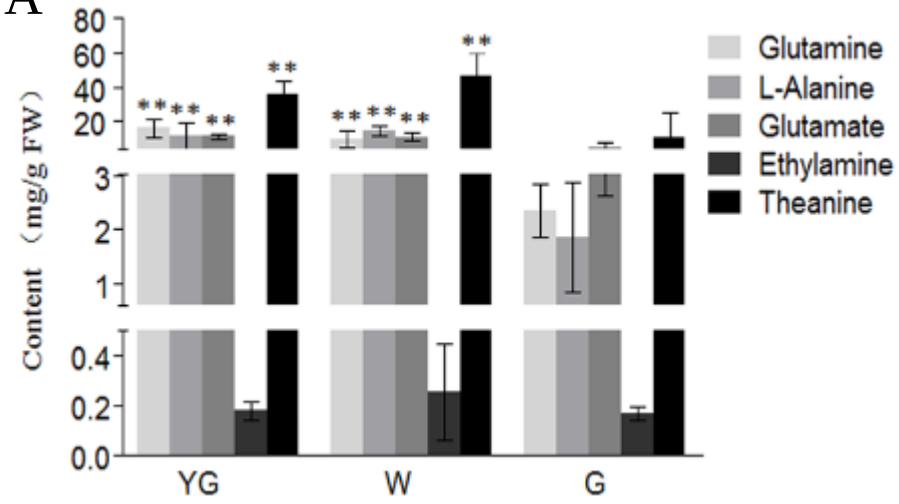
Cluster analysis of all DEGs

The chlorophyll biosynthesis pathway (71)

Results

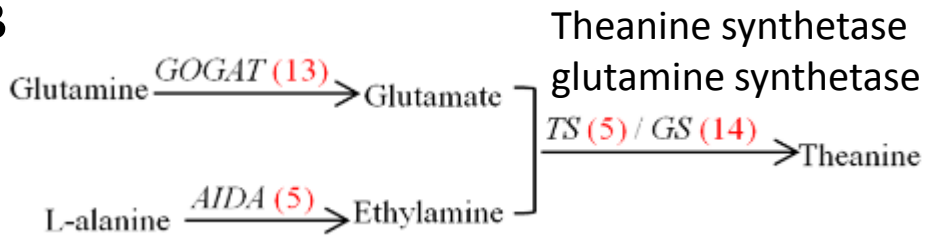
Theanine concentration and the unigenes involved in theanine biosynthesis at different stages

A



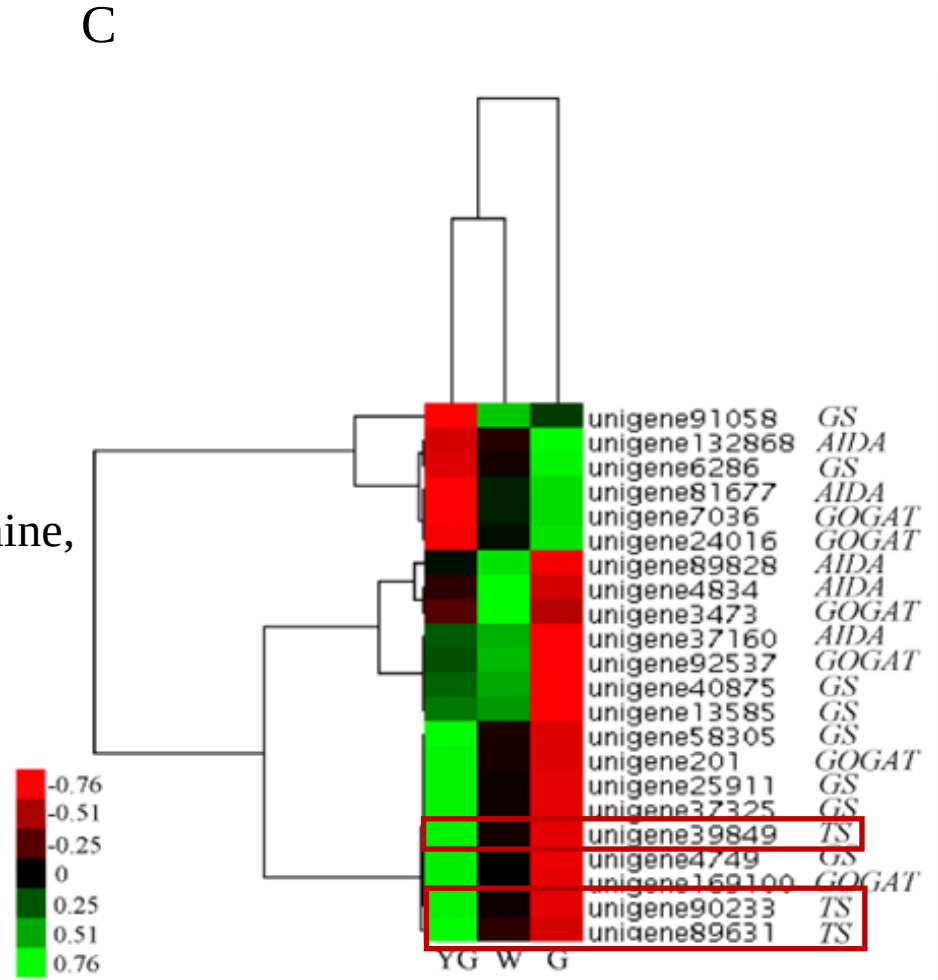
The concentrations of glutamine, glutamate, alanine, ethylamine, and theanine at different stages

B



The theanine biosynthesis pathway (37)

C



Cluster analysis of all DEGs

Conclusion

- The metabolic and transcriptomic profiles were highly divergent between the abscent stages and green stage.

- The main differential metabolic pathways included carbon fixation in photosynthetic organisms and the phenylpropanoid and flavonoid biosynthesis pathways.

- The carbohydrate and amino acid metabolic pathways were disturbed during the albescent stages.

- The differentially expressed unigenes were mainly involved in metabolic pathways, biosynthesis of secondary metabolites, phenylpropanoid biosynthesis, and carbon fixation in photosynthetic organisms.

Acknowledgement

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