

Supplementary material-1

Supplementary method S1.

LC-MS analysis of components in tea extracts

Instrument model: Accela UHPLC system (Thermo Scientific, San Jose, CA) combine with Velos Pro mass spectrometer (Thermo Scientific, San Jose, CA)

Identification conditions: chromatographic column: Acquity BEH C18 column (1.7 μm , 2.1mm \times 100mm);

Mobile phase A: 0.1% formic acid, B: acetonitrile; Column temperature is 45 $^{\circ}\text{C}$; Wavelength: 200~600 nm;

Sample volume: 1.0 μl .

gradient elution:

0 ~ 0.25min: 99% A;

0.25~12 min: 99~50% A;

12~16 min: 50~1% A;

16~20 min: 1~99% A.

Mass spectrometry conditions: ESI negative ion mode; ESI voltage is 2.0kv; The gas flow rate of atomizer is 6.5; The offset is 80; Ion source temperature is 120 $^{\circ}\text{C}$, desolvation temperature melting point is 450 C, atomization gas flow rate is 800 L/h and temperature is 800 C; Testing voltage: 1600v; Scanning quality range: 100 m/z ~ 1200 m/z.

Supplementary Table S1.

Primers for RT-qPCR analyzing MPs biosynthetic genes

Primers	Sequences (5'→3')	References
<i>β-actin F</i>	5'-TTCGAGACCTTCAACGCCC-3'	(Wang et al., 2012)
<i>β-actin R</i>	5'-ACCCTCGTAGATGGGAACGA-3'	
<i>MpPKS5 F</i>	5'-TGTCCGACGAGTTTCTGCAA-3'	(Wang et al., 2015)
<i>MpPKS5 R</i>	5'-TATCAACGCTGCTTGGGCAT-3'	
<i>MpFasA2 F</i>	5'-ATGGATCGCCCGATCTTGTC-3'	(Wang et al., 2015)
<i>MpFasA2 R</i>	5'-CTTTGTCGAGTCCGCTGGAT-3'	
<i>MpFasB2 F</i>	5'-CCTCCAGGGATTACAACCCG-3'	(Wang et al., 2015)
<i>MpFasB2 R</i>	5'-ATTCAATGCCAGGTGCTCCA -3'	
<i>mppA F</i>	5'-TCCCGTTTCTTGGACGTGAG-3'	(Wang et al., 2015)
<i>mppA R</i>	5'-ACGTGCCATGGTTCTGTCTT-3'	
<i>mppB F</i>	5'-CGTCTCGCCCGATAACTTCA-3'	(Wang et al., 2015)
<i>mppB R</i>	5'-TTGACAGACGGGTCGAAGTC -3'	
<i>mppC F</i>	5'-CAGTCCTCGTCCCTTCCAGT -3'	(Wang et al., 2015)
<i>mppC R</i>	5'-CCACGGTGAAGGATGTCGAG -3'	
<i>mppD F</i>	5'-TCAACACGGGAGATGCTGTC-3'	(Wang et al., 2015)
<i>mppD R</i>	5'-GCCAAAGGACAGGAGCAGAT-3'	
<i>mppE F</i>	5'-CTTCCCGATGCCGTTGTGAT-3'	(Wang et al., 2015)
<i>mppE R</i>	5'-CGTCTCGTGGATCATCTCGT-3'	
<i>mppR1 F</i>	5'-TCTGCAGTATGCCATGTGGG-3'	(Wang et al., 2015)
<i>mppR1 R</i>	5'-ATGGCACCGTCACTTAGCTC-3'	
<i>mppR2 F</i>	5'-ACGAAACCCTCCATGACACC-3'	(Wang et al., 2015)
<i>mppR2 R</i>	5'-TGCAGACAGCCTTGTGGTAG-3'	

References

- Wang, C., Chen, D., Chen, M., Wang, Y., Li, Z., Li, F., 2015. Stimulatory effects of blue light on the growth, monascin and ankaflavin production in *Monascus*. *Biotechnol. Lett.* 37, 1043–1048. doi:10.1007/s10529-014-1763-3
- Wang, C., Yang, H., Chen, M., Wang, Y., Li, F., Luo, C., Zhao, S., He, D., 2012. Real-time quantitative analysis of the influence of blue light on citrinin biosynthetic gene cluster expression in *Monascus*. *Biotechnol. Lett.* 34, 1745–1748. doi:10.1007/s10529-012-0962-z

Table S2

Overview of *Monascus* transcriptome in Con and T11 groups

Sample	Clean reads	Clean bases	Error rate(%)	Q20(%)	Q30(%)	GC content(%)
Con_1	45194782	6698176143	0.026	97.62	93.18	52.6
Con_2	50446790	7518122982	0.0267	97.37	92.58	52.27
Con_3	46183040	6887952800	0.0268	97.32	92.48	52.52
T11_1	47779162	7134560832	0.0263	97.51	92.92	53.51
T11_2	44364026	6609621245	0.0262	97.55	93.02	53.56
T11_3	49019986	7303425179	0.026	97.61	93.15	53.08

Table S3

Annotated number of expressed genes

DEG Set	Total	GO	KEGG	COG	NR	Swiss-Prot	Pfam	Total_anno
Con vs. T11	9058(1)	5356	3502	8004	8229	5504	6549	8262
transformants		(0.5913)	(0.3866)	(0.8836)	(0.9085)	(0.6076)	(0.723)	(0.9121)

Table S4

Expression of key genes for *Monascus pigments* secondary metabolism

Genes Name	Gene ID	Homologous genes ID (NR)	Log ₂ (FC)
<i>MpFasA2</i>	BL30022203	AGL44429.1	1.18
<i>MpFasB2</i>	BL30015972	AGL44430.1	1.01
<i>MpPKS5</i>	BL30008298	ALN44200.1	1.32
<i>mppA</i>	BL30025317	ALN44201.1	-0.04
<i>mppB</i>	BL30004761	AGI63864.1	0.73
<i>mppC</i>	BL30011727	PSN75407.1	0.32
<i>mppD</i>	BL30003060	APZ73941.1	0.08
	BL30022209	APZ73942.1	0.06
<i>mppE</i>	BL30012672	APZ73943.1	-0.08
<i>mppR1</i>	BL30025323	AGL44390.1	0.43
<i>mppR2</i>	BL30022206	APZ73944.1	0.16

Figure. S1. Hierarchical cluster plot base on PCA

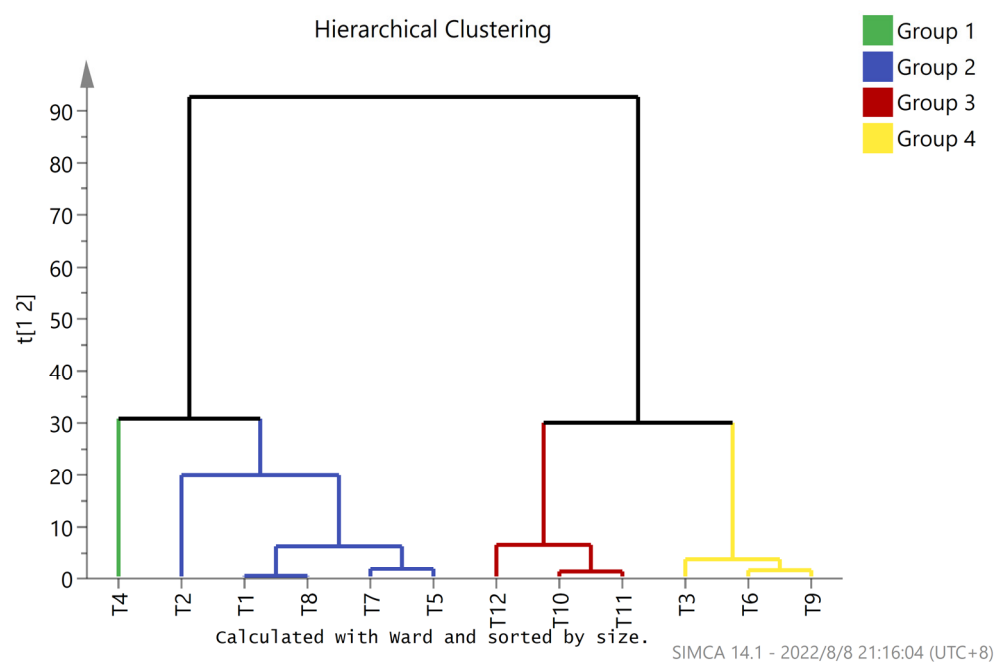


Figure. S2

Heat map of pearson correlction of genes and transcripts between Con and T11.

(A): Gene; B: transcript.

