

Supporting Information

Metabolomic profiling of drought-tolerant and susceptible peanut (*Arachis hypogaea* L) genotypes in response to drought stress

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Table S1. Number of putatively identified metabolites in TAG 24 and JL 24 genotypes in control and stress using GC-MS

Detail of sample	No of metabolites produced
TSL	65
TCL	97
JSL	104
JCL	94
TSR	61
TCR	56
JSR	30
JCR	50

Where, JCL= JL 24 leaf (Control), TCL= TAG 24 leaf (Control), JSL= JL 24 leaf (Stress), TSL= TAG 24 leaf (Stress), JCR= JL 24 root (Control), TCR= TAG 24 root (Control), JSR= JL 24 root (Stress), TSR= TAG 24 root (Stress).

Table S2: Phenolics identified and quantified in TAG 24 and JL 24 genotypes of peanut in control and stress using UPLC-MS/MS

Polyphenol (ppm)	Leaf				Root			
	Control		Stress		Control		Stress	
	JL 24	TAG 24	JL 24	TAG 24	JL 24	TAG 24	JL 24	TAG 24
Cinnamic acid	0.488	0.44	1.08	182.008	4.424	95.78	0.632	109.5
Caffeic acid	0.316	0.184	0.432	0.7	1.12	0.352	0.324	0.668
Salicylic acid	3.692	0.436	2.524	2.08	4.112	3.548	0.732	23.948
Gallic acid	0.44	0.504	0.408	1.396	0.712	2.528	0.636	2.704
Ferulic acid	85.412	0.504	50.248	2.796	57.636	0.72	60.828	2.584
Quercetin	0.256	0.256	0.192	0.3	0.24	0.48	0.272	0.22
Catechol	1.168	0.976	1.24	1.18	1.084	1.256	1.076	1.088
Chlorogenic acid	0.364	0.272	0.316	0.372	0.248	0.276	0.236	0.236
Coumaric acid	326.676	0.252	372.488	1.424	708.124	0.196	255.284	1.876
Syringic acid	0.848	0.424	0.74	4.544	1.156	0.672	0.32	2.772
Kaempferol	1.088	1.004	0.96	1.12	1.088	1.204	1.164	1.144
Vanillic acid	2.764	0.46	2.988	19.808	0.888	1.12	8.92	5.376
Catechin	1.516	0.036	1.42	0.484	0.772	0.984	0.892	1.444
Epicatechin	0.94	0.424	0.344	0.612	0.896	0.364	0.616	0.412
Epigallocatechin	0.716	0.552	0.548	0.468	0.648	0.496	0.968	0.324

Table S3: Polyamine concentration determined using HPLC in TAG 24 and JL 24 genotypes of peanut in control and stress

Polyamines (ppm)	Leaf				Root			
	Control		Stress		Control		Stress	
	JL 24	TAG 24	JL 24	TAG 24	JL 24	TAG 24	JL 24	TAG 24
Agmatine	276.52	51.71	56.08	520.24	420.81	191.06	165.24	236.69
Putrescine	bdl	0.67	0.09	bdl	bdl	0.88	bdl	bdl
Cadaverine	bdl	0.84	0.73	0.6	bdl	bdl	0.07	2.08
Spermidine	bdl	4.64	bdl	bdl	3.97	2.92	3.51	1.16
Spermine	bdl	2.65	bdl	bdl	1.45	bdl	2.3	bdl

bdl=Below detection limit of instrument.

Note: Too many zeroes or missing values (bdl) cause difficulties for downstream analysis. MetaboAnalyst 4.0 software offers several different methods for this purpose. The default method replaces all the missing and zero values with a small value (the half of the minimum positive values in the original data) assuming to be the detection limit. The assumption of this approach is that most missing values are caused by low abundance metabolites (i.e. below the detection limit). In addition, since zero values may cause problem for data normalization (i.e. log), they are also replaced with this small value.

Table S4: Details of gradient mobile phase used for elution of phenolics

Time (min)	A (%)	B (%)
Initial	5	95
1	20	80
3	35	65
5	50	50
6	75	25
8	75	25
10	50	50
12	15	85
14	5	95
15	5	95

Where **A**: Methanol, **B**: 1% Acetic acid in water