

**New insights of low-temperature plasma effects on seeds
germination of *Platycodon grandiflorum***

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Supplementary material

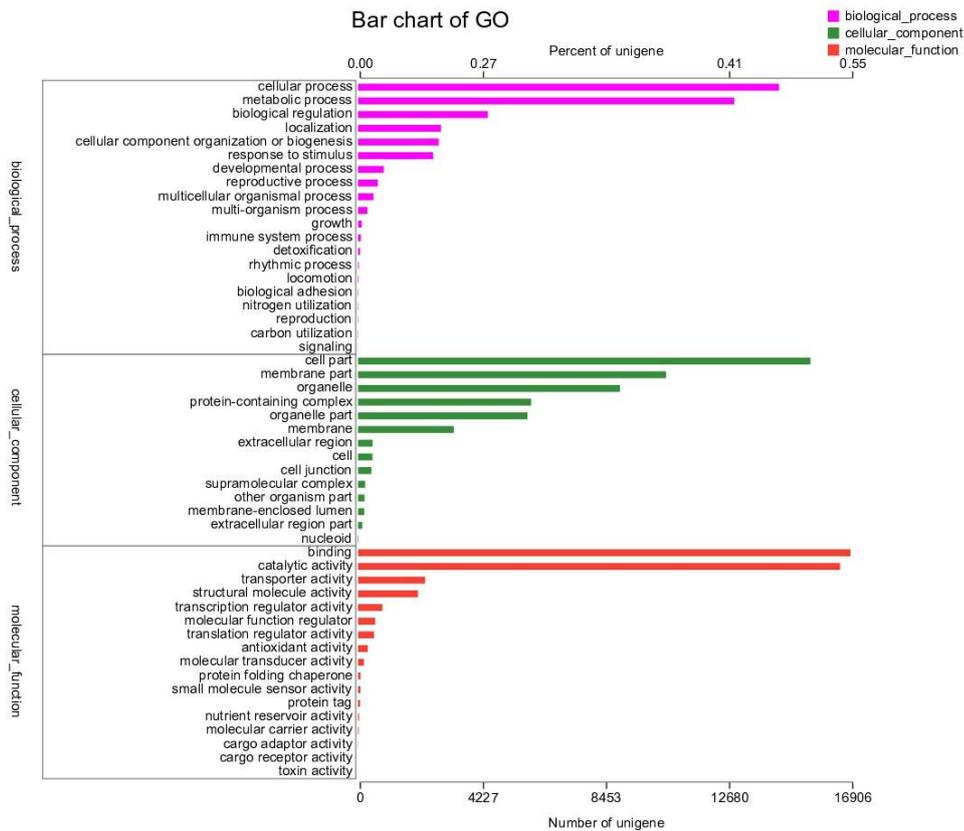


Figure S1. GO classification. The horizontal axis shows secondary nodes of three categories in GO. Left the vertical axis displays different genes in this secondary classification of GO is a percentage of the total annotated genes and right the vertical axis displays the numbers different genes of annotated genes in this secondary classification of GO. Three colors displays the three categories in GO (biological process, cellular component and molecular function).

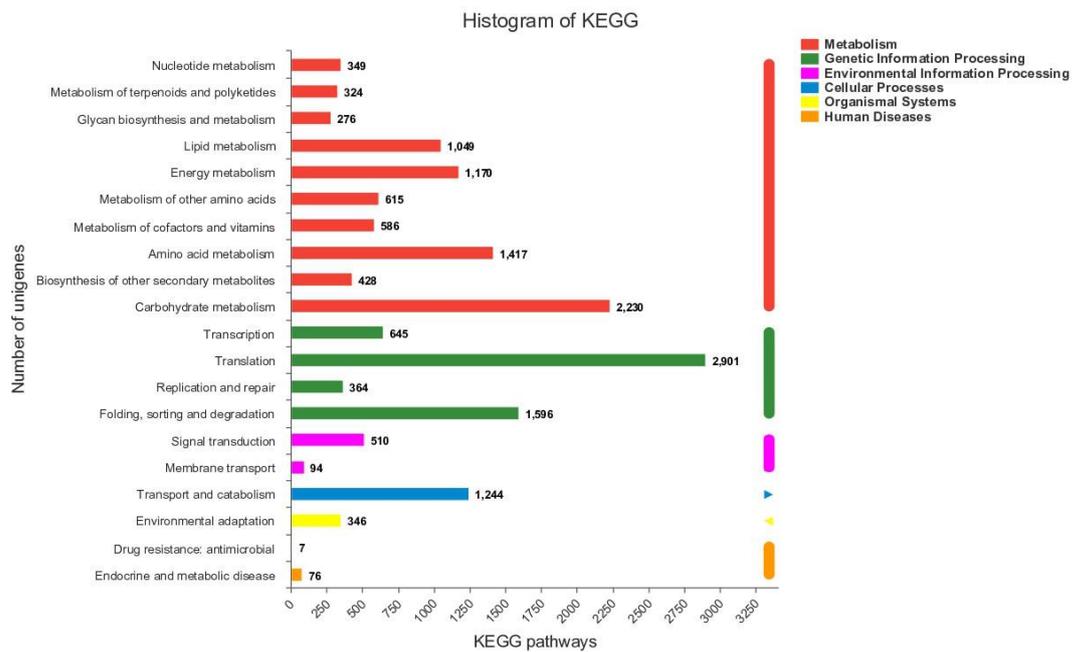


Figure S2. KEGG pathways. The gene numbers of KEGG pathways are shown on the horizontal axis and The categories of the KEGG are plotted on the vertical axis.

Table S1. Factor level coding table.

code	Treatment power (Kv)	Treatment time(s)
+1.07809	16.5	20.1
+1	16.4	20.0
0	14.8	18
-1	13.2	16
-1.07809	13.0	15.8
Change Interval	1.64	2

Table S2. Selected genes and primers for quantitative qRT-PCR.

Gene ID	Gene	Annotation	Primer sequence 5'-3'	Tm
TRINITY_DN28475_c0_g1	CAT	hypothetical protein Lal_00001570	F:ATGAGCTTCACCTTGTAGACG	54.3
			R:TTTCGCATCCCCTGTTCTC	54.5
TRINITY_DN20745_c0_g3	SOD	superoxidedismutase	F:ACAAGTCCACAACTCCCTG	53.7
			R:CCAAGGGCGTTAGAGTAGAAG	52.9
TRINITY_DN26350_c0_g1	SOD	iron/manganese superoxide dismutase	F:GTACCCGTGCAAGTCCAG	54.5
			R:GTTGATTTTGCCCATGCCG	53.5
TRINITY_DN19111_c1_g1	IDH	Isocitrate dehydrogenase(F:GTTGTAGGCTGTACTCTCACTG	52.9
TRINITY_DN47526_c0_g1	SOD	superoxide dismutase [Cu-Zn] 2 isoform X1	R:TTCGCAACGGATAAGATCGG	52.8
			F:GAGCTGGACACCATTCTG	53.6
TRINITY_DN29432_c0_g3	GYS	glycogen [starch] synthase-like	R:AAAGGTTAAGTTGAGGCTGC	53.3
			F:CGCTCTACAGTCACTACAAGTC	54.6
TRINITY_DN23668_c0_g1	GYG	glycogenin-2-like	R:GGAAATGGATGCTCAAACGTG	54.4
			F:GATGTTCCCTCTCGCTGTCTG	55.6
TRINITY_DN42038_c0_g2	TREH	putative trehalase	R:TGCTTCGAGACCATGAACC	55.1
			F:TTCTGGAACGACATCGCG	54.3
TRINITY_DN33795_c0_g1	TSL	putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 106 kDa subunit	R:GATCCTCCAGAGCGAGTAATC	54.9
			F:TCTTAAACACTAGAAGCGGCC	53.7
TRINITY_DN48162_c0_g1	TREH	lpha,alpha-trehalose-phosphate synthase [UDP-forming]-like	R:GTGATATACATGGAGCTGTGG	53.4
			F:TAGTGAAGTATCAATGGCAG	52.6
Action			R:GACAGAGTGTAGCAATTCAGC	52.8
			F:CTGAACCTTTCTGACCCAAT	52.7
			R:ACCTCACCGACCACCTAATG	53.4

Table S3. Summary for raw reads of two samples.

Samples	Read Number	Clean Data	GC Content	%≥Q30
CK	48,425,663	7,136,469,725	45.62%	94.39%
LTP	46,942,152	6,905,283,908	45.55%	94.26%

Note: GC content: Clean Data G and C percentage of the total bases; Q30:Quality Score of base is greater than or equal to 30% of the total bases.

Table S4. Summary of Illumina transcriptome assembly for *coix*.

Length Range	Transcript	Unigene
200-500	39,017(53%)	44,210(46%)
501-1000	15,164(21%)	21,478(22%)
1001-1500	7,195(10%)	11,764(12%)
1501-2000	4,985(7%)	8,039(8%)
2000+	6,910(9%)	10,752(13%)
Total Number	73,271	96,243
Total Length	60,441,462	88,799,710
N50 Length	1,415	1,518
average Length	8.249	922.66

Note: 39,017 transcripts were obtained. The total length was 60,441,462Mb, the average length was 8.249 bp, and the N50 length was 1,415.

Table S5. Different regulating patterns LTP_VS_CK for DEGs associated with plant hormone signal transduction-related genes.

Gene ID of maize genome database	NR	LTP_VS_CK	
		Log 2 FC	P Value
TRINITY_DN9754_c0_g2	Auxin-responsive protein SAUR24(SAUR)	2.88783	$P < 0.01$
TRINITY_DN37642_c0_g1	probable protein phosphatase 2C 51(PP2C)	5.93056	$P < 0.01$
TRINITY_DN12843_c0_g1	pathogenesis-related protein 1(PR1)	-2.495700	$P < 0.01$
TRINITY_DN11477_c0_g2	unnamed protein product, partial(TGA)	2.107612	$P < 0.01$
TRINITY_DN2205_c0_g1	hypothetical protein F0562_020491(SAUR)	3.435799	$P < 0.01$
TRINITY_DN33027_c0_g1	hypothetical protein F0562_020491(SAUR)	4.435799	$P < 0.01$
	mitogen-activated protein kinase homolog	6.146292	$P < 0.01$
TRINITY_DN29483_c0_g1	NTF3(ERK)		
TRINITY_DN4140_c0_g1	protein ABSCISIC ACID-INSENSITIVE 5(ABF)	2.095012	$P < 0.01$
TRINITY_DN11892_c0_g1	pathogenesis-related protein 1B-like(PR1)	5.930564	$P < 0.01$

Table S6. Different regulating patterns LTP_VS_CK for DEGs associated with peroxisome genes.

Gene ID of maize genome database	NR	LTP_VS_CK	
		Log 2 FC	P Value
TRINITY_DN16312_c0_g2	superoxide dismutase [Cu-Zn]-like (SOD)	6.830987	<i>P</i> < 0.01
TRINITY_DN16312_c0_g1	superoxide dismutase [Cu-Zn] (SOD)	7.193557	<i>P</i> < 0.01
TRINITY_DN8127_c0_g2	hypothetical protein FH972_021485(SOD)	-4.830987	<i>P</i> < 0.01
TRINITY_DN38931_c0_g2	isocitrate dehydrogenase [NADP](IDH)	-3.309034	<i>P</i> < 0.01
TRINITY_DN36553_c0_g2	catalase-1-like, partial(CAT)	-4.830987	<i>P</i> < 0.01
TRINITY_DN57189_c0_g1	hypothetical protein FH972_021485(SOD)	-4.724071	<i>P</i> < 0.01
TRINITY_DN33856_c0_g1	superoxide dismutase [Cu-Zn] (SOD)	5.930522	<i>P</i> < 0.01
TRINITY_DN42653_c0_g2	hypothetical protein Lal_00014973(SOD)	5.515485	<i>P</i> < 0.01
TRINITY_DN38931_c1_g2	isocitrate dehydrogenase [NADP] (IDH)	-4.667488	<i>P</i> < 0.01
TRINITY_DN50176_c0_g1	superoxide dismutase [Cu-Zn] (SOD)	6.638342	<i>P</i> < 0.01
TRINITY_DN26350_c0_g1	isocitrate dehydrogenase [NADP] (IDH)	-6.578221	<i>P</i> < 0.01
TRINITY_DN1700_c1_g1	manganese superoxide dismutase(SOD)	8.476213	<i>P</i> < 0.01
TRINITY_DN33846_c0_g1	superoxide dismutase [Fe] (SOD)	5.85901	<i>P</i> < 0.01
TRINITY_DN54652_c0_g1	catalase-1-like(CAT)	2.941602	<i>P</i> < 0.01
TRINITY_DN12191_c0_g3	NADP+-isocitrate dehydrogenase(IDH)	5.368685	<i>P</i> < 0.01
TRINITY_DN37217_c0_g5	peroxisomal catalase-like(CAT)	3.26914	<i>P</i> < 0.01
TRINITY_DN47526_c0_g1	superoxide dismutase [Cu-Zn] 2 isoform X1 (SOD)	8.402632	<i>P</i> < 0.01
TRINITY_DN14917_c0_g1	hypothetical protein FH972_026518 (SOD)	5.063830	<i>P</i> < 0.01
TRINITY_DN8127_c0_g3	hypothetical protein FH972_021485 (SOD)	2.045630	<i>P</i> < 0.01
TRINITY_DN19111_c0_g1	isocitrate dehydrogenase [NADP] (IDH)	6.809257	<i>P</i> < 0.01
TRINITY_DN20745_c0_g3	superoxide dismutase(SOD)	4.998735	<i>P</i> < 0.01
TRINITY_DN13998_c0_g1	iron/manganese superoxide dismutase(SOD)	5.063830	<i>P</i> < 0.01
TRINITY_DN42653_c0_g1	hypothetical protein Lal_00014973(SOD)	-5.224295	<i>P</i> < 0.01
TRINITY_DN39222_c0_g2	hypothetical protein F8388_016571(SOD)	-4.676807	<i>P</i> < 0.01
TRINITY_DN36375_c0_g2	isocitrate dehydrogenase/citrate hydrolyase(IDH)	5.368685	<i>P</i> < 0.01
TRINITY_DN28475_c0_g1	hypothetical protein Lal_00001570(CAT)	9.185821	<i>P</i> < 0.01
TRINITY_DN19111_c1_g1	Isocitrate dehydrogenase(IDH)	7.918882	<i>P</i> < 0.01
TRINITY_DN45986_c1_g2	superoxide dismutase [Cu-Zn] 2 isoform X3(SOD)	2.850836	<i>P</i> < 0.01
TRINITY_DN29164_c0_g2	hypothetical protein Lal_00009091(SOD)	5.976367	<i>P</i> < 0.01

Table S7. Different regulating patterns LTP_VS_CK for DEGs associated with Oxidative phosphorylation genes.

Gene ID of maize genome database	NR	LTP_VS_CK	
		Log 2 FC	P Value
TRINITY_DN29149_c0_g2	ATP synthase subunit H, mitochondrial-like	6.483063	$P < 0.01$
TRINITY_DN10066_c1_g1	ATP synthase subunit beta, mitochondrial-like	3.925721	$P < 0.01$
TRINITY_DN30170_c0_g2	NADH dehydrogenas	-6.233085	$P < 0.01$
TRINITY_DN31557_c0_g3	ATP synthase subunit 9, mitochondrial-like	4.760597	$P < 0.01$
TRINITY_DN41787_c1_g1	ATP synthase subunit alpha, mitochondrial-like	6.11109	$P < 0.01$
TRINITY_DN30578_c0_g2	ATP synthase subunit beta, mitochondrial-like	6.801051	$P < 0.01$
TRINITY_DN45668_c0_g1	V-type proton ATPase subunit E-like	-6.11109	$P < 0.01$
TRINITY_DN8274_c0_g2	ATP synthase subunit gamma, mitochondrial-like	7.000912	$P < 0.01$
TRINITY_DN57568_c0_g1	ATP synthase subunit delta, mitochondrial-like	5.830987	$P < 0.01$
TRINITY_DN18096_c0_g3	V-type proton ATPase catalytic subunit A	-4.60859	$P < 0.01$
TRINITY_DN32485_c0_g1	V-type proton ATPase subunit c'2	-5.778519	$P < 0.01$
TRINITY_DN1879_c1_g1	V-type proton ATPase 16 kDa proteolipid subunit-like	-5.345560	$P < 0.01$
TRINITY_DN16958_c0_g2	ATP synthase subunit f, mitochondrial-like	4.830987	$P < 0.01$
	nascent polypeptide-associated complex subunit		$P < 0.01$
TRINITY_DN57309_c0_g1	alpha-like	-6.345560	
TRINITY_DN36353_c0_g1	PREDICTED: V-type proton ATPase subunit a3-like	-5.608594	$P < 0.01$
TRINITY_DN46891_c0_g1	V-type proton ATPase subunit C-like isoform X3	4.783722	$P < 0.01$
TRINITY_DN29305_c0_g2	ATP synthase subunit gamma, mitochondrial	8.583698	$P < 0.01$
TRINITY_DN25132_c0_g2	vacuolar ATPase subunit B	4.883258	$P < 0.01$
	NADH-ubiquinone oxidoreductase 49 kDa subunit,		$P < 0.01$
TRINITY_DN54963_c0_g1	mitochondrial-like	2.382873	
	NADH dehydrogenase [ubiquinone] iron-sulfur		$P < 0.01$
TRINITY_DN3040_c0_g1	protein 5-B-like	2.442031	
TRINITY_DN48948_c0_g1	ATP synthase subunit O, mitochondrial-like	6.998735	$P < 0.01$
TRINITY_DN12809_c0_g1	ATP synthase subunit beta, mitochondrial	9.790148	$P < 0.01$
	NADH dehydrogenase [ubiquinone] flavoprotein 1,		$P < 0.01$
TRINITY_DN40245_c1_g1	mitochondrial	4.883258	
	NADH dehydrogenase [ubiquinone] 1 beta		$P < 0.01$
TRINITY_DN9790_c0_g2	subcomplex subunit like	5.834348	
	NADH-ubiquinone oxidoreductase 23 kDa subunit,		$P < 0.01$
TRINITY_DN43032_c0_g2	mitochondrial-like	2.155170	
TRINITY_DN4804_c0_g1	V-type proton ATPase subunit G-like	2.624066	$P < 0.01$
TRINITY_DN23959_c0_g2	V-type proton ATPase subunit a-like	2.595277	$P < 0.01$
	NADH-ubiquinone oxidoreductase 78 kDa subunit,		$P < 0.01$
TRINITY_DN11874_c0_g1	mitochondrial-like	2.205955	
TRINITY_DN50791_c0_g1	Vacuolar H ⁺ -ATPase V1 sector, subunit E	4.435799	$P < 0.01$
TRINITY_DN22644_c0_g1	V-type proton ATPase catalytic subunit A-like	3.109262	$P < 0.01$
	NADH-ubiquinone oxidoreductase 51 kDa subunit,		$P < 0.01$
TRINITY_DN34068_c0_g1	mitochondrial-like	2.45301	

	NADH dehydrogenase [ubiquinone] 1 alpha		
TRINITY_DN56623_c0_g1	subcomplex subunit 9, mitochondrial	4.205186	<i>P</i> < 0.01
	NADH-ubiquinone oxidoreductase 30.4 kDa subunit,		
TRINITY_DN13148_c0_g1	mitochondrial-like	2.541964	<i>P</i> < 0.01
TRINITY_DN54444_c0_g1	hypothetical protein CDL12_30575	4.020764	<i>P</i> < 0.01
TRINITY_DN34961_c0_g1	V-type proton ATPase subunit F-like	2.096662	<i>P</i> < 0.01
TRINITY_DN57342_c0_g1	V-type proton ATPase subunit c'2	6.146292	<i>P</i> < 0.01
TRINITY_DN6706_c0_g2	ATP synthase subunit alpha, mitochondrial-like	3.073223	<i>P</i> < 0.01

Table S8. Different regulating patterns LTP_VS_CK for DEGs associated with starch and sucrose genes.

Gene ID of maize genome database	NR	LTP_VS_CK	
		Log 2 FC	P Value
TRINITY_DN29432_c0_g3	glycogen [starch] synthase-like (GYS)	-5.54719	<i>P</i> < 0.01
TRINITY_DN23668_c0_g1	glycogenin-2-like (GYG)	5.66749	<i>P</i> < 0.01
TRINITY_DN23668_c0_g2	glycogenin-2-like (GYG)	5.97783	<i>P</i> < 0.01
TRINITY_DN42038_c0_g2	putative trehalase (TREH)	5.93052	<i>P</i> < 0.01
TRINITY_DN55684_c0_g1	glycogen [starch] synthase-like (GYS)	-4.27156	<i>P</i> < 0.01
TRINITY_DN43195_c0_g1	glycogen phosphorylase-like (PYG)	6.54719	<i>P</i> < 0.01
	probable glucan endo-1,3-beta-glucosidase eglC (EGLC)	5.205186	<i>P</i> < 0.01
TRINITY_DN52727_c0_g1	alpha-glucosidase-like (malZ)	2.298296	<i>P</i> < 0.01
TRINITY_DN34003_c0_g2	alpha-glucosidase-like (malZ)	3.080704	<i>P</i> < 0.01
TRINITY_DN34003_c0_g1	alpha-glucosidase-like (malZ)	3.080704	<i>P</i> < 0.01
TRINITY_DN22999_c0_g3	probable alpha/beta-glucosidase agdC (malZ)	4.883258	<i>P</i> < 0.01
TRINITY_DN46398_c1_g1	alpha-glucosidase-like (malZ)	5.49993	<i>P</i> < 0.01
TRINITY_DN33678_c0_g1	1,4-alpha-glucan-branching enzyme-like (GBE1)	3.106899	<i>P</i> < 0.01
TRINITY_DN19808_c0_g2	alpha-glucan phosphorylase, H isozyme (PYG)	4.976368	<i>P</i> < 0.01
TRINITY_DN22296_c0_g9	glycogen phosphorylase-like (PYG)	2.604698	<i>P</i> < 0.01
TRINITY_DN16888_c0_g1	alpha-amylase-like (AMY)	3.336264	<i>P</i> < 0.01
TRINITY_DN29432_c1_g1	glycogen [starch] synthase-like (GYS)	3.120298	<i>P</i> < 0.01
	probable glucan endo-1,3-beta-glucosidase eglC (EGLC)	2.83619	<i>P</i> < 0.01
TRINITY_DN15372_c0_g1	trehalose-phosphatase-like (TPS)	2.625025	<i>P</i> < 0.01
TRINITY_DN1119_c0_g2	trehalose-phosphatase-like (TPS)	2.625025	<i>P</i> < 0.01
TRINITY_DN31150_c0_g1	endoglucanase 1-like (CBH2)	4.191381	<i>P</i> < 0.01
TRINITY_DN48217_c0_g1	glucoamylase-like (SGA1)	5.676808	<i>P</i> < 0.01
TRINITY_DN46738_c0_g1	alpha-glucosidase-like (IMA)	2.146293	<i>P</i> < 0.01
TRINITY_DN42135_c0_g1	glucoamylase-like (SGA1)	3.473199	<i>P</i> < 0.01
TRINITY_DN23703_c0_g3	glycogen debranching enzyme-like(AGL)	2.883258	<i>P</i> < 0.01
TRINITY_DN23971_c0_g1	alpha-glucosidase-like (IMA)	4.883258	<i>P</i> < 0.01
	putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 106 kDa subunit (TSL1)	2.020163	<i>P</i> < 0.01
TRINITY_DN31074_c0_g1	alpha,alpha-trehalose-phosphate synthase [UDP-forming] 1-like (TPS)	8.546223	<i>P</i> < 0.01
TRINITY_DN56735_c0_g1			