

# The Effect of Mitochondria on *Ganoderma lucidum* Growth and Bioactive Components Based on Transcriptomics

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## Title page

**Figure 1. The process of constructing isonuclear alloplasmic.**

**Figure 2. The PCR results of isonuclear alloplasmic strain S1-S5.** (A) The PCR results of samples strain by the primers of nuclear genome. M indicates the 2,000 bp DNA marker; lane 1-5, 6-10, 11-15, 16-20, and 21-25 template DNA was S1-S5 in each group and primer were Nc-119, Nc-TL, Nc-WBL, Nc-SL4, and Nc-SL10, separately; lane 26 is negative control with ddH<sub>2</sub>O instead of DNA. (B) The PCR results of samples strain by the primers of mtDNA. M indicates the 2,000 bp DNA marker; lane 1-4 template DNA was S1 and primer were primer 6-9 in table s1; lane 5-8 template DNA was S2 and primer were primer 6-9 in table s1; lane 9-12 template DNA was S3 and primer were primer 6-9 in table s1; lane 13-16 template DNA was S4 and primer were primer 6-9 in table s1; lane 17-20 template DNA was S5 and primer were primer 6-9 in table s1; lane 21 is negative control with ddH<sub>2</sub>O instead of DNA.

**Figure 3. Biological characteristics of five isonuclear alloplasmic strains.** (A). colony and fruit bodies morphology. (B) mycelial growth rate in PDA. (C) mycelial growth rate in solid-state fermentation. The same letters mean not significantly different ( $p>0.05$ ).

**Figure 4. Correlation and DEGs analysis between strain S1 and S5.** (A) Pearson correlation analysis between samples of strain S1 and S5. (B) DEGs between strain S1 and S5.

**Figure 5 Enrichment analysis of DEGs.** (A) GO enrichment of DEGs. (B) Bubble plot of KEGG enrichment of DEGs.

**Figure 6. Polysaccharide and triterpenoid related pathways of isonuclear alloplasmic based on transcriptome analysis.** (A) pentose and glucuronate interconversions pathway. (B) starch and sucrose metabolism pathway. (C) steroid biosynthesis pathway; (D) Changes in expression of genes involved in pathways.

**Table 1.** Mushroom yield, basidiospores yield, and polysaccharide and triterpenoid

content in isonuclear alloplasmic strains S1-S5.

**Table S1.** Specific primers for nonconserved regions among nucleus DNA and mtDNA of *G.lucidum* strains.

Table S2. Summary of RNA-Seq data.

**Figure S1.** Pearson correlation analysis between samples among strain S1-S5.

**Supplementary tables and figures**

Table S1. Specific primers for nonconserved regions among nucleus DNA and mtDNA of *G.lucidum* strains.

Primer number	Primer name	Strain	Location	Primer sequence (5'→3')	Production size (bp)
1	Nc-119	M119-M71	nucleus DNA	F:GACAACCAGTCACGCTCAAG; R:CTATCCCATCCGTACTCCTG	418
2	Nc-TL	MTL	nucleus DNA	F:TTCACATCCCTCTCGTCTATGC; R:TACTCCCCTCCTGATCTTTCCT	643
3	Nc-WBL	MWBL	nucleus DNA	F:CGCAACACACAGGAGAATCAAC; R:CAACTCAGACTTTCC	594
4	Nc-SL10	MSL10	nucleus DNA	F:GTACATCCGTTCCGGCTTCG; R:TGCTTTGGTGGGGTTCAAG	449
5	Nc-SL4	MSL4	nucleus DNA	F:ACCAAAACCATGAAATCCAACAG; R:GGAGGGAGATAATCAAACGAAAA	465
6	Mito-119-TL	MTL; M119-M71	mtDNA	F:TAGCGGTCTTAAGTATGAGGA; R:GGTATTCCATCTTTTCGTCAT	MTL:261; M119-M71:1933
7	Mito-119-WBL	MWBL; M119-M71	mtDNA	F:AACCATATCTCACACACCATCT; R:ATCAGCACTTTTTGTAAATTC	MWBL:1117; M119-M71:824
8	Mito-119-SL10	MSL10; M119-M71	mtDNA	F:GATAGGTACTGCATTCTTGGG; R:CAGGAACAATAGATGCTGGTG	MSL10:1491; M119-M71:401
9	Mito-119-SL4	MSL4; M119-M71	mtDNA	F:TATCAGCACCTGGAGTGCAAGT; R:CATCTCCTTCAATTAACCCTGC	MSL4:253; M119-M71:1528

Table S2. Summary of RNA-Seq data.

Sample	Raw Reads	Raw Bases	Clean Reads	Clean Bases	Error Rate	Q20	Q30	GC Content
S1_1	21559906	3.23G	21464430	3.22G	0.03%	97.60%	93.68%	59.67%
S1_2	25145530	3.77G	25033436	3.76G	0.03%	97.54%	93.54%	59.56%
S1_3	22296198	3.34G	22206522	3.33G	0.03%	97.56%	93.60%	59.70%
S2_1	27409858	4.11G	27312980	4.1G	0.03%	97.72%	93.95%	59.62%
S2_2	30734054	4.61G	30620530	4.59G	0.03%	97.55%	93.63%	59.52%
S2_3	22500770	3.37G	22421140	3.36G	0.03%	97.72%	93.90%	59.41%
S3_1	24568268	3.68G	24468368	3.67G	0.03%	97.72%	93.91%	59.53%
S3_2	23816140	3.57G	23720756	3.56G	0.03%	97.65%	93.84%	59.55%
S3_3	20727876	3.1G	20650116	3.1G	0.03%	97.80%	94.09%	59.50%
S4_1	22344306	3.35G	22264820	3.34G	0.03%	97.79%	94.00%	59.66%
S4_2	30760148	4.61G	30650670	4.6G	0.03%	97.79%	94.08%	59.63%
S4_3	26272338	3.94G	26165408	3.92G	0.03%	97.51%	93.63%	59.60%
S5_1	28972968	4.34G	28860520	4.33G	0.03%	97.53%	93.64%	59.70%
S5_2	19012984	2.85G	18930552	2.84G	0.03%	97.61%	93.68%	59.50%
S5_3	24246148	3.63G	24147638	3.62G	0.03%	97.55%	93.67%	59.61%

Figure S1. Pearson correlation analysis between samples among strain S1-S5.

