外源硒缓解甜瓜幼苗镉毒害的抗氧化抑镉机制

邵勤[1,2] 徐富豪[1] 曾俊涛[1] 罗浩[1] 李晓鹏[1,2] 陈娜[1,2*]

（1. 宜春学院生命科学与资源环境学院，宜春 336000；2. 江西省教育厅赣西特色作物种质资源创新与绿色高值利用重点实验室，宜春 336000）

Antioxidant and Cadmium Accumulation Inhibition Mechanisms of Exogenous Selenium in Alleviating Cadmium Toxicity in Muskmelon Seedlings

SHAO Qin[1,2] XU Fu-hao[1] ZENG Jun-tao[1] LUO Hao[1] LI Xiao-peng[1,2] CHEN Na[1,2*]

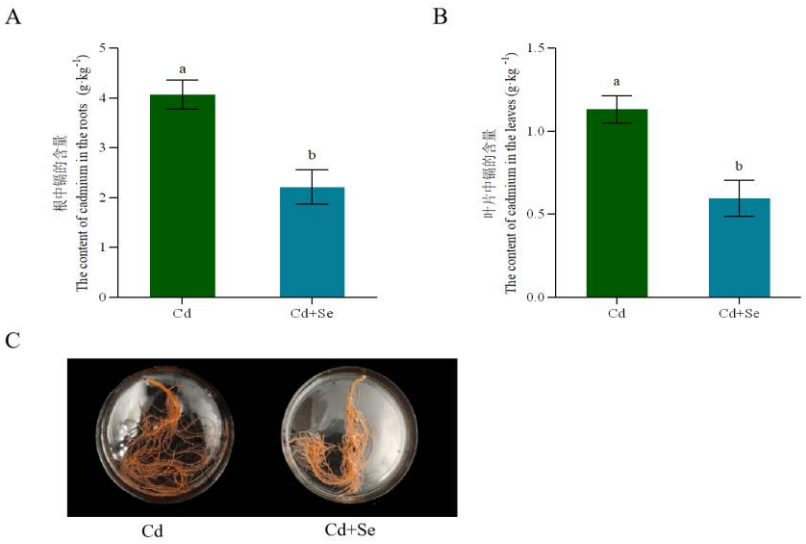
(1. *School of Life Sciences and Environmental Resources*, *Yichun University*, *Yichun* 336000; 2. *Key Laboratory of Germplasm Innovation and Green High-Value Utilization for Specialty Crops in Western Jiangxi*, *Jiangxi Education Department*, *Yichun* 336000)

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表 S1 转录组测序数据质量统计

Table S1 Quality statistics of transcriptome sequencing data

样本名称 Sample name	原始数据 Raw Reads	Clean Reads	Clean Base (G)	比对到参考基因组的 reads 数 Reads mapped	唯一比对到参考基因组的 reads 数 Unique mapped	Q20 (%)	Q30 (%)	Error Rate (%)
CK-1	45289866	43525128	6.53	41244415 (94.76%)	40473992 (92.99%)	96.97	91.93	0.03
CK-2	45311536	43919138	6.59	41317945 (94.08%)	40579982 (92.40%)	96.72	91.53	0.03
CK-3	51359066	49547402	7.43	46840722 (94.54%)	46003671 (92.85%)	97.03	92.23	0.03
Cd-1	53090126	50416374	7.56	47757331 (94.73%)	46770257 (92.77%)	96.98	91.98	0.03
Cd-2	50263826	46929912	7.04	43531129 (92.76%)	42739011 (91.07%)	97.06	92.14	0.03
Cd-3	54056220	51211048	7.68	48801917 (95.30%)	47934550 (93.60%)	97.14	92.29	0.03
Cd+Se-1	47049928	45007690	6.75	42572174 (94.59%)	41725515 (92.71%)	96.91	91.83	0.03
Cd+Se-2	49474072	46760976	7.01	44179505 (94.48%)	43404361 (92.82%)	97.06	92.14	0.03
Cd+Se-3	59377530	57171838	8.58	54174343 (94.76%)	53005462 (92.71%)	96.99	91.99	0.03

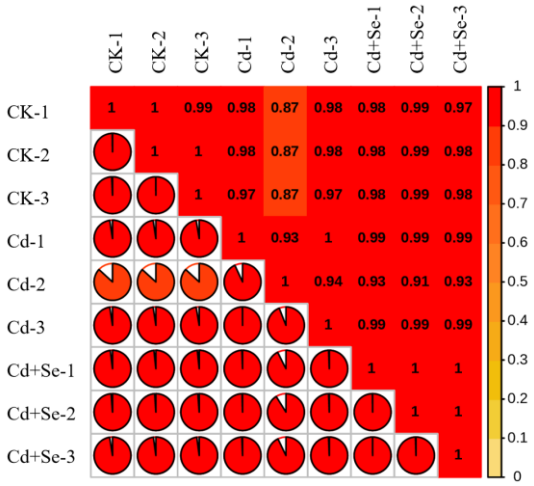


A：甜瓜根中镉的含量；B：甜瓜叶片中镉的含量。C：使用二硫化物（二苯基硫脲）法对甜瓜根部镉积累进行组织化学染色。数据为三个生物重复样本的平均值±标准误（SE）。不同字母表示各组间具有统计学显著差异（Tukey's honest significant difference test, $P < 0.05$）

A: The cadmium content in the roots of melons; B: The cadmium content in the leaves of melons. C: Histochemical staining of Cd accumulation in melon roots using dithizone (diphenylthiocarbazone) method. Data are means of three biological replicates ± standard error (SE). Different letters indicate statistically significant differences among groups (Tukey's honest significant difference test, $P < 0.05$)

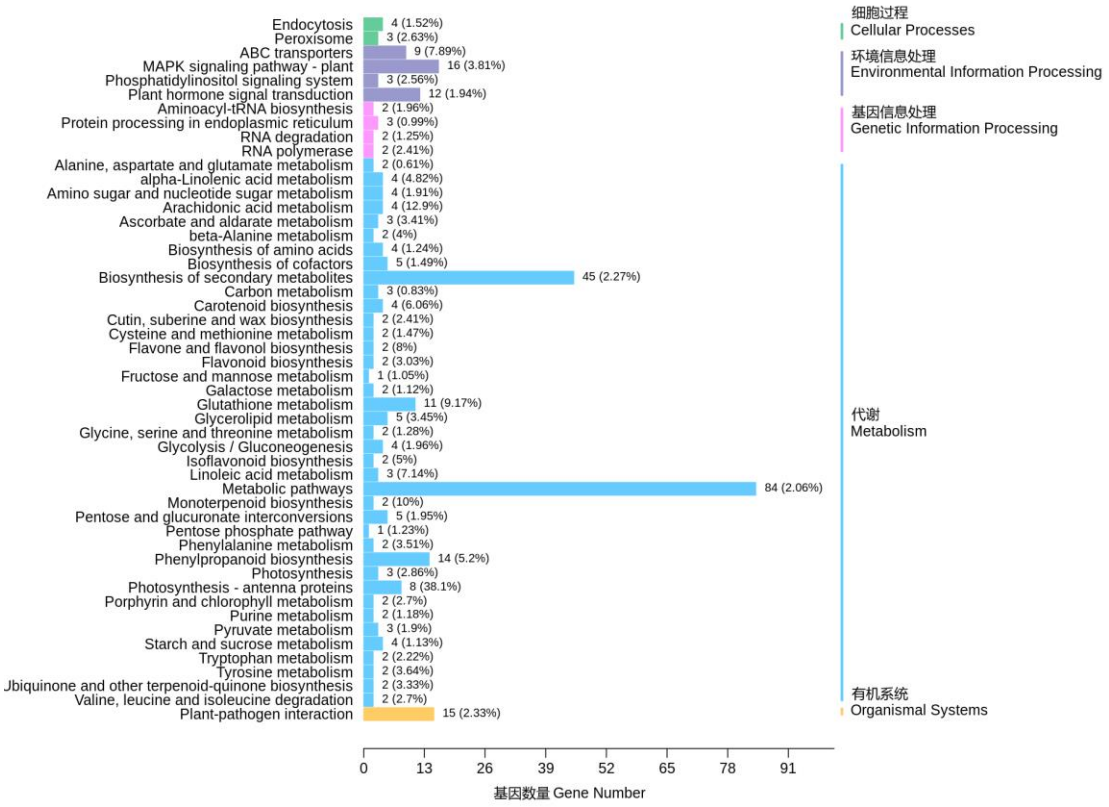
图S1　硒处理对镉胁迫下甜瓜幼苗镉积累的影响

Fig. S1　The effect of Se treatment on the accumulation of Cd in melon seedlings under Cd stress



图S2　不同处理组转录组间的Pearson相关分析

Fig. S2　Pearson correlation analysis between transcriptomes of different treatment groups

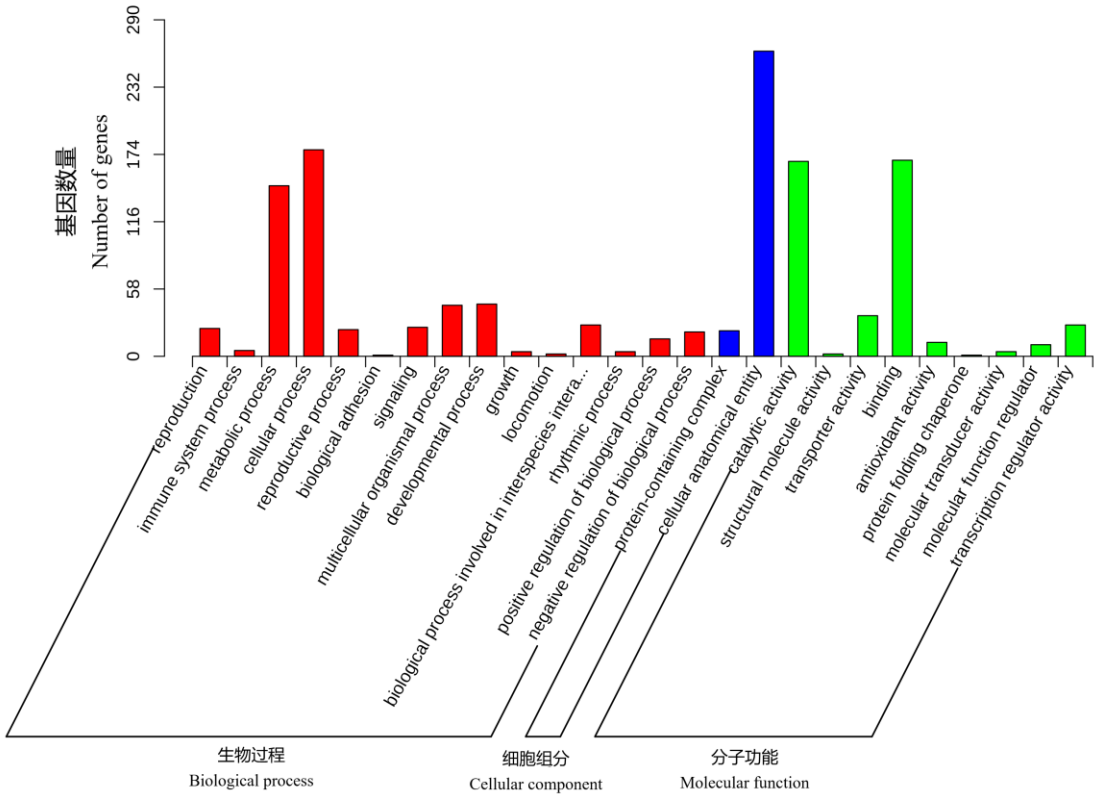


括号内为注释到该通路的差异表达基因数占注释到该背景通路的背景基因数的百分比

The parentheses represents the percentage of differentially expressed genes annotated to this pathway compared to the background genes annotated to this pathway

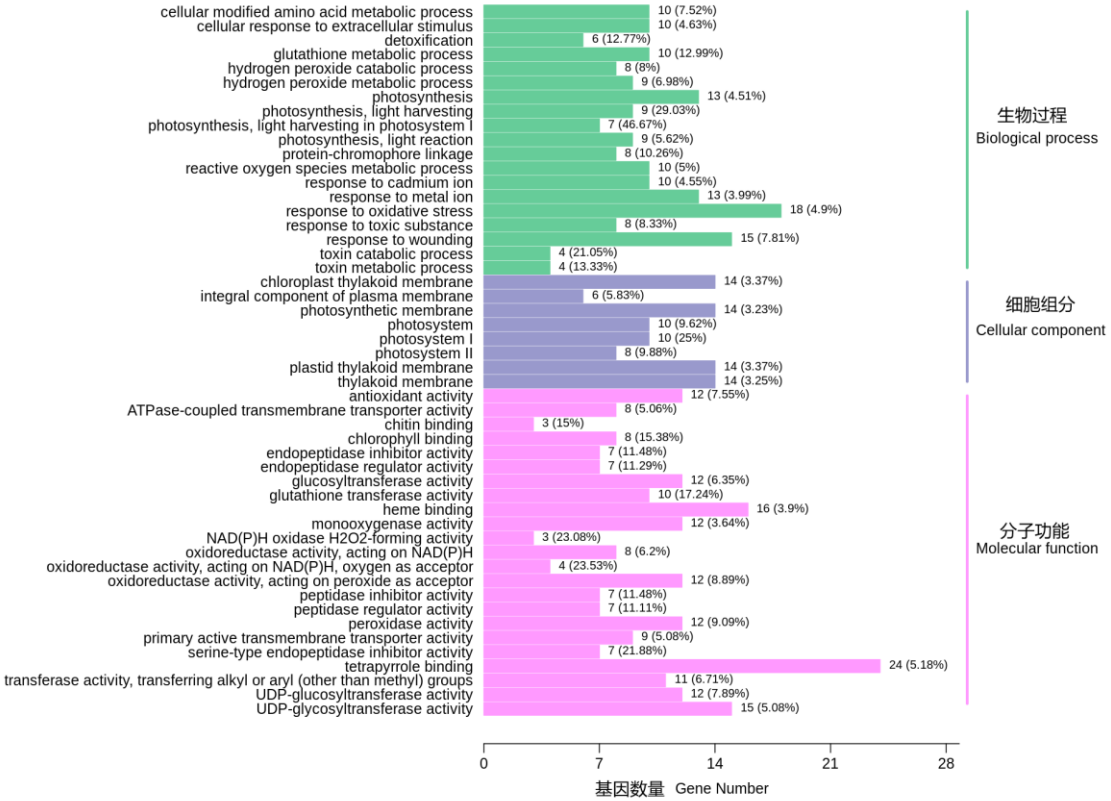
图S3　差异表达基因KEGG分类

Fig. S3　Bar chart of KEGG classification of differentially expressed genes



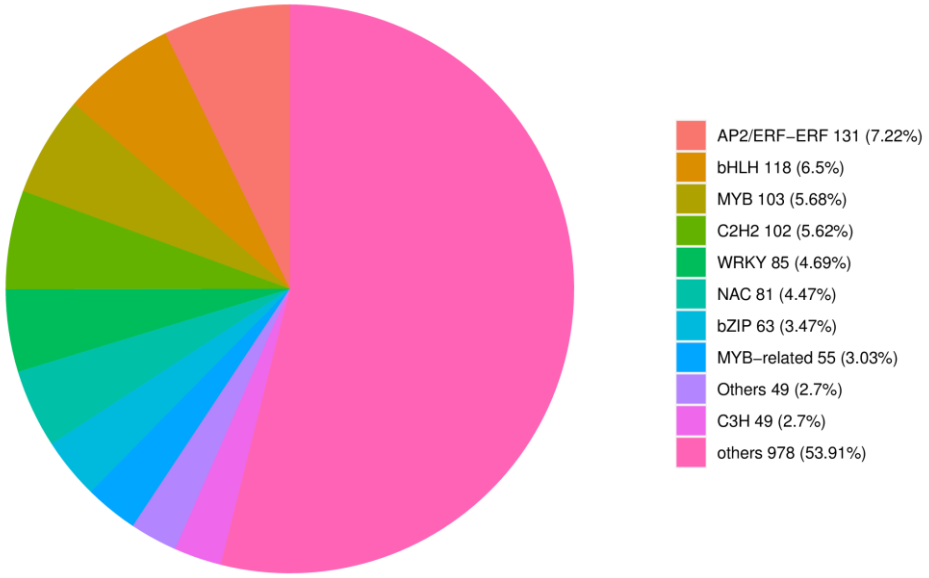
图S4　差异表达基因GO分类

Fig. S4　Differentially expressed gene GO classification



图S5　差异表达基因GO富集

Fig. S5　Differentially expressed gene GO enrichment



图S6　转录因子家族统计

Fig. S6　Statistics of transcription factor families