**α-Linolenic acid alleviates aluminum toxicity in RAW264.7 cells by antioxidative and anti-inflammatory effects**

**Qiqi Jia,b, Ling Hana, Tianyuan Zhangc, Xiaoyang Xia\*a, Xia Xiang\*a**

a Oil Crops Research Institute, Chinese Academy of Agricultural Sciences, Oil Crops and Lipids Process Technology National & Local Joint Engineering Laboratory, Key Laboratory of Oilseeds processing, Ministry of Agriculture and Rural Affairs, Hubei Key Laboratory of Lipid Chemistry and Nutrition, Wuhan 430062, China.

b Key Laboratory of Plant Resource Conservation and Germplasm Innovation in Mountainous Region (Ministry of Education), Collaborative Innovation Center for Mountain Ecology & Agro-Bioengineering (CICMEAB), College of Life Sciences/Institute of Agro-bioengineering, Guizhou University, Guiyang, Guizhou, PR China.

c State Key Laboratory of Agricultural Microbiology, College of Life Science and Technology, Huazhong Agricultural University, Wuhan, Hubei 430070, China

\*Corresponding author

*E-mail:* [xiangxia0130@163.com](mailto:xiangxia0130@163.com)*;* [xia\_xiaoyang@126.com](mailto:xia_xiaoyang@126.com;)

*Tel:* +86-27-86711526.



**Fig. S1. Effects of Al and ALA on cell apoptosis.** (A) Analysis of apoptosis in RAW264.7 cells by using DAPI staining. (B) The cell apoptosis was observed with flow cytometry by using Annexin V-FITC/PI. The data obtained from three individual experiments were collected shown as mean ± SD. \**P*<0.05, \*\*\**P*<0.001 compared with the control group. ###*P*<0.001 compared with the Al group.

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| Table S1. Sequences of primers used for real-time polymerase chain reaction | | |
| Target | Direction | Sequence 5'———3’ |
| Trib3 | FORWARD | TGCCTGCGTGATGACTGGAT |
| REVERSE | CATCAGCCGCTTTGCCAGAG |
| Myc | FORWARD | ACTTCTCCACCGCCGATCAG |
| REVERSE | GTCTCGTCGTCAGGATCGCA |
| Traf1 | FORWARD | CCCTTTGCAGGTGTTGGCTG |
| REVERSE | AGCAGGTACAGGTGGGAGGA |
| Birc3 | FORWARD | GCGCCTTTCTAGCCAAGCTG |
| REVERSE | CAGCACGAGCCAGACTCCTT |
| Osm | FORWARD | GCTGCAGAATCAGGCGAACC |
| REVERSE | AGTTGCCGGAGTGTGTCCTC |
| Cd40 | FORWARD | TGCGGCGTTCACTGTAAGGA |
| REVERSE | AGCCAGTACCCTGCTGATGG |
| Nfkbia | FORWARD | CGGTGGACCTGCAGAATCCT |
| REVERSE | GCTGCTGCTGTATCCGGGTA |
| Cxcl2 | FORWARD | CCACCAACCACCAGGCTACA |
| REVERSE | ATGACTTCTGTCTGGGCGCA |
| Tnfaip3 | FORWARD | ATCCTACTGCTGCCAGCTGG |
| REVERSE | AGATGTGCTCCGCCTACGTC |
| tnf | FORWARD | CCAGCCGATGGGTTGTACCT |
| REVERSE | CAAATCGGCTGACGGTGTGG |

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| Table S2. Summary of Mus musculus transcriptome raw data sequenced by the Illumina platform | | | | | |
| Sample name | Total reads | Total bases | GC content | Q20 | Q30 |
| Al1 | 51,473,474 | 7,721,021,100 | 51.32% | 97.78% | 93.82% |
| Al2 | 50,072,094 | 7,510,814,100 | 50.88% | 97.53% | 93.28% |
| Al3 | 44,024,250 | 6,603,637,500 | 51.06% | 97.62% | 93.47% |
| ALA1 | 43,487,772 | 6,523,165,800 | 51.28% | 97.55% | 93.37% |
| ALA2 | 41,643,244 | 6,246,486,600 | 51.23% | 97.84% | 94.00% |
| ALA3 | 44,199,900 | 6,629,985,000 | 51.12% | 97.72% | 93.70% |
| Al+ALA1 | 44,952,906 | 6,742,935,900 | 51.02% | 97.93% | 94.17% |
| Al+ALA 2 | 45,189,056 | 6,778,358,400 | 51.03% | 97.85% | 93.98% |
| Al+ALA3 | 41,642,674 | 6,246,401,100 | 51.00% | 97.81% | 93.89% |
| Control1 | 41,625,988 | 6,243,898,200 | 51.19% | 97.84% | 93.99% |
| Control2 | 41,504,958 | 6,225,743,700 | 51.15% | 97.71% | 93.76% |
| Control3 | 40,888,278 | 6,133,241,700 | 51.14% | 97.71% | 93.70% |
| Total | 530,704,594 | 79,605,689,100 |  |  |  |

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| Table S3. Summary of Mus musculus transcriptome clean data sequenced by the Illumina platform | | | | | |
| Sample name | Total reads | Total bases | GC content | Q20 | Q30 |
| Al1 | 50,427,948 | 7,564,192,200 | 51.31% | 97.80% | 93.84% |
| Al2 | 48,818,838 | 7,322,825,700 | 50.85% | 97.57% | 93.33% |
| Al3 | 42,646,984 | 6,397,047,600 | 51.03% | 97.65% | 93.51% |
| ALA1 | 42,363,716 | 6,354,557,400 | 51.24% | 97.58% | 93.41% |
| ALA2 | 40,849,088 | 6,127,363,200 | 51.22% | 97.86% | 94.02% |
| ALA3 | 43,033,632 | 6,455,044,800 | 51.10% | 97.75% | 93.74% |
| Al/ALA1 | 43,514,128 | 6,527,119,200 | 50.99% | 97.97% | 94.23% |
| Al/ALA 2 | 43,666,102 | 6,549,915,300 | 51.00% | 97.88% | 94.01% |
| Al/ALA3 | 40,193,762 | 6,029,064,300 | 50.96% | 97.83% | 93.92% |
| Control1 | 40,452,512 | 6,067,876,800 | 51.17% | 97.88% | 94.03% |
| Control2 | 40,389,652 | 6,058,447,800 | 51.12% | 97.74% | 93.79% |
| Control3 | 39,980,940 | 5,997,141,000 | 51.11% | 97.73% | 93.73% |
| Total | 516,337,302 | 77,450,595,300 |  |  |  |

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| Table S4. KEGG pathway enrichment of DEGs in control group versus Al group | | | | |
| ID | Description | GeneRatio | BgRatio | p-value |
| ko04110 | Cell cycle | 45/649 | 124/7678 | 2.93E-18 |
| ko03030 | DNA replication | 20/649 | 35/7678 | 2.53E-13 |
| ko03460 | Fanconi anemia pathway | 20/649 | 51/7678 | 1.65E-09 |
| ko04115 | p53 signaling pathway | 21/649 | 66/7678 | 4.96E-08 |
| ko04111 | Cell cycle - yeast | 19/649 | 60/7678 | 2.36E-07 |
| ko04113 | Meiosis - yeast | 16/649 | 53/7678 | 4.30E-06 |
| ko03430 | Mismatch repair | 10/649 | 22/7678 | 4.40E-06 |
| ko03440 | Homologous recombination | 11/649 | 28/7678 | 8.16E-06 |
| ko04668 | TNF signaling pathway | 24/649 | 110/7678 | 1.14E-05 |
| ko05166 | Human T-cell leukemia virus 1 infection | 44/649 | 277/7678 | 2.76E-05 |
| ko04060 | Cytokine-cytokine receptor interaction | 42/649 | 261/7678 | 3.07E-05 |
| ko03410 | Base excision repair | 10/649 | 33/7678 | 0.000268 |
| ko04064 | NF-kappa B signaling pathway | 18/649 | 93/7678 | 0.000667 |
| ko05203 | Viral carcinogenesis | 34/649 | 228/7678 | 0.000738 |
| ko03420 | Nucleotide excision repair | 11/649 | 44/7678 | 0.000833 |
| ko05322 | Systemic lupus erythematosus | 22/649 | 127/7678 | 0.000876 |
| ko05222 | Small cell lung cancer | 16/649 | 84/7678 | 0.001558 |
| ko00240 | Pyrimidine metabolism | 18/649 | 100/7678 | 0.001606 |
| ko00480 | Glutathione metabolism | 12/649 | 57/7678 | 0.002453 |
| ko05202 | Transcriptional misregulation in cancer | 25/649 | 164/7678 | 0.00264 |
| ko04114 | Oocyte meiosis | 19/649 | 113/7678 | 0.002738 |
| ko04710 | Circadian rhythm | 8/649 | 31/7678 | 0.003415 |
| ko05200 | Pathways in cancer | 49/649 | 395/7678 | 0.00374 |
| ko04010 | MAPK signaling pathway | 34/649 | 252/7678 | 0.00408 |
| ko02010 | ABC transporters | 10/649 | 46/7678 | 0.004323 |
| ko05332 | Graft-versus-host disease | 11/649 | 54/7678 | 0.004791 |
| ko04978 | Mineral absorption | 9/649 | 40/7678 | 0.005246 |
| ko04940 | Type I diabetes mellitus | 12/649 | 63/7678 | 0.005805 |
| ko05219 | Bladder cancer | 9/649 | 41/7678 | 0.00623 |
| ko04914 | Progesterone-mediated oocyte maturation | 15/649 | 89/7678 | 0.007187 |
| ko04015 | Rap1 signaling pathway | 29/649 | 215/7678 | 0.007689 |
| ko05330 | Allograft rejection | 11/649 | 58/7678 | 0.008375 |
| ko04672 | Intestinal immune network for IgA production | 9/649 | 43/7678 | 0.008619 |
| ko05168 | Herpes simplex virus 1 infection | 28/649 | 208/7678 | 0.008958 |
| ko05323 | Rheumatoid arthritis | 14/649 | 83/7678 | 0.009173 |
| ko05321 | Inflammatory bowel disease (IBD) | 11/649 | 59/7678 | 0.009533 |
| ko05140 | Leishmaniasis | 12/649 | 67/7678 | 0.009572 |
| ko04514 | Cell adhesion molecules (CAMs) | 23/649 | 164/7678 | 0.0106 |
| ko05150 | Staphylococcus aureus infection | 10/649 | 52/7678 | 0.010606 |
| ko04145 | Phagosome | 24/649 | 177/7678 | 0.013645 |
| ko05020 | Prion diseases | 7/649 | 32/7678 | 0.015512 |
| ko04068 | FoxO signaling pathway | 19/649 | 134/7678 | 0.017143 |
| ko05161 | Hepatitis B | 20/649 | 145/7678 | 0.019454 |
| ko04151 | PI3K-Akt signaling pathway | 40/649 | 341/7678 | 0.020126 |
| ko04933 | AGE-RAGE signaling pathway in diabetic complications | 15/649 | 101/7678 | 0.021916 |
| ko05145 | Toxoplasmosis | 16/649 | 113/7678 | 0.027574 |
| ko04360 | Axon guidance | 17/649 | 126/7678 | 0.035751 |
| ko04210 | Apoptosis | 12/649 | 81/7678 | 0.038514 |
| ko04350 | TGF-beta signaling pathway | 12/649 | 83/7678 | 0.045285 |
| ko04640 | Hematopoietic cell lineage | 12/649 | 84/7678 | 0.048961 |
| ko00982 | Drug metabolism - cytochrome P450 | 10/649 | 66/7678 | 0.0491 |
| ko05205 | Proteoglycans in cancer | 24/649 | 200/7678 | 0.049867 |
| ko04630 | JAK-STAT signaling pathway | 19/649 | 159/7678 | 0.077321 |

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| Table S5. KEGG pathway enrichment of DEGs in Al group versus Al+ALA group | | | | |
| ID | Description | GeneRatio | BgRatio | p-value |
| ko03030 | DNA replication | 15/267 | 35/7678 | 1.55E-13 |
| ko04110 | Cell cycle | 18/267 | 124/7678 | 2.33E-07 |
| ko04111 | Cell cycle - yeast | 12/267 | 60/7678 | 7.71E-07 |
| ko03460 | Fanconi anemia pathway | 11/267 | 51/7678 | 1.01E-06 |
| ko04113 | Meiosis - yeast | 11/267 | 53/7678 | 1.52E-06 |
| ko03410 | Base excision repair | 8/267 | 33/7678 | 1.25E-05 |
| ko04060 | Cytokine-cytokine receptor interaction | 21/267 | 261/7678 | 0.00028 |
| ko01230 | Biosynthesis of amino acids | 10/267 | 78/7678 | 0.000341 |
| ko04115 | p53 signaling pathway | 9/267 | 66/7678 | 0.000423 |
| ko00480 | Glutathione metabolism | 8/267 | 57/7678 | 0.000725 |
| ko03430 | Mismatch repair | 5/267 | 22/7678 | 0.000793 |
| ko05323 | Rheumatoid arthritis | 9/267 | 83/7678 | 0.002248 |
| ko00240 | Pyrimidine metabolism | 10/267 | 100/7678 | 0.002399 |
| ko03440 | Homologous recombination | 5/267 | 28/7678 | 0.002495 |
| ko00670 | One carbon pool by folate | 4/267 | 19/7678 | 0.003667 |
| ko00051 | Fructose and mannose metabolism | 5/267 | 34/7678 | 0.005962 |
| ko03320 | PPAR signaling pathway | 8/267 | 80/7678 | 0.006399 |
| ko04640 | Hematopoietic cell lineage | 8/267 | 84/7678 | 0.008547 |
| ko05150 | Staphylococcus aureus infection | 6/267 | 52/7678 | 0.008894 |
| ko00680 | Methane metabolism | 4/267 | 27/7678 | 0.013355 |
| ko04064 | NF-kappa B signaling pathway | 8/267 | 93/7678 | 0.015302 |
| ko05166 | Human T-cell leukemia virus 1 infection | 17/267 | 277/7678 | 0.016187 |
| ko03420 | Nucleotide excision repair | 5/267 | 44/7678 | 0.017575 |
| ko00052 | Galactose metabolism | 4/267 | 31/7678 | 0.021493 |
| ko04922 | Glucagon signaling pathway | 8/267 | 100/7678 | 0.022753 |
| ko00980 | Metabolism of xenobiotics by cytochrome P450 | 6/267 | 64/7678 | 0.02323 |
| ko00030 | Pentose phosphate pathway | 4/267 | 32/7678 | 0.023911 |
| ko00100 | Steroid biosynthesis | 3/267 | 19/7678 | 0.026677 |
| ko00010 | Glycolysis / Gluconeogenesis | 6/267 | 67/7678 | 0.028389 |
| ko05340 | Primary immunodeficiency | 4/267 | 35/7678 | 0.032123 |
| ko05144 | Malaria | 5/267 | 52/7678 | 0.033669 |
| ko04668 | TNF signaling pathway | 8/267 | 110/7678 | 0.037371 |
| ko05332 | Graft-versus-host disease | 5/267 | 54/7678 | 0.038763 |
| ko00900 | Terpenoid backbone biosynthesis | 3/267 | 22/7678 | 0.039292 |
| ko00710 | Carbon fixation in photosynthetic organisms | 3/267 | 24/7678 | 0.049101 |
| ko04630 | JAK-STAT signaling pathway | 8/267 | 159/7678 | 0.188872 |