|  |  |  |
| --- | --- | --- |
| **Table S1 Primer pairs for real time quantitative PCR in *p.citri.*** | | |
| **Gene name** | **Primer sequence (5′-3′)** | **Length (bp)** |
| c22254.graph\_c0 | F:CGAGACGGTCTTGTGGTCAG | 173 |
| R:GAGGCCATGTCGATCTGTGA |
| c23144.graph\_c0 | F:ACTTCTGGTCGGTTCATCAT | 170 |
| R:CATCTCAACATTAGCCAATCCTT |
| c21051.graph\_c0 | F:TCTCGCCGCTAATCTGGAA | 179 |
| R:GCCGTCGTGTAGTTGTATGAAT |
| c22729.graph\_c1 | F:AGAGGTTGGATTAGCAGATATGGA | 179 |
| R:TGGAATAAAGTGACATCGCAGTTT |
| c21570.graph\_c0 | F:ATTGTCAACTCTTGTGAATAACTG | 183 |
| R:CCATCTTCGTCGTCATCTC |
| c23311.graph\_c0 | F:ATGCCTCAAGAAACGGCTCTA | 220 |
| R:GTCGCGGCGAATGTATCAA |
| c22508.graph\_c0 | F:TCGTGTCTATGCCCTTGTTTCT | 119 |
| R:GAGTCGCTCATTCATTGGTTCA |
| c17984.graph\_c0 | F:CAGATTCTTTGGCGGTGAT | 156 |
| R:TGTGTCAAGGCAGAGTCA |
| c20663.graph\_c0 | F:GGATTGGTGGCTGATTCG | 181 |
| R:CTGCTGTGGTCAATAGAAGAG |
| c20525.graph\_c0 | F:CCTGGTCAACTGTCATTGGTAA | 169 |
| R:CAAGGCGGTCGGAAGAAT |
| *ELF1α* | F:GGCACTTCGTCTTCCACTTC | 164 |
| R:ATGATTCGTGGTGCATCTCA |
| β-actin | F:CGGGACGAACGACTGGTATTGT | 180 |
| R:CAGCGGTTGTGGTGAAGGAGTA |

**Table S2. Indoor toxicity test of amitraz with three different synergists PBO, DEM, DEF in SS and RS.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Strain | Regression equation | Correlation coefficient R | χ2 | LC50 (95% CI) (mg L-1) |
| SS | y=3.7045+0.8913x | 0.9073 | 7.8564 | 28.42 (15.76-51.23) |
| SS+PBO | y=3.6510+1.0145x | 0.9078 | 7.7622 | 21.37 (13.68-33.38) |
| SS+DEM | y=3.2109+1.1787x | 0.9528 | 5.6122 | 32.95 (20.08-54.07) |
| SS+DEF | y=3.1092+1.3296x | 0.97 | 4.2406 | 26.43 (17.91-37.00) |
| RS | y=0.3404+1.4185x | 0.9608 | 12.4144 | 1926.65 (1507.70-2462.02) |
| RS+PBO | y=2.1936+0.9839x | 0.9385 | 10.8905 | 711.53 (548.01-923.84) |
| RS+DEM | y=1.3373+1.1595x | 0.9613 | 9.046 | 1441.51 (1111.82-1868.96) |
| RS+DEF | y=1.3504+1.2341x | 0.9679 | 7.4168 | 906.39 (727.97-1128.54) |



Figure S1. COG, KOG and eggNOG functional classification of differentially expressed genes. The abscissa represents the classification content, and the ordinate represents the number of genes. In different functional classification, the quantity of gene number reflects the metabolism or physiological tendencies of mites in the corresponding period and environment