**Figure S1** A flow diagram of the experiment design were used for the plant treatments, and sample collection, along with plant ages and time lines.

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**Figure S2** TYLCV copy numbers in two tomato genotypes (Moneymaker and *Mi-1.2*) before releasing whitefly for TYLCV acquisition when grown under ambient CO2 and elevated CO2. Different lowercase letters indicate significant differences between ambient CO2 and elevated CO2 within the same genotype. Different uppercase letters indicate significant differences between genotypes within the same CO2 treatment. Means were compared with Tukey’s multiple range test at P < 0.05.

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**Table S1.** Primer sequences used for real-time quantitative PCR.

|  |  |  |
| --- | --- | --- |
| Gene name | Primer sequence（5’-3’） | Function |
| *PI* | *F*:GCC AGA ACT TAT TGG TGT A *R*:TGA CAT ATT GTG GCT GCT T | JA defense related |
| *LOX* | *F*:ATG GCG ACA AGA AAG ATG AGG*R*: CTT AAA GTA GGG CGA TTA GGG | JA defense related |
| *PAL* | *F*:AGA TTG AAG TCA TTC GTG CTG*R:*ACC CGT TGT TGT AAT AGT CGT TG | SA defense related |
| *PR* | *F*:TAC GCT ACC AAC CAA TGT G*R*:TCC AGT TGC CTA CAG GAT C | SA defense related |
| *β-actin* | *F:* GTT GGA ATG GGT CAG AAA GAT*R:* TTC AGT AAG CAG AAC AGG GTG | Housekeeping gene |

**Table S2**. *F* and *P* values from MANOVAs for the effect of CO2 level, tomato genotypes on growth traits in two tomato genotypes.

|  |  |  |
| --- | --- | --- |
| Plant traits | Value | Treatment(df1,df2)a |
| CO2b(1,92) | Genoc(1,92) | CO2×Genod(1,92) |
| Biomass | *F* | 26.3 | 22.4 | 6.57 |
| *P* | <0.001\*\*\* | <0.001\*\*\* | 0.012 |
| Stem diameter | *F* | 0.901 | 1.44 | 1.21 |
| *P* | 0.345 | 0.234 | 0.275 |
| Height | *F* | 28.4 | 25.9 | 0.374 |
| *P* | <0.001\*\*\* | <0.001\*\*\* | 0.542 |
| Photosynthetic rate | *F* | 87.5 | 4.13 | 7.35 |
| *P* | <0.001\*\*\* | 0.045\* | 0.008\*\* |
| adf1:The degrees of freedom for treatments.df2: The degrees of freedom for error.bAmbient CO2 vs. elevated CO2. cTwo genotypes of Tomato (Moneymaker vs. *Mi-1.2*).d The interaction between CO2 level and tomato genotypes.Asterisk denotes significant P values: \*<0.05, \*\*<0.01, \*\*\*<0.001. |

**Table S3**. *F* and *P* values from MANOVAs for the effect of CO2 level, tomato genotype on disease severity by artificially inoculation in two tomato genotypes.

|  |  |  |
| --- | --- | --- |
| Plant traits | Value | Treatment(df1,df2)a |
| CO2b(1,28) | Genoc(1,28) | CO2×Genod(1,28) |
| Disease incidence | *F* | 45.3 | 19.6 | 10.1 |
| *P* | <0.001\*\*\* | <0.001\*\*\* | 0.002\*\* |
| Disease index | *F* | 39.4 | 10.1 | 31.7 |
| *P* | <0.001\*\*\* | 0.004\*\* | <0.001\*\*\* |
| adf1:The degrees of freedom for treatments. df2: The degrees of freedom for error.bAmbient CO2 vs. elevated CO2. cTwo genotypes of Tomato (Moneymaker vs. *Mi-1.2*).d The interaction between CO2 level and tomato genotypes. Asterisk denotes significant P values: \*<0.05, \*\*<0.01, \*\*\*<0.001. |

**Table S4**. *F* and *P* values from MANOVAs for the effect of CO2 level, tomato genotype and whitefly density on disease incidence and index of two tomato genotypes.

|  |  |  |
| --- | --- | --- |
| Measured indices | Value | Treatment(df1,df2)a |
| CO2b(1,36) | Genoc(1,36) | Dend(2,36) | CO2×Genoe(1,36) | CO2×Denf(1,36) | Geno×Deng(1,36) | CO2×Geno×Denh(1,36) |
| Disease incidence | *F* | 7.19 | 4.64 | 9.63 | 18.5 | 4.04 | 0.397 | 4.37 |
| *P* | 0.011\*\* | 0.038\* | <0.001\*\*\* | <0.001\*\*\* | 0.052 | 0.531 | 0.041\* |
| Disease index | *F* | 4.98 | 0.013 | 12.2 | 12.4 | 5.04 | 0.031 | 0.025 |
| *P* | 0.032\* | 0.910 | <0.001\*\*\* | <0.001\*\*\* | 0.031\* | 0.861 | 0.874 |
| a df1:The degrees of freedom for treatments. df2: The degrees of freedom for error.bAmbient CO2 vs. elevated CO2. cTwo genotypes of tomato (Moneymakervs.*Mi-1.2*). dWhitefly density for TYLCV transmission.e The interaction between CO2 level and tomato genotypes. f The interaction between CO2 level and whitefly densities.g The interaction between tomato genotypes and whitefly densities.Asterisk denotes significant P values: \*<0.05, \*\*<0.01, \*\*\*<0.001. |

**Table S5**. *F* and *P* values from MANOVAs for the effect of CO2 level, tomato genotype and virus infection on whitefly population abundance and fecundity of two tomato genotypes.

|  |  |  |
| --- | --- | --- |
| Measured indices | Value | Treatment(df1,df2)a |
| CO2b(1,120) | Genoc(1,120) | TYLCVd(1,120) | CO2×Genoe(1,120) | CO2×TYLCVf(1,120) | Geno×TYLCVg(1,120) | CO2×Geno×TYLCVh(1,120) |
| Populationi | *F* | 5.09 | 9.01 | 15.6 | 3.77 | 13.3 | 1.21 | 5.99 |
| *P* | 0.028\* | 0.004\*\* | <0.001\*\*\* | 0.057 | <0.001\*\*\* | 0.272 | 0.015\* |
| Fecundityj | *F* | 4.38 | 0.978 | 21.3 | 0.480 | 26.3 | 29.4 | 8.44 |
| *P* | 0.041\* | 0.327 | <0.001\*\*\* | 0.491 | <0.001\*\*\* | <0.001\*\*\* | 0.004\*\* |
| a df1:The degrees of freedom for treatments. df2: The degrees of freedom for error.bAmbient CO2 vs. elevated CO2. cTwo genotypes of tomato (Moneymakervs.*Mi-1.2*). dInfected or non-infected with TYLCV .e The interaction between CO2 level and tomato genotypes. f The interaction between CO2 level and TYLCV infection. g The interaction between tomato genotypes and TYLCV infection. h The interaction among CO2 level, tomato genotypes and TYLCV infection.iWhitefly population abundance. j Whitefly fecundity.Asterisk denotes significant P values: \*<0.05, \*\*<0.01, \*\*\*<0.001. |

**Table S6**. *F* and *P* values from MANOVAs for the effect of CO2 level, tomato genotype and virus acquisition/transmission time on TYLCV acquisition and transmission of two tomato genotypes.

|  |  |  |
| --- | --- | --- |
| Measured indices | Value | Treatment(df1,df2)a |
| CO2b(1,180) | Genoc(1,180) | Timed(2,180) | CO2×Genoe(1,180) | CO2×Timef(2,180) | Geno×Timeg(2,180) | CO2×Geno×Timeh(2,180) |
| Acqusitioni | *F* | 0.853 | 0.150 | 3.85 | 9.84 | 3.28 | 16.9 | 7.12 |
| *P* | 0.357 | 0.699 | 0.023\* | 0.002\*\* | 0.04\* | <0.001\*\*\* | 0.001\*\* |
| Transmissionj | *F* | 0.144 | 8.08 | 7.93 | 7.73 | 13.0 | 19.2 | 15.8 |
| *P* | 0.705 | 0.005\*\* | <0.001\*\*\* | 0.006\*\* | <0.001\*\*\* | <0.001\*\*\* | <0.001\*\*\* |
| a df1:The degrees of freedom for treatments. df2: The degrees of freedom for error.bAmbient CO2 vs. elevated CO2. cTwo genotypes of tomato (Moneymakervs.*Mi-1.2*). dVirus acquisition/transmission time . e The interaction between CO2 level and tomato genotypes. f The interaction between CO2 level and Virus acquisition/transmission time.g The interaction between tomato genotypes and virus acquisition/ transmission time. h The interaction among CO2 level, tomato genotypes and virus acquisition/ transmission time .iVirus acquisition. jVirus transmission. Asterisk denotes significant P values:\*<0.05, \*\*<0.01, \*\*\*<0.001. |

**Table S7**. *F* and *P* values from MANOVAs for the effect of CO2 level, tomato genotype and virus infection on phytohormone and enzymes activities in leaves of two tomato genotypes.

|  |  |  |
| --- | --- | --- |
| Measured indices | Value | Treatment(df1,df2)a |
| CO2b(1,24) | Genoc(1,24) | TYLCVd(1,24) | CO2×Genoe(1,24) | CO2×TYLCVf(1,24) | Geno×TYLCVg(1,24) | CO2×Geno×TYLCVh(1,24) |
| SAi | *F* | 35.4 | 3.52 | 28.9 | 38.5 | 4.88 | 0.288 | 10.9 |
| *P* | <0.001\*\*\* | 0.073 | <0.001\*\*\* | <0.001\*\*\* | 0.037\* | 0.596 | 0.003\*\* |
| JAj | *F* | 0.333 | 7.59 | 0.226 | 0.124 | 10.9 | 0.622 | 45.6 |
| *P* | 0.569 | 0.011\* | 0.639 | 0.728 | 0.003\*\* | 0.438 | <0.001\*\*\* |
| PALk | *F* | 14.2 | 0.023 | 12.6 | 0.011 | 0.494 | 7.03 | 1.14 |
| *P* | <0.001\*\*\* | 0.879 | <0.001\*\*\* | 0.916 | 0.489 | 0.014\* | 0.295 |
| LOXl | *F* | 16.7 | 0.592 | 0.076 | 2.38 | 5.18 | 0.298 | 0.859 |
| *P* | <0.001\*\*\* | 0.449 | 0.785 | 0.136 | 0.032\* | 0.590 | 0.363 |
| a df1:The degrees of freedom for treatments. df2: The degrees of freedom for error.b Ambient CO2 vs. elevated CO2. cTwo genotypes of tomato (Moneymakervs.*Mi-1.2*).d Infected or non-infected with TYLCV . e The interaction between CO2 level and tomato genotypes. f The interaction between CO2 level and TYLCV infection. g The interaction between tomato genotypes and TYLCV infection. h The interaction among CO2 level, tomato genotypes and TYLCV infection.  d Salicylic acid. e Jasmonic acid. f Phenylalanine ammonia lyase . g Lipoxygenase.Asterisk denotes significant P values:\*<0.05, \*\*<0.01, \*\*\*<0.001. |

**Table S8**. *F* and *P* values from MANOVAs for the effect of CO2 level, tomato genotype and virus infection time on gene expression on phytohormone-mediated signaling pathwayin leaves of two tomato genotypes.

|  |  |  |
| --- | --- | --- |
| Measured indices | Value | Treatment(df1,df2)a |
| CO2b(1,48) | Genoc(1,48) | Timed(3,48) | CO2×Genoe(1,48) | CO2×Timef(3,48) | Geno×Timeg(3,48) | CO2×Geno×Timeh(3,48) |
| PALi | *F* | 10.7 | 9.78 | 6.98 | 22.9 | 4.05 | 5.06 | 12.2 |
| *P* | 0.002\*\* | 0.003\*\* | <0.001\*\*\* | <0.001\*\*\* | 0.012\* | 0.004\*\* | <0.001\*\*\* |
| PR1j | *F* | 14.5 | 18.4 | 27.6 | 7.94 | 20.9 | 3.56 | 15.6 |
| *P* | <0.001\*\*\* | <0.001\*\*\* | <0.001\*\*\* | 0.007\*\* | <0.001\*\*\* | 0.021\*\* | <0.001\*\*\* |
| LOXk | *F* | 0.964 | 0.93 | 6.38 | 7.94 | 2.01 | 5.71 | 1.55 |
| *P* | 0.331 | 0.34 | 0.009\*\* | 0.005\*\* | 0.125 | 0.002\*\* | 0.213 |
| PIl | *F* | 3.59 | 56.3 | 5.06 | 24.5 | 5.71 | 26.1 | 19.7 |
| *P* | 0.064 | <0.001\*\*\* | 0.004\*\* | <0.001\*\*\* | 0.002\*\* | <0.001\*\*\* | <0.001\*\*\* |
| a df1:The degrees of freedom for treatments. df2: The degrees of freedom for error.b Ambient CO2 vs. elevated CO2. cTwo genotypes of tomato (Moneymakervs.*Mi-1.2*). dVirus acquisition/transmission time . e The interaction between CO2 level and tomato genotypes. f The interaction between CO2 level and Virus acquisition/transmission time. g The interaction between tomato genotypes and virus acquisition/ transmission time. h The interaction among CO2 level, tomato genotypes and virus acquisition/ transmission time .iPhenylalanine ammonia lyase. jPathogen related protein. kLipoxygenase.lProteinase inhibitor.Asterisk denotes significant P values:\*<0.05, \*\*<0.01, \*\*\*<0.001. |