**Supporting information**

**Heterologous WRKY and NAC transcription factors triggered resistance in *Nicotiana benthamiana***

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**Fig. S1.** Hypersensitive response initiated by *ptHR759* gene. **(A-B)** *L. esculentum* leaves treated with **(A)** Empty vector and **(B)** *ptHR759*. **(C-D)** *G. hirustum* leaves treated with **(C)** Empty vector and **(D)** *ptHR759*. **(E-F)** *P. ternata* leaves treated with **(E)** Empty vector and **(F)** *ptHR759*. Each experiment was repeated thrice. Representative pictures are shown here.

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**Fig. S2.** Phylogenetic tree of *ptHR* genes from *P. ternata*. The nucleotide sequences were aligned with ClustalW and phylogenetic tree was built by using MEGA X and the maximum likelihood method. Tree clades were marked with distinct color linesalong bootstrap indication on nodes. iTOL, an online tool was used to edit the phylogenetic tree.

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**Fig. S3.** Relative expression levels of PR-genes. *N. benthamiana* leaves were pressure infiltrated with *ptHR759* and an empty vector. At different time intervals, samples were collected to extract total RNA for qRT-PCR. Empty vector infiltrated leaves were used as a control. *EF-1α* served as an indigenous control. **(A-G)** Relative expression levels of **(A)** *PR-1a*, **(B)** *PR-5*, **(C)** *PDF1.2*, **(D)** *NPR1*, **(E)** *PAL*, **(F)** *RBOHB* and **(G)** *ERF1* compared with empty vector control. The results are the averages from three individual experiments. Vertical bars represent SD. Significance analysis was done by t-test: \**P*<0.05, \*\**P*<0.01.

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**Fig. S4.** Mass spectra for the detected bioactive compounds in *ptHR293* transformed plants. **(A)** Ethoxzolamide, **(B)** Pyrrolidine, **(C)** Lignocerane, **(D)** 3,4-Dichloromaleimide, **(E)** Sulfanilamide and **(F)** 2-Undecanone.

**Table S1.** List of qRT-PCR primers**.**

|  |  |  |
| --- | --- | --- |
| **Gene** | **Forward Primer（5’—3’）** | **Reverse Primer（5’—3’）** |
| **TF** | TACAGGTTACTGAATCACTTGCGCTA | CCGTAGTTTAATGTCTTCGGGACA |
| ***EF-1α*** | TGTGATGTTTTTGTTCGGTCTTTAA | TCAAAAGAAAATGCAGACAGACTCA |
| ***PR-1a*** | CCTCGTACATTCTCATGGTCAAT | CCATTGTTACACTGAACCCTAGC |
| ***PR-5*** | CCGAGGTAATTGTGAGACTGGAG | CCTGATTGGGTTGATTAAGTGCA |
| ***PDF1.2*** | GGAAATGGCAAACTCCATGCG | ATCCTTCGGTCAGACAAACG |
| ***NPR1*** | ACATCAGCGGAAGCAGTAG | GTCGGCGAAGTAGTCAAAC |
| ***PAL*** | GTTATGCTCTTAGAACGTCGCCC | CCGTGTAATGCCTTGTTTCTTGA |
| ***RBOHB*** | TTTTCTCTGAGGTTTGCCAGCCACCA | GCCTTCATGTTGTTGACAATGTCTTT |
| ***ERF1*** | GGCGAATTTTCCGGGAGACT | GGCTCCGATTTTACTTCGCC |
| ***ptHR293*** | GCTCCATACCCACCAATCTG | GGTCTGAACCACCACCCTTG |
| ***ptHR759*** | AGAAAACAATAGGCGAAACTGC | CACCTTTTATTCGGTCTTCCA |

**Table S2.** NCBI blast results exhibiting homology with transcription factors.

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene** | **Length (bp)** | **Homology** | **Identity (%)** |
| ***ptHR293*** | 749 | PREDICTED: *Setaria italica* WRKY transcription factor WRKY24 (LOC101782717), mRNA | 80 |
| ***ptHR759*** | 363 | PREDICTED: *Musa acuminata* subsp. malaccensis NAC domain-containing protein 21/22-like (LOC103993629), mRNA | 90 |

**Table S3.** List of detected bioactive compounds in *ptHR293* transformed plants.

|  |  |  |  |
| --- | --- | --- | --- |
| **Compounds** | **Retention time (min)** | **m/z [M+H]+** | **Molecular weight  (g/mol)** |
| Ethoxzolamide | 4.46 | 774.06 | 258.31 |
| Pyrrolidine | 2.36 | 72.05 | 71.12 |
| Lignocerane | 6.01 | 562.86 | 338.66 |
| 3,4-Dichloromaleimide | 7.61 | 97.99 | 165.95 |
| Sulfanilamide | 2.47 | 90.53 | 172.20 |
| 2-Undecanone | 6.02 | 50.81 | 170.29 |