**Supporting information**

**Salivary protein NlSP7of the brown planthopper functions as an effector for mediating tricin metabolism in rice plants**

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Declarations of interest: none.

图表

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**Fig. S1** Posterior probabilities predicted by the TMHMM server for NLSP7 and prediction of transmembrane helices in NLSP7 protein. Prediction of transmembrane helices in NLSP7protein. Transmembrane position is 1–20 base pairs of *NLSP7.*

**图表

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**Fig. S2** Signal peptide (sec/ Signal Peptidase I) prediction of NLSP7 using the SignalP 5.0 server. A-B cleavage site between pos. 20 and 21: AMA -GP (sequence position). Probability: 0.9477.

图表, 条形图

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**Fig. S3** Brown planthoppers were injected with specific double-stranded RNA. A BPHs after three days of three different treatments. B the expression level of *NLSP7* was determined at 24 h intervals. Data are represented as the mean ± SD from three biological replicates. Asterisks (\*\*) indicate significant difference (P < 0.01, *t*-test).

图表, 折线图

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**Fig. S4** Mortality rate of BPHs fed TN1 rice, repeated three times, respectively. Each treatment repeated with 100 brown planthoppers. Data are represented as the mean ± SD (*P* < 0.01, Duncan’s multiple range test).

图表, 折线图

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**Fig. S5** Mortality rate of BPHs fed an artificial diet with 0 mg/l tricin, repeated three times. Each treatment repeated with 100 brown planthoppers. Data are represented as the mean ± SD (*P* < 0.01, Duncan’s multiple range test).

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**Fig. S6** Effect of *NLSP7* expression silencing on salivary flanges based on an artificial diet with different tricin concentrations. Significant differences were observed for different concentrations of tricin. Each bar represents the mean ± SD from 30 replicates. Bars with different letters indicate significant differences among the three treatments (*P* < 0.01, Duncan’s multiple range test).**Table S1.**Primers used for qRT-PCR and PCR.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Description** | **Forward primer (5'-…-3')** | **Reverse primer (5'…-3')** |  |  |  |  |  |  |  |  |  |  |  |
| *NLSP7* | QPCR | AAGAAAGGCAAGAGCAAG | GTAGGCTGCACATAAGGA |  |  |  |  |  |  |  |  |  |  |  |
| *NLSP7* | Cloning | ATGAGGGCTGCCCTGATT | TAGACAACCTGTGGTCCA |  |  |  |  |  |  |  |  |  |  |  |
| *NLSP7* | dsRNA synthesis | GGATCCTAATACGACTCACTATAGG  ATGAGGGCTGCCCTGATT | GGATCCTAATACGACTCACTATAGG  TAGACAACCTGTGGTCCA |  |  |  |  |  |  |  |  |  |  |  |
| *GFP* | dsRNA synthesis | GGATCCTAATACGACTCACTATAGGAA  GGGCGAGGAGCTGTTCACCG | GGATCCTAATACGACTCACTATAGGCA  GCAGGACCATGTGATCGCGC |  |  |  |  |  |  |  |  |  |  |  |