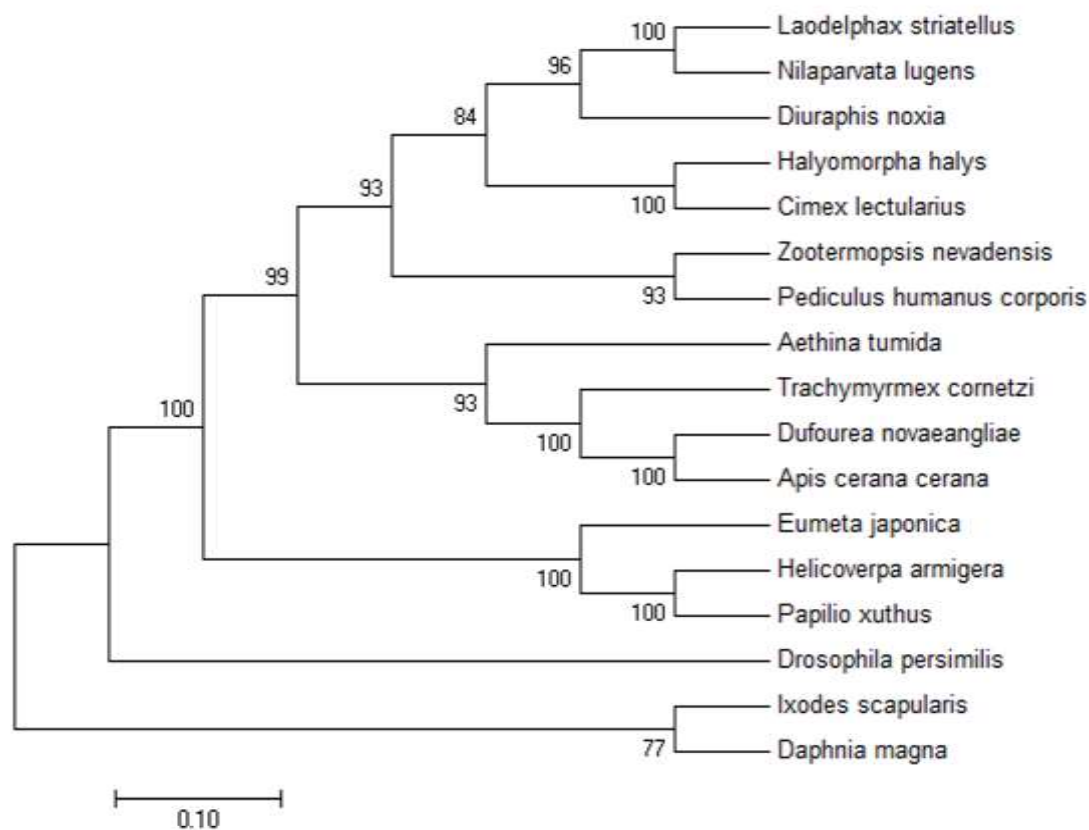


TCGCCGGGTATTCTCTACTTCGCCGTCGGTTTTGCCGCCGAAAGCAGTAGCAGGGCATTGTACTATATGG
AGATGAACACACGACACGGCGAAAACGCCGGACGGCGCTGTCCCCACCCATGCCACTTCTTTATTTATTAAC
ATTTGTAACGTTAAACAATGGGTAGGGTAGGGTTACAAGGGTAGGTTACAAGGGTAGGGTTGTAAGTAGGG
1 ATGGGTTGGAAAGGTGGAACACAATGGGCCAGTCCAGAAATGGAGGCTCTGGACGAACGT
1 M G W K G G T Q W A S P E M E A L D E R
61 CACGACCAGGAATTGCTGAAAGCCGTCCAGGAAAGCATGGCAGCCTGGGAGAGGAGGAAA
21 H D Q E L L K A V Q E S M A A W E R R K
121 GCTAGTCATAGCCATCGGCAAAAGAGGGCAGACTCACCAGGGGTATGTTATGACGGTGTG
41 A S H S H R Q K R A D S P G V C Y D G V
181 GGGTGTCTCAAGGAGTCTGGACCCTATGGTTACATCGATATGTTACCTAGTTCTCCCGAA
61 G C F K E S G P Y G Y I D M L P S S P E
241 GAGGTGGACACCCGTTTCTTGATGTACAGTTCGAAAAAGAACAGACGCTCGGATACACCC
81 E V D T R F L M Y S S K K N R R S D T P
301 CTGTTAGACGTAGGCTTCGCCAACCTGACTGCCGTCTACACGTGGGCTGGCAAAGCGTTC
101 L L D V G F A N L T A V Y T W A G K A F
361 AACGTGTCAGCCCCACCAAGGTCATAGTTCACGGGTTTGGCTCATCTGCTCGCATGTC
121 N V S A P T K V I V H G F G S S C S H V
421 TGGGTCTACGAGATGCGGAGTGCCTCATGTCTGTTGAAGAATGCAACGTAATCTGCGTG
141 W V Y E M R S A L M S V E E C N V I C V
481 GACTGGGAGAACGGTGCCACATTCCCCAACTACGTCCGAGCCGAGCCAATACAAGATTG
161 D W E N G A T F P N Y V R A A A N T R L
541 GTTGGCAAACAGTTGTCAATGCGGATAGCTGGCCTCCATGAGAAGCTGCACTTACCCTG
181 V G K Q L S M R I A G L H E K L H L P L
601 CATAAAGTGCATATCATTGGGTTCTCTTGGCGCTCATGTGGCTGGCTTTGCCGGGGCT
201 H K V H I I G F S L G A H V A G F A G A
661 CAACTCAAGAATATCAGCAGGATTACTGGTCTAGACCCAGCAGGCCCCCTGTTGAGAGC
221 Q L K N I S R I T G L D P A G P L F E S
721 CAAGACCCGAGCCCGTCTGGACTCGAGTGACGCCAGCTTTGTGATGTGATTCACTCC
241 Q D P R A R L D S S D A S F V D V I H S
781 AACGGGGAGAACCTCATCCTGGGTGGCCTGGGGTCATGGCAGCCTATGGGACACGTCGAC
261 N G E N L I L G G L G S W Q P M G H V D
841 TATTACCCCAACGGGGGGCGCATGCAGAAGGGGCTGTGCAACCTGTTTGTGGGTGCTGTC
281 Y Y P N G G R M Q K G C S N L F V G A V
901 ACCGATATATTGGTCTGTATCAGAAGCAGAAGGCAGGAGCCTGTGCAATCATAGGCGA
301 T D I L W S V S E A E G R S L C N H R R
961 GCCTACAAGTTCTTACAGACAGCGTCTCGCCACGTTGCCATTTCCCTGCACTCTCTGTC
321 A Y K F F T D S V S P R C H F P A L S C
1021 GACAGCTTCGATAAATACCTGGCAGGCAACTGCTTCCCATGCACCGATCAGGATAACTGC
341 D S F D K Y L A G N C F P C T D Q D N C
1081 GGCAACATGGGATATTATGCCGACAAGGCTAAGGGGAGAGGCACGCTCTATCTGGTCACT
361 G N M G Y Y A D K A K G R G T L Y L V T
1141 AGGGATGAGGAACCTTTTTGTGGATCGATGTCAAAGAATCTATGTCAAACGAGGACACCG
381 R D E E P F C G S M S K N L C Q T R T P

1201 ACGAAAGAGGCCTGCGACAGTCCAGAAATAGTGGCCTCAACTCTAACTCAATTGGATAAA
401 T K E A C D S P E I V A S T L T Q L D K
1261 AGGGTAGATGTCAAACGAGGCCACCGACGAAAGAGTTTGTCTAGTATGCAAAAAGAGGGCT
421 R V D V K R G H R R K S L S V C K R G L
1321 GTTCTGGAGTCTGGCATAGCGGCTCTACTGCCACTTTATCCTGGGAACTGCAAGCATCAA
441 V L E S G I A A L L P L Y P G N C K H Q
1381 TCTGATAGTACTCCGTCGGTACTTGGAAACAATAATGTGACATTACCAAAGATCCCATCC
461 S D S T P S V T W N N N V T L P K I P S
1441 GACAACACCACCCGCTACATCCCGACCCAAGTGGTACACCTGGGTGACGAAATCGTGTTC
481 D N T T R Y I P T Q V V H L G D E I V F
1501 AACAGCTCGTTAACCGACAGGAAACAAAATGGCAGCGACAAACACGACGACAACTACCTC
501 N S S L T D R K Q N G S D K H D D N Y L
1561 AGCTACAACCTGGCAACCGTTCTGAGTACCCAGAAGTCTCCGGCAACTCAGGAAACGAC
521 S Y N W Q P V P E Y P E V S G N S G N D
1621 CTTGAGTCCACAAATCTCAACCTGAGGATGTTGGTCGAGGGTTCCTTAACGTGAAACAG
541 L E S T N L N L E D V G R G F L N V K Q
1681 GTTAGCAGCAGCTGGAACCTCACTAGAAACACAACCGGTTTAGAGGAAAGGTTTGGGAAC
561 V S S S W N S T R N T T G L E E R F G N
1741 AGCACAACCCTGGACAAGAGGTCACCGGGGAAGGATTTGTTGGGTAATGCAACCCGTA
581 S T T L D K R S P G K D L L G N A T R K
1801 ATGGATGACAAAAAGGAGAGGATCCTCAGGAAGGATGAACCCTACAAGTTTGAAGCGATT
601 M D D K K E R I L R K D E P Y K F E A I
1861 ATGTTGAGTGACGAACCGGTTCAACCGGTTCTACAAGTTCAGGGAACGACACAACA
621 M L S D E P V Q T G S T S S G N D T T T
1921 CGTCCAGAAATCAAGGAACCTATCTACCTCAACAACACCTCGTGTAGCTTCCAACCGG
641 R P E I K E P I L P S T T P R V A S N R
1981 TCACCCAAATCAGACCTCACACCACCTTCTGTGACCGCCACAGAATCGTGGTACCACTGG
661 S P K S D L T P P S V T A T E S W Y H W
2041 GAGAGCTCCACCAACAATGGCAAAAAGACTAAAAAGTTGAACCTGGATTCTGTGCCCTCT
681 E S S T N N G K K T K K L N L D S V P S
2101 GCAGCTGCTGCAACTTCCAATGAAACTTCTCCGAAAGGTCTCTGGTGGTACAACCTTTTC
701 A A A A T S N E T S P E R S L V V Q L F
2161 CCGCAGAGGTTGGTCAGTTTGTGGAGCAGGCTGAAAGGTATGCAAGGTTGGCGTTTTCT
721 P Q R L V S L L E Q A E R Y A R L A F S
2221 CCGTTTGTGTCTCAAGGTGATAACTCGGAGTCAAGAGTGCAGAGGATGTTGAAGTATTTG
741 P F V S Q G D N S E S R V Q R M L K Y L
2281 CCGACATTTTGGACACATAGTGATCAACATGCAGCATCTTCGGCCAAACGGGCCAACCGG
761 P T F W T H S D Q H A A S S A K R A N R
2341 CATATAGATGTTGCCAAACCTGGGGAAAACCAACCTGACAATCCATACAAGATGGAAACC
781 H I D V A K P G E N Q P D N P Y K M E T
2401 CCTGATCCCAATTCAGGCTACAAGATGGAAAACCTGATTCCAATTCAGGTTACAAGATG
801 P D P N S G Y K M E N P D S N S G Y K M
2461 GAGAACCACCTGATAGGGATCCCAATCCAGGTTTAAAACCTAGTCCAGGACCTTCCCCT
821 E N H P D R D P N P G L K P S P G P S P

2521 GTGGGTGAACACCAAACCTGTTTCTTTTGACAACAGGGGGGATTCCACATTACCTACAAA
 841 V G E H Q T V S F D N R G D S T L P Y K
 2581 CTACAAACCCAGCAAACCTAGAGGAAAACCTCTAAAGTGGTTGCAATTCCTTACAAACTA
 861 L Q T Q Q T L E E N S K V V A I P Y K L
 2641 GCCGACCAGAAGAGGGTGGATAAGTTTCATCAAAGTTCATCCCTGTTTTGCATGAAACA
 881 A D Q K R V D K F H P K F I P V L H E T
 2701 GATAAAGGTTTCGACGGAGGAAAGTCTGTAAAGTTGTGTTAGATTTTAAATCGACCTGAG
 901 D K G S T E E S P V K V V L D F N R P E
 2761 GGTGTGGTTGACCATATGGAGACTCCCTTGGCTCAGGAGGAGTCGGAGTATGAAGGTGT
 921 G V V D H M E T P L A Q E E S E Y E G V
 2821 GAGAAGACAACCTGTGAAAGAGGGTACGAGATGAGGAGAATGGTGATTCCAGTAGAAAATT
 941 E K T T V K E G T R *
 2881 TTATTGAAATATGTGTATCACACACTAATCATGAAAACCTCAGAGTAGAGA

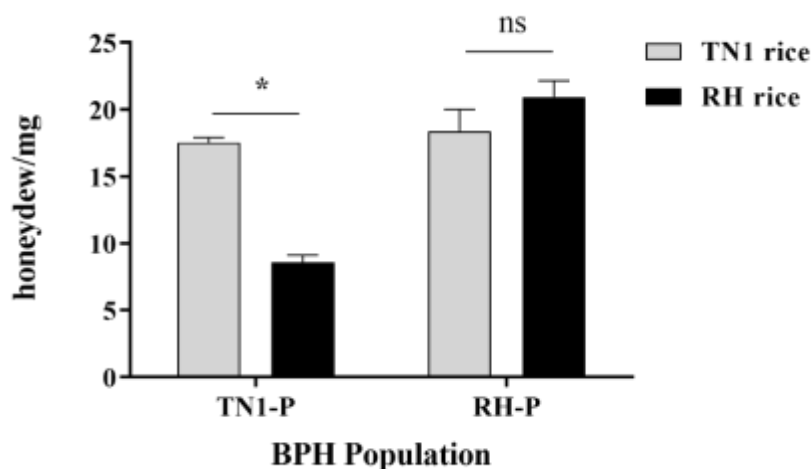
Appendix A Nucleotide and amino acid sequences of *NIPTL*. Red: catalytic triad TCT---GAC---CAT; yellow: Nucleophilic elbow GGGTTCTCTCTTGG; blue: active site flap/lid TGCAGC-----CTGTGC; gray: Pancreatic lipase-like enzyme domain.



Appendix B Phylogenetic analysis of insect *NIPTL* genes. The phylogenetic tree was constructed by MEGA7 (<http://www.megasoftware.net/>) using the neighbor-joining method. The

Jones-Taylor-Thornton model for amino acid substitution was used and the test of phylogeny was performed using the bootstrap method with 500 replications; bootstrap values > 50% are shown on each node of the tree. The GenBank accession numbers for the PTL sequences are as follows.

Laodelphax striatellus (RZF32036.1); *Nilaparvata lugens* (XP_022199696.1); *Helicoverpa armigera* (PZC85279.1); *Drosophila persimilis* (EDW29655.1); *Halyomorpha halys* (XP_014294180.1); *Zootermopsis nevadensis* (XP_021914803.1); *Cimex lectularius* (XP_014250894.1); *Ixodes scapularis* (EEC12502.1); *Aethina tumida* (XP_019875174.1); *Pediculus humanus corporis* (XP_002423272.1); *Zootermopsis nevadensis* (XP_021914883.1); *Diuraphis noxia* (XP_015377095.1); *Papilio xuthus* (KPI98004.1) ; *Daphnia magna* (KZS15767.1) ; *Eumeta japonica* (GBP32831.1) ; *Dufourea novaeangliae* (KZC08766.1) ; *Apis cerana cerana* (PBC32093.1) ; *Trachymyrmex cornetzi* (KYN23410.1).



Appendix C The secretion of honeydew by two kinds of BPH on different resistant rice

Appendix D PCR primers used in this study.

Primer Name	Sequence
5'-RACE	TGGAAAGGTGGAACACAATGG
5'-RACE	GGAACACAATGGGCCAGTCCAGAAATGG
3'-RACE	GTACCACTGGGAGAGCTCCA
3'-RACE	ACAGAATCGTGGTACCACTGGGAGAGCT
PTL-F	AATTGGGCGAATTACAGGTTTGG

PTL-R	TGAGCACGTAAGTGAGAACAAGT
dsGFP-F	TAATACGACTCACTATAGGGCGGACT
dsGFP-R	TAATACGACTCACTATAGGGCGATGC
dsPTL-F	GGATCCTAATACGACTCACTATAGGAATTGGGCGAATT ACAGGTTTGG
dsPTL-R	GGATCCTAATACGACTCACTATAGGTGAGCACGTAAGT GAGAACAAGT
<i>NLPTL</i> -QPCR-F	TCAATCCTGTCGGTCATGTTGAT
<i>NLPTL</i> -QPCR-R	TCATGAGCACGTAAGTGAGAACA
Qactin-F	ATGAAACCGTCTACAACCTCG
Qactin-R	GCATCCTGTCGGCAATAC
