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|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
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| Table S1: Genome assembly metrics for B ( MI47H and 5DH ) and C-strain (MI12H; gray) *Hamiltonella defensa* isolates | | | | | | | | | | | | | | | | |
| strains | 5DH | | | | | | MI47H | | | | | | MI12H | | | |
|  | Chromo | P1 | P2 | P3 | P4 | P5 | Chromo | P1 | P2 | P3 | P4 | P5 | Chromo | CHR2 | P1 | P2 |
| Size (bps) | 2029888 | 91765 | 57467 | 44404 | 27768 | 14565 | 2039134 | 91008 | 57469 | 47817 | 27761 | 12812 | 1078250 | 1047506 | 84572 | 42981 |
| Total GC % | 40.4 | 42.1 | 46 | 43.5 | 45.5 | 43 | 40.4 | 42 | 46 | 43 | 45 | 43.1 | 41.2 | 40.2 | 42.6 | 46.5 |
|  | 1968 | 106 | 64 | 45 | 32 | 17 | 1977 | 104 | 64 | 47 | 32 | 14 | 1029 | 1058 | 85 | 52 |
| Pseudo-genes no. | 128 | 33 | 3 | 13 | 3 | 2 | 139 | 36 | 3 | 15 | 3 | 0 | 131 | 77 | 17 | 3 |
| # of reads | 107939 | | | | | | 115370 | | | | | | 114000 | | | |
| N50 read length | 27215 | | | | | | 39073 | | | | | | 38583 | | | |
| Mapped read | 100304 | | | | | | 105337 | | | | | | 107668 | | | |
| Mean coverage | 427 | | | | | | 708 | | | | | | 762 | | | |
| Mean Read length | 10412 | | | | | | 21127 | | | | | | 20510 | | | |
| Plasmid designations P1: pHDMI47H.1/pHD5DH.1/pHDMI12.1, P2: pHDMI47H.2/pHD5DH.2/pHDMI12.2, P3: pHDMI47H.3/pHD5DH.3, P4: pHDMI47H.4/pHD5DH.4, P5: pHDMI47H.5/pHD5DH.5) | | | | | | | | | | | | | | | | |

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| **Table S2:** Accession numbers used in this study. | | | | | | | | |
| Accession numbers for loci used in phylogenetic analyses | | | | | | | | |
|  | **accD** | **ptsI** | **hrpA** | **gyrB** | **murE** | | **rpoS** | **recJ** |
| H. defensa Co26-S.avenae | KM375951.1 |  | KM375983.1 | KM375967.1 | KM375999.1 | | KM376031.1 | KM376015.1 |
| H. defensa Co08-S.avenae | KM375948.1 |  | KM375980.1 | KM375964.1 | KM375996.1 | | KM376028.1 | KM376012.1 |
| H. defensa 16-Utamphorophora | KM375956.1 |  | KM375988.1 | KM375972.1 | KM376004.1 | | KM376036.1 | KM376020.1 |
| H. defensa Sc02-S.fragariae | KM375954.1 |  | KM375986.1 | KM375970.1 | KM376002.1 | | KM376034.1 | KM376018.1 |
| H. defensa Co37-S.avenae | KM375952.1 |  | KM375984.1 | KM375968.1 | KM376000.1 | | KM376032.1 | KM376016.1 |
| H. defensa Co23-S.avenae | KM375950.1 |  | KM375982.1 | KM375966.1 | KM375998.1 | | KM376030.1 | kM376014.1 |
| H. defensa up11-S.fragariae | KM375955.1 |  | KM375987.1 | KM375971.1 | KM376003.1 | | KM376035.1 | KM376019.1 |
| H. defensa 402-A.fabae | KM375947.1 |  | KM375979.1 | KM375963.1 | KM375995.1 | | KM376027.1 | KM376011.1 |
| H. defensa-U.nigrotuberculatum | EU021767.1 | EU021874.1 | EU0218971 | EU021847.1 | EU021794.1 | | EU021741.1 | EU021821.1 |
| H. defensa -U.pieloui | EU021768.1 | EU021875.1 | EU021898.1 | EU021848.1 | EU021795.1 | | EU021742.1 | EU021822.1 |
| H. defensa-U. reynoldense | EU021772.1 | EU021879.1 | EU021902.1 | EU021852.1 | EU021799.1 | | EU021746.1 | EU021826.1 |
| H. defensa UA001-U.ambrosiae | EU021764.1 | EU021871.1 | EU021894.1 | EU021844.1 | EU021791.1 | | EU021738.1 | EU021818.1 |
| H. defensa B-U.ambrosiae | EU021763.1 | EU021870.1 | EU021893.1 | EU021843.1 | EU021790.1 | | EU021737.1 | EU021817.1 |
| H. defensa 5ATac-A.craccivora | EU021758.1 | EU021865.1 | EU021888.1 | EU021838.1 | EU021785.1 | | EU021732.1 | EU021812.1 |
| H. defensa-Geopemphigus | EU021760.1 | EU021867.1 | EU021890.1 | EU021840.1 | EU021787.1 | | EU021734.1 | EU021813.1 |
| H. defensa N4-Chaitophorus | EU021774.1 | EU021881.1 | EU021904.1 | EU021854.1 | EU021801.1 | | EU021828.1 | EU021748.1 |
| H. defensa-U.sonchi | EU021770.1 | EU021877.1 | EU021900.1 | EU021850.1 | EU021797.1 | | EU021744.1 | EU021824.1 |
| H. defensa-U.escalantii | EU021771.1 | EU021878.1 | EU021901.1 | EU021851.1 | EU021798.1 | | EU021745.1 | EU021825.1 |
| H. defensa N5-Cinara | EU021775.1 | EU021882.1 | EU021905.1 | EU021855.1 | EU021802.1 | | EU021829.1 | EU021749.1 |
| H. defensa-M.euphorbiae | EU021761.1 | EU021868.1 | EU021891.1 | EU021841.1 | EU021788.1 | | EU021735.1 | EU021814.1 |
| Various MLST from pea aphid *H. defensa* new to this study | OQ835201- OQ835276 | | | | | | | |
| Various loci from pea aphidAPSE new to this study | OQ835276- OQ835308, OQ836610- OQ836625 | | | | | | | |
| Accession number for bacterial genome | | | | | |
| H. defensa MI47H -A. pisum | PRJNA398079 | | | | |
| H. defensa 5DH -A. pisum | PRJNA388069 | | | | |
| H. defensa Mii12H -A. pisum | PRJNA398080 | | | | |
| H. defensa 3053-Ci.curtihirsuta | PRJEB31187 | | | | |
| H. defensa 3402-Ci.curvipes | PRJEB31188 | | | | |
| F. symbiotica 5DX-A.pisum | PRJNA388070 | | | | |
| Y. pestis CO92 | PRJNA235224 | | | | |
| R. insecticola 5.15-M.persicae | PRJNA65437 | | | | |
| R. insecticola LSR-A.pisum | PRJNA39723 | | | | |
| H. defensa AS3-A.pisum | PRJNA345370 | | | | |
| H. defensa A2C-A.pisum | PRJNA345370 | | | | |
| H. defensa A1A-A.pisum | EU021781.1 | | | | |
| H. defensa 2801-Ci.confinis | PRJEB15504 | | | | |
| H. defensa NY26-A.pisum | PRJNA345370 | | | | |
| H. defensa 5AT-A.pisum | PRJNA31259 | | | | |
| H. defensa MED-B.tabaci | PRJNA80993 | | | | |
| H. defensa MEM-B.tabaci | PRJNA312470 | | | | |
| Accession numbers for loci associated with APSE virulence cassette region | | | | | |
| ‘Original’ APSE1 | NC\_000935.1 | | | | |
| A. craccivora APSE4 | EU794051.1 | | | | |
| U. rudbeckiae APSE5 | EU794050.1 | | | | |
| Various *A. pisum* APSE VCR sequences used in this study | OR452418-OR452422 | | | | |

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| **Table S3:** Models used in phylogenetic trees | | |
| Pea aphid *H. defensa* phylogeny | | |
| ptsI | Phosphoenolpyruvate-protein phosphotransferase | F81+F+I |
| recJ | Single-stranded-DNA-specific exonuclease | K2P+I |
| accD | Acetyl-coenzyme A carboxyl transferase beta chain | K2P+I |
| hrpA | ATP-dependent RNA helicase | HKY+F |
|  | | |
| *H. defensa* phylogeny across multiple aphid species | | |
| ptsI | Phosphoenolpyruvate-protein phosphotransferase | K2P+G4 |
| accD | Acetyl-coenzyme A carboxyl transferase beta chain | K2P+G4 |
| gyrB | DNA topoisomerase (ATP-hydrolyzing) subunit | TIM3e+I |
| hrpA | ATP-dependent RNA helicase | K2P+G4 |
| murE | UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase | K2P+G4 |
| recJ | Single-stranded-DNA-specific exonuclease | K2P+G4 |
| rpoS | RNA polymerase sigma factor | K3P+G4 |
| APSE phylogenies | | |
| Module 1: P51 | Phage Protein | TVMe+I+G4 |
| Module 2: P3 | P3 ATPase | TPM3+F+G4 |
| Module 4: P19 | Phage portal protein | TVMe+G4 |

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| **Table S4**: Average amino acid identity (AAI: black) and average nucleotide identity (ANI: red) comparisons among *H. defensa* isolates from all five strain groups. Brackets indicate the number of orthologous proteins (black) or number of nucleotide fragments (red) from which the percent averages were derived. | | | | | | | | | | |
|  | **B clade** | | **A clade** | | **C clade** | **E clade** | **D clade** | | **whitefly isolates** | |
|  | **5DH** | **MI47H** | **NY26** | **5AT** | **MI12H** | **ZA17** | **AS3** | **A2C** | **MED** | **MEAM** |
| **5DH** | X | 99.32  (2002) | 96.77  (1472) | 96.98  (1572) | 96.62  1692 | 96.66  (1572) | 97.63  (1565) | 97.43  (1548) | 93.56  (1313) | 94.28  (1284) |
| **MI47H** | 99.95  (10796) | X | 96.73  (1486) | 96.97  (1577) | 96.55  1717 | 96.51  (1581) | 97.43  (1579) | 97.32  (1568) | 93.70  (1319) | 94.30  (1290) |
| **NY26** | 98.60  (8367) | 98.56  (8458) | X | 99.96 | 97.55 (1492) | 97.56  (1443) | 97.53  (1442) | 97.62  (1416) | 93.41  (1220) | 93.78  (1187) |
| **5AT** | 98.60  (8388) | 98.57  (8525) | 99.98  (10264) | X | 97.57 (1582) | 97.48  (1524) | 97.69  (1522) | 97.69  (1503) | 93.80  (1276 | 94.29  (1245) |
| **MI12** | 98.3  (8702) | 98.37  8676) | 98.78  8551) | 98.80 (8570) | X | 98.48  1700 | 97.75  1595 | 97.59  1579 | 94.01 () | 94.47  1327 |
| **ZA17** | 98.36  (8663) | 98.37  (8644) | 98.80  (8581) | 98.77  (8563) | 99.17  (9706) | X | 97.62  (1551) | 97.68  (1525) | 94.00  (1297) | 94.39  (1265) |
| **AS3** | 98.87  (8748) | 98.88  (8787) | 98.71  (8491) | 98.65  (8609) | 98.53  (8793) | 98.57  (8680) | X | 99.94  (1731) | 94.04  (1281) | 94.68  (1233) |
| **A2C** | 98.88  (8620) | 98.87  (8662) | 98.72  (8252) | 98.70  (8312) | 98.52  (8502) | 98.51  (8578) | 99.98  (10704) | X | 94.28  (1261) | 94.79  (1218) |
| **MED** | 96.60  (6195) | 96.92  (6208) | 96.98  6003) | 97.01  (5973) | 96.92  6225 | 96.92  (6120) | 96.95  (6026) | 97.11  (5891) | X | 99.72  (1369) |
| **MEM** | 96.85  (6752) | 96.78  (6776) | 96.99  6494) | 96.98  (6408) | 96.75  6817 | 96.75  (6759) | 96.86  (6630) | 96.99  (6425) | 99.99  (7532) | X |

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| **Table S5a: Genes present in MI47H but absent in 5DH** (Both B *H. defensa*) | |
| **Locus tag in MI47H** | **Description** |
| CJJ18\_03675 | IS200/IS605 family transposase |
| CJJ18\_03690 | Hypothetical protein |
| CJJ18\_03695 | Dehydrogenases with different specificities |
| CJJ18\_03700 | D-lactate dehydrogenase (EC 1.1.1.28) |
| CJJ18\_03705 | DUF378 domain-containing protein |
| CJJ18\_03725 | Glyoxalase |
| CJJ18\_03740 | Hypothetical protein |
| CJJ18\_03745 | Hypothetical protein |
| CJJ18\_03750 | Beta-lactamase (EC 3.5.2.6) |
| CJJ18\_03755 | Hypothetical protein |
| CJJ18\_03760 | PlcB ORFX ORFP ORFB ORFA ldh gene |
| CJJ18\_03765 | Hypothetical protein |

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| **Table S5b: Genes in MI47H that are pseudogenized in 5DH** | |
| **Locus tag in 5DH** | **Description** |
| CCS40\_01055 | Conjugal transfer protein TrbB |
| CCS40\_08120 | Hypothetical protein |
| CCS40\_08565 | Hypothetical protein |
| CCS40\_08595 | pilus assembly protein HofM |
| CCS40\_10400 | Hypothetical protein |
| CCS40\_11135 | conjugal transfer protein TraH |
| CCS40\_11505 | Hypothetical protein |

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| **Table S5c: Genes in 5DH that are pseudogenized in MI47H** | |
| **Locus tag in MI47H** | **Description** |
| CJJ18\_02030 | RTX toxin RtxA |
| CJJ18\_03505 | Hypothetical protein |
| CJJ18\_04720 | Possible Yersinia enterocolitica-like Orf1 |
| CJJ18\_04830 | Octanoate-[acyl-carrier-protein]-protein-N-octanoyltransferase |
| CJJ18\_07170 | FIG002708: Protein SirB1 |
| CJJ18\_07180 | Methionine ABC transporter ATP-binding protein (metN) |
| CJJ18\_08000 | Homoserine lactone synthase (ypeI) |
| CJJ18\_08105 | RTX toxin |
| CJJ18\_08200 | Heat shock protein (ftsJ) |
| CJJ18\_08205 | Transcription elongation factor (greA) |
| CJJ18\_09185 | Hypothetical protein |
| CJJ18\_10035 | Ferric siderophore transport system periplasmic binding (tonB) |
| CJJ18\_10330 | Glutamate--cysteine ligase |
| CJJ18\_10570 | DNA-binding response regulator |
| CJJ18\_10640 | Hypothetical protein |
| CJJ18\_10675 | 3-oxoacyl-ACP synthase |
| CJJ18\_10925 | RepB family plasmid replication initiator protein |
| CJJ18\_11285 | colicin V synthesis protein |

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| Table S6: Summary of **prophage and prophage islands** among isolates of B- ( MI47H & 5DH ) and C-clade (MI12H; gray background) strains of *H. defensa.* | | | | | | | |
| **Group** | **Genome** | **start** | **stop** | **length** | **G+C** | **Total CDS** | **description** |
| **Phage Island Group S** | **MI47H** | **236708** | **237277** | **570** | **45.3** | **2** | **Tail protein, Hypothetical protein** |
| **5DH** | **236709** | **237238** | **570** | **45.3** | **2** |
| **MI12H(K1)** | **478075** | **478320** | **246** | **42.7** | **1** | **Tail Protein** |
| **Phage Island Group O** | **MI47H** | **424287** | **425708** | **1422** | **36.2** | **3** | **Tail protein, Hypothetical protein** |
| **5DH** | **428640** | **430061** | **1422** | **36.2** | **3** |
| **MI12H(K1)** | **980304** | **981687** | **1384** | **35.9** | **3** | **Hypothetical protein** |
| **Phage Island Group G** | **MI47H** | **449680** | **450771** | **2252** | **45.2** | **4** | **Hypothetical protein** |
| **5DH** | **454033** | **456318** | **2252** |
| **MI12H(K2)** | **728211** | **741086** | **12876** | **40.7** | **20** | **Hypothetical protein, YqaJ-like viral recombinase, ATP binding protein** |
| **Phage Island Group C** | **MI47H** | **452133** | **454510** | **2414** | **47** | **5** | **Holin, Lysozyme, Muraminidase** |
| **5DH** | **456486** | **458863** | **2414** |
| **MI12H(K2)** | **430449** | **440886** | **10438** | **42.6** | **18** | **Hypothetical protein, Lysozyme, Holin, ATP binding protein** |
| **MI12H(K2)** | **746705** | **765832** | **19128** | **44.7** | **31** | **Hypothetical protein, Lysozyme, Holin, ATP binding protein,peptidase, exonuclease, DNA adenine methylase** |
| **Phage Island group B (Myoviridae of Type 1 Cluster 3, HK97-like)** | **MI47H** | **454676** | **472389** | **17714** | **53** | **26** | **Capsid protein, Tail protein, Terminase, Baseplate protein, Transcriptional regulator, Head tail adaptor protein** |
| **5DH** | **459029** | **476742** | **17714** |
| **MI12H(K1)** | **645305** | **665375** | **20071** | **54.7** | **26** |
| **MI12H(K2)** | **405687** | **430154** | **24468** | **52.8** | **30** |
| **Phage Island group A (Myoviridae of Type 1 Cluster 8, Mu-like)** | **MI47H** | **472571** | **480698** | **8128** | **45.2** | **9** | **Integrase, Exicionase, Hypothetical protein, Antirepressor** |
| **5DH** | **476924** | **485051** | **8128** |
| **MI12H(K1)** | **189329** | **192245** | **2917** | **55.8** | **3** | **Restriction endonuclease, DNA (cytosine-5-)-methyltransferase CDS** |
| **MI12H(K1)** | **665801** | **680488** | **14688** | **48.9** | **18** | **Terminase, Integrase, Hypothetical protein, endolysin, Autotransporter** |
| **MI12H(K2)** | **779408** | **817809** | **38402** |  | **51** | **Hypothetical protein, Terminase, Integrase, DEAD/DEAH box helicase, Head protein, Late control protein, Phage tail protein, Base plate protein** |
| **Phage Island Group F** | **MI47H** | **783775** | **784897** | **1123** | **48** | **3** | **Terminase, HNN endonuclease, Hypothetical protein** |
| **5DH** | **771779** | **772901** | **1123** |
| **MI12H(K1)** | **147837** | **149099** | **1263** | **49.4** | **4** | **Hypothetical prtein, HNN endonuclease, Phage terminase** |
| **Phage Island Group D** | **MI47H** | **1477709** | **14780353** | **2645** | **38.9** | **3** | **Phage lysin, Holin, Phosphoesterase** |
| **5DH** | **1465771** | **1468415** | **2645** |
| **MI12H(K2)** | **237140** | **241136** | **3968** | **41.2** | **5** | **Hypothetical protein, Phosphoesterase, Lysozyme, Holin** |
| **Phage Island Group E** | **MI47H** | **1509727** | **1516723** | **6997** | **48.5** | **10** | **Phage tail protein, Baseplate assembly protein, HNN endonuclease, Hypothetical protein** |
| **5DH** | **1497788** | **1504784** | **6997** | **48.5** | **10** |
| **MI12H(K1)** | **607301** | **619938** | **12638** | **45.7** | **15** |
| **Phage Island Group I** | **MI47H** | **1517259** | **1521073** | **3815** | **34** | **6** | **Hypothetical protein** |
| **5DH** | **1505320** | **1509134** | **3815** | **34** | **6** |
| **MI12H(K1)** | **620489** | **624435** | **3947** | **34** | **6** |
| **Phage Island Group G** | **MI47H** | **1521123** | **1532495** | **11373** | **42.2** | **17** | **YqaJ-like viral recombinase, ATP-binding protein, DNA-binding protein, Hypothetical protein** |
| **5DH** | **1509184** | **1520556** | **11373** |
| **MI12H(K1)** | **602272** | **607117** | **4846** | **43.6** | **9** | **Hypothetical protein, Holin, Lysozyme, Peptidase** |
| **MI12H(K1)** | **680525** | **686919** | **6395** | **43.3** | **4** | **Hypothetical protein** |
| **Phage Island Group C** | **MI47H** | **1539851** | **1549330** | **9480** | **45.2** | **18** | **ATP-binding protein, HNN endonuclease, Holin, Lysozyme, Phage protein, Hypothetical protein** |
| **5DH** | **1527912** | **1537391** | **9480** |
| **Phage Island group D (Myoviridae of Type 1 Cluster 6, lambda -like)** | **MI47H** | **1549524** | **1554439** | **4911** | **45** | **8** | **Hypothetical protein, ATP-binding protein, Exonuclease** |
| **5DH** | **1537585** | **1542500** | **4911** |
| **MI12H(K1)** | **627576** | **645011** | **17436** | **44** | **26** | **Hypothetical protein, ATP-binding protein, Exonuclease, Integrase, Lysozyme** |
| **Phage Island Group K** | **MI47H** | **1656528** | **1665628** | **9101** | **42.7** | **15** | **Integrase, Exonuclease, Hypothetical protein, ATP-binding protein, Transcriptional regulator** |
| **5DH** | **1644592** | **1653692** | **9101** |
| **MI12H(K1)** | **524893** | **527697** | **2805** | **50.4** | **6** | **Hypothetical protein, ATP-binding protein, Exonuclease** |
| **Phage Island Group H** | **MI47H** | **1677715** | **1694986** | **15861** | **44.3** | **27** | **Late control protein, Hypothetical protein, XRE family transcriptional regulator** |
| **5DH** | **1667190** | **1683050** | **15861** | **44.3** | **26** |
| **MI12H(K1)** | **687089** | **691434** | **4346** | **40.9** | **4** | **Hypothetical protein, Integrase** |
| **MI12H(K2)** | 821146 | 837234 | 16089 | **42.3** | **25** | **Hypothetical protein, Phage repressor protein, Glycosyl hydrolase, Exicionase** |
| **Phage Island Group L** | **MI47H** | **1739069** | **1740943** | **1876** | **39.6** | **3** | **SAM-dependent methyltransferase, Hypothetical protein** |
| **5DH** | **1727134** | **1729007** | **1876** |
| **MI12H(K2)** | 936510 | 946604 | 10095 | **51.2** | **17** | **Hypothetical protein, Head protein, Baseplate assembly protein, Phage tail protein, addiction module antitoxin RelB** |
| **Phage Island Group H** | **MI47H** | **1741657** | **1748069** | **6422** | **45.4** | **12** | **Phage antirepressor protein, Integrase, Exonuclease, Hypothetical protein** |
| **5DH** | **1729721** | **1736133** | **6422** |
| **Phage Island Group H** | **MI47H** | **1760554** | **1764910** | **4355** | **40.8** | **3** | **Integrase, Hypothetical protein** |
| **5DH** | **1748618** | **1752974** | **4355** |
| **APSE** | **MI47H** | **1820393** | **1856477** | **36522** | **43.9** | **45** | **APSE1** |
| **5DH** | **1808190** | **1846893** | **38742** | **42.9** | **47** | **APSE8** |
| **MI12H(K1)** | **746982** | **766816** | **36936** | **43.9** | **43** | **APSE9** |
| **Phage Island Group A** | **MI47H** | **1856915** | **1875327** | **18413** | **49.4** | **26** | **Phage tail protein, Phage baseplate assembly protein, Phage capsid protein, Terminase, Phage integrase, DNA helicase phage protein** |
| **5DH** | **1847609** | **1865994** | **18386** |
| **MI12H(K1)** | **784430** | **790910** | **6481** | **40.9** | **7** | **Hypothetical Protein, DEAD/DEAH helicase, Integrase** |
| **MI12H(K1)** | **966456** | **970212** | **3757** | **50.9** | **4** | **Hypothetical Protein, DEAD/DEAH helicase, Integrase, Autotransporter** |
| **Phage Island Group H** | **MI47H** | **1977445** | **1982039** | **4595** | **45.9** | **13** | **Phage repressor protein, Exicionase, Phage tail protein, Hypothetical protein** |
| **5DH** | **1968135** | **1972729** | **4595** |
| **MI12H(K2)** | 951091 | 956598 | 5508 | **34.9** | **12** | **Hypothetical protein** |
| **MI12H(K2)** | 990273 | 991555 | 1238 | **40.3** | **4** | **Hypothetical protein, Integrase** |
| **Phage Island group N** | **MI12H(K1)** | **177524** | **178493** | **634** | **53.9** | **1** | **Phage tail protein** |
| **Phage Island group M** | **MI12H(K1)** | **624485** | **626979** | **2495** | **42.5** | **5** | **Hypothetical protein, Integrase, YqaJ-like viral recombinase** |

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| **Table S7**: Summary of **plasmid islands** among isolates of B ( MI47H and 5DH ) and C-clade (MI12H; gray background) strains of *H. defensa.* | | | | | | | |
| Name (homologous plasmids) | Genome | start | stop | length | G+C | Total CDS | Description |
| Plasmid Island Group A (pHD5D.2/pHD5AT/pHDAS3.1 /pHDA2C.1/pHDA2C.3) | MI47H | 220192 | 234951 | 14765 | 46.4 | 18 | VapB antitoxin, VapC toxin, DNA binding protein, TrbC, TrbB, TrbA, Surface Exclusion protein, TraY, TraX, TraW, pilS,pilV |
| 5DHH | 220195 | 234952 | 14763 | 46.4 | 18 |
| MI12(K1) | 479781 | 523717 | 43937 | 48.7 | 54 | TrbA, TrbB, TrbC, MobA, PilS, PilV, TraY, TraX, TraR, TraH, TraT, TraO, TraM, TraN, TraJ, PilQ, PilO, PilV, PIlN |
|  | 1008030 | 1018834 | 10805 | 48.2 | 14 | PilN, PilR, PilQ, PilO, PilP, PilM, PilV, Prepillin peptidase |
| Plasmid Island Group J (pPSR1 from Pseudomonas syringae) | MI47H | 349505 | 366992 | 17488 | 45.3 | 23 | VirD4, virB4, VirB5, virB8, virB9, virB10,virB11,VagC, VapC toxin, pilM, staB |
| 5DH | 349507 | 366994 | 17488 | 45.3 | 23 |
| MI12H(K1) | 1018914 | 1034943 | 16030 | 45.8 | 23 | Conjugal transfers Proteins, VirB11, Hypothetical protein, type II toxin and antitoxin system, MobB |
| Plasmid Island Group C | MI47H | 387972 | 394998 | 7027 | 38.5 | 8 | pilR, pilQ, pilT, prepilin, Hypothetical protein, addiction module toxin RelE, RepB |
| 5DH | 387975 | 395001 | 7027 | 38.5 | 8 |
| MI12H(K1) | 157799 | 166156 | 8358 | 39.6 | 9 | Hypothetical protein, cupin superfamily protein, Transcriptional regulator |
| Plasmid Island Group D (pHD5D.1) | MI47H | 397742 | 402120 | 4379 | 43.1 | 6 | Heat shock protein, Resolvase, Plasmid stabilization protein, Prevent host death protein |
| 5DH | 397745 | 402123 | 4379 | 43.1 | 6 |
| MI12H(K1) | 1065845 | 1071515 | 5671 | 42.5 | 8 | Hypothetical protein, Replication initiation protein, Plasmid stabilization protein |
| Plasmid Island Group M | MI47H | 403658 | 406064 | 2407 | 35.2 | 2 | Hypothetical protein, Fructose 1,6-bisphosphatase |
| 5DH | 403661 | 408585 | 5104 | 42.3 | 7 |
| MI12H(K1) | 1073178 | 1078150 | 4973 | 43.2 | 4 | Hypothetical protein |
| Plasmid Island Group H (pHDZA17.2) | MI47H | 406469 | 407351 | 1196 | 54.3 | 2 | Hypothetical protein, type II secretion protein, heat shock protein |
| 5DH | 409031 | 412012 | 2982 | 43.3 | 5 |
| MI12H(K1) | 974386 | 978874 | 4489 | 52.1 | 7 | Type II secretion protein E, PilR, lytic transglycosylase, Hypothetical protein |
| Plasmid Island Group B (pHDZA17.2) | MI47H | 407736 | 422788 | 15053 | 43.5 | 18 | pilR, Hypothetical protein, Prepillin, Heat shock protein, Lytic transglycosylase |
| 5DH | 412086 | 426881 | 15056 | 43.5 | 17 |
| Plasmid Island Group K (Plasmid island 5 (Degnan et al 2009)) | MI47H | 732987 | 772909 | 39925 | 40.7 | 53 | class A beta-lactamase, glyoxalase, hydroxyacid dehydrogenase, cytochrome o ubiquinol oxidase subunit I, Hypothetical protein, HicA, type II restriction endonuclease, Transcriptional regulator, DNA mismatch repair protein MutL |
| 5DH | 737339 | 760913 | 23575 | 40.6 | 32 | Hypothetical protein, HicA, type II restriction endonuclease, Transcriptional regulator, |
| Plasmid Island Group K (Plasmid island 5 (Degnan et al 2009)) | MI47H | 786395 | 804697 | 18303 | 39.5 | 27 | Hypothetical protein, Replication initiation protein, traY, Transcriptional regulator, RelE/StbE |
| 5DH | 774399 | 792754 | 18356 | 39.4 | 27 |
| MI12H (K1) | 105653 | 146559 | 40907 | 40.2 | 59 | Hypothetical protein, ABC transporter, Transcriptional regulator, Replication protein RepA |
| Plasmid Island Group D (pHDZA17.2 / pHD5D.1) | MI47H | 817602 | 823484 | 5883 | 43.3 | 9 | Heat shock protein, RepB,VapB protein |
| 5DH | 805660 | 811542 | 5883 | 43.3 | 9 |
| Plasmid Island Group A (pHD5D.3/pHD5AT/pHDAS3.1/ pHDA2C.1/pHDA2C.3) | MI47H | 1555083 | 1580102 | 25020 | 49.2 | 34 | PilL, PilO, PilP, PilB, pulF, PilS, VapB/VapC, PilV, PilM, PilT,TraH, TraL, TraM, TraN, TraO |
| 5DH | 1543144 | 1568163 | 25020 | 49.2 | 34 |
| Plasmid Island Group L (Plasmid island 9 (Degnan et al 2009)) | MI47H | 1875955 | 1901451 | 25497 | 38.2 | 31 | TraI, stab/staC, VapC, MobC |
| 5DH | 1866622 | 1892138 | 25517 | 38.2 | 31 |
| MI12H (K1) | 11275 | 93571 | 24438 | 38.3 | 31 | Hypothetical Protein, resolvase, PIN domain containing protein |

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| **Table S8**: Identify and copy number of **IS elements** among isolates of B- ( MI47H and 5DH ) and C-clade (MI12H; gray background) strains of *H. defensa.* | | | | | | | | | | |
|  | **5DH** | | **MI47H** | | **MI12H** | | | **Totals** | | |
|  | **CHR** | **Plasmid** | **CHR** | **Plasmid** | **CHR-K1** | **CHR-K2** | **Plasmid** | **MI12** | **5DH** | **MI47H** |
| **IS630** | **47** | **4** | **51** |  |  |  |  |  | **51** | **51** |
| **IS3 ssgr IS3** | **15** | **7** | **20** |  | **21** | **4** |  | **25** | **22** | **20** |
| **IS6** | **10** | **1** | **11** |  |  |  |  |  | **11** | **11** |
| **IS5** |  |  |  |  | **11** | **6** | **1** | **18** |  |  |
| **IS5 ssgr IS427** | **11** | **3** | **16** |  |  |  | **5** | **5** | **11** | **11** |
| **ISNCY** | **9** | **9** |  | **18** | **10** | **1** | **6** | **17** | **18** | **18** |
| **Tn3** | **5** | **8** |  | **15** | **10** | **3** | **3** | **16** | **13** | **14** |
| **IS3** |  |  |  |  | **8** | **4** |  | **12** |  |  |
| **IS110 ssgr IS1111** | **3** | **1** | **4** |  | **2** | **2** |  | **4** | **4** | **4** |
| **IS21** | **3** | **1** | **4** |  | **1** | **3** |  | **4** | **4** | **4** |
| **Others** |  |  |  |  |  |  |  |  |  |  |
| **IS4 ssgr IS50** | **1** | **3** | **3** |  |  |  |  |  | **4** | **3** |
| **IS256** |  |  |  |  |  |  | **5** | **5** |  |  |
| **IS4** |  |  |  |  | **2** | **1** |  | **3** |  |  |
| **IS6** |  |  |  |  | **2** | **1** |  | **3** |  |  |
| **IS5 ssgr IS1031** |  |  |  |  |  | **2** |  | **2** |  |  |
| **IS481** | **1** |  | **1** |  |  |  |  |  | **1** | **1** |
| **IS5/IS1182** | **1** | **1** | **2** |  |  |  |  |  | **2** | **2** |
| **IS200/IS605** |  |  | **1** |  |  |  | **1** | **1** | **0** | **1** |
| **ISNCY ssgr ISPlu15** |  |  |  |  |  |  | **1** | **1** |  |  |
| **IS 701** | **2** | **1** | **3** |  |  | **1** |  | **1** | **3** | **3** |
| **IS91** | **1** |  | **1** |  | **1** |  |  | **1** | **1** | **1** |
| **IS982** | **1** | **2** | **2** | **1** | **1** |  | **2** | **3** | **3** | **3** |
| **ISKra4 ssgr ISAzba1** |  | **1** |  | **1** |  |  |  |  | **1** | **1** |
| **Retron type RNA directed DNA polymerase** | **3** | **1** |  | **5** |  |  |  |  | **4** | **5** |
| **Transpoases** | **1** |  |  |  |  |  |  |  | **1** | **1** |
| **New family** |  |  |  |  | **3** |  |  | **3** |  |  |
|  |  |  |  |  |  |  |  | **125** | **154** | **154** |

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| Table S9: Presence of colicin-bearing plasmids in *H. defensa* isolates from the *five H. defensa* strains (A-E) | | | | |
| Symbiont status | *H. defensa*  clades | Colicin plasmid  Yes/No | *H. defensa*  clade | Colicin plasmid  Yes/No |
| *H. defensa* only | A (N =45)  C (N= 17)  D (N = 24)  E (N= 3) | 0/63 | B (N= 135) | 7/0 |
| *H. defensa* +  *F. symbiotica* | 0/3 | 123/4 |
| *H. defensa* with  other symbionts | 0/23 | 1/0 |
| total | 0/89 | 131/4 |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Amino Acid Biosynthesis | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Clade | Genome | aroH | aroB | aroQ | aroE | aroK | aroA | aroC | pheA | aspC | thrA | asd | dapD | dapE | dapF | lysA | carA | carB | thrA | thrB | | thrC | glyA | serA | serC | cysE | cysK | aspC | proC | iscS | asnB | putA |
| B | 5DH |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |
| MI47H |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |
| C | MI12H |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |
| E | ZA17 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |
| D | AS3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |
| A2C |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |
| A | 5AT |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |
| NY26 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |
|  | | Amino Acid Transportation | | | | | | | | | | | | | | | | | | | | | | | Vitamin/Peptide Transport | | | | | | | |
| Clade | Genome | metQ | metI | metN | glnQ | glnP | glnH | artM | artQ | artI | artP | TC.LICVS | sdaC | putP | proY | lysP | mtr | tyrP | aroP | | ABC.PA.S | ABC.PA | ABC.PA.P | gltL | panF | thiB | thiP | thiQ | sapF | sapD | sapC | sapB |
| B | 5DH |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |
| MI47H |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |
| C | MI12H |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |
| E | ZA17 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |
| D | AS3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |
| A2C |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |
| A | 5AT |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |
| NY26 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |
| Other Transportation | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Clade | Genome | lolC E | lolD | lolF | lptG | lptB | ABC-2LPSE.P | ABC-2LPSE.A | mlaC | mlaE | mlaF | ABC.FEV.P | ABC.FEV.A | ABC.FEV.S | feoC | feoB | feoA | tonB | znuA | | znuC | znuB | sitD | sitC | sitB | sitA | pstB | pstA | pstC | pstS | mgtA | corC |
| B | 5DH |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |
| MI47H |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |
| C | MI12H |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |
| E | ZA17 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |
| D | AS3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |
| A2C |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |
| A | 5AT |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |
| NY26 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | |  |  |  |  |  |  |  |  |  |  |  |  |

**Figure S1**. Comparison of metabolic pathway among sequenced *H. defensa* from all five strain groups. Green indicates intact genes, gold boxes indicate pseudogenes, and gray boxes indicate absent genes.

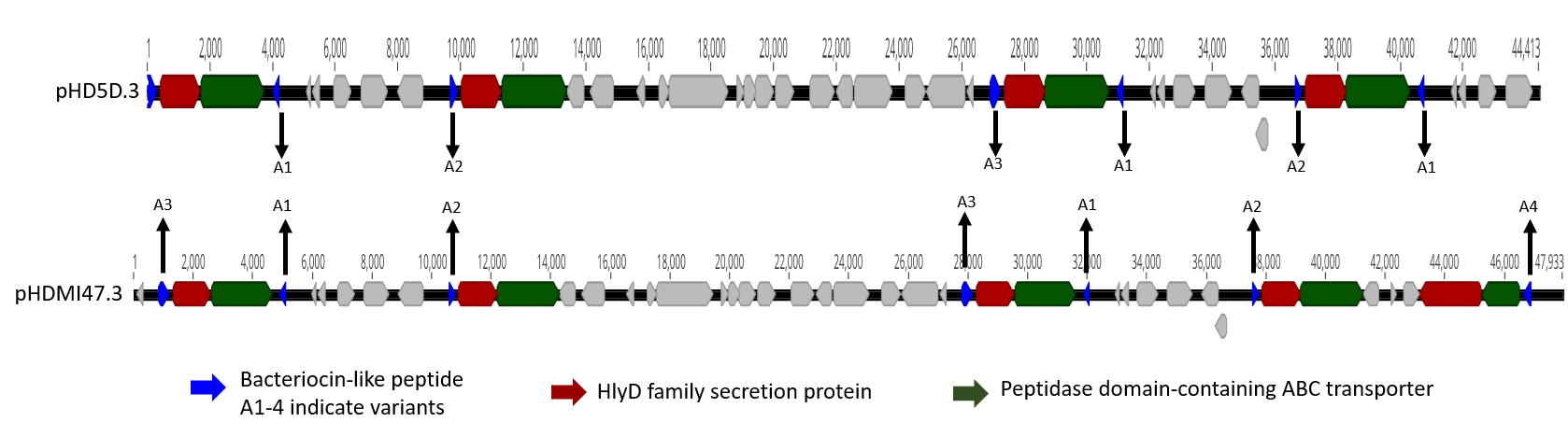
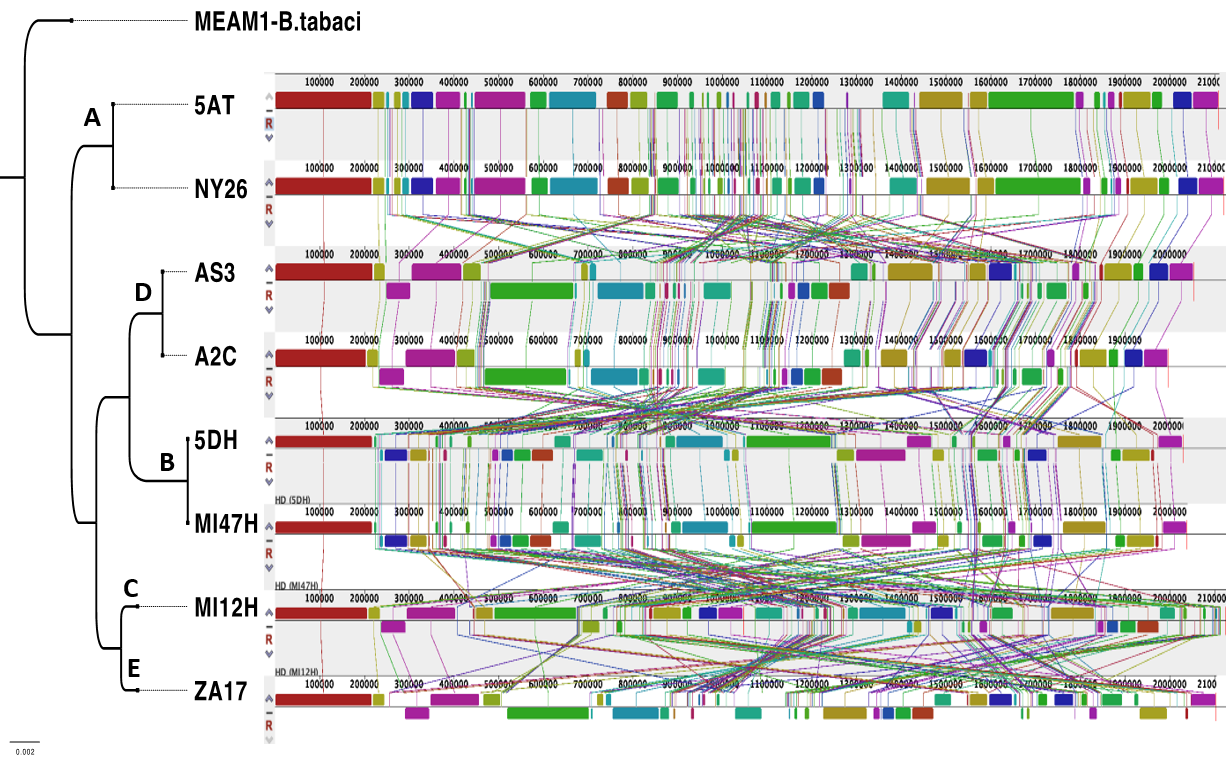
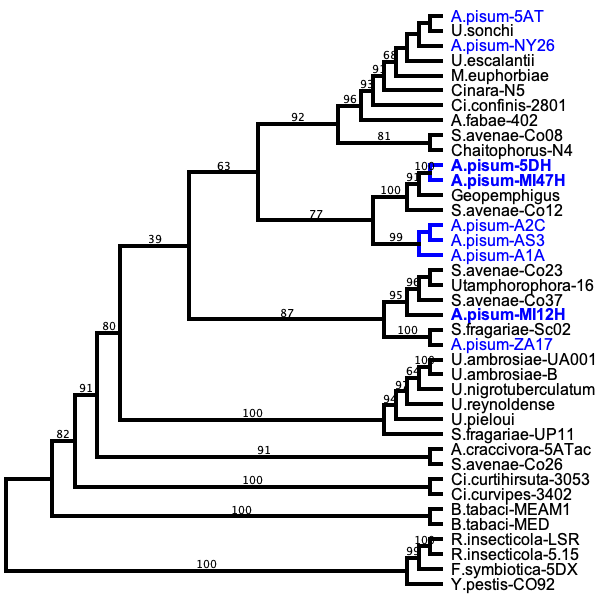


Figure S2. Genomes of bacteriocin-containing plasmids unique to B-strain *H. defensa*. Repeats of Type 1 secretion system components (HylD, ABC transporter) and up to four bacteriocins variants are present on each plasmid.



**Figure S3.** Mauve alignment showing that within-clade genomes highly similar in content and architecture, while among-clade strains vary in these respects.



A

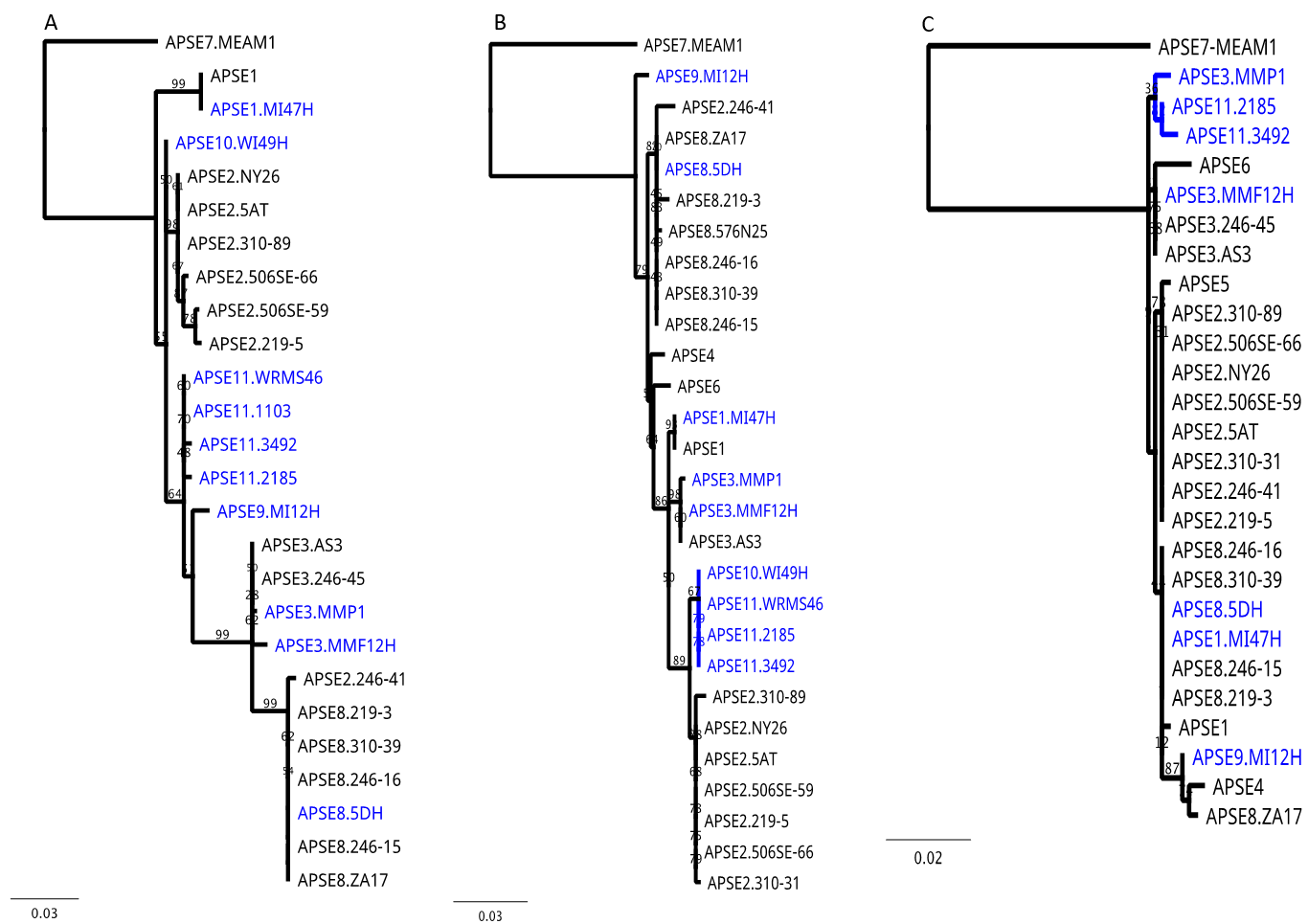
B

D

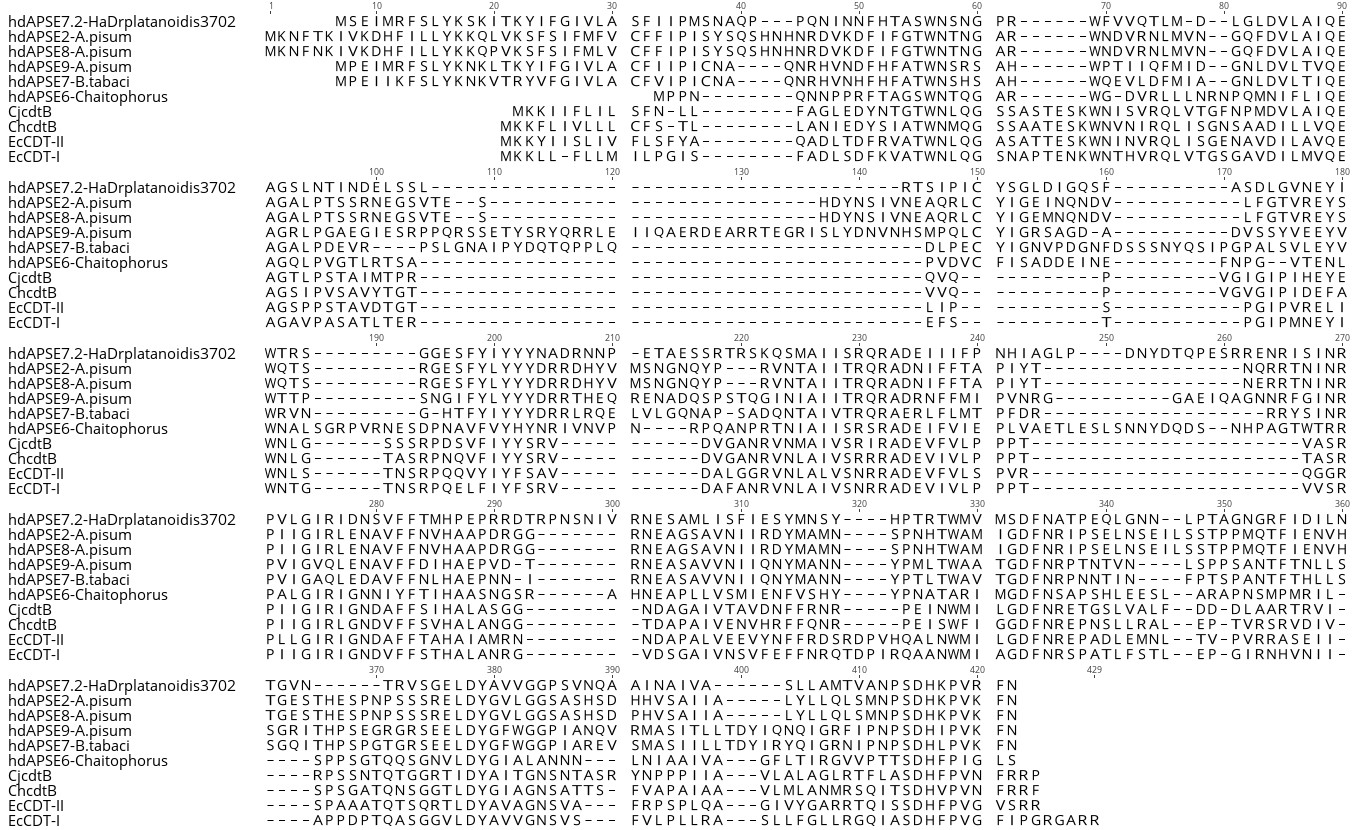
C

E

**Figure S4**. A maximum likelihood phylogenetic analysis of *H. defensa* isolates inferred from five partial single copy orthologous genes nucleotide sequences with partitioned model for each locus. Branch support indicated by 10,000 bootstrap replicates. Blue text indicates *H. defensa* isolates with sequenced genome.



**Figure S5**. A maximum likelihood phylogenetic analysis of APSE (A) module 1:P51 gene (B) Module 2: P3gene (C) Module 4: P19 gene of APSE. Branch support indicated by 10,000 bootstrap replicates. Blue text indicates isolates new to this study.



**Figure S6.** Amino acid sequences of CdtB from *H. defensa* and other bacteria aligned by using Maftt L-INS-I strategy along with scoring matrix BLOSUM62. Key active residues (boxes and arrows) are conserved in otherwise dissimilar alleles.

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| Table S10: Data from parasitism assays | | | | | |
| Assay 1 | E8, B8 and B10 vs uninfected control (all same aphid genotype = 5DAB) | | | | |
| code | aphid line | mummy | aphids | mortality |  |
| UC | 5DAB | 9 | 3 | 8 |  |
| UC | 5DAB | 11 | 2 | 7 |  |
| UC | 5DAB | 16 | 3 | 1 |  |
| UC | 5DAB | 14 | 3 | 7 |  |
| UC | 5DAB | 18 | 2 | 0 |  |
| UC | 5DAB | 12 | 1 | 7 |  |
| UC | 5DAB | 18 | 0 | 1 |  |
| UC | 5DAB | 10 | 2 | 8 |  |
| E8 | ZA17 | 11 | 4 | 5 |  |
| E8 | ZA17 | 10 | 4 | 6 |  |
| E8 | ZA17 | 1 | 8 | 11 |  |
| E8 | ZA17 | 4 | 7 | 9 |  |
| E8 | ZA17 | 9 | 5 | 7 |  |
| E8 | ZA17 | 6 | 5 | 8 |  |
| E8 | ZA17 | 8 | 5 | 7 |  |
| E8 | ZA17 | 9 | 9 | 2 |  |
| E8 | ZA17 | 11 | 5 | 4 |  |
| B8 | 5DH | 5 | 4 | 11 |  |
| B8 | 5DH | 4 | 6 | 10 |  |
| B8 | 5DH | 9 | 5 | 6 |  |
| B8 | 5DH | 6 | 4 | 10 |  |
| B8 | 5DH | 7 | 2 | 11 |  |
| B8 | 5DH | 6 | 9 | 5 |  |
| B8 | 5DH | 4 | 12 | 4 |  |
| B8 | 5DH | 5 | 6 | 9 |  |
| B8 | 5DH | 6 | 9 | 5 |  |
| B8 | 5DH | 5 | 5 | 10 |  |
| B10 | WI49H | 6 | 10 | 4 |  |
| B10 | WI49H | 6 | 11 | 3 |  |
| B10 | WI49H | 6 | 11 | 3 |  |
| B10 | WI49H | 0 | 14 | 6 |  |
| B10 | WI49H | 1 | 16 | 3 |  |
| B10 | WI49H | 1 | 11 | 8 |  |
| B10 | WI49H | 0 | 6 | 14 |  |
| B10 | WI49H | 3 | 6 | 11 |  |
| B10 | WI49H | 4 | 12 | 4 |  |
| B10 | WI49H | 0 | 17 | 3 |  |
|  |  |  |  |  |  |
| Assay 1B | B3 vs. uninfected control (all same aphid genotype = 5DAB) | | | | |
| code | aphid line | mummies | aphids alive | dual mortality |  |
| UC2 | 5DAB | 16 | 2 | 2 |  |
| UC2 | 5DAB | 13 | 3 | 4 |  |
| UC2 | 5DAB | 17 | 0 | 3 |  |
| UC2 | 5DAB | 13 | 4 | 3 |  |
| UC2 | 5DAB | 13 | 3 | 4 |  |
| UC2 | 5DAB | 17 | 1 | 2 |  |
| UC2 | 5DAB | 9 | 7 | 4 |  |
| UC2 | 5DAB | 15 | 4 | 1 |  |
| B3 | MMP1 | 14 | 7 | 0 |  |
| B3 | MMP1 | 11 | 4 | 5 |  |
| B3 | MMP1 | 14 | 5 | 1 |  |
| B3 | MMP1 | 10 | 4 | 6 |  |
| B3 | MMP1 | 6 | 11 | 3 |  |
| B3 | MMP1 | 11 | 4 | 5 |  |
| B3 | MMP1 | 10 | 4 | 6 |  |
| B3 | MMP1 | 10 | 5 | 5 |  |
|  |  |  |  |  |  |
| Assay 2 | B1 vs uninfected control in MI47AB aphid genotype | | | |  |
| code | aphid line | mummies | aphids alive | dual mortality |  |
| UC | MI47HAB | 13 | 3 | 4 |  |
| UC | MI47HAB | 18 | 1 | 1 |  |
| UC | MI47HAB | 10 | 3 | 7 |  |
| UC | MI47HAB | 15 | 3 | 2 |  |
| UC | MI47HAB | 12 | 5 | 3 |  |
| UC | MI47HAB | 16 | 2 | 2 |  |
| UC | MI47HAB | 18 | 2 | 0 |  |
| UC | MI47HAB | 17 | 3 | 0 |  |
| B1 | MI47H | 0 | 10 | 10 |  |
| B1 | MI47H | 0 | 18 | 2 |  |
| B1 | MI47H | 0 | 12 | 8 |  |
| B1 | MI47H | 0 | 18 | 2 |  |
| B1 | MI47H | 0 | 20 | 0 |  |
| B1 | MI47H | 0 | 10 | 10 |  |
| B1 | MI47H | 0 | 14 | 6 |  |
| B1 | MI47H | 0 | 20 | 0 |  |
|  |  |  |  |  |  |
| Assay 3 | C9 vs UC control (AS3AB genotype) | | | |  |
| code | aphid line | mummies | aphids alive | dual mortality |  |
| UC | AS3AB | 19 | 2 | 0 |  |
| UC | AS3AB | 16 | 1 | 3 |  |
| UC | AS3AB | 11 | 3 | 6 |  |
| UC | AS3AB | 19 | 1 | 0 |  |
| UC | AS3AB | 14 | 4 | 2 |  |
| UC | AS3AB | 20 | 0 | 0 |  |
| UC | AS3AB | 16 | 0 | 4 |  |
| UC | AS3AB | 15 | 0 | 5 |  |
| UC | AS3AB | 15 | 0 | 5 |  |
| UC | AS3AB | 17 | 4 | 0 |  |
| C9 | MI12H-AS3AB | 0 | 13 | 7 |  |
| C9 | MI12H-AS3AB | 0 | 15 | 5 |  |
| C9 | MI12H-AS3AB | 0 | 20 | 0 |  |
| C9 | MI12H-AS3AB | 0 | 15 | 5 |  |
| C9 | MI12H-AS3AB | 0 | 15 | 5 |  |
| C9 | MI12H-AS3AB | 1 | 20 | 0 |  |
| C9 | MI12H-AS3AB | 0 | 18 | 2 |  |
| C9 | MI12H-AS3AB | 1 | 17 | 2 |  |
| C9 | MI12H-AS3AB | 1 | 15 | 4 |  |
|  |  |  |  |  |  |
| Assay 3B | C9 vs UC (2I84AB genotype) | | | |  |
| code | aphid line | mummies | aphids alive | dual mortality |  |
| UC | 2184AB | 12 | 0 | 8 |  |
| UC | 2184AB | 10 | 0 | 10 |  |
| UC | 2184AB | 10 | 0 | 10 |  |
| UC | 2184AB | 11 | 0 | 9 |  |
| UC | 2184AB | 12 | 0 | 8 |  |
| UC | 2184AB | 9 | 0 | 11 |  |
| UC | 2184AB | 11 | 0 | 9 |  |
| UC | 2184AB | 12 | 0 | 8 |  |
| C9 | 2184H | 0 | 6 | 14 |  |
| C9 | 2184H | 0 | 8 | 12 |  |
| C9 | 2184H | 0 | 8 | 12 |  |
| C9 | 2184H | 1 | 8 | 11 |  |
| C9 | 2184H | 0 | 7 | 13 |  |
| C9 | 2184H | 0 | 8 | 12 |  |
| C9 | 2184H | 0 | 8 | 12 |  |
| C9 | 2184H | 0 | 5 | 15 |  |