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ao-801      .... MKAI YGRNFKPQDLNAKYTHVLFHAFVKI NQQLCEI GLADWADIDI EWDFE VDFG . IN 59
kaf3934333 . . . . NSAGYRTVGYYYVDWAI YGRNFKPQDLKADQFTH LFAFLKI NRETCHEI TLADWADVIDI RWDFE VDFG . IN 71
kaf3910283 M STATAGYRTVGYYYVDWAI YGRNFKPQDLNASQFTH LFAFLVNI NPSICEVLIADWADIDI EWDFE VDFG . NN 75
kaf3910915 . . . . MAPAYRTI GYYVDWAI YGRNFKPQDLNGSQFTH LFAFLVKI NPSICEI TLADWADIDI EWDFE VDFG . IN 71
eps44564    . . . . NATGFRTVGYYYVDWAI YGRNFKPQDLKADQFTH LFAFLVKI NRDICEI QLADWADIDI EWDFE VDFVAGVIN 73
kaf3902836 . . . . NSPGRFTI GYYVDWAI YGRNFKPQDLVAQNFTH LFAFLVNI DGDSCEI VKLADSWADIDI EWDFE VDFG . IN 72

ao-801      LFCII FVQLYKLRANR RLRVLMK I CGWTYS QDGLPGGASTPERRDTTEARTAVEMVRNE CLIDCVVDWEYFNDATEVA 137
kaf3934333 VYCIIFVQLYRLKQTR RLRVLLS I CGWTYS QDGFAGGASTPERRDRGARSAMEMVKNYCLIDG DLDWEYFVDATEAA 149
kaf3910283 LYCIIFVQLWLRKQTR RLRVLLS VCGWTYS QDGNFPNGVDNPKRRDTTEARTAVEMVKNFCLIDG DLDWEYFVDSIQAA 153
kaf3910915 LYCIIFVQLYKLRKSN RLRVLLS I CGWTYS QDGNFPNGANTPEKREKARSAMEMVKNFCLIDG DLDWEYFKDATEAA 149
eps44564    VYCIIFLQDFRLRKHVHRNLRITMS I CGWTYS QDGSFAAGASTPERRDRGARSAMQVMDHCLIDG DLDWEYFVDATEAA 151
kaf3902836 VYCIIFKQLYLRKANR RLRITLS I CGWTYS QNCSLPNAASTPERRDRGARSAMAMENFCLIDG DLDWEYFANADAA 150

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ao-801      NYNDLLRRI FQYLDI LNP . . . . RFEIS I VAPCCGLDQLQKLDAAAGNDKYLSE WNIWAYDFSCPWSSVSGHASN VHY 208
kaf3934333 NYNDLLR LRFYLDVNP . . . . SFEIS I VAPCCGPKI TKLD PGMQYLD WNIWAYDFSCWSSVSGHANFYA 220
kaf3910283 NYNDLLR LRFYLDVNP . . . . RFEIS I VAPCCGPKI SKLD PGMQYLD WNIWAYDFSCWSSVSGHANYP 224
kaf3910915 NYNDLLRKRREHINALSAGYGATRPHE I S VAPCCAEVNYTKLD RGMQYLD WNIWAYDFSCWSSVAGHANYP 227
eps44564    NYNDLLR LRFYLDVNP . . . . AFEIS I VAPCCADKI QKLD PGMQYLD WNIWAYDFSCWSSVAGHANYP 222
kaf3902836 NYNDLLR LRFYLDKLR . . . . NFEIS I VAPCCADNVRNMD PGMQYLD WNIWAYDFSCWSSVYTCANLXP 221

ao-801      SKTNPAS IDYSF DKTIDFFKGS. VKPERLVM CVPLYGRCHADTEGP . . . . CKPYNGCGAGI WEACVWDYKDLPLAGSKVN 283
kaf3934333 STSNP GSDFAFDDSKLYSAVD . . . . PPKI V CVPLYGRCHASTEGV . . . . CKPYS GSGAGI WEACVWDYKDLPLQAGAVH 294
kaf3910283 SPDNPAS IPIFSF DASIKMYSAV . . . . NPKRLV V CVPLYGRCHADTEGP . . . . CKPFS CVCGI WEACVWDYKDLPLAGSOVF 298
kaf3910915 SITI PCSI IPIFSF EKOIEDYLHAGI RSDKI V CVPLYGRCHADTEGP . . . . CKGYS CGCAGI WEPVWDYKDLPLPGSOVS 303
eps44564    STSNPAS IPIFSF DTAIRMYSAVN . . . . PPKL V CVPLYGRCHADTEGP . . . . CKPYCGT CQWETVWDYKDLPLPGSOEY 296
kaf3902836 SITNPAS IPIFSF DASIQLYHADV . . . . PPKI V CVPLYGRCHADTEGP ELAQPNVNLPEIWEACVWDYKDLPLPGSOEY 297

ao-801      EDPYAI AAWSYEATKLVN S YETI N VAKKAOYI KAKGLCGAMWHEIS CDK GSEI I VCTVI DALGGTRALDTHKNTI 361
kaf3934333 EDPQLLASVSYDNRQLM S YETI N ARLKAQYI I SGLCGAMWHEIS CDK GADSI VQVNI VDTFGGANGLDLSKLNII 372
kaf3910283 EDERVI CSYCYDSSRMV S YETI N AMI KAIYI KFLCGAMWHEIS CDK GSNII QSVI NALGGQDNLDTQNTII 376
kaf3910915 DDQKM ASWYD AARLM S YETI N VAKKAAVI KQGLCGAMWHEIS CDK GPDI I VEHVI DSLGGQALDHRGNL 381
eps44564    QDDQL ASYSYD AQRLL S YETI H AELKAKYI NSRGLCGAMWHEIS CDK GAGSI VCTVI DTFPKKRTTAAPAKK 374
kaf3902836 EDDKLVASVYDNRQLL S YETI N VAKLKAQYI NSGLCGAMWHEIS CDK GHGSI VCTVI DTFVPLKPMVAVPAP 375

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ao-801      AYPGS KYDNVRSACA . . . . . 376
kaf3934333 AYPQSKFDNI RSYKP . . . . . 387
kaf3910283 SYPDS KYDNVRSFK . . . . . 390
kaf3910915 SYPGS KYDNI RA . . . . . 393
eps44564    KVRVKLAQDLSLSTEEEQEVRLEAFDYFTDPEELGKDI I QSKDLKKAFAALGFNLSPEI KEI KETI DPDDEGFI VYEL 452
kaf3902836 VAVTAPAPPNNAPKPKDPKPKPKAPKPKTKLQWANDLLDKLLKRNGE . . . . . 425

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Supplementary Fig. S3. Alignments of amino acid sequences of chitinases among the different nematophagous fungi. The chitinases are from *Dactylella cylindrospora* (kaf3934333), *Drechslerella brochopaga* (kaf3910283), *Dactylella cionopaga* (kaf3910915), *Dactylella haptotyla* (eps44564) and *Arthrobotrys entomopaga* (kaf3902836), respectively. Areas shaded in black are high degree homology (100%) and unshaded areas are regions of variability between the chitinases; ***represent chitinase conserved sequence.