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Appendix A

Solutions, media and their compositions used in this study.

The following table provides details of the composition of media and solutions used during this research. Recipe for a given volume is shown.

Solution/Media	Recipe
Fries Culture Medium (FCM)	KH ₂ PO ₄ , 1 g; MgSO ₄ ·7H ₂ O, 0.5 g; NaCl, 0.1 g; CaCl ₂ , 0.13 g; MnSO ₄ ·4H ₂ O, 1 mg; Boric acid, 1 mg; CuSO ₄ , 0.1mg; ZnSO ₄ , 0.1 mg; FeSO ₄ , 20mg, NO ₃ NH ₄ , 1 g; ammonium tartrate, 5 g; Glucose 30g; distilled H ₂ O 1000 mL. Autoclaved at 121 °C for 30 min.
Phosphate Buffered Fries Culture Medium (PFCM)	As for FCM except that 200 mM phosphate buffer pH 6.8 was used instead of H ₂ O.
200 mM Phosphate Buffer pH 6.8	49.7 mL K ₂ HPO ₄ (200 mM), 50.3 mL KH ₂ PO ₄ (200 mM) in 1000 mL distilled H ₂ O.
LB (Luria-Bertani Broth; liquid growth media)	1% (w/v) Bacto [®] -tryptone, 0.5% (w/v) Bacto [®] -yeast extract, 1% (w/v) NaCl, pH 7.0
LB plates (solid growth media)	1% (w/v) Bacto [®] -tryptone, 0.5% (w/v) Bacto [®] -yeast extract, 1% (w/v) NaCl, 1.2% (w/v) Bacto [®] -agar, pH 7.0
LB + ampicillin + IPTG + X-Gal (AIX) plates	LB plate ingredients, with ampicillin added to a final concentration of 100µg/mL and supplemented with 0.5mM IPTG and 80µg/mL X-gal
TAE buffer (50x)	2M Tris-acetate, 50mM EDTA, pH 8.0
TE buffer (50x)	100mM Tris-Cl, 10mM EDTA, pH 8.0

Appendix B-Protein homology

B1. Proteins showing potential homology to the peptide fragments from the 48 kDa protein extracted from culture filtrates of *Pyrenophora teres* f. *maculata*. The accession number, area of overlap, homology and e value are shown for each.

Accession No, Putative protein function, (organism)	Overlap (amino acids)	% homology – e value
1. ATTAMSGNNVARYK NP_966376.1, Regulatory protein RepA (<i>Wolbachia endosymbiont</i>) NP_436022.1, Putative ABC transporterpermease protein, (<i>Sinorhizobium</i> sp.) ZP_01508215.1, (2Fe-2S) binding, (<i>Burkholderia phytofirmans</i>)	ATTAMSGNN (9aa) AMSGNNVARYK (11aa) TTAMSGN (7aa)	88, +320 81, +429 100, +575
2. ATTAYGANNVGGFTR ABC transporter, permease protein (<i>Burkholderia pseudomallei</i>) Ste12-like transcription factor CpST12 (<i>Cryphonectria parasitica</i>)	ATTAYGANNVGGFTR (14aa) AYGANNV (7aa)	78, +3.9 100, +574
3. ATLDCGYQLGGSGEPGAR ZP_01640025.1, Surface adhesion protein, (<i>Pseudomonas putida</i>) XP_370099.2, Hypothetical protein MGG-06614, (<i>Magnaporthe grisea</i>)	ATLDCGYQLGGSGEP GAR (18aa) GGSGEPGAR (9aa)	68, +131 88, +316

Appendices

Accession No, Putative protein function, (organism)	Overlap (amino acids)	% homology – e value
<p>4. ATGPPLVPMYQGLR</p> <p>XP_001272449.1, MFS monosaccharide transporter, (<i>Neosartorya fischeri</i>)</p> <p>XP_746835.1, MFS monosaccharide transporter, (<i>Aspergillus fumigatus</i>)</p> <p>XP_366861.1, Hypothetical protein MGG-02937, (<i>Magnaporthe grisea</i>)</p> <p>EAT82204.1, Hypothetical protein SNOG_10810, (<i>Phaeospharia nodorum</i>)</p>	<p>LVPMYQG (7aa)</p> <p>LVPMYQG (7aa)</p> <p>PLVPMYQGLR (10aa)</p> <p>LVPMYQ (6aa)</p>	<p>100, +99</p> <p>100, +99</p> <p>80, +429</p> <p>100, +575</p>
<p>5. ATGDGAYNNYQGLR</p> <p>ZP_01643492.1, TonB-dependent receptor, (<i>Stenotrophomonas maltophilia</i>)</p> <p>EAT84642, Hypothetical protein SNOG_08366, (<i>Phaeospharia nodorum</i>)</p>	<p>GDGAYNNYQGL (11aa)</p> <p>TGDGAYNNY (9aa)</p>	<p>90, +1.2</p> <p>88, +99</p>
<p>6. RHSMNPPVGAGPSLTAR</p> <p>ZP_01547224.1, Peptide ABC transporter, periplasmic peptide binding protein (<i>Stappia aggregate</i>)</p>	<p>SMNPPVGAGP (10aa)</p>	<p>80, +98</p>
<p>7. DVLDMTGVPVPLSGGHR</p> <p>XP_001413674.1, Hypothetical protein MGG-11346, (<i>Magnaporthe grisea</i>)</p> <p>EAT78790.1, Hypothetical protein SNOG_13766, (<i>Phaeospharia nodorum</i>)</p>	<p>DVLDMTGVPVPP (11aa)</p> <p>TGPVPLSG (9aa)</p>	<p>72, +176</p> <p>88, +176</p>

Appendices

Accession No, Putative protein function, (organism)	Overlap (amino acids)	% homology – e value
8. Q/KHALPQ/KGPLGDTDLNPQ/K XP_001248024.1, Hypothetical protein CIMG_01795, (<i>Coccidioides immitis</i>) XP_001268892.1, oligopeptide transporter, OPT family protein, (<i>Aspergillus fumigatus</i>) EAT86152.1, Hypothetical protein SNOG_6321, (<i>Phaeospharia nodorum</i>) XP_001228238.1, Hypothetical protein CHGG_10311, (<i>Chaetomium globosum</i>) XP_390895.1, Hypothetical protein (<i>Gibberella zeae</i>)	ALPKGPLGDTDLN (13aa) LGDTDLNP (8aa) LGDTDLNP (8aa) LGDTDLNP (8aa) LGDTDLNP (8aa)	76, +73 87, +317 87, +317 87, +317 87, +317
9. NPDEELMVPPDNSHHCAR XP_001023650.1, Zinc finger protein (<i>Tetrahymena thermophila</i>) XP_364468.1, Hypothetical protein MGG-09313, (<i>Magnaporthe grisea</i>)	ELMVPPDNS (9aa) EELMVPPD (10aa)	88, +9.3 80, +236
10. CWLSPGQVDTGSLAEK XP_001271003.1, Forkhead domain protein, (<i>Aspergillus clavatus</i>) XP_754617.1, Forkhead domain protein, (<i>Aspergillus fumigatus</i>) NP_783993.1, ABC transporter, ATP binding protein (<i>Lactobacillus</i> sp.)	WLSPGQV (7aa) WLSPGQV (7aa) GQVDTGSLAE (11aa)	100, +177 100, +177 81, +318
11. DVLSPYGPVPPGGPMHK XP_759578.1, Hypothetical protein UM03431.1, (<i>Ustilago maydis</i>) YP_714064.1, Putative ABC transport protein, ATPase component (<i>Frankia alni</i>) XP_001226167.1, Hypothetical protein CHGG_10900, (<i>Chaetomium globosum</i>)	YGPVPPGGPM (10aa) GPVPPGGP (8aa) GPVPPGGP (8aa)	90, +9.3 100, +98 100, +98

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Accession No, Putative protein function, (organism)	Overlap (amino acids)	% homology – e value
12. GAFSLSRPVGFRYTSR XP_001272086.1, Alkaline phytoceramidase, (<i>Aspergillus clavatus</i>) XP_759317.1, Hypothetical protein UM03170.1, (<i>Ustilago maydis</i>) XP_362484.1, Hypothetical protein MGG_08067, (<i>Magnaporthe grisea</i>)	FSLSRPVGFR (10aa) GAFSLSRPV (9aa) AFSLSRP(7aa)	90, +41 88, +318 100, +769
13. WCLSGSPMQGPSLAEK XP_001268048.1, SNF2 family helicase/ATPase, (<i>Aspergillus clavatus</i>) XP-388776.1, Hypothetical protein FG08600.1, (<i>Gibberella zeae</i>) XP_368791.2, Hypothetical protein MGG_00453, (<i>Magnaporthe grisea</i>) EAT86485.1, Hypothetical protein SNOG_06654, (<i>Phaeospharia nodorum</i>)	WCLSGSPMQ (9aa) WCLSGSPMQ (9aa) WCLSGSPMQ (9aa) WCLSGSPMQ (9aa)	88, +2.9 88, +2.9 77, +17 77, +17
14. VDLSNPPPVPGQPGVFK XP_751134.1, AAAfamily ATPase, (<i>Aspergillus fumigatus</i>) XP_365329.2, Hypothetical protein MGG_02031, (<i>Magnaporthe grisea</i>) YP_001133367.1, Virulence factor MCE family protein, (<i>Mycobacterium gilvum</i>) XP_001271351.1, Conserved hypothetical protein, (<i>Aspergillus clavatus</i>) XP_754231.1, Conserved hypothetical protein, (<i>Aspergillus fumigatus</i>) YP_716212.1, Putative transport associated protein (<i>Frankia alni</i>)	DLSNPPPVPGQP (12aa) PPPVPQGPGV (10aa) PPPVPQGPG (9aa) PVPGQPGVF (9aa) PVPGQPGVF (9aa) PPPVPQGPG (9aa)	75, +30 90, +54 88, +54 88, + 73 88, + 73 88, + 73

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Accession No, Putative protein function, (organism)	Overlap (amino acids)	% homology – e value
15. YQSSCPPVKGPGPVMK XP_644669.2, Hypothetical protein DDBDRFAT_0217202, (<i>Dictyostelium discoideum</i>) ZP_00952836.1, TonB-dependent receptor (<i>Oceanicuilis alexandrii</i>) EAQ70787.1, Hypothetical protein MGH7_ch7g194, (<i>Magnaporthe grisea</i>)	SSCPPVKGPGPV (12aa) SCPPVKGPGP(11aa) QSSCPPVKGPGPVM (14aa)	75, +318 81, +573 64, +573
16. CAANLFQEGEGGGEQ/KFLNAGR YP_611537.1, ABC transporter related, (<i>Silicibacter</i> sp.) XP_757422.1, Hypothetical protein UM01275.1, (<i>Ustilago maydis</i>) XP_363747.2, Hypothetical protein MGG_01673, (<i>Magnaporthe grisea</i>)	NLFQEGEGG (9aa) AANLFQE (7aa) GEGGGEQFL (9aa)	77, +314 100, +421 88, +421
17. NMFVTQRNESTEEEAR ABK_88691.1, Sp185/333, (<i>Strongylocentrotus</i> <i>purpuratus</i>) YP_141507.1, Cell division ABC transport permease, (<i>Streptococcus</i> sp.)	QRNESTEEEAR (11aa) MFVTQRNEST (10aa)	72, +23 80, +73
18. YGLLTLLNQADCLTWNK EAT79852.1, Hypothetical protein SNOG_12554, (<i>Phaeosphaeria nodorum</i>)	YGLLTLLNQAD (12aa)	75, +17
19. QMLCCYFDYFCLLK CT122_CONPE, T-1-conotoxin Pn- B01122 precursor, (<i>Conus pannaceus</i>)	CCYFDYFCCL (10aa)	80, +2.9
20. SLCMVVYMGCMYQNGDDYTMLK ZP_01637531.1, Outer membrane porin, (<i>Pseudomonas putida</i>)	MGCMYQNGD (9aa)	77, +234

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Accession No, Putative protein function, (organism)	Overlap (amino acids)	% homology – e value
21. MQLDVLRMCGDPANDLLK EAT79852.1, Hypothetical protein SNOG_12554, (<i>Phaeosphaeria nodorum</i>) ZP_01412332.1, Putative transport system permease ABC transporter, (<i>Sinorhizobium medicae</i>) XP_661832.1, Hypothetical protein AN4228.2, (<i>Aspergillus nidulans</i>)	CGDPANDLLK (10aa) VLRMCGDPA (9aa) DVLRMCGDPANDLL (11aa)	81, +5.2 88, +73 73, +236
22. VLRNDDDDGDCMYVQPGHR EAT78245.1, Hypothetical protein SNOG_14374, (<i>Phaeosphaeria nodorum</i>)	NDDDGDCMYVQPG (13aa)	76, +17
23. YGLLTLMANQNLLTNWK XP_660062.1, Hypothetical protein AN2458.2, <i>Aspergillus nidulans</i> NP_578172.1, Putative membrane transport protein, (<i>Pyrococcus furiosus</i>)	GLLTLMANQNLL (11aa) LMANQNLL (8aa)	81, +98 87, +131
24. FWLTLFANHADGCDTLK XP_001223848.1, Hypothetical protein CHGG_04634 (<i>Chaetpmium globosum</i>) EAT183988.1, Hypothetical protein SNOG_08820, (<i>Phaeosphaeria nodorum</i>)	LFANHAD (7aa) FWLTLF (6aa)	100, +318 100, +426
25. YGLLTLLSHAGMLTYHK ZP_01438661.1, ABC Mn+2/Fe+2 transporter inner membrane subunit, (<i>Fulvimarina pelagi</i>) YP_484708.1, ABC transporter, ATP binding protein (<i>Synechococcus</i> sp.)	YGLLTLLSHAGMLT (14aa) LLTLLSHAG (9aa)	71, +73 88, 237

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Accession No, Putative protein function, (organism)	Overlap (amino acids)	% homology – e value
26. TLDDPESSSPRLSSPMLNQR XP_383750.1, Hypothetical protein FG03574.1, (<i>Gibberella zeae</i>) EAT87607.1, Predicted protein, (<i>Phaeosphaeria nodorum</i>) XP_364693.1, Hypothetical protein MGG_09538, (<i>Magnaporthe grisea</i>)	PESSSPRLSSP (11aa) SSSPRLSSPMLNQR (14aa) PESSSPRLSSP (11aa)	72, +54 64, +97 81, +175
27. WWQTAPDGCFLGAMHSLK EAT78337.1, Hypothetical protein SNOG_14100, (<i>Phaeosphaeria nodorum</i>) ZP_01746647.1, Oligonucleotide ABC transporter, (<i>Sagitula stellata</i>)	LGAMHSLK (8aa) WQTAPD (6aa)	87, +425 100, +765
28. YPWTLLLMSNLLTYHK NP_619459.1, Oligonucleotide ABC transporter, (<i>Methanosporium acetivorans</i>) BAE61869.1, Unnamed protein product, (<i>Aspergillus oryzae</i>)	MSNLLTYHK (11aa) PWTLLLMSNLL (12aa)	83, +7.0 81, +30
29. RNHGRGSVEELSGLPMNR XP_001389883.1, Hypothetical protein An01g14950, (<i>Aspergillus niger</i>) AAX09986.1, Non ribosomal protein synthase, (<i>Cochliobolus heterostrophus</i>) EAT88582.1, Predicted protein, (<i>Phaeosphaeria nodorum</i>) XP_001275339.1, Fungal specific transcription factor domain protein, (<i>Aspergillus clavatus</i>)	VEELSGLPMNR (11aa) RNHGRGSVEELSGLPMNR (20aa) RNHGRGSVEELSGLPM (16aa) SVEELSGL (9aa)	72, +131 55, +236 56, +236 88, +317

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Accession No, Putative protein function, (organism)	Overlap (amino acids)	% homology – e value
30. LEDFTMVDALPVRTADGSR EDJ98817.1 Predicted protein (<i>Magnaporthe grisea</i>) NP_768911.1, Sugar ABC transport permease protein (<i>Bradyrhizobium japonicum</i>) XP_659140.1, Hypothetical protein AN1536.2, (<i>Aspergillus nidulans</i>) XP_384795.1, Hypothetical protein FG04619.1, (<i>Gibberella zeae</i>) YP_001196193.1, TonB-dependent receptor, (<i>Flavobacterium johnsoniae</i>) NP_879560.1 Putative inner membrane sensor for iron transport, (<i>Bordetella pertussis</i>)	TMVDALPVRTADG (14aa) DALPVRTAD (9aa) EDFTMVDAL (9aa) MVDALPVR (8aa) LPVRTADGS (8aa) DALPVRTADGS (11aa)	78, +40 88, +54 77, +54 87, +131 88, +175 71, +235
31. ELAGPSRMTENCWFLETGHSWESR XP_38962.1, Hypothetical protein FG09445.1, (<i>Gibberella zeae</i>)	TENCWF (6aa)	100, +173
32. NQPFTQMATAWEFAPAMSK XP_001262986.1, Fungal specific transcription factor, (<i>Neosartorya fischeri</i>) YP_968308.1, Signal transduction histidine kinase, (<i>Desulfovibrio vulgaris</i> sub. <i>vulgaris</i>) EAT83708.1, Hypothetical protein SNOG_08540, (<i>Phaeosphaeria nodorum</i>)	FTQMATA (7aa) FTQMATA (7aa) ATAWEFAPAM (10aa)	100, +235 100, +235 100, +235
33. ECHYAPMTWNMPGLVGALVATLAASK ZP_01602324.1, Chromate transporter, (<i>Shewenella pealeana</i>)	LVGALVATLA (10aa)	100, +6.8

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Accession No, Putative protein function, (organism)	Overlap (amino acids)	% homology – e value
EAT79238.1, Hypothetical protein SNOG_13354, (<i>Phaeosphaeria nodorum</i>) YP_929402.1, molybdenum ABC ATPase protein, (<i>Shewanella amazonensis</i>)	ECHYAPMTWNMPGL VGALV (12aa) PMTWNMPGLVGALV (11aa)	54, +12 68, +22
34. THPQMYMGPLNWCFMLMYLYGSR YP_841775.1, Nitrate nitrite transporter (<i>Ralstonia eutropha</i>) XP_001276744.1, Methylmalonate-semialdehyde dehydrogenase, (<i>Aspergillus clavatus</i>)	CFMLMY (6aa) MGPLNWCFML (10aa)	100, 72 80, +129
35. GGFNGTLPAASMECAPLDLMR EAT79997.1, Predicted protein, (<i>Phaeosphaeria nodorum</i>) YP_919100.1, Abortive infection protein, (<i>Thermophilum pendens</i>) YP_200521.1, Serine protease, (<i>Xanthomonas oryzae</i> pv. <i>oryzae</i>) XP_383113.1, Hypothetical protein FG02937.1, (<i>Gibberella zeae</i>)	ECAPLDLM (7aa) GGFNGTLPAAS (10aa) NGTLPAASME (10aa) GFNGTLPAA (8aa)	87, +314 58, +314 80, +314 81, +421
36. THTNWEFATNMHVVDQVGAYSWFR YP_731561.1, Serine protease, trypsin family protein, (<i>Synechococcus</i> sp.) XP_390968.1, Hypothetical protein FG10792.1, (<i>Gibberella zeae</i>)	TNMHVVDQV (9aa) THTNWEFATNM (11aa)	88, +129 72, +232

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Accession No, Putative protein function, (organism)	Overlap (amino acids)	% homology – e value
37. CQYSNDDGDAACWSNHR XP_001220540.1, Predicted protein, (<i>Chaetomium globosum</i>) XP_751248.1, Class V chitinase, (<i>Aspergillus fumigatus</i>) XP_962424.1, Hypothetical protein, (<i>Neurospora crassa</i>)	DGDAACWSN (9aa) QYSNDDGD (8aa) CQYSNDDGD (9aa)	88, +30 87, +236 77,+317
38. TQPGAZGGASSAVPK YP_555381.1, ABC aliphatic sulphonates transporter, periplasmic ligand b (<i>Burkholderia xenovorans</i>) XP_368359.1, Hypothetical protein MGG_00885, (<i>Magnaporthe grisea</i>)	PGAZGGASSA (10aa) QPGAZGGASSAVP (10aa)	83, +319 72, +772
39. LAALNSYCHQQGMNR XP_363962.1, Hypothetical protein MGG_01889, (<i>Magnaporthe grisea</i>)	LNSYCHQQGMN (9aa)	69, +17
40. HMVGMAVRSNWCLAQMTR XP_367873.2, Hypothetical protein MGG_07777, (<i>Magnaporthe grisea</i>) ZP_01035987.1, Glutamate/aspirate ABC transporter ATP binding protein (<i>Roseovarius</i> sp.).	HMGMAVRSNWCLAQM (11aa) MAVRSNWCLAQ (11aa)	64, +12 72, +176
41. QTGSACSHSLEPNDNK ZP_01703635.1, Aminotransferase (<i>Methanospirillum hungatei</i>) EAT90560.1, Hypothetical protein SNOG_02348, (<i>Phaeosphaeria nodorum</i>) XP_384411.1, Hypothetical protein FG04641.1, (<i>Gibberella zeae</i>) XP_365021.1, Hypothetical protein MGG_09866, (<i>Magnaporthe grisea</i>)	TGSACSHSLEP (10aa) SLEPNDN (7aa) SHSLEPNDNK (10aa) EPNDNK (6aa)	83, +237 100, +318 87, +1385 100, +1859

B2 Proteins showing potential homology to peptide fragments from the 48 kDa protein extracted from culture filtrates of *Pyrenophora teres f. teres*. The accession number, area of overlap, homology and e value are shown for each.

Accession No, putative protein function, (organism)	Overlap (amino acids)	% homology – e value
1. KIVVGMPLYGRA		
BAE57828.1, Unnamed protein product, (<i>Aspergillus oryzae</i>)	KIVVGMPLYGRA (12aa)	100, +0.003
XP_368023.1, Hypothetical protein MGG_07927, (<i>Magnaporthe grisea</i>)	KIVVGMPLYGRA (11aa)	91, +0.036
XP_662475.1, Hypothetical protein AN4871.2, (<i>Aspergillus nidulans</i>)	KIVVGMPLYGRA (10aa)	83, +0.21
XP_390905.1, Hypothetical protein FG10729.1, (<i>Gibberella zeae</i>)	KIVVGMPLYGR (10aa)	90, +0.28
XP_369158.1, Hypothetical protein MGG_00086, (<i>Magnaporthe grisea</i>)	KIVVGMPLYGR (10aa)	90, +0.28
2. KYGTGYCDSQCPHDIKF		
CAK18913.1, Cellulose 1,4-beta-cellobiosidase precursor, (<i>Pleurotus sp.</i>)	KYGTGYCDSQCPHDI KF (17aa)	100, -0.09
EAT83824.1, Predicted protein, (<i>Phaeosphaeria nodorum</i>)	KYGTGYCDSQCPHDI KF (17aa)	100, -0.09
BAA76363.1, Cellulase, (<i>Irpex lacteus</i>)	KYGTGYCDSQCPHDI KF (17aa)	100, -0.09
EAU85437.1, Hypothetical protein CC1G_12410, (<i>Coprinopsis cinerea</i>)	KYGTGYCDSQCPHDI KF (16aa)	94, -0.07
XP-001220726.1, Hypothetical protein CHGG_01505, (<i>Chaetomium globosum</i>)	KYGTGYCDSQCPHDI KF (16aa)	94, -0.07
XP_001272622.1, Cellobiohydrolase D, (<i>Aspergillus clavatus</i>)	KYGTGYCDSQCPHDI KF (15aa)	88, -0.06

Appendices

Accession No, Putative protein function, (organism)	Overlap (amino acids)	% homology – e value
3. BSTPTNSFGSDFGK		
NP_600713.1, ATPase of the AAA+ class, (<i>Corynebacterium glutamicum</i>)	BSTPTNSFGSDFGK (12aa)	66, 133
XP_001268708.1, C6 transcription factor (UaY), putative, (<i>Aspergillus clavatus</i>)	STPTNSFGSDF (11aa)	81, 239
BAE66156.1, Unnamed protein product, (<i>Aspergillus oryzae</i>)	SFGSDFGK (8aa)	87, 578
JC7140, Protoxin, (<i>Bacillus thuringiensis</i>)	STPTNSF (7aa)	100, 578
ANN16462.1, Insecticidal protein Cry1C, (<i>Bacillus thuringiensis</i>)	STPTNSF (7aa)	100, 578
XP_00123975.1, Hypothetical protein CIMG_09396, (<i>Coccidioides immitis</i>)	SFGSDFG (7aa)	100, 776
XP_759952.1, Hypothetical protein UM03805.1, (<i>Ustilago maydis</i>)	STPTNSFGSDF (11aa)	72, 776
XP_643147.1, Hypothetical protein DDBDRAFT_0167082, (<i>Dictyostelium discoideum</i>)	SFGSDFG (7aa)	100, 776
4. BTSPTNSFGSDFGK		
XP_001221952.1, Hypothetical protein CHGG_05857, (<i>Chaetomium globosum</i>)	BTSPTNSFGSDFG (10aa)	66,41
XP_001271076.1, Dynactin Arp1 p62 subunit RO2, putative, (<i>Aspergillus fumigatus</i>)	TSPTNSFGSDFG (12aa)	66, 74
XP_001134588, Putative actin binding protein, (<i>Dictyostelium discoideum</i>)	TSPTNSF (7aa)	100, 578
XP_360210.2, Hypothetical protein MGG_05584, (<i>Magnaporthe grisea</i>)	TSPTNSFGS (9aa)	100, 776

Appendices

Accession No, Putative protein function, (organism)	Overlap (amino acids)	% homology – e value
5. BSYGPLYDAQLQGVK EAT855854.1, Predicted protein, (<i>Phaeosphaeria nodorum</i>) EAU90730.1, Predicted protein, (<i>Coprinopsis cinerea</i>) XP_958989.1, Hypothetical protein, (<i>Neurospora crassa</i>)	YGPLYDAQLQGVK (12aa) YDAQLQGVK (8aa) PLYDAQLQGV (9aa)	75, +74 87, +321 77, +321
6. BLDPPSDLAGFSNTK XP_751403.2, Conserved hypothetical protein, (<i>Aspergillus fumigatus</i>) ZP_01102349.1, TonB-dependent receptor, (<i>Gamma proteobacterium</i>)	LDPPSDLAGFSN (12aa) DLAGFSNT (8aa)	66, +133 87, +577

Appendix C- Publications

Sarpeleh, A., Wallwork, H., Catcheside, D. E. A., Tate, M. E., and Able, A. J. 2007. Proteinaceous metabolites from *Pyrenophora teres* contribute to symptom development of barley net blotch. *Phytopathology* 97: 907-915.

Sarpeleh, A., Wallwork, H., Catcheside, D., and Able, A. J. 2006. Different fungal proteins contribute to the net form and spot form of the barley net blotch disease. 8th International Congress of Plant Molecular Biology, Adelaide, Australia.

Sarpeleh, A., Wallwork, H., Catcheside D., and Able, A. J. 2005. .Involvement of proteins produced by *Pyrenophora teres* in symptom development of net blotch of barley. 15th Australasian Phytopathology Society Conference, Geelong, Australia.

Little, A., Sarpeleh, A., Graig, A., Boettcher, A., Stonor, J., and Able, A. J. 2005. Understanding how barley interacts with *Rhynchosporium secalis* and *Pyrenophora teres* as a basis for improving disease resistance to necrotrophic fungal pathogens. 12th Australian Barley Technical Symposium Proceedings, Hobart, Australia.