SI Text

Primers for inverse PCR for *AMA1* were CCATCTGGGGTATCGGTTGC and TTGGGATTGTGAGGTTTAGAGGTC, and for *PHA1* CGTCAACCGTCTCCTC and ACGCATGGGCAGTCTAC.

For 3’ RACE, initial and nested primers from GeneRacer (Invitrogen) were used. For the other 3’ *AMA1* RACE primers, the initial primer was CCCATTCGAACCTAACTCCAAGAC and the nested primer was CCTCTAAACCTCACAATCCCAATG . For 5’ RACE of the *AMA1* cDNA, the initial primer was GCCCAAGCCTGATAACGTCCACAACT and the nested primer was TATCGCCCACTACTTCGTGTCATA. For *PHA1*, the 3’ initial primer was GACCTCTGCTCTAAATCACAATG and the 3’ nested primer was ATCAATGCCACCCGTCTTCCTG. The 5’ initial *PHA1* primer was CGGATCATTTACGTGGGTTTTA and the 5’ nested primer was AACTTGCCTTGACTAGTGGATGAGAC.

Degenerate primers for amplification of toxin genes from *A. phalloides* were ATGTCNGAYATYAAYGCNACNCG (forward) and AAGGSYCTCGCCACGAGTGAGGAGWSKRKTGAC (reverse), in which W indicates A or T, S indicates C or G, K indicates G or T, R indicates A or G, and Y indicates T or C.

Primers to amplify a portion of the *A. bisporigera* tubulin gene were ACCTCCATCTCGTCCATACCTTCC and TGTTTGCCACGCTGCATACTA.

Sequences orthologous to human prolyl oligopeptidase (POP) in *A. bisporigera* and other fungi. The following genome survey sequences were identified in the *A. bisporigera* genome (subject) by TBLASTN using human POP (GenBank NP_002717) as query:

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>ECGK9LO02JKSHR R length=112
          Length = 112

 Score = 47.8 bits (112), Expect = 4e-06
 Identities = 20/33 (60%), Positives = 26/33 (78%)
 Frame = +3

Query: 436 QTVQIFYPSKDGTKIPMFIVHKKSIKLDGSHPA 468
           ++ Q++Y SKDGTK+PMFIV  KS K DG+ PA
Sbjct: 3   ESTQVWYESKDGTKVPMFIVRHKSTKFDGTAPA 101

>contig26093 length=206   numReads=6
          Length = 206

 Score = 41.2 bits (95), Expect = 3e-04
 Identities = 18/32 (56%), Positives = 23/32 (71%)
 Frame = +1

Query: 440 IFYPSKDGTKIPMFIVHKKSIKLDGSHPAFLY 471
           ++Y S DGTKIPMFIV  K+ K +G+ PA  Y
Sbjct: 109 VWYDSYDGTKIPMFIVRHKNTKFNGTAPAIQY 204

>ECIMO1V02I2IO5 S length=107
          Length = 107

 Score = 35.8 bits (81), Expect = 0.014
 Identities = 18/27 (66%), Positives = 21/27 (77%), Gaps = 1/27 (3%)
 Frame = +2

Query: 546 KRLTINGGSNGGLLVAAC-ANQRPDLF 571
           ++L I+GGSNGGLLV A    QRPDLF
Sbjct: 26  EKLAISGGSNGGLLVGASRLTQRPDLF 106


>ECIMO1V01CKHE5 R length=94
          Length = 94

 Score = 35.4 bits (80), Expect = 0.019
 Identities = 16/27 (59%), Positives = 19/27 (70%)
 Frame = +2

Query: 120 SDDGTVALRGYAFSEDGEYFAYGLSAS 146
           S DGT +L  Y FS  G+YFAYG+S S
Sbjct: 2   SSDGTASLSMYDFSHCGKYFAYGISLS 82

>EEISCGG02IHTSV R length=106
          Length = 106

 Score = 33.1 bits (74), Expect = 0.093
 Identities = 14/20 (70%), Positives = 15/20 (75%)
 Frame = -2

Query: 669 PLLIHVDTKAGHGAGKPTAK 688
           PLL+ VD KAGHG GK T K
Sbjct: 105 PLLLRVDKKAGHGGGKSTEK 46
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```
>ECIMO1V02H2WNR S length=78
          Length = 78

 Score = 28.9 bits (63), Expect = 1.7
 Identities = 12/16 (75%), Positives = 13/16 (81%)
 Frame = +2

Query: 446 DGTKIPMFIVHKKSIK 461
           DGTK+PMFIV  KS K
Sbjct: 2   DGTKVPMFIVRHKSTK 49
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Orthologs of human POP in other Basidiomycetes are: *Coprinus cinereus* (GenBank CC1G_09936), *Ustilago maydis* (GenBank UM05288), *Cryptococcus neoformans* (GenBank XP_567311 and XP_567292), *Laccaria bicolor* (Lacbi1|303722), *Phanerochaete chrysosporium* (Phchr1|1293), *Puccinia graminis* (PGTG_14822.2), and *Sporobolomyces roseus* (Sporo1|33368).

The genome sequences of *L. bicolor*, *P. chrysosporium*, and *S. roseus* are available at http://genome.jgi-psf.org/. The genome sequence of *P. graminis* is available at http://www.broad.mit.edu/annotation/genome/puccinia_graminis.