S2 Fig. Maximum likelihood phylogeny of *Rps3*. Phylogenetic analysis of orf540, orf551 and orf551 from *C. austroafricana*, *C. cubensis* and *C. deuterocubensis* which show sequence similarity to *C. parasitica* S5 ribosomal protein/maturase fusion protein. Sequences used in this phylogeny were retrieved from GenBank using BLAST. The LG+G model of substitution was used. Branch support for was calculated using the bootstrap method with 1000 replicates. *S3H* stands for *rps3*/HEG fusion protein. Blue stars indicate *S5* proteins sequences grouping with *rps3* proteins.

Chaetomium thermophilum S3
Podospora anserina S3
100
Madurella mycetomatis S3
75
Sphaeronaemella fimicolaS3
100 *Neurospoa crassa S5* ★
97 *Gelasinospora tetrasperma S3*
Annulohypoxylon stygium S3
Ophiostoma minima S3H
100 *Ceratocystiopsis brevicomis S3H*
Ophiostoma distortum S3H
78
Leptographium truncatum S3H
100 *Grosmannia europhioides S3H*
100
Graphilbum curvicolle S3H
100 *Graphilbum nigrum S3*
Chrysoporthe austroafricana orf540
94
Chrysoporthe deuterocubensis orf551
Chrysoporthe cubensis orf551
100
Cryphonectria parasitica S5 ★
100
Trichoderma reesei S5 ★
Pochonia chlamydosporia S3
94
99 *Metarhizium robertsii s3*
Fusarium graminearum S3
100
73 *Hirsutella minnesotensis S3*
Beauveria bassiana S3
100
Cordyceps brongniartii S3
80
100 *Lecanicillium muscarium S3*
Cornuvesica falcata S3
99
92 *Ceratocystis cacaofunesta S3*
Colletotrichum graminicolaS3

rps3

Sclerotinia sclerotiorum S5
Arthroderma uncinatum S5
Arthroderma obtusum S5
100
77 99 *Trichophyton mentagrophytes S5*
89 *Trichophyton rubrum S5*
83 81 *Microsporum gypseum S5*
Microsporum canis S5
Blastomyces gilchristii S5
Penicillium chrysogenum S5
100
Neosartorya fischeri S5
83
87 *Aspergillus oryzae S5*
95 *Aspergillus clavatus S5*
Aspergillus ustus S5
91
Talaromyces stipitatusS5
100 *Talaromyces marneffei S5*
Parastagonospora nodorum S5

rps5

0.2