**Table S1** Primers for *in vitro* synthesis of *Austropuccinia psidii (Ap)* and *Coleosporium plumeriae (Cp)*-specific dsRNA*.*Transcripts per million (TPM) was calculated from unpublished RNAseq data. We amplified *28S*-2with conserved primers for rust fungi, namely Rust28SF (Aime et al., 2018) and LR3 (Vilgalys and Hester, 1990). *28S*-1 was also amplified with LR3 but a new forward primer was designed to make a shorter amplicon. The T7 promoter sequence, which was added to the primers for *in vitro* RNA transcription is shown in bold.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Target gene | Putative function | TPM | Primer sequence | Length (bp) |
| *28S*-1 | Large fungal ribosomal subunit | 1,000,000 | F:**TAATACGACTCACTATAGGG**CAAACAAGTACCGTGAGGG R:**TAATACGACTCACTATAGGG**TCCGTGTTTCAAGACGGG | 340 (*A. psidii)* and 347 (*C. plumeriae*) |
| *Ap28S*-2 | Large fungal ribosomal subunit | 1,000,000 | **F:TAATACGACTCACTATAGGG**TTTAAGACCTCAAATCAGGTG  **R:TAATACGACTCACTATAGGG** CCGTGTTTCAAGACGGG | 685 |
| *ApEF1-A*  *CpEF1-A* | Translation elongation factor | 113,841 | F:**TAATACGACTCACTATAGGG**ATGCTCCTGGACATCGTG R:**TAATACGACTCACTATAGGG**CCAACCTTCTTGACAAAGTTGG  F:**TAATACGACTCACTATAGG**GCCTGGACATCGTGATTTCA  R:**TAATACGACTCACTATAGGG**CCGACCTTCTTGACAAAGTTG | 268  337 |
| *ApB-TUB*  *CpB-TUB* | Beta-tubulin | 107,221 | F:**TAATACGACTCACTATAGGG**AGCCGAATTAGTGGACTCTG R:**TAATACGACTCACTATAGGG**CGGAGACAGGTGGTAATACC F:**TAATACGACTCACTATAGGG**CGAGGGTGCTGAGCTTGTAG  R:**TAATACGACTCACTATAGGG**CGGAGACAAGTGGTAATTCCG | 398  402 |
| *GFP* | Green fluorescent protein | N/A | **F:TAATACGACTCACTATAGGG**AGGACGACGGCAACTACAAG **R:TAATACGACTCACTATAGGG**TCTCGTTGGGGTCTTTGCTC | 339 |
| *ApATC* | Acetyl-CoA transferase | 29,227 | **F:TAATACGACTCACTATAGGG**CCAACCTGCGTCGTCGTC **R:TAATACGACTCACTATAGGG** CGCATCTTTCGCACACGTTC | 227 |
| *ApCYP450* | Cytochrome P450 | 26,106 | **F:TAATACGACTCACTATAGGG**CCGCAAAAATACGAGCCCG **R:TAATACGACTCACTATAGGG**CGAACAAGCTGTCGAAGATAAC | 403 |
| *ApGCS-H* | Glycine cleavage system-H | 209,855 | **F:TAATACGACTCACTATAGGG**CGGGTAATTGCAGTCGAACTC **R:TAATACGACTCACTATAGGG**GACCTCTGTCACAGTACCCG | 331 |
| *ApMAPK* | Mitogen-activated protein kinase | 57,014 | **F:TAATACGACTCACTATAGGG**CTTCTGCCTTGGCCATTGAC **R:TAATACGACTCACTATAGGG**GGTTGCTTTATTCAATCTCGTGG | 507 |
| *ApHAUS01136* | Haustorial target 01136 | 25,185 | **F:TAATACGACTCACTATAGGG** CTCCAATGTATGGCATTCCT  **R:TAATACGACTCACTATAGGG** GAGGTCTTCAGGCTGAGTGTA | 317 |
| *ApHAUS01215* | Haustorial target 01215 | N/A | **F:TAATACGACTCACTATAGGG** GCGAATACTCTGGCAATGCAG  **R:TAATACGACTCACTATAGGG** TCAGTTTCACCAATAATCATT | 296 |
| *ApHAUS12890* | Haustorial target 12890 | 43,164 | **F:TAATACGACTCACTATAGGG** CACCAGTAGGATCGAACATG  **R:TAATACGACTCACTATAGGG** GTGATGCAAGCTTCGCCACA | 298 |

AIME, M. C., BELL, C. D. & WILSON, A. W. 2018. Deconstructing the evolutionary complexity between rust fungi (Pucciniales) and their plant hosts. *Studies in Mycology,* 89**,** 143-152.

VILGALYS, R. & HESTER, M. 1990. Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several Cryptococcus species. *J Bacteriol,* 172**,** 4238-46.