**Conidial morphogenesis and septin-mediated plant infection require Smo1, a Ras GTPase-activating protein in *Magnaporthe oryzae***

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**Supplemental Table and Figure Legends**

**Table S1** Smo1 mutants used in this study and characteristics of the genome sequences generated

**Table S2** Primers used in this study

**Figure S1.** Multiple sequence alignment using Clustal X (Larkin et al. 2007) showing GTPase activating proteins from *M. oryzae* in Maximum likelihood phylogenetic tree created using PhyML. Bootstrap support values of 70 or greater are indicated on tree.

**Figure S2.** Complementation of the *smo1* mutant restores wild type phenotypes. (A) Micrographs showing spore morphology of Guy11 and *smo1* mutant complemented with the Smo1-GFP fusion construct, and the *smo1-* strain CP750 complemented with wild type *SMO1* allele. Bar = 10 m (B) Photographs of leaves from infected seedlings of rice cultivar CO-39 inoculated with conidial suspensions (1 x 105 ml-1) of wild type Guy11, *smo1* and *smo1* mutant complemented with *SMO1-GFP*.

**Figure S3.** Cellular localisation of H1-RFP by live cell imaging in (A) a wild type Guy11 background and (B) the *smo1* mutant background, visualized by epifluorescence microscopy over a time course of infection related development. Bar = 10 m. (C) Calcofluor-white staining of conidia, germ tubes and appressoria of the wild type strain Guy11 and *smo1* mutant at 24 hpi. Bar = 10 m.