

Table S2 Coverage of conserved eukaryotic genes in *M. oryzae* isolate Ina168 and 70-15 genome sequences analyzed by CEGMA.

Strain	Complete*	Partial*
Ina168	236 (95.2%)	242 (97.6%)
70-15	236 (95.2%)	242 (97.6%)

* Number of genes that exhibited a homology to the protein sequences from the 248 core eukaryotic genes with 'complete' and 'partial' coverage for the CEGMA analysis.