**Table S1:** Summary of genes and genomic regions employed in phylogenetic studies of *Armillaria* species

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| Gene or genomic region | Comments |
| IGS-1 | * The first region used in *Armillaria* phylogenetics * Does not provide sufficient resolution for discriminating some *Armillaria* species * 5S gene is inverted in African taxa, the region can therefore not be used for a global phylogenetic analysis * Intra-strain nucleotide heterogeneity present in some individuals |
| ITS | * Does not provide sufficient resolution for discriminating some *Armillaria* species * Intra-strain nucleotide heterogeneity present in some individuals |
| *tef*-1α | * In general, provides sufficient resolution to discriminate *Armillaria* species, it is now widely used in *Armillaria* phylogenetic studies * Some individuals, however, reported to have intra-strain heterozygous sites |
| *rpb2* | * Cannot discriminate between certain species, for example *A. calvescens* and *A. gallica* |
| β–tubulin | * Does not provide sufficient resolution to separate *Armillaria* species |
| SWAPP | * Phylogenetic analysis of a matrix in which these sequences were combined yielded a phylogenetic tree that resolved the phylogenetic history of the North American species * Has not been employed in other phylogenetic studies of *Armillaria* |
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