

**Supplementary Figure S3**. Maximum parsimony tree (semi-strict consensus) of *A. niger* clade species using three-locus (*CaM, BenA*, and *RPB2*) phylogenies. Genealogical non-discordance criterion: The lineages that were well supported by at least one *locus* but not contradicted by any other locus are identified as independent evolutionary lineages (coloured boxes). Bootstrap values (BS) and/or posterior probabilities values (pp) higher than 70% and 0.70, respectively, are shown. *A. carbonarius* is the outgroup.