 **Supplementary Figure S2.** Maximum parsimony tree (MR 50%) of *A. niger* clade species using the *loci* *CaM, BenA*, and *RPB2*. Genealogical Concordance criterion: The lineages that occur in most of the single *loci* are highlighted in coloured boxes, and these lineages were identified as independent evolutionary lineages. Bootstrap values (BS) and/or posterior probabilities values (pp) higher than 70% and 0.70, respectively, are shown. *A. carbonarius* is the outgroup.