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ERRATUM

Geosmithia Fungi are Highly Diverse and Consistent Bark Beetle Associates: Evidence from their Community Structure in Temperate Europe

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In the original version of this article, Fig. 2 was misprinted with the missing part. The caption of the tree (vertical numbered lines at the right side) must be present. The correct version of Fig. 2 is given here.

The online version of the original article can be found at http://dx.doi.org/10.1007/s00248-007-9251-0.

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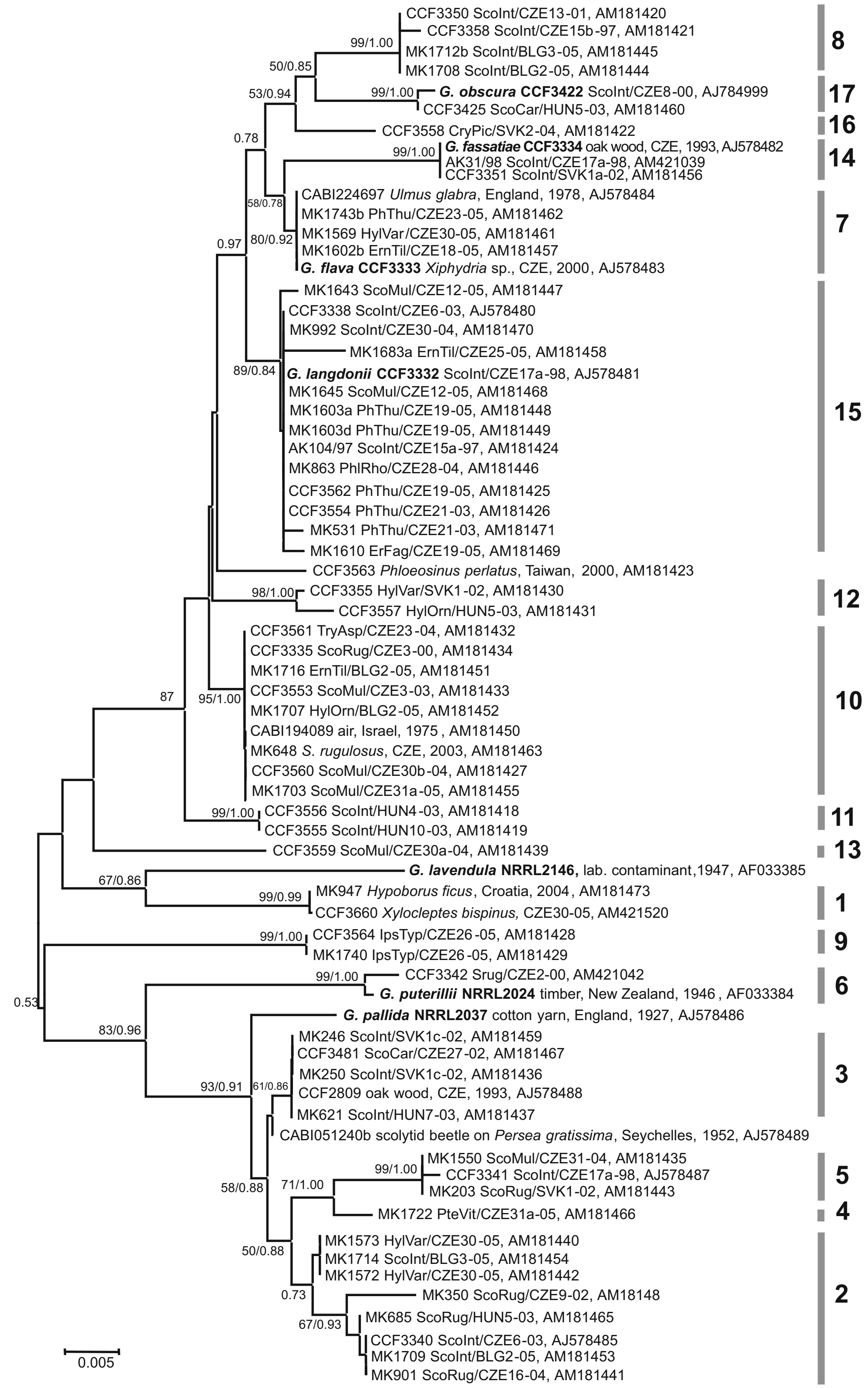

Figure 2 Neighbor-joining tree of 70 *Geosmithia* strains covering morphological and genetic variability of strains from temperate Europe and their comparison with reference strains from culture collections. The clusters representing different OTUs, 1–17, are marked on the right side. The alignment of ITS-rDNA sequences contained 562 positions, of which 488 were constant. The tree was constructed by NJ analysis and is unrooted. Bootstrap values from NJ (>50%) and Bayesian posterior probabilities (>0.5) from Bayesian MCMC are shown at the nodes. Individual sequence codes are identified as follows: strain/substrate/locality code (as in Table 1) and GenBank No. Ex-type strains are printed in bold. GenBank accession numbers beginning with "AM" were obtainedduring this study