Distances between trees with 11 taxa obtained by different methods for particular markers to trees (F, G and H) based on the concatenated alignment of all markers. The maximum distance = 16. When some methods proposed several equally probable topologies, we averaged the calculated distances for these trees. The eight phylogenetic approaches were applied: Bayesian analyses in MrBayes (MB) and PhyloBayes (PB), maximum likelihood analyses with partitioned data in TreeFinder (TF) and not partitioned in PAUP (ML) as well as neighbour joining (NJ), minimum evolution (ME), weighted least squares (WLS) and maximum parsimony (MP) in PAUP.

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