

Aspergillus nanangensis: updated description with phenotypic and ecological comparison to other species of section *Janorum*

František Sklenář, Željko Jurjević, Vít Hubka

Czech Mycology 77(1): 1–16, 2025

Electronic supplement

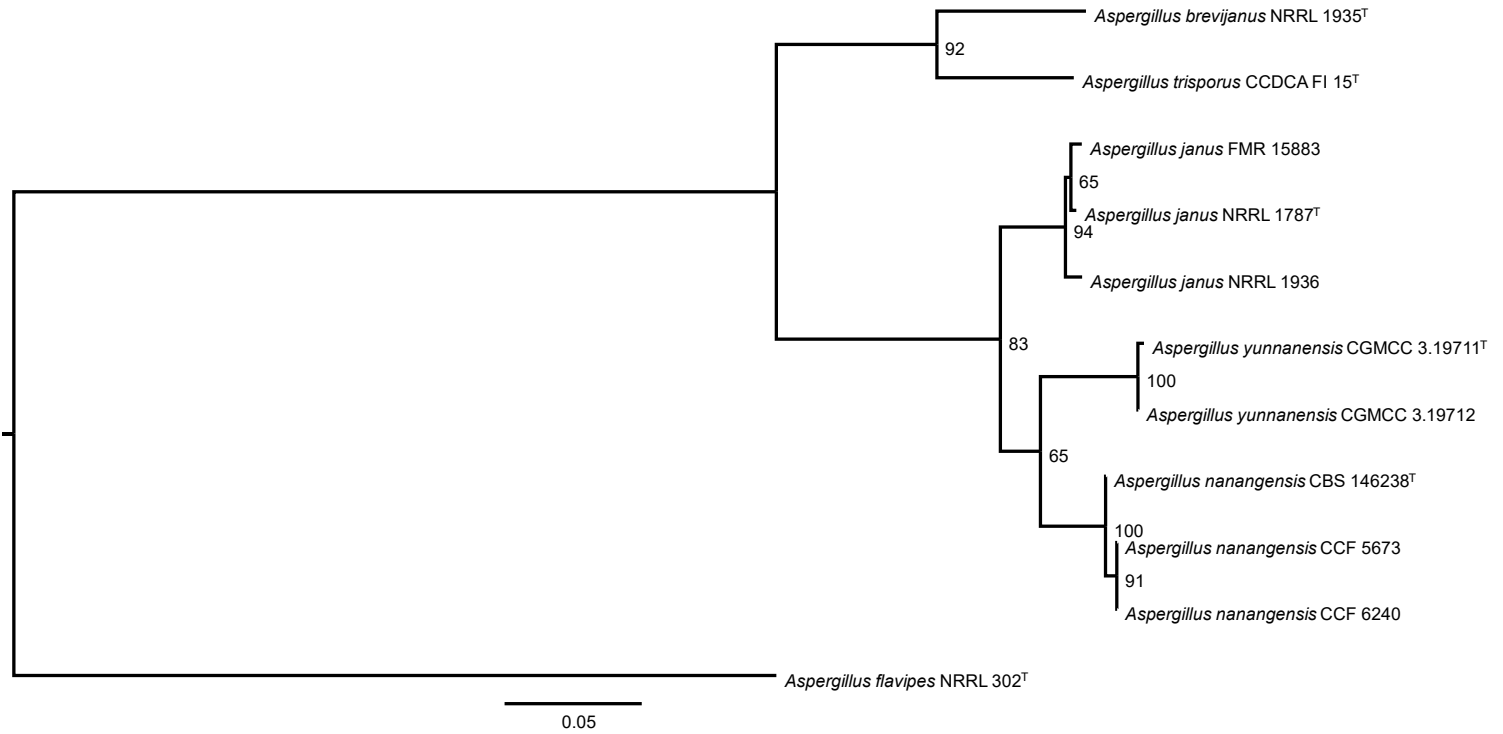


Figure S1. Phylogenetic tree based on *benA* sequences of section *Janorum* strains. The tree was inferred in IQ-TREE 2.2.0 (Minh et al. 2020). Support values were calculated with 1000 standard nonparametric bootstrap replicates. K80+G was selected in jModelTest 2.1.7 (Posada 2008) as the most suitable model of evolution. Ex-type strains are indicated by a T in superscript.

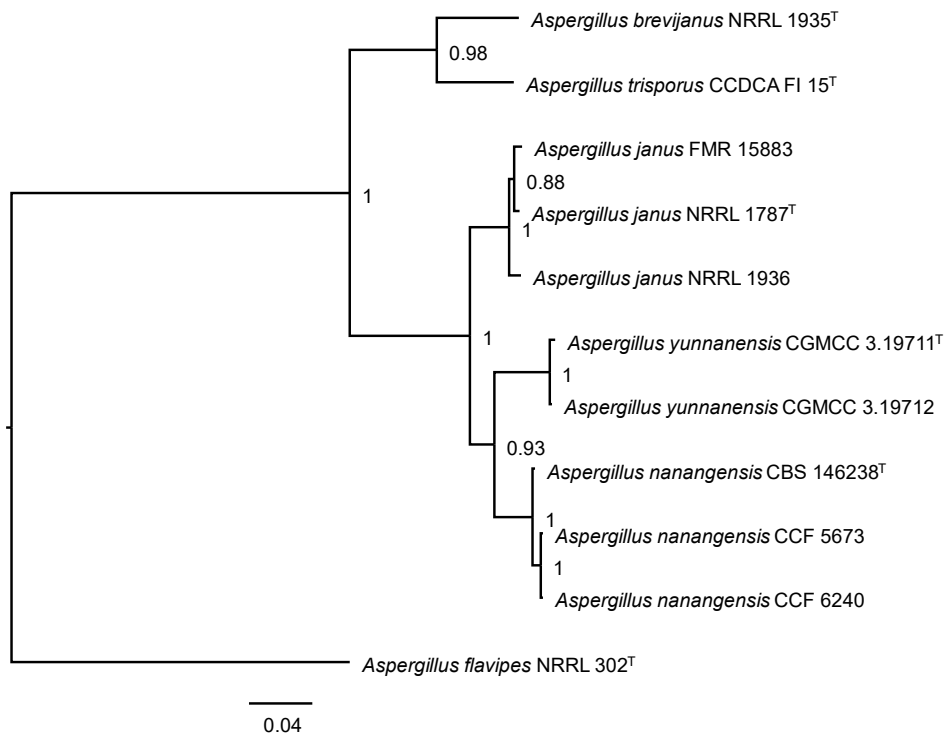


Figure S2. Phylogenetic tree based on *benA* sequences of section *Janorum* strains. The tree was inferred in MrBayes 3.2.7 (Ronquist et al. 2012). The analysis was split into two runs each with 40,000 generations. K80+G was selected in jModelTest 2.1.7 (Posada 2008) as the most suitable model of evolution. Ex-type strains are indicated by a T in superscript.

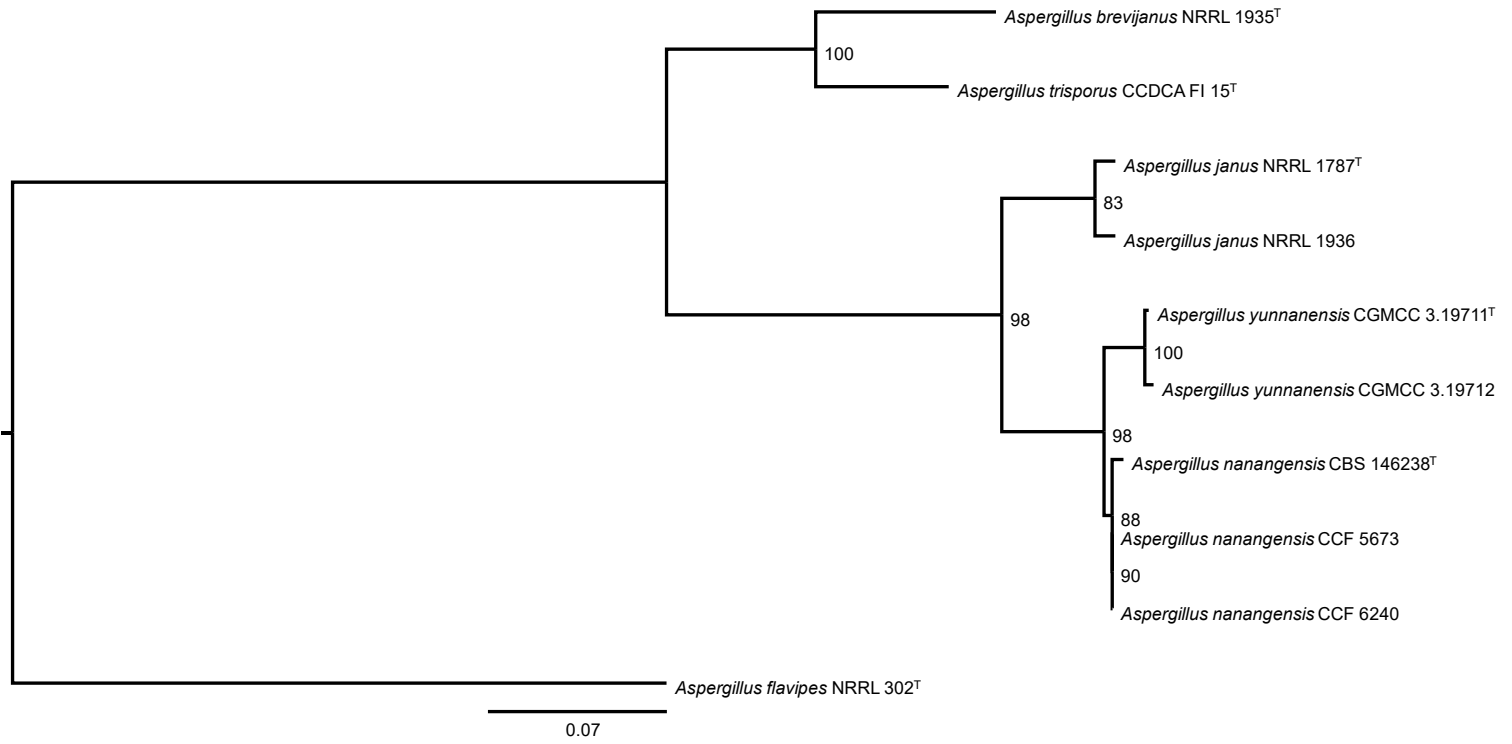


Figure S3. Phylogenetic tree based on *CaM* sequences of section *Janorum* strains. The tree was inferred in IQ-TREE 2.2.0 (Minh et al. 2020). Support values were calculated with 1000 standard nonparametric bootstrap replicates. TrNef+G was selected in jModelTest 2.1.7 (Posada 2008) as the most suitable model of evolution. Ex-type strains are indicated by a T in superscript.

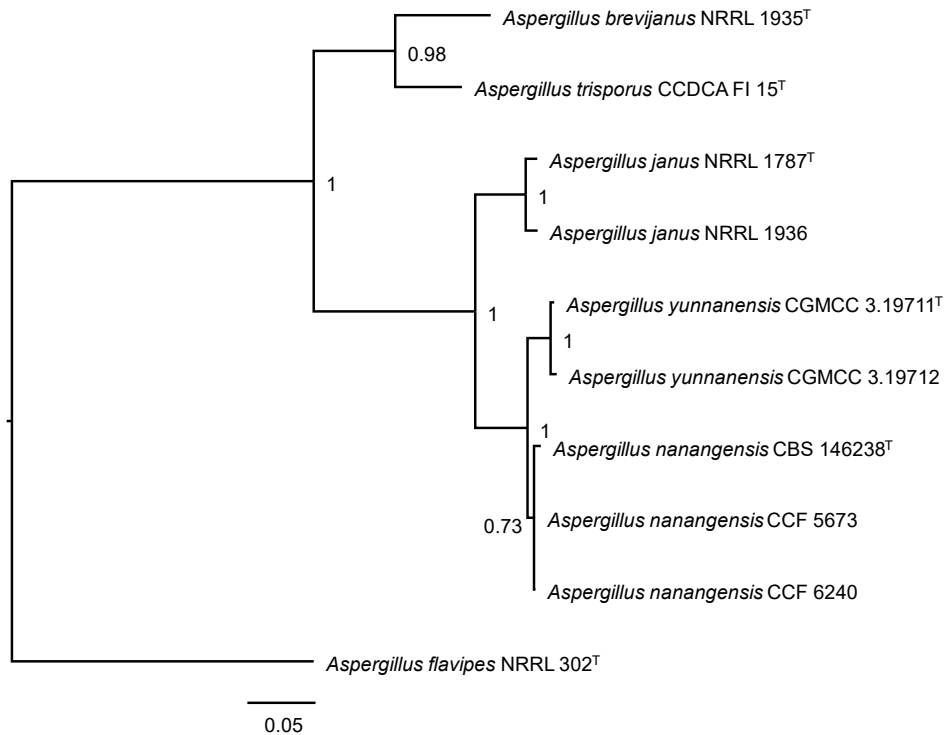


Figure S4. Phylogenetic tree based on *CaM* sequences of section *Janorum* strains. The tree was inferred in MrBayes 3.2.7 (Ronquist et al. 2012). The analysis was split into two runs each with 40,000 generations. TrNef+G was selected in jModelTest 2.1.7 (Posada 2008) as the most suitable model of evolution. Ex-type strains are indicated by a T in superscript.

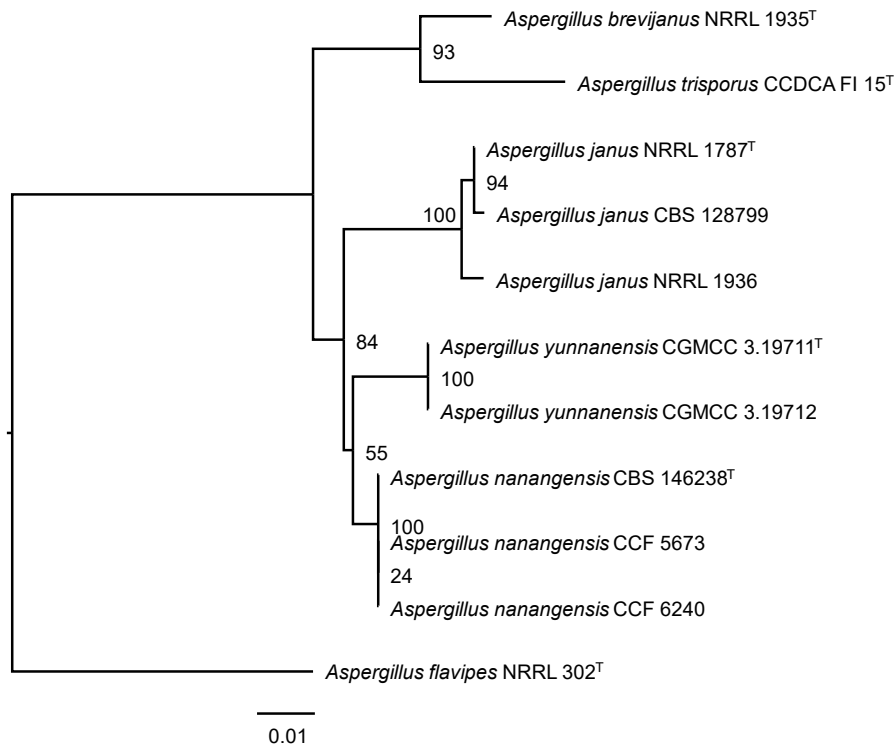


Figure S5. Phylogenetic tree based on ITS sequences of section *Janorum* strains. The tree was inferred in IQ-TREE 2.2.0 (Minh et al. 2020). Support values were calculated with 1000 standard nonparametric bootstrap replicates. TVM+I was selected in jModelTest 2.1.7 (Posada 2008) as the most suitable model of evolution. Ex-type strains are indicated by a T in superscript.

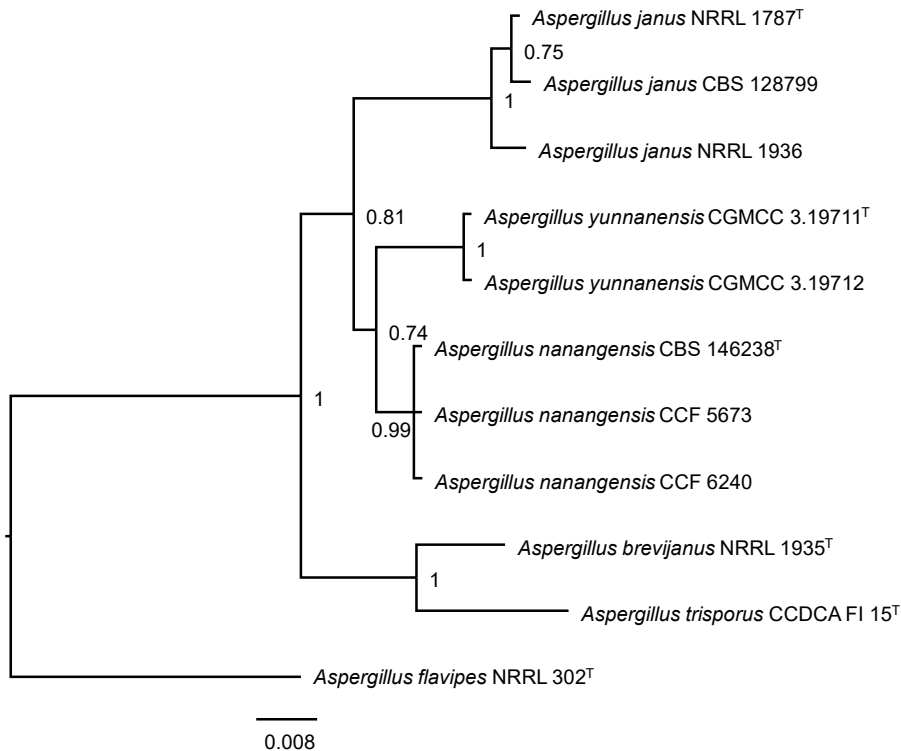


Figure S6. Phylogenetic tree based on ITS sequences of section *Janorum* strains. The tree was inferred in MrBayes 3.2.7 (Ronquist et al. 2012). The analysis was split into two runs each with 40,000 generations. TVM+I was selected in jModelTest 2.1.7 (Posada 2008) as the most suitable model of evolution. Ex-type strains are indicated by a T in superscript.

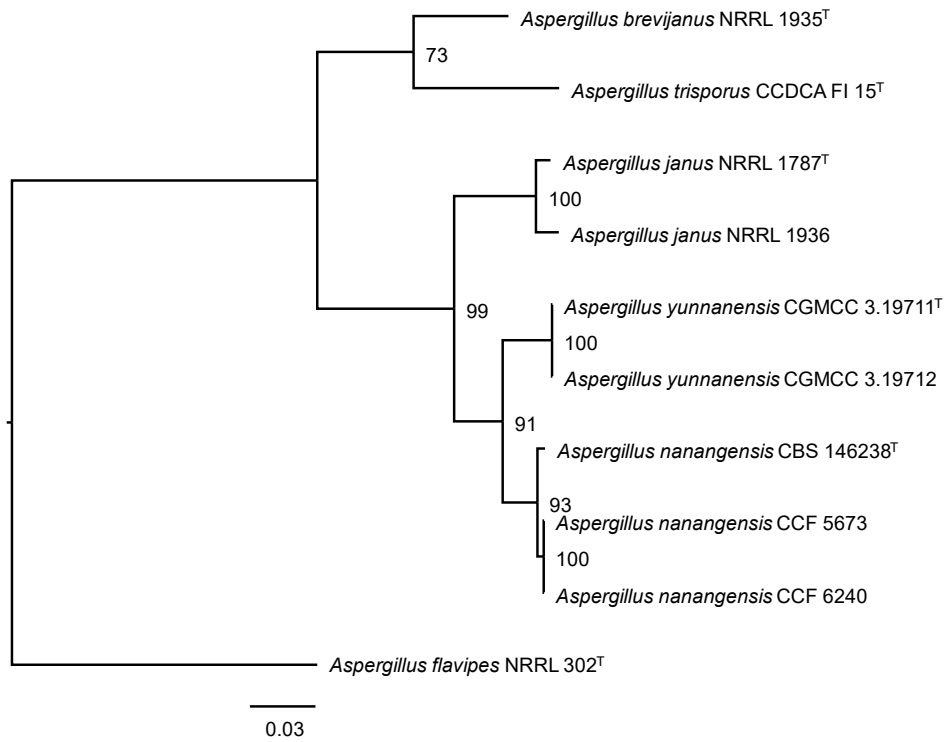


Figure S7. Phylogenetic tree based on *RPB2* sequences of section *Janorum* strains. The tree was inferred in IQ-TREE 2.2.0 (Minh et al. 2020). Support values were calculated with 1000 standard nonparametric bootstrap replicates. TrNef+G was selected in jModelTest 2.1.7 (Posada 2008) as the most suitable model of evolution. Ex-type strains are indicated by a T in superscript.

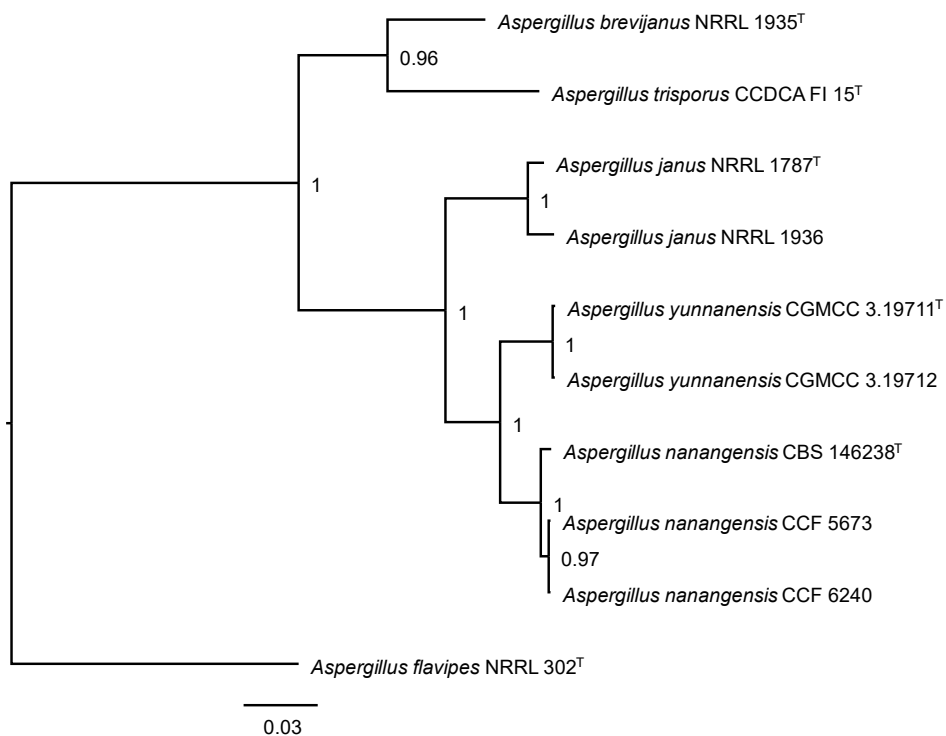


Figure S8. Phylogenetic tree based on *RPB2* sequences of section *Janorum* strains. The tree was inferred in MrBayes 3.2.7 (Ronquist et al. 2012). The analysis was split into two runs each with 40,000 generations. TrNef+G was selected in jModelTest 2.1.7 (Posada 2008) as the most suitable model of evolution. Ex-type strains are indicated by a T in superscript.