

Phylogenetic relationships within the stem and gall-forming plant parasitic nematodes (Tylenchida: Anguinidae) as inferred from analyses of the ITS-rDNA sequences



Sergei A. Subbotin¹, Eino L. Krall², Ian T. Riley³, Vladimir N. Chizhov⁴, Ariane Staelens⁵, Marc De Loose⁵ and Maurice Moens⁶

¹Institute of Parasitology of RAS, Leninskii prospect 33, Moscow, 117071, RUSSIA, s.subbotin@clo.fgov.be ,

²Institute of Plant Protection, Estonian Agricultural University, 51014 Tartu, ESTONIA,

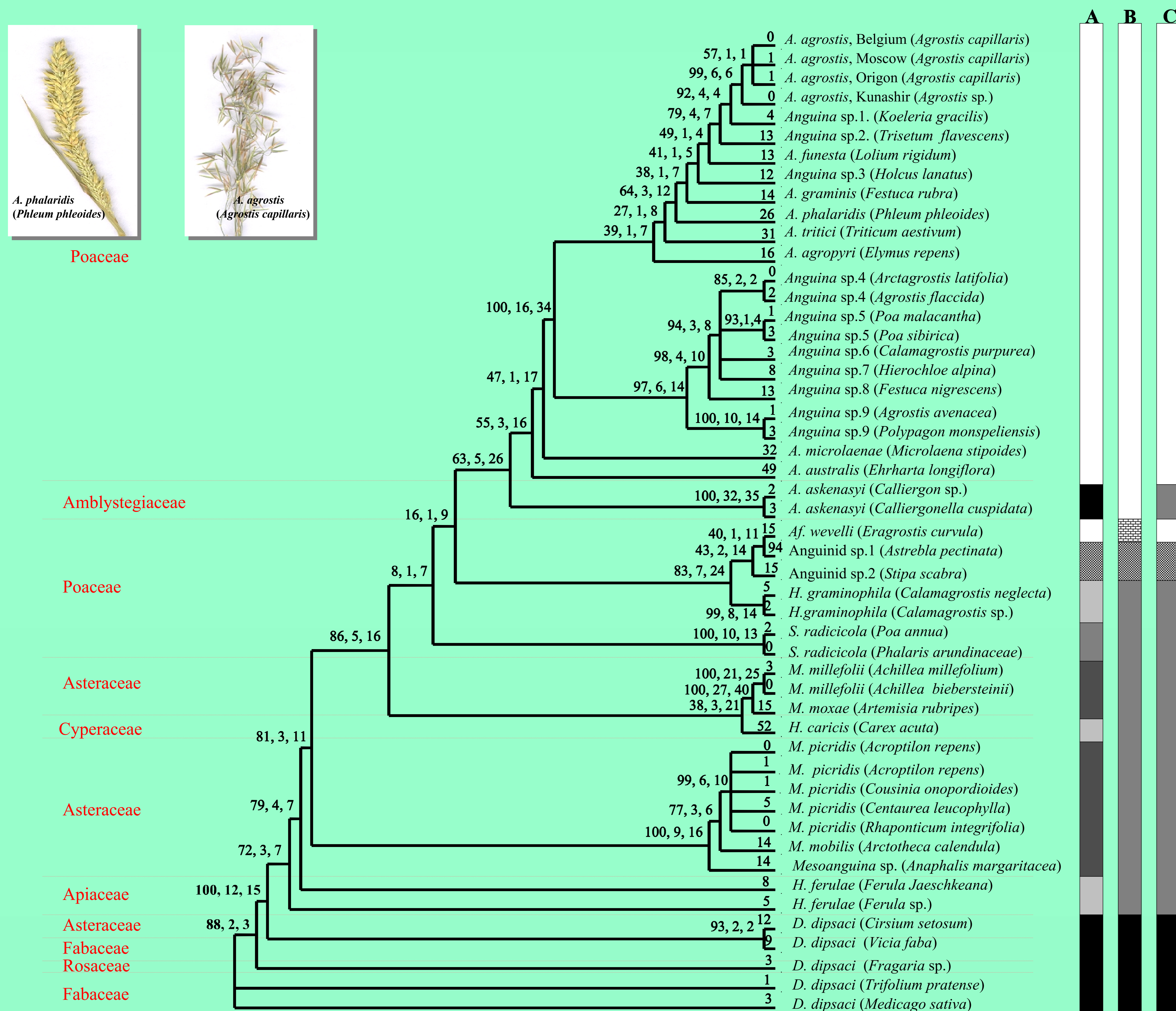
³Applied and Molecular Ecology, Adelaide University, PMB1, Glen Osmond, SA 5064, AUSTRALIA,

⁴Prospect Mira 184-1-53, Moscow, 129301, RUSSIA,

⁵Agricultural Research Centre, Department of Plant Genetics and Breeding, Caritasstraat 21, B-9090 Melle, BELGIUM,

⁶Agricultural Research Center, Crop Protection Department, Burg. Van Gansberghelaan 96, B-9820 Merelbeke, BELGIUM

Internal transcribed spacer (ITS) sequences of rDNA from 53 populations and species of gall-forming nematodes of the subfamily Anguininae, along with five populations of the *D. dipsaci* species complex were used for phylogenetic analyses. The molecular analyses support a concept of narrow specialisation for seed-gall nematodes and reveal distinction of at least nine undescribed species of *Anguina* inducing seed galls, previously identified as *A. agrostis*, and two species within the *D. dipsaci* species complex. Both the maximum parsimony and maximum likelihood analyses of the ITS data strongly support monophyly of the genus *Anguina*. Also, non-monophyly for *Subanguina* in the broad sense of Brzeski (1981) and of *Mesoanguina* and *Heteroanguina* according to Chizhov and Subbotin's (1985, 1990) classification was indicated. Morphological and biological characters are congruent with the anguinid groups supported by the ITS phylogeny. The test of topologies conducted by maximum likelihood analyses shows that the monophyletic origin of anguinids parasitising grasses and sedges could not be rejected. The main anguinid groups are generally associated with plant hosts belonging to the same or related systematic groups.



Strict consensus of 14 equally parsimonious trees from analyses (unweighted parsimony analyses with gaps treated as missing data) of ITS sequence data for 50 species and populations of Anguinidae. Number above the branches indicates bootstrap percentage, decay index and number of character state changes.

Classification of stem and gall nematodes according to **A** - Chizhov and Subbotin (1985, 1990), **B** - Brzeski (1981), **C** - Siddiqi (2000)



REFERENCES

Subbotin, S.A., Krall, E.L., Riley, I.T., Chizhov, V.N., Staelens, A., De Loose, M. & Moens, M. Evolution of the gall-forming plant parasitic nematodes (Tylenchida: Anguinidae) and their relationships with hosts as inferred from Internal Transcribed Spacer sequences of nuclear ribosomal DNA. *Molecular Phylogenetics and Evolution* (submitted).