Phylogeny and historical ecology of some mushroom-associated mites of the genus *Sancassania* (Acari: Acaridae), with some new generic synonymies

Mariam Lekveishvili, Pavel B. Klimov & Barry M. OConnor

University of Michigan, Museum of Zoology, 1109 Geddes Ave., Ann Arbor, MI


Polyporus hirsutus

Abstract:

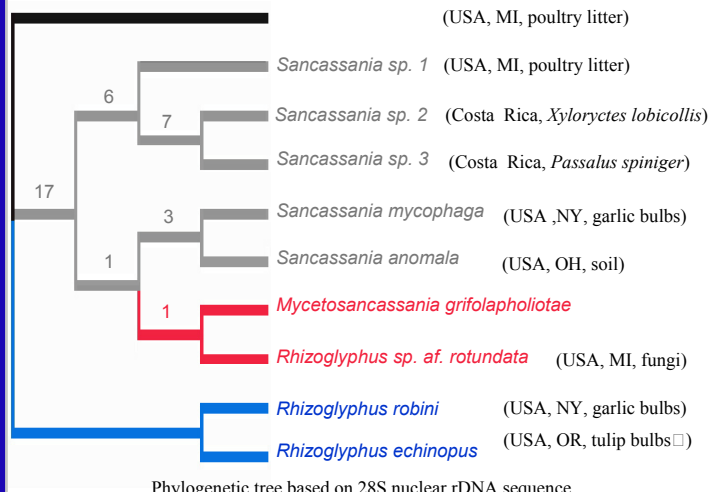
Phylogenetic analyses of molecular data has shown that several mushroom-associated acarid mites previously assigned to the genera *Rhizoglyphus*, *Rhizoglyphoides* and *Mycetosancassania* represent a monophyletic group within the genus *Sancassania*. Based on our phylogenetic reconstruction of the clade (*nidicola* (*grifolapholiotae* (*germanica*+sp3) (sp1 (*rotundata*+sp2))))), the lineage probably originated from relatively advanced *Sancassania* with setiform supracoxal setae. *Sancassania grifolapholiotae* n. comb. and *S.* sp1 inhabit several species of basidiomycete fruiting bodies; *S. rotundata* n. comb. is restricted to mushrooms in relatively wet acid bog habitats. Dispersal is via phoretic deutonymphs which have been found on millipedes and carabid beetles.

Introduction:

The genera *Rhizoglyphus* and *Sancassania* contain some of the most important pest mites in the family Acaridae, damaging bulbs, potatos and other crops in fields and storehouses (species of the genus *Sancassania* feed on other stored products as well). Several taxa of mushroom associated mite species in North America, Europe, and Asia that have been placed in the genera *Rhizoglyphoides*, *Mycetosancassania* and *Rhizoglyphus* appear related to these genera, but morphological characters show homoplasy and do not resolve the phylogenetic placement of these species. For example, the mites have a spiniform seta *ba* on tarsus I (as in *Rhizoglyphus*), and the anus is displaced anteriorly (as in *Sancassania*). Because of these morphological features, species of this group had been assigned either to *Rhizoglyphus* or to new genera by previous authors. We used molecular characters to resolve this conflict. We then used morphological characters to hypothesize relationships among species in the mushroom-associated clade.

Molecular phylogeny.

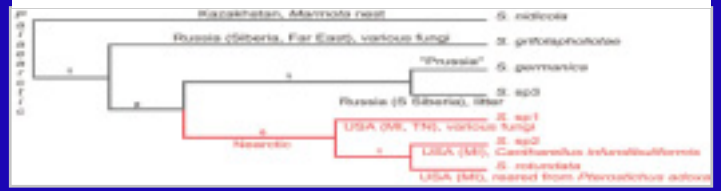
We used 28S nuclear rDNA gene sequence and morphological data for phylogenetic analyses. We obtained 701 bp of PCR product from 10 species of mites using primers D23□F and d6R (Park & OFoighil, 2000). Phylogenetic analyses were conducted using PAUP* 4.0b10 with *Acarus siro* as an outgroup. Analyses performed as exhaustive search yielded a single most parsimonious tree (length 491, CI=0.7413, RI=0.0608) where *Mycetosancassania grifolapholiotae* and *Rhizoglyphus* sp. af. *rotundata* form a monophyletic clade within the genus *Sancassania*.



Phylogenetic tree based on 28S nuclear rDNA sequence

Internal phylogeny and historical ecology:

Thirty-six morphological characters of 7 species were analyzed using PAUP* v.4.0b10. The exhaustive search produced two shortest trees (length=37, ci=0.68, ri=0.67). The most parsimonious topology is shown on the right. The ancestor (not shown), like several other habitat generalists in the genus *Sancassania*, was polyphagous, dispersing on a variety of hosts. *S. nidicola*, the most primitive species of the clade, may retain the ancestral ecology. The other species have specialized to feed on mushrooms and have some adaptations to their phenology. Palaearctic *S. grifolapholiotae* (the biology of *S. germanica* and *S.* sp3 is unknown) and Nearctic *S.* sp1 do not show a preference for particular fungus species/habitat, but species in the more advanced lineage *rotundata*+sp2 appear to be more specialized. *S. rotundata* is adapted to relatively wet peat bog habitats; biology of *S.* sp2 is unknown, but, probably it inhabits very restricted habitat. The Nearctic species, which form a separate clade, appear to have evolved from an unspecialized fungivorous Palaearctic ancestor.



Sancassania anomala

Rhizoglyphus robini

Rhizoglyphus sp. af. rotundatus

Mycetosancassania grifolapholiotae


Sancassania berlesei - female


Sancassania berlesei -male

Conclusions

- Mushroom associated mites previously assigned to the genera *Rhizoglyphus, Rhyzoglyphoides* and *Mycetosancassania* comprise a monophyletic lineage within the genus *Sancassania.*
- Basal lineages occur in the Palaearctic region, with all three North American species forming a single derived clade, suggesting a Palaearctic origin for the group.
- The generic names *Rhizoglyphoides* and *Mycetosancassania* are considered as junior synonyms of the genus *Sancassania*, syn. n. Four new combinations are proposed: *Sancassania rotundata* (Nesbitt, 1944), comb. n. (from *Rhizoglyphus*); *Sancassania germanica* (Berlese, 1921), comb. n. (from *Rhizoglyphus*); *Sancassania nidicola* (Volgin, 1978), comb. n. (from *Rhizoglyphoides*); *Sancassania grifolapholiotae* (Klimov, 2000), comb. n. (from *Mycetosancassania*).

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