



<http://dx.doi.org/10.11646/zootaxa.3931.4.1>

<http://zoobank.org/urn:lsid:zoobank.org:pub:DCDE8326-74F5-4C80-B802-8A05C0B4C4A7>

Molecular phylogenetics, systematics and host-plant associations of the *Bruchidius albosparsus* (Fåhraeus) species group (Coleoptera, Chrysomelidae, Bruchinae) with the description of four new species

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Abstract

Bruchidius Schilsky is a large paraphyletic genus of seed beetles (Coleoptera: Chrysomelidae: Bruchinae) which consists of multiple lineages that are usually associated with narrow sets of host-plants. In this study we focus on a group that mostly develops on wattle trees (acacias) belonging to the genus *Vachellia* Wight & Arn. This group originally included nine species and was designated as the *Bruchidius centromaculatus* (Allard) species group, but recent phylogenetic analyses revealed that these species belong to a much wider group of species with similar morphologies. For reasons of anteriority we call this enlarged group *Bruchidius albosparsus* (Fåhraeus). Here we review the morphology of species in this group and provide new diagnoses and ecological data for 10 species. The following combinations and synonymies are proposed: *Bruchidius tanaensis* (Pic, 1921) (= *Bruchus tanaensis* Pic, 1921) **comb. nov.** and *Bruchidius albosparsus* (Fåhraeus, 1839) (= *Bruchus spadiceus* Fåhraeus, 1839) **syn. nov.** Four new species are also described: *B. eminingensis* **sp. nov.**, *B. gerrardiicola* **sp. nov.**, *B. glomeratus* **sp. nov.** and *B. haladai* **sp. nov.** Finally we carried out molecular phylogenetic analyses on a multi-marker dataset of 59 specimens and 35 species, including 14 species from the group. The resulting trees allow us to confirm the monophyly of the group of interest and provide a more detailed picture of their evolutionary relationships.

Key words: *Bruchidius*, molecular phylogenetics, morphology, systematics, *Vachellia*

Introduction

With more than 250 species, the genus *Bruchidius* Schilsky is one of the two most diverse seed beetle genera (the other being *Acanthoscelides* Schilsky; Kergoat 2004); it is widely distributed in the Old World where it reaches a high level of diversity both in temperate and tropical regions (Udayagiri & Wadhi 1989). *Bruchidius* species are specialized seed feeders with a narrow host-plant range that usually encompasses plants from the same genus or botanical tribe (Jermy & Szentesi 2003; Delobel *et al.* 2004; Kergoat *et al.* 2004; Delobel & Delobel 2006; Delobel & Le Ru 2008; Tuda 2008; Delobel 2014); most species are associated with legume plants (Fabaceae) but a few species are also known to develop on Apiaceae (*B. cinerascens* (Gyllenhal)) or Cistaceae (e.g. *B. biguttatus* (Olivier) or *B. cisti* (Fabricius)). Several molecular phylogenetic analyses (Kergoat & Silvain 2004; Kergoat *et al.* 2005a, 2007, 2008) have revealed that the genus *Bruchidius* is clearly paraphyletic and consists of multiple lineages with distinctive host preferences. Some of these lineages partially correspond to species groups that have been defined on the basis of morphological characters (e.g. Borowiec 1985, 1988; Anton & Delobel 2003).

Host plant preferences. Collectively species in the *B. albosparsus* group are known to develop on 38 mimosoid species (Table 3): 28 *Vachellia* spp., six *Senegalia* spp., two *Prosopis* spp., one *Acacia* and one *Dichrostachys*. The host record of *B. raddiana*e on *Hydnocarpus* in Iran is somewhat questionable because Achariaceae have never been recorded as valid hosts for seed beetles. In addition, because members of *B. albosparsus* group are only known to feed on mimosoids, a shift toward a plant from a distinct family seems quite unlikely. Nonetheless this case is worth investigating because shifts toward unrelated plants have been documented in seed beetles, as in the case of a unique specimen of *B. emarginatus* Allard that has been reared from *Tribulus terrestris* Linnaeus (Zygophyllaceae) instead of a regular legume host (Delobel & Delobel 2005). Regarding the level of specialization of species from the group, nine species appear strictly monophagous (Table 3). Because most of them are not commonly sampled (e.g. *B. arabicus*, *B. basilewskyi*) we cannot exclude the possibility that additional hosts may be discovered in the future; however in the case of the abundant *B. aurivillii* the strict association with *Vachellia tortilis* seems real. Other species in the group have between two and 10 distinct host plant species (10 for *B. albosparsus*). All species but six are exclusively associated with *Vachellia* species, which are well characterized by the sequestration in their seeds of the nonprotein amino acid N-acetyldjenkolic acid (Seigler 2003; Or & Ward 2004). Only a few species are able to develop on *Vachellia* and on plants with distinct toxic secondary compounds, such as *Senegalia* spp. which rely on the nonprotein amino acid albizziine as their main toxic compounds (Evans *et al.* 1977, 1979; Bisby *et al.* 1994; Seigler 2003) or *Dichrostachys* spp. which rely on dichrostachinic acid (Bisby *et al.* 1994). This high level of specialization can be likely explained by the fact that multiple detoxification abilities (e.g. Bleiler & Rosenthal 1988; Rosenthal 1990; Zhu-Salzman *et al.* 2003; Moon *et al.* 2004) are required for species that are more generalist. The latter likely involves major evolutionary trade-offs (*sensu* Cornell and Hawkins 2003) that constrain most seed-beetle species to feed on restricted set of plants that share similar toxic metabolites (Kergoat *et al.* 2005a, 2007b, 2008).

Acknowledgments

We would to thank the editor Matthias Schöller, Michael Schmitt and one anonymous referee for their constructive comments on a previous version of the manuscript. We thank the Curators of MNHN, MRAC and NHRS Coleoptera collections for the loan of types, and other persons and institutions mentioned in the text for the loan of additional specimens. We are grateful to the *Boyekoli Ebale Congo Expedition* organized in 2010 by a consortium of three Belgian institutions: the Royal Museum of Central Africa, the Royal Belgian Institute of Natural Sciences, and the National Botanical Garden of Belgium, in collaboration with the University of Kisangani (UNIKIS), in the Democratic Republic of Congo who allow us to participate to the expedition and collect many interesting specimens. The authors thank Alexandre Dehne Garcia for his help on the CBGP HPC computational platform. Sequencing of new specimens was supported by the Plant Health and Environment Division of INRA (project INRA-SPE EVOSEED).

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