



<http://dx.doi.org/10.11646/zootaxa.3920.1.6>

<http://zoobank.org/urn:lsid:zoobank.org:pub:27B038B1-34DA-4688-836E-657833F300A2>

Revision of the African pollen beetle genera *Tarchonanthogethes* and *Xenostromylogethes*, with insect-host plant relationships, identification key, and cladistic analysis of the *Anthystrix* genus-complex (Coleoptera: Nitidulidae: Meligethinae)

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Abstract

The Afrotropical endemic pollen beetle genera *Tarchonanthogethes* Audisio & Cline and *Xenostromylogethes* Audisio & Cline, of the *Anthystrix* genus-complex, are revised. Eleven new species of *Tarchonanthogethes* (*T. autumnalis*, **sp. nov.**, *T. bisignatus*, **sp. nov.**, *T. fasciatus*, **sp. nov.**, *T. gratiellae*, **sp. nov.**, *T. hermani*, **sp. nov.**, *T. hystrix*, **sp. nov.**, *T. lilliputianus*, **sp. nov.**, *T. maasai*, **sp. nov.**, *T. manconiae*, **sp. nov.**, *T. pectinipes*, **sp. nov.**, *T. thalycrifformis*, **sp. nov.**) and one new *Xenostromylogethes* (*X. cychramoides*, **sp. nov.**) are described, illustrated and compared with related taxa. *Tarchonanthogethes hirtus* Kirejtshuk & Easton, 1988 is synonymized with *T. martini* (**syn. nov.**). *Meligethes assutus* Easton, 1960 from Kenya is transferred from *Afrogethes* Audisio & Cline to *Tarchonanthogethes* (**comb. nov.**). *Meligethes singularis* Grouvelle, 1919 from southern Africa is transferred from *Tarchonanthogethes* to *Meligethinus* Grouvelle, 1906 (**comb. nov.**). Larval host-plants for *Tarchonanthogethes* and *Xenostromylogethes* include dioecious bushes and trees of Tarchonantheae Asteraceae (genera *Brachylaena* R.Br. and *Tarchonanthus* L.). All species currently attributed to the genera *Anthystrix* Kirejtshuk, *Sebastiangethes* Audisio, Kirk-Spriggs & Cline, *Tarchonanthogethes* and *Xenostromylogethes* (*Anthystrix* genus-complex) are included in a morphology-based cladistic analysis to provide a rigorous hypothesis of phylogenetic relationships. An identification key to all 25 known species in the *Anthystrix* genus-complex, including all available data on insect host plant relationships, is presented.

Key words: Pollen beetles, new species, distribution, key to identification, Asteraceae, Africa

Introduction

Meligethinae, commonly known as ‘pollen beetles’, develop in flower buds of both monocot and dicot plants. Some species are of economic importance as feeders and pollinators of widely cultivated crops including mustard-oil plants (Brassicaceae), grass-clover and lucerne (Fabaceae), oil palms (Arecaceae), and bulrush millet (Poaceae) (Hatch 1957; Jourdeuil 1962; Kelm 1976; Kirk-Spriggs 1985, 1996; Jelínek 1992; Audisio 1993; Howard *et al.* 2001; Hansen 2003). However, other species are known pests of ornamental plants such as roses and blackberries (Rosaceae) (Ormerod 1874; Hayashi 1978; Audisio 1993).

Recently the generic classification of Meligethinae has been discussed and largely revised from results obtained by both morphological and molecular data analyses (Strika 2004; Mancini *et al.* 2008; Audisio *et al.* 2009a, b, 2011a, b, 2014; Lamanna 2009; Trizzino *et al.* 2009). In this context, Audisio *et al.* (2008, 2009b) proposed the ‘*Anthystrix* genus complex’ to include *Anthystrix* Kirejtshuk, 1981, and three closely related southern African genera, namely: *Sebastiangethes* Audisio, Kirk-Spriggs & Cline, 2008, *Tarchonanthogethes* Audisio and Cline, 2009, and *Xenostromylogethes* Audisio & Cline, 2009. A recent contribution (Kirejtshuk & Kirejtshuk 2012), mainly based on subjective and unsupported argumentation, suggested that the three latter genera should be included in a single, more comprehensive, and highly heterogeneous genus *Anthystrix*. However, the actual status of this generic complex and its close relationship with the Afrotropical *Chromogethes* Kirejtshuk, 1989 received strong support from molecular data based on mitochondrial and nuclear genes (Trizzino *et al.* 2009; Audisio *et al.* 2014). A comparative analysis of ITS2 sequences and secondary structures in Meligethinae highlighted a distinctive elongation (due to simple-sequence repeats) of the apical portion of ITS2 domain ‘D1’ in members of the ‘*Anthystrix* genus complex’ and *Chromogethes*, as well as the exclusive presence of a ‘signature sequence’ at the 3’ portion of the D1 insertion (‘GAUUCAC’), which was absent in all other Meligethinae (Lamanna 2009; Trizzino *et al.* 2009). Even the partial data from larval morphology of Meligethinae suggest a similar phylogenetic pattern. In fact, all examined members of the ‘*Anthystrix* genus complex’ and *Chromogethes* share mouthpart synapomorphies of 3rd instar larvae (e.g., shape of the inner mandibular edge: Reibaldi 2013; Audisio *et al.* unpublished data).

Tarchonanthogethes and *Xenostromylogethes* were originally erected to accommodate five and one species, respectively, from southern Africa, which were originally ascribed to *Anthystrix*, *Meligethinus* Grouvelle, 1906, *Pria* Stephens, 1830, and *Meligethes* Stephens, 1830. *Anthystrix* currently includes six southern African species, all associated with Asteraceae trees (Grouvelle 1899; Kirejtshuk 1981; Kirejtshuk & Easton 1988; Audisio *et al.* 2009a); *Meligethinus* includes numerous Palearctic and Palearctic species (Cooper 1980; Jelínek 1992; Audisio *et al.* 2009b; Kirejtshuk 2011), true examples of which are strictly associated with male inflorescences of palms (Arecaceae) in larval stages (Jelínek 1992; Audisio 1993; Audisio *et al.* 2009b); *Pria* includes approximately 100 described and undescribed species, mostly distributed in Palearctic areas and associated with flowers of several

Colonnelli, and M. Mei (Rome, Italy), M. Biondi (L'Aquila, Italy), R. Manconi (Sassari, Italy), R. Fochetti and M. Zapparoli (Viterbo, Italy), and A. Freidberg (Tel Aviv, Israel). Special thanks are due to N. Falchi (Rome) for helping prepare the colour plates, and to M. Tisato (Verona) for helping prepare the final format of pictures, SEM photos, and maps; to P. Maltzeff (Rome) for help in translations of a series of scientific papers published in Russian; and to the botanist P.P.J. Herman (Pretoria) for providing us with reprints of his important papers on African Tarchonantheae-Asteraceae, and detailed information on distribution and flowering time of several species of this group in South Africa. We thank Josef Jelínek and Gareth Powell for their insightful reviews of the manuscript.

This paper was partially supported by grants from Italian Ministero dell'Istruzione, dell'Università e della Ricerca (PRIN 2004057217 'Zoogeography of Mediterranean-southern African disjunct distributions by a multimethod approach'), from University of Rome 'La Sapienza' (60% funds 'Aspetti genetici e morfometrici della biodiversità animale in aree africane e medio-orientali a basso impatto antropico'), and from MiPAAF - National Forest Service, CNBF National Centre for Forestry Biodiversity, Verona, Italy.

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APPENDIX 1. Data matrix for the phylogenetic analysis and list of characters and character states. Characters are ordered from head to abdomen, from dorsal to ventral side, from anterior to posterior appendages of each body region, from male to female genital parts. Character states separated by “/” may be co-present in the same species; question marks refer to unknown character states (one of the two sexes being unknown).