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Abstract

Until recently the *subaptera*-group of *Phyllodromica* contained only one species. The revision of the *subaptera*-group herein consists of the two newly described bisexual species, *P. iberica* and *P. quadracantha*, endemic to the Iberian Peninsula and a parthenogenetic species, *P. subaptera* (Rambur, 1838), which is widely distributed over most of the Mediterranean countries and islands. Within *P. iberica* three conspecific morphotypes are distinguished. The morphological characteristics of the *subaptera*-group are described. The species and their distributions are described and depicted. A key for the morphological determination of *P. quadracantha* and the morphotypes of *P. iberica* is given. DNA sequences of the mitochondrial cytochrome c oxidase subunit I (COI) gene are included in the species descriptions. The sequence data are suitable for species identification (DNA barcodes). A cladistic analysis of the morphological data and a phylogenetic analysis of the DNA sequences were performed to infer the phylogenetic relationships between the species of the *subaptera*-group.

Key words: Blattoptera, Blattellidae, Ectobiinae, *Phyllodromica*, new species, thelytoky, geographic parthenogenesis, mtDNA, COI, DNA sequences, DNA barcodes, molecular phylogeny

Introduction

The phenomenon of parthenogenesis has been observed in several cockroach species (Roth & Willis 1956, Corley *et al.* 1999). Obligatory parthenogenesis was only known in *Pycnoscelus surinamensis* which is assumed to be sexually isolated from its presumed bisexual ancestor *Pycnoscelus indicus* (Roth 1967). The parthenogenesis of the *subaptera*-group of *Phyllodromica* (Blatellidae: Ectobiinae) is the second case of obligatory thelytokous parthenogenesis observed in cockroaches (Knebelsberger & Bohn 2003).

This paper presents a revision of the *subaptera*-group and provides new information on the origin and evolution of parthenogenesis in Blattoptera.

The bisexual and the parthenogenetic forms of the *subaptera*-group exhibit different geographical distributions. The bisexual forms are endemic to the Iberian peninsula, whereas the parthenogens can be found in most of the Mediterranean countries and islands (Knebelsberger & Bohn 2003). This distribution pattern is consistent with the term "geographic parthenogenesis" first proposed by Vandel (1928). Morphological investigations have shown that males of the *subaptera*-group exhibit remarkable morphological variation mainly in the glandular structures of tergites 7 and 8 (Knebelsberger & Bohn 2003). Four morphotypes ('morphs') with partially overlapping distributions were distinguished. In contrast to the males, the bisexual and the parthenogenetic females for the most part cannot be distinguished by their external features.

To investigate the taxonomical state of the identified 'morphs' an extended morphological analysis was performed based on the material in the collection of Horst Bohn and T. K., and as a whole covered most of the mountain regions of the Iberian Peninsula.

Analysis of DNA sequence data provided information about the degree of the separation of the morphs which may possibly even represent new species. In cockroaches the investigation of DNA sequence variation was already used to detect new species and species boundaries. Kambhampati *et al.* (1996) investigated the sequence variation of two mitochondrial rRNA genes to obtain evidence for newly detected sibling species of *Cryptocercus punctulatus*. Based on this study Nalepa *et al*. (1997) and Burnside *et al*. (2000) described new species of *Cryptocercus* and the latter included sequence data (12S rRNA and 16S rRNA) in the descriptions of new species.

In this paper two new bisexual species are described. The parthenogenetic strain (species) retains the name *Phyllodromica subaptera* (Rambur 1838) because the holotype specimen is most likely a parthenogenetic female. The complete sequences of the mitochondrial COI gene are included in the description of each species. One important aim of the genetic characterisation of the species is to support the potential use of the sequence information as a taxonomic tool for subsequent species re-identification as recommended by Tautz