



Nota breve | Short note

First genetic data for *Bandeirenica caboverda* (Pierrard, 1987) (Diplopoda: Odontopygidae) from Cabo Verde

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The species *Bandeirenica caboverda* (Pierrard, 1987) (Diplopoda: Odontopygidae) represents a unique case of a diplopod adapted to agricultural ecosystems in Cabo Verde (Decker 2026, Pierrard 1987, Nascimento 2005). The presence of this species in the archipelago remained unknown until 1982 (Harten 1993). Even though it was originally described as *Spinotarsus caboverdus*, Enghoff (1982) temporarily assigned it as *Tibiomus* sp. based on similarities to mainland African species (Enghoff 1993). Reported as a common agricultural pest from a small collection of millipedes from Santo Antão Island, the species was transferred to the Angolan genus *Bandeirenica* following detailed morphological analyses, particularly the absence of dorsal paraproctal spines – a trait distinguishing this taxon from other Odontopygidae groups (Enghoff 1993, Hoffman 2000).

Studies on *B. caboverda* remain scarce, and its origin remains a mystery, with some authors even considering it an exotic species. Available literature focuses predominantly on morphological description, ecology in cropping systems (Neves & Viereck 1987, Faria *et al.* 1990) and biological control trials (Brito 1994). To date, there is no genetic data available for the *B. caboverda* populations from Cabo Verde, and online databases (<https://portal.boldsystems.org/>) contain only three sequences from Kenya (USNM ENT 00980560–62), which raises some doubts because its distribution is known only at Cabo Verde (Enghoff 1993).

The scarce molecular data available hinder understanding of its evolutionary history and systematics within the family Odontopygidae. The present study aims at addressing this knowledge gap by providing the first genetic data for *B. caboverda* from Cabo Verde.

Four samples were collected in agricultural fields from Vila das Pombas, Santo Antão (Fig. 1A). Total DNA extraction was performed from fresh specimens using the E.Z.N.A. Mollusc & Insect DNA Kit (Omega Bio-Tek). Amplification of a ~641 bp fragment of the cytochrome *c* oxidase subunit I region was performed using the universal primers pair LCO1490/ HCO2198 (Folmer *et al.* 1994) via PCR conducted following Lopes *et al.* (2025). The PCR products were submitted for Sanger sequencing in both forward and reverse sense by StabVida (Portugal). Raw outputs were

validated via BoldSystems portal (www.boldsystems.org), edited, manually aligned in MEGA X and employed for similarity analyses against others *B. caboverda* sequences on 05 March 2026. A maximum likelihood phylogenetic tree (GTR+I model) was performed using the PhyML software (Guindon *et al.* 2010), including *Prionopetalum krapelini* and *Chaleponcus netus* as outgroups. All *B. caboverda* COI sequences obtained were deposited in GenBank under accession numbers PZ412605–PZ412608.

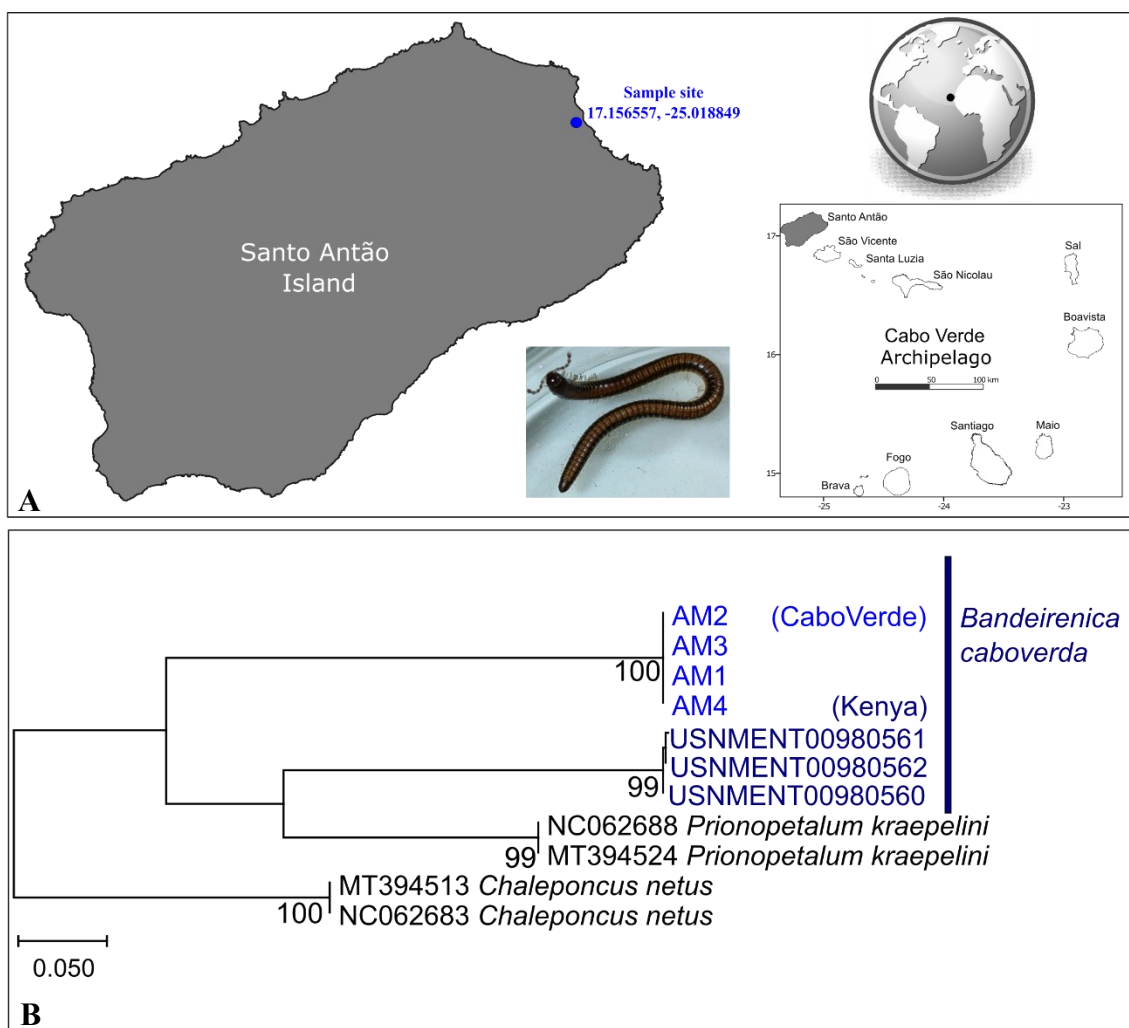


Fig. 1. Sampling site and phylogenetic relationships between the sequences obtained in this study and those retrieved from GenBank/ BOLD databases. **A)** Geographical location of the *B. caboverda* specimen collection site on Santo Antão Island in February 2026 (point in blue), of the sampled island in the Cabo Verde Archipelago (in grey), and of the country (black point). A photograph of one of the sampled specimens (AM4) is also provided (photo by E. Lopes). **B)** Maximum likelihood (ML) consensus tree for the 641 bp COI sequences of *B. caboverda* shows two clades and high divergence between the Cabo Verdean samples and the tree samples from the African continent (Kenya). Numbers at nodes represent statistical support values (ML bootstrap). GenBank/BOLD Systems accession codes are provided for all sequences from other studies. Scale bar indicates substitutions per site.

The Cabo Verde sequences formed a distinct clade well-separated from Kenya samples (Fig. 1B), exhibiting >20% genetic divergence (BS = 100). These results have not enabled identification of the ancestral mainland population, reinforcing the need for

more genetic studies in Africa. This study provides the first molecular data for *B. caboverda* from Cabo Verde, a reference baseline for future studies on interspecific genetic diversity, population structure and evolutionary dynamics in an insular context.

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