

ABSTRACT

The ability to delimit species boundaries is essential in taxonomic studies. However, different methods of delimitation may give ambiguous or contradictory results, thus integration of multiple approaches is often necessary for correct species recognition. This is especially true for taxa originated in recent radiations that may not have had sufficient time to accumulate morphological apomorphies, in which case a strictly morphology based approach would underestimate the real species diversity. In this regard, molecular methods became a useful tool for species delineation. The woodlouse hunter spider *Dysdera erythrina* is considered a sibling species complex with wide geographic distribution (Iberian Peninsula to Georgia). Three species have been separated from *D. erythrina* in the past, however their current taxonomic position remains unclear. In this study an integrative approach combining molecular (one nuclear, four mitochondrial genes) and morphological data is used for species delimitation. Molecular data are further used in order to reconstruct the phylogenetic relationships among the lineages and estimation of the time frame of their diversification. In the phylogenetic analyses *Dysdera fervida* and *D. lantosquensis* formed independent monophyletic clades supported also by morphology, but *D. erythrina* and *D. provincialis* individuals were placed in a single clade. Up to 39 independent lineages within the entire *erythrina* complex were detected by the two molecular species delimitation approaches. These lineages may correspond to cryptic species, however a better sampling and implementation of additional lines of evidence are necessary in order to assess their status (for subsequent progress on this topic see Supplementary File 2). The results also revealed one previously unknown lineage endemic to Sardinia, sister to the entire *erythrina* group (subsequently described as *D. shardana*; see Supplementary File 1). The divergence time analyses show that most of the *erythrina/provincialis* clade lineages originated during the Plio-pleistocene glacial cycles, suggesting that the possible isolation of populations in different refugia could have promoted the diversification. On the other hand, the separation of *D. cf. erythrina* (*D. shardana*), *D. fervida* and *D. lantosquensis* dates further back to the past. The current distribution of *D. erythrina* species complex shows no clear geographic pattern. The overlapping of the lineages may be caused by the range expansion of previously separated populations; however human mediated introduction cannot be ruled out in some cases.