

Poster Abstracts

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and provide the species identification and bioinformatics functions. The database and bioinformatics platform are designed loose coupled, and the connection are through web services and/or http services. Nevertheless, the mirror site in China is more than a duplication of BOLD. To meet the Chinese users' need, we are developing the Chinese tags for the data, and making translation between English and Chinese. We also placed some basic information of DNA barcode and some useful links (in Chinese) to let Chinese society to know DNA barcode better. Moreover, the mirror site is seamless to connect our information system, which contains the data submission system for Chinese collaborators and may provide further information of a given species and/or DNA barcode. Thus, our mirror site also functions as data transformer to transform the data from Chinese collaborators into BOLD system. Currently, we have integrated the international data from BOLD into our mirror site, that contains over 140,000 data entries. Those data can be accessed either by taxon search or by BLAST. We are developing the data transform rules to make the collections of fish, birds and fungi data in China into BOLD system. By now, the mirror site is still under construction.

PHYLOGENY OF MESOBUTHUS EUPEUS (C.L.Koch, 1839) IN IRAN USING CO1 SEQUENCES

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The genus *Mesobuthus* belonging to family Buthidae is most diverse in Central Asia and Iran. The scorpion *M.eupeus* is one of the most naturally widespread members of the family Buthidae, being present in eastern Turkey, Caucasia, southern Russia, Middle East, Central Asia, southern Mongolia and northern China. Additionally, considerable morphological variation has been attributed to populations of *M.eupeus* within this extensive geographic distribution and 21 recognized valid subspecies have been described. A recent comprehensive update or revision of *M.eupeus* is not available.

In this study, the first molecular phylogeny assessment of *M.eupeus* in Iran based on sequence data of a ~700bp fragment of Cytochrome C oxidase, subunit I is presented. Fifteen populations collected from different localities within Iran were included in the study. Phylogenetic relationships were inferred using neighbour-joining (p-distance) and maximum likelihood under GTR+ Γ substitution model. The results support monophyly for *M.eupeus*, but they do show a clear deep split between northern and southern clades within the species. The northern clade included *M.e.eupeus*, *M.e.philippovitschi*, *M.e.afghanus*, and *M.e.thersites*, while the southern clade comprised *M.e.phillipsi* and *M.e.kirmanensis*. In the topology observed, the "southern clade" has a basal position relative to the "northern clade". Accordingly, some scenarios for the evolution and phylogeographic structure of this species based on the paleogeography and geological history of Iranian plateau were proposed and tested. In addition to the intraspecific divergence, our topology showed a deeper phylogenetic split within the genus *Mesobuthus*. Here, a "western clade" consisting of *M.gibbosus* and *M.cyprius* is separated from an "eastern clade" containing *M.*

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eupeus and *M.caucasicus*. Finally, the molecular clock hypothesis using the likelihood ratio test was applied in order to test the constancy of the evolutionary rates across the tree.