

Molecular genetic analysis of some mesothel spiders (Heptathelidae)

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Island populations of Heptathelidae in Japan and the Ryuku-Islands have been either classified as subspecies (Haupt, 1983) or as separate species (Ono & Nishikawa, 1989). Taxonomic and phylogenetic studies were mainly based on morphological data.

In this study a molecular genetic analysis is used to clarify the relationship of several representatives of Heptathelidae from Kyushu and Okinawa.

An 800 bp sequence from the 28S DNA was amplified by the polymerase chain reaction (PCR) by using two highly conserved primers flanking the D1 and D2 domains (Beye & Moritz, 1994). The PCR product were digested with several four-base enzymes. The samples were electrophoretically separated in a 7% acrylamide gel, stained with ethidium bromide, and visualised over an UV-lamp. Restriction fragment analyses showed a considerable variation within and between different populations of the *Heptathela kimurai* group from Kyushu and Northern Okinawa, but no variation between populations of *Ryuthela nishihirai* from different localities in South Okinawa.

References

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