Molecular philogeny of the old world porcupines (family hystricidae) using mitochondrial cytochrome b gene / Jeffrine Japning Rovie-Ryan, Faisal Ali Anwarali Khan, Zainal Zahari Zainuddin, Abdul Hamid Ahmad, Millawati Gani, Ahmad Mashur Julaihi, Salman Saaban

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Abstrak

The Old World porcupines (Family Hystricidae) are generally large terrestrial rodents. The major threats to their survival includes over-hunting primarily due to high demand for their meat that is thought to be of high medicinal value. This threat is further impacted by mass habitat destruction where forest is converted into agricultural land or human settlements. Despite their large and unique appearance, little is known with regards to their intrafamilial phylogenetic relationships. This is hampered by the limited DNA sequences that are available on public databases for species identification and comparison.

In this study, the phylogenetic relationships among eight out of eleven extant species of Hystricidae were examined using a partial cytochrome b gene of the mitochondrial DNA. The first reference record of DNA sequence for all four species of porcupines in Malaysia (Atherurus macrourus, Hystrix brachyura, Thecurus crassispinis, and Trichys fasciculata) were made available in GenBank database. These reference sequences are crucial for species identification in a forensic case framework. The phylogeny supported the monophyly of the family Hystricidae. Except for Thecurus, the genera within Hystricidae: Atherurus, Hystrix, and Trichys formed distinct groups supporting their genus status with Trichys forming the basal group. Based on the positioning of Thecurus crassispinis within the Hystrix species group in the phylogeny tree, we suggested that Thecurus crassispinis to be systematically classified as Hystrix crassispinis. Within the genus Hystrix, further studies are needed to elucidate the relationships by including the remaining three species within the genus (Hystrix javanica, Hystrix pumila, and Hystrix sumatrae). Furthermore within Hystrix brachyura, additional studies are needed to investigate the regional populations structuring within their range countries in Southeast Asia to assist in the sustainable management and conservation of the species.