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ANALYSIS OF INTRASPECIFIC VARIATION IN *TAENIA TAENIAEFORMIS*
AND *ECHINOCOCCUS MULTILOCULARIS* BY DNA FINGERPRINTING

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Intraspecific variation in genome DNA of *Taenia taeniaeformis* and *Echinococcus multilocularis* were investigated. DNA fingerprints were generated from 18 isolates of *Taenia taeniaeformis* and 7 isolates of *E. multilocularis* using (CAC)₅ non-radioactive oligonucleotide probes. The fingerprint patterns of the following 18 *T. taeniaeformis* isolates were compared; 1 of *Clethrionomys rufocanus bedfordiae* in Hokkaido, 1 of *Rattus norvegicus* from Malaysia, 1 of a mouse from Belgium, 13 of *R. norvegicus* and 2 of cats from 8 different areas of Hokkaido. The DNA fingerprint patterns of *T. taeniaeformis* isolates from *C. rufocanus bedfordiae* in Hokkaido, *R. norvegicus* from Malaysia, and the mouse from Belgium could be differentiated easily from one another. Although very similar fingerprint patterns were observed for all of the isolates from *R. norvegicus* and cats in Hokkaido, slight individual pattern variation was noted among the parasites that were isolated from different hosts in the same area.

The fingerprint patterns were then numerically analysed by cluster analysis and dendrograms were constructed. *T. taeniaeformis* isolates from *R. norvegicus* and cats in Hokkaido formed one cluster, and the other isolates could be grouped into 3 clusters.

The DNA fingerprints of 7 isolates of *Echinococcus multilocularis* were also compared. The patterns of the 5 isolates from different hosts such as swine, *C. rufocanus bedfordiae*, and *R. norvegicus* in Hokkaido were identical despite the difference in host species. The patterns of the 2 remaining isolates, which originated from *Microtus oeconomus* and *Clethrionomys rutilus* in Alaska, were identical to each other but distinctly different from the isolates from Hokkaido.

Therefore, DNA fingerprinting, with further modifications, may be used to elucidate the intraspecific variation of taeniids.