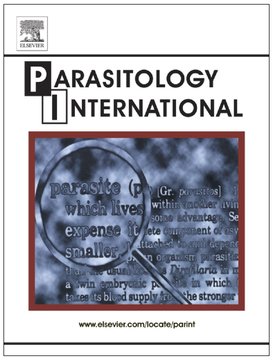

Use of molecular data in species-level taxonomy of parasites: A commentary

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Use of molecular data in species-level taxonomy of parasites: a commentary.

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An ideal systematic/taxonomic study should employ both morphological and molecular data sets to inform conclusions. But should we regard molecules as more accurate than morphology? A recent study by Banzai-Umehara and colleagues provides food for thought [1]. These authors obtained plerocercoids from anadromous surf-smelt in Japan and fed them to hamsters. Twenty adult cestodes in the genus *Diphyllobothrium* were obtained from the hamsters. Various morphological features of intact worms and in histological sections of proglottids were examined. Banzai-Umehara et al. [1] tried to use criteria established by Yazaki et al. [2] to distinguish between species. Particular importance was placed on the angle between the long axis of the cirrus sac and that of the seminal vesicle. However, their specimens showed morphological characteristics that overlapped those of *D. hottai* and *D. ditremum*, according to this and other criteria. They stated: “Thus, the use of morphometric characteristics of plerocercoids and eggs is not suitable for the differentiation of *D. hottai* from *D. ditremum*” and “… differentiation of the two cestode species based on these histologically-obtained parameters may not be very reliable”. Nevertheless, they assigned seven worms to *D. hottai* and one to *D. ditremum* based on the angle between the cirrus sac and the seminal vesicle. They were not confident about the identities of the remaining worms, one of which exhibited angles typical of *D. hottai* in some proglottids and typical of *D. ditremum* in others. Working on the assumption that they had correctly identified (morphologically) one specimen as *D. ditremum*, Banzai-Umehara et al. [1] then sequenced mitochondrial *cox1* and *cob* from their named specimens. Their sequences from the Japanese worm determined as *D. ditremum* were almost identical with those from their *D. hottai*. However, all the Japanese sequences were distinct from those of *D. ditremum* from Europe. They regarded the genetic distance between Japanese *D. hottai*