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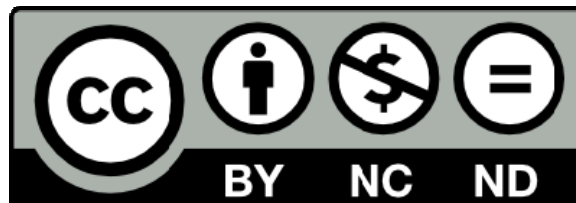
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Response to Nakao *et al.* – is *Echinococcus intermedius* a valid species?

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The aim of our Opinion article [1] was to stimulate discussion on the taxonomic status of the G6, G7, G8, and G10 genotypes of *Echinococcus granulosus*, and we therefore welcome the letter from Nakao *et al.* (2015) [2]. They make two main points, one concerning the separation of the G8 and G10 (cervid) genotypes, and one concerning the nomenclature of the G6/G7 (camel and pig) genotypes. With both these points there are aspects which we can agree upon, but others about which we must disagree. However, the areas of disagreement can be settled empirically with further data, and we hope that such data will be forthcoming soon.

Nakao *et al.*[2] propose that it is premature to regard the G8 and G10 genotypes as separate species because their sympatric distribution suggests that cross-hybridization between them is easily possible. Our point was that it is because these genotypes maintain their genetic distinctiveness in sympatry that they should be regarded as separate species. Nakao *et al.*[2] suggest that the G8 and G10 genotypes are different mitochondrial lineages only (i.e., there is no evidence that they are not recombining) because nuclear DNA differences between them at several loci are minor and do not separate monophyletic groups [3], whereas we believe that morphological and life-history differences between them suggest that these genotypes are different evolutionary lineages. Neither arguments are yet entirely convincing; the nuclear DNA data for G8 and G10 come from a very limited set of

specimens, and we do not know the extent to which differences in morphological and life-history characters between the genotypes are influenced by the environment. Further detailed genetic and morphological studies on isolates collected in strictly sympatric situations (i.e., in the same locality) should provide a more definitive answer. A good place to look for such isolates may be in western Canada where individual wolf hosts harboring both mitochondrial DNA genotypes have been found [4].

Nakao *et al.*[2] believe that the name *Echinococcus intermedius*, which we suggested for the G6/G7 genotype, is inappropriate because of confusion over the provenance of the isolates used in the original description, and the loss of the type specimens. We agree that the original morphological descriptions [5] were inadequate and that the apparent absence of the type specimens makes it almost impossible to match the original description to contemporary isolates. However, we do not think that is the most important issue. As we pointed out in our original Opinion article, we were not seeking to formally propose names, simply to make some suggestions – before we tackle the issue of nomenclature we need to decide whether the G6/G7 group is deserving of species status. We suggested that morphological and life-history characteristics provided no evidence that the G6 and G7 genotypes were on evolutionarily different pathways, but that they were evolutionarily distinct from the G8 and G10 genotypes. This question is rather more difficult to settle with genetic data than the G8/G10 problem because the G6/G7 genotypes have distributions which are largely allopatric to the two cervid genotypes. However, the G6, G8, and G10 genotypes have been found in parts of eastern Russia [6], and this may be an area in which appropriate genetic, morphological, and life-history data could be collected.

In summary, our Opinion article was stimulated by a conviction that scientific names are required in the medical and veterinary sciences for effective communication, and a nomenclature that reflects evolutionary reality has important public policy implications. Our concern is that we believe the genotypes G6, G7, G8, and G10 were unified as *Echinococcus canadensis* without due consideration of the well-documented biological and epidemiological factors that separate G6/G7, G8, and G10. This has created a confusing and controversial situation that hinders understanding of transmission

patterns in endemic areas. If this discussion provokes a search for empirical data that unambiguously resolve the species status of these four genotypes, then it will have been well worthwhile. The sooner this situation is resolved the better because a correct taxonomy has serious public policy implications, as documented in our original article [1].

References

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