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The disjunct distribution of *Echinoderes ohtsukai* (Kinorhyncha) explained by human-mediated dispersal across the Pacific Ocean

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The dispersal ability of kinorhynchs, like many other meiofaunal groups, is inferred to be limited because they are endobenthic direct developers (i.e., without planktonic larval stages). However, the distribution of certain species of kinorhynchs extends over vast geographical areas, for example in *Echinoderes ohtsukai*. This species was originally described from Japan, but is has also been found in several localities in the northeastern Pacific Ocean (British Columbia). To evaluate the unexpected biogeographical pattern in *E. ohtsukai*, we sequenced two mitochondrial genes (*Cytochrome* c oxidase subunit I, COI; and *Cytochrome* b) and one nuclear gene (Ribosomal internal transcribed spacer, ITS) in 95 isolates from three different populations in Japan, including the species type locality in the Seto inland Sea, and three populations off the British Columbia coast. Haplotype networks and phylogenetic trees show that most individuals collected from Japan and British Columbia share the same haplotypes at all three molecular markers, and only few mutations separate diverged haplotypes in individuals separated by the Pacific Ocean. We interpret this high sequence similarity as the first evidence of a highly disjunct geographical distribution in kinorhynchs that is consistent with human-mediated dispersal. The coast of British Columbia has historically had a high level of maritime traffic from the coast of Japan, thus we infer that aquacultural related activities could have played a key role in transporting kinorhynchs across the Pacific Ocean.

Keywords: Kinorhyncha, human-mediated dispersal, Pacific Ocean, molecular markers