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Morphological and genetic differentiation of heteromorphy in *Labidocera rotunda* (Copepoda, Calanoida, Pontellidae)

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Abstract

The pontellid calanoid *Labidocera rotunda* Mori, 1929 is relatively widespread in the inshore surface waters of East Asia. In this study, some heteromorphic specimens have been observed with extreme morphological discrepancies in the female, including the genital double-somite, the second urosomite, the caudal rami, and the fifth leg. To evaluate the validity of species assignment of the morphological variants, we analyzed the DNA sequences of two mitochondrial genes, 16S rRNA and cytochrome oxidase subunit I (mtCOI). The specimens were collected in the Yellow Sea, the East China Sea and the East Sea (Sea of Japan) around Korea. They differed by <2.9% for mt16S rRNA and by 3.7%–4.7% for mtCOI, suggesting that they are conspecific despite their considerable morphological differences. In contrast, *Labidocera japonica* Mori, 1935, a morphologically similar species to *L. rotunda*, displayed interspecific variation of 6.1%–7.2% for mt16S rRNA and 15.1%–16.7% for mtCOI.

Key words: Calanoida, neustonic copepods, mitochondrial genes, genital structure, zoogeography

Introduction

The genus *Labidocera* Lubbock, 1853 is comprised of 52 species, and occurs mostly in the surface waters (0–30 cm surface layer) from tropical to warm temperate regions (Sherman 1963, 1964; Razouls *et al.* 2013). The genus is divided into five species-groups such as *detruncata*, *kröyeri*, *minuta*, *pectinata*, and an unnamed group, on the basis of its morphological characteristics (Fleminger *et al.* 1982; Othman 1986; Mulyadi 1997, 2003). *Labidocera rotunda*, included in the *pectinata* group, was originally described by Mori (1929) from Pusan, Korea and distinguished from *L. bipinnata* of Sagami Bay, Japan (Tanaka, 1936). Sewell (1948) suggested that both species are synonymous with *L. pectinata*. However, Fleminger (1967) retained *L. rotunda* and *L. pectinata* as separate species, while *L. bipinnata* was synonymized with *rotunda* because of their minor difference in the presence or absence of lateral cephalic hooks (Fleminger *et al.* 1982). Likewise, *L. rotunda* displays some extreme morphological variability as reported by Chen & Zhang (1965), Fleminger *et al.* (1982) and Othman & Toda (2006).

Morphological identification is hampered by many instances of subtle or considerable morphological characters overlapping, as well as the overlap of geographical distributions among closely related species (Fleminger & Hulsemann 1974; Fleminger *et al.* 1982). When morphological characteristics are not practical for routine identification to species level, molecular analysis can provide unambiguous taxonomic discrimination (Bucklin & Wiebe 1998; Lee & Frost 2002; Eyun *et al.* 2007; Soh *et al.* 2012). In particular, sequence analysis of mitochondrial genes can reveal intraspecific or interspecific variations (Bucklin *et al.* 1995, 1998; Goetze 2003). The present study compares the morphological differences between the typical form of *L. rotunda* and the variants, and evaluates the validity of species assignment of morphological variants using two mitochondrial genes, 16S rRNA and cytochrome oxidase subunit I (mtCOI).

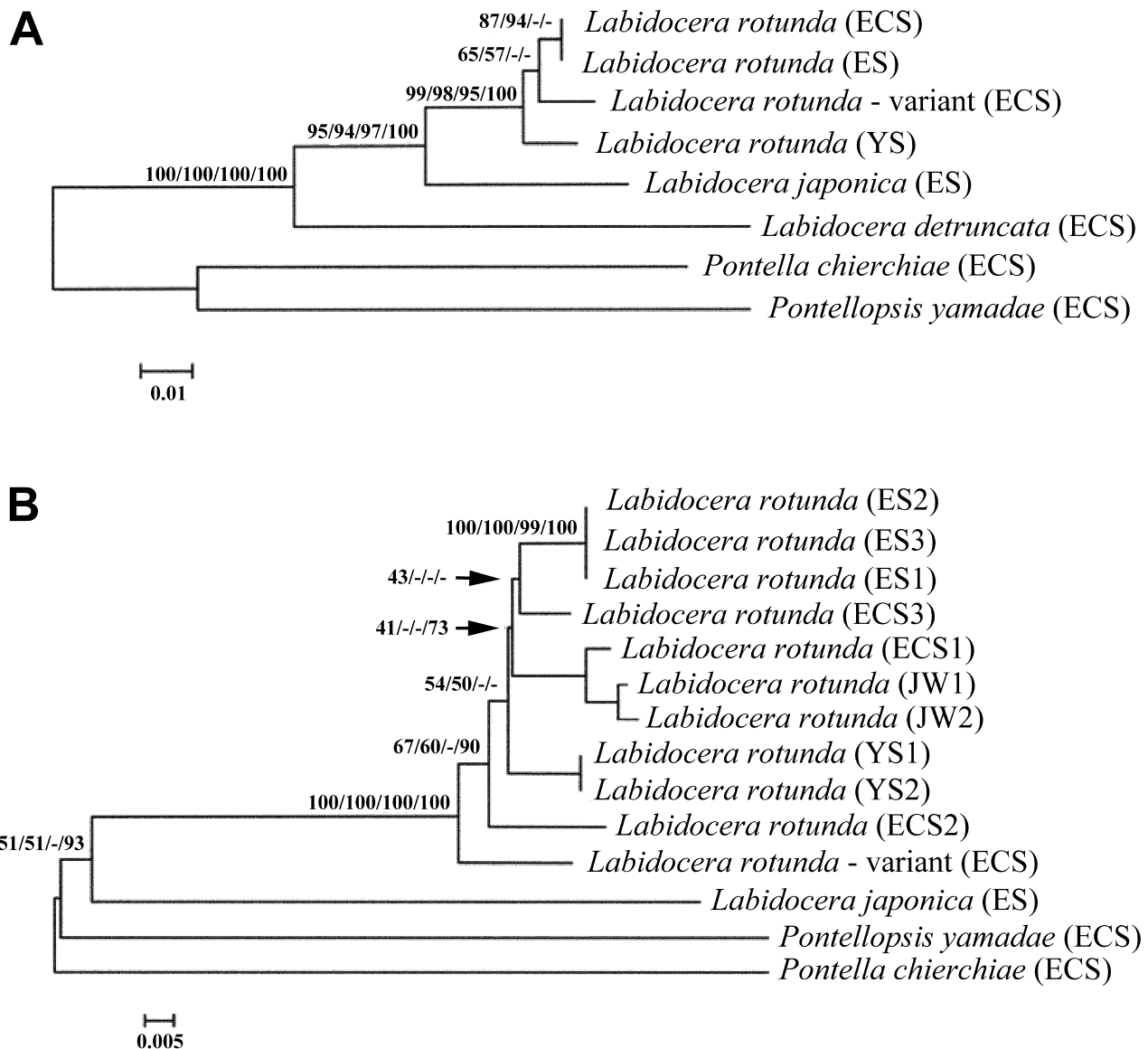


FIGURE 5. Cladograms for 16S rRNA (A) and mtCOI (B) between individual females of *Labidocera rotunda* and *L. japonica* based on NJ analysis. *Pontellopsis yamadae* and *Pontella chierchiae* are outgroups. Numbers at branch point indicate bootstrap values for NJ/ML/MP/BP analyses among 1000 pseudoreplicates.

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