

pure morphs was found in the two sampling areas. However, both pure morphs mated at random with the hybrid morph. A female hybrid sexual disadvantage also contributed to the incipient reproductive isolation between both pure morphs, but no such trend was found in males. The assortative mating behaviour and the female sexual selection components were probably caused by different biological phenomena.

These results confirm the conspecific status of the *L. saxatilis* Galician morphs, but also suggest the possibility of a further evolving towards complete speciation. The division of mating behaviour in three independent components represents a useful tool for the study of the reproductive isolation between incipient species.

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Phylogenetic reconstruction of the genus *Littorina* using mitochondrial DNA sequence data

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A gene phylogeny of eighteen of the nineteen known species of *Littorina* was reconstructed using sequence data from three mitochondrial genes (small ribosomal RNA gene, large ribosomal RNA gene and cytochrome *b* gene). Using the sister genus *Nodilittorina* as the outgroup, the monophyly of the genus *Littorina* was supported. The problematical species *L. striata* was resolved in a basal position within *Littorina*, supporting classification in this genus. Data from one species of the enigmatic tropical genus *Mainwaringia* showed that it was not closely related to *Littorina*. Within *Littorina*, the terminal pairings of *L. brevicula* and *L. mandshurica*, *L. squalida* and *L. littorea*, *L. sitkana* and *L. horikawai* were resolved, as was the monophyly of the species of the subgenus *Neritrema* in the Atlantic. However, the branching sequence in the middle region of the tree was poorly resolved, suggesting that perhaps a short period of rapid cladogenesis may have taken place at this point in the phylogenetic history of the group. The phylogenetic trees generated from the sequence data are consistent with a revised morphological cladogram for the genus (Reid, 1990a and in prep.). The molecular phylogeny shows that the northern Atlantic species were derived from a minimum of two Pacific ancestors, supporting the hypothesis of trans-Arctic migration of this genus (Reid, 1990b).

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Researches on the demecology of two species of Pacific *Littoraria* (Gastr. Pros.)

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