

Data from: To remain or leave: dispersal variation and its genetic consequences in benthic freshwater invertebrates

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Abstract

Variation in dispersal capacity may influence population genetic variation and relatedness of freshwater animals and hence provide insights on patterns and processes that influence biodiversity. The majority of studies addressing this issue have focused on dispersal variation in fish inhabiting riverine systems whose dendritic nature and upstream/downstream gradients facilitate characterizing populations along networks. We undertook extensive, large-scale investigations of two freshwater bryozoans species whose dispersive propagules (statoblasts) are either attached to surfaces (*Fredericella sultana*) or are released as buoyant stages (*Cristatella mucedo*). Characterizing population genetic structure in multiple sites within each of three (or four) UK regions enabled us to test hypotheses regarding how dispersal variation and hydrological connectivity impact genetic variation in colonial freshwater invertebrates that primarily inhabit lotic (*F. sultana*) or lentic (*C. mucedo*) habitats. We found that hydrological connectivity enhanced genetic diversity and gene flow in

and amongst *C. mucedo* populations but not in *F. sultana*. Higher overall measures of clonal diversity and greater genetic divergence suggest accumulation of genetic variation over time within *F. sultana* populations – perhaps reflecting constraints of releasing propagules that might eventually be swept to sea. Our study provides more nuanced views about drivers of population genetic structures in freshwater invertebrates and illustrates how a range of demographic and evolutionary processes reflect life history attributes. Growing evidence that genetic divergence may commonly characterise populations of a diversity of riverine taxa highlights how organisms inhabiting lotic systems may be particularly challenged by environmental change.

Usage Notes

Genotype datafiles for the manuscript "To remain or leave: dispersal variation and its genetic consequences in benthic freshwater invertebrates", Ruggeri Paolo, Pasternack Ellen, Okamura Beth

The Excel file contains two folders with monoclonal multilocus genotypes per individual at the 10 microsatellite loci typed. The first column indicates the sample ID. Names in the first row are referring to the names of the microsatellite loci here used. The last folder contains a summary of general information concerning the localities associated with the samples ID in the folders *C. mucedo* and *F. sultana*.

Dryad_CrisFred.xlsx

References

This dataset is supplement to <https://doi.org/10.1002/ece3.5656>

Location



Cumbria



United Kingdom



Greater Glasgow



Norfolk Broads



Northern Ireland

Keywords

gene flow, *Cristatella mucedo*, *Fredericella sultana*, Dispersal ability, Holocene, statoblasts, hydrological connectivity

Files

1 files for this dataset

Dryad_CrisFred.xlsx	90.08 kB	application/vnd.openxmlformats-officedocument.spreadsheetml.sheet
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