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 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

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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

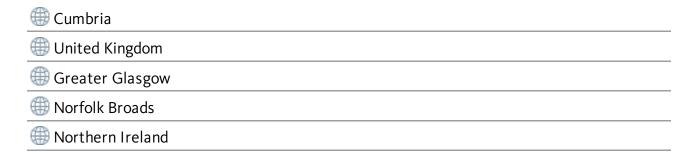
The Excel file contains two folders with monoclone multilocus genotypes per individual at the 10 microsatellite loci typed. The first column indicates the sample ID. Names in the first row are referring to the names of the microsatellite loci here used. The last folder contains a summary of general infomation 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



Keywords

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

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Files

1 files for this dataset

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

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