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Predicting shifts in the climate space of freshwater fishes in Great Britain due to climate change

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ABSTRACT

The implications of climate change for terrestrial and aquatic taxa are for their dispersal pole-wards and/ or to higher altitudes as they track their climate niches. Here, bioclimatic models are developed to predict how projected climate change scenarios for a northern temperate region (Great Britain) shift the climate spaces (i.e. areas of suitable thermal habitat) for 12 freshwater fishes of the Salmonidae, Percidae, Esocidae and Cyprinidae families. Climate envelope models developed in Biomod2 used the current species' distributions and their relationships with current climatic variables, and projected these onto the BCC-CSM1-1 and HadGEM2-AO climate change scenarios (low and high emissions, 2050 and 2070) in full and no dispersal scenarios. Substantial contractions in climate spaces were predicted for native salmonid fishes, with decreases of up to 78% for Atlantic salmon *Salmo salar*, with these largely unchanged between the dispersal scenarios. Conversely, for the majority of cyprinid fishes, expansions were predicted, including into northern regions where they are current not present biogeographically. Only under the no dispersal scenarios did their predicted distributions remain the same as their current distributions. For all non-salmonid species, the most important climate variables in the model predictions related to temperature; for salmonids, they were a combination of temperature and shifts in annual mean precipitation. As these predictions suggest that there is potential for considerable alterations to the climate spaces of freshwater fishes in Great Britain during this century then regulatory and mitigation conservation actions should be undertaken to minimise these.

1. Introduction

Freshwater environments and their fishes are especially sensitive to the effects of climate change as the persistence and quality of aquatic habitats are strongly reliant on climatic and hydrologic regimes (Morrongiello et al., 2011). The vulnerability of freshwater fish communities to altered climatic patterns is highlighted by their isolation and fragmentation within terrestrial landscapes that typically result in river basins acting as biogeographic islands (Fausch et al., 2002; Gozlan et al., 2010; Olden et al., 2011). This reliance on climate patterns for their thermal regimes and hydrology suggest that they will be particularly vulnerable to changes that result from the alterations in air temperatures and precipitation patterns that are projected to occur during this century (Johnson et al., 2009; Hobday and Lough, 2011).

The predicted effects of climate change on fishes are associated with their thermal tolerances (Rahel and Olden, 2008); where these are due to be either surpassed or optimised for species due to warming then range shifts and expansions can be expected (Graham and Harrod, 2009; Morrongiello et al., 2011; Comte and Grenouillet, 2013, Comte et al., 2013). The species-specific effects of temperature changes on distributions of freshwater fishes are a reflection of the interactions of their changing hydrological and thermal habitats with their physiological and life-history characteristics, and thus potentially result in considerable effects at the species level that will then affect patterns of freshwater biogeography at larger spatial scales (Heino et al., 2009). In general, climate change predictions for both terrestrial and aquatic taxa tend to be for movements pole-wards and/or to higher altitudes (Chen et al., 2011; Comte and Grenouillet, 2013; Holding et al., 2015), as species attempt to track their climate niches (Crimmins et al., 2011).

In predicting how climate change will alter the distribution of species, bioclimatic envelopes assess the responses of a species to current climatic conditions in order to predict how their distribution will then alter in projected future climate scenarios (Berry et al., 2002; Heikkinen et al., 2006). Bioclimatic envelopes assume that climate is the primary factor determining species' distributions, and that range shifts will occur promptly in response to climate change (Woodward and Beerling, 1997; Hampe, 2004). For freshwater fishes to track their climate niche then they must either be able to disperse through suitable corridors that connect their isolated habitats (Poff et al., 2002) or they will require some managed translocations, a continuing source of debate (e.g. Olden et al., 2010, 2011; Schwartz et al., 2012). Thus, the utility of bioclimatic models for the conservation management of freshwater fishes is arguably their identification of how the areas of

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suitable thermal habitat available to species (hereafter referred to as their climate space) will alter, highlighting the species and spatial areas of their existing ranges that are most vulnerable to the adverse effects of climate change (Staudt et al., 2013). The identification of the fishes and basins at most risk of alterations in their distribution of their species can then be prioritised for immediate management actions that should then provide the greatest long-term conservation benefits.

The aim of this study was thus to develop bioclimate models to predict how climate change could alter the available climate space for a range of freshwater fishes across a number of families with varying thermal preferences in a northern temperate region during this century (2050 and 2070). The model region was Great Britain, which has sufficient latitude, longitudinal and altitudinal ranges to provide marked differences in regional climates, and the model fishes were 12 species from across four families of varying thermal tolerances and with strong data on their presence/absence. It was predicted that the available climate space for each fish species would shift northwards under the modelled climate change scenarios, but the extent of the changes would vary at both species and family levels.

2. Materials and methods

The modelled fishes were from the families Salmonidae (*Salmo trutta*, *Salmo salar*), Percidae (*Perca fluviatilis*), Esocidae (*Esox lucius*) and Cyprinidae (*Cyprinus carpio*, *Carassius carassius*, *Scardinius erythrophthalmus*, *Rutilus rutilus*, *Squalius cephalus*, *Abramis brama*, *Leuciscus leuciscus* and *Gobio gobio*). For the latter five species of the Cyprinidae family, data were reported initially in Ruiz-Navarro et al. (2016). However, their model predictions are included here in order to provide comprehensive comparisons across the four fish families and to present some new results from the models. Where the data from in Ruiz-Navarro et al. (2016) for these five cyprinid fishes are used in the Results, this original source has been cited appropriately.

As the 12 fishes were selected on the basis of their conservation, recreational and/ or socio-economic importance, this meant that species without these interests, such as minnow *Phoxinus phoxinus* and stone loach *Barbatula barbatula*, were not modelled. The modelled fishes included species with preferences for relatively cold waters (<15 °C, e.g. *S. salar*, *S. trutta*), cool waters (≤20 °C, e.g. *R. rutilus*, *S. erythrophthalmus*) and relatively warm waters (>20 °C, e.g. *C. carpio*) (Rahel and Olden, 2008; www.Fishbase.org). Other than *C. carpio*, all of the modelled species have native ranges in Great Britain. Due to their non-native status, *C. carpio* would normally not be suitable for climate modelling using the methodology outlined below, as they do not have a natural biogeographic range in Great Britain. However, their introduction history means they are considered naturalised in parts of Britain (primarily England) and have attained a widespread distribution during the last 100 years that suggests they are now present in all regions that are climatically suitable for their persistence (Britton et al., 2010).

Within the bioclimate models, data on the occurrences of the fishes within Great Britain were obtained from the 'Database for the Atlas of Freshwater Fishes', provided by the Biological Records Centre, available at the NBN Gateway website (https://data.nbn.org.uk/Datasets/GA000174). The majority of the records ranged from 1950 to 2003 in the British National Grid spatial reference system (based on the 1936 Ordnance Survey Great Britain datum, OSGB_36) at a 10 × 10 km resolution. They represent an accumulation of the recordings of each species over time within these grid squares and so all of the data were utilised in the models. The British National Grid spatial references were then converted to the World Geodetic System WGS_84 grid system so that the occurrence data matched the available climatic data. Species absences were considered to be sampled locations in Great Britain where fish species other than the fishes were present in the 'Database for the Atlas of Freshwater Fishes', i.e. squares that have not been visited by fish recorders were not considered for use in the modelling (Ruiz-Navarro et al., 2016).

The climate data utilised baseline (1950–2000) and future global projections of climate data (annual values) obtained from the WorldClim website (http://www.worldclim.org/, Hijmans et al., 2005), version 1.4 (release 3), at a 5-min resolution in the WGS_84 grid system. Climate projections for the years 2050 and 2070, under low (rcp 2.6) and high (rcp 8.5) emission scenarios were obtained from two different climate prediction models: BCC-CSM1-1 and HadGEM2-AO. BCC-CSM1-1 was produced by the Beijing Climate Center, China Meteorological Administration, whereas the Hadley Centre of the Meteorological Office of the UK produced HadGEM2-AO. The use of projections from both climate models thus provides 8 climate change scenarios for application to the bioclimate models and so a wider range of modelled scenarios than if only one climate model was used.

A 'UK outline polygon', obtained from the OS Opendata website (https://www.ordnancesurvey.co.uk/opendatadownload/products.html), was used to clip the climatic data to the area of Great Britain. The 19 climatic variables available, derived from the monthly temperature and rainfall values, were reduced to six through analysis of their correlations so that only variables with low pairwise correlations were used in the models (Dormann et al., 2013). This was completed through use of Pearson's correlation coefficient, with a threshold of $r = 0.70$ used to remove highly correlated variables from the climate data set (Ruiz-Navarro et al., 2016). As a result, the climatic variables used were: annual mean temperature (°C), mean diurnal range of temperature (°C), isothermality (100 $*$ (mean diurnal range / annual range of temperature)), mean temperature of wettest quarter (°C), mean temperature of driest quarter (°C), and annual precipitation (mm). The rationale for retaining these variables rather than their correlates was because they represent the two primary properties of the climate, energy and water that tend to be physiologically limiting factors for aspects of the biology and ecology of ectotherms, such as fish (Chu et al., 2005). It is, however, acknowledged that these climate variables are not the only determinants of fish distribution (Pont et al., 2006), with a range of other abiotic and biotic variables also often being important parameters that it was not possible to model here (Ruiz-Navarro et al., 2016).

Fish species distributions in Great Britain were modelled using seven algorithms available in the *biomod2* package (Thuiller et al., 2014) in R: (1) generalized linear models (GLM), (2) generalized additive models (GAM), (3) multivariate adaptive regression splines (MARS), (4) classification tree analysis (CTA), (5) boosted regression trees (BRT), (6) random forests (RF), and (7) artificial neural networks. In all models, the default options of *biomod2* were selected, with the exception of restricting the GAM smoothing to 4 knots to avoid over-fitting the data. Evaluation of the models was through the area under the ROC curve (AUC), using an 80:20 split of training to test data and 50 evaluation repetitions. AUC values range between 0 and 1, where 1 indicates excellent model performance and values lower than 0.5 indicate predictive discrimination that is no better than a random guess (Ruiz-Navarro et al., 2016). Marmion et al. (2009) outlined that the usefulness and accuracy of bioclimate models for conservation, i.e. their robustness, were improved when 'consensus' models were used, i.e. ensemble models. This was because ensemble models overcome the variability of predictions that can occur between single models. Thus, ensemble models were created in *biomod2* by weighting the single models by their AUC score, with only single models that had individual AUC evaluation scores of ≥0.7 included in the calculation. Where a single model had an AUC evaluation score below this then it would be excluded from the ensemble.

For the ensemble model of each species, the importance of the included climate predictors (i.e. annual mean temperature, mean diurnal range of temperature, isothermality, mean temperature of wettest quarter, mean temperature of driest quarter and annual precipitation) were then determined using the variables importance function, with the importance values converted to proportions (%) to facilitate their interpretation. These were run 10 times per species, with their mean (± SE) calculated.