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Assessment of future habitat suitability and ecological vulnerability of *Collichthys* at population and species level

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Abstract

Background Global warming and extreme weather events driven by greenhouse gas emissions are significantly impacting fish survival and reproduction, leading to dramatic consequences for marine biodiversity and ecosystem stability. Comparative analysis of closely related species from a phylogenetic perspective provides valuable insights for biodiversity conservation efforts. The study investigates the effects of climate change on the suitability of habitat and ecological vulnerability of two important sibling fishes, *Collichthys lucidus* and *Collichthys niveatus*, in the western Pacific.

Results This study found that the main driver of ecological niche differences between the two species is the niche contraction of *C. niveatus*. Predictions from species distribution models indicate that *C. lucidus* has a wider distribution and greater adaptability under future climate scenarios. Both species will experience significant habitat loss and heightened ecological vulnerability in the southern Yellow Sea. Additionally, the two populations of *C. lucidus* in the Yangtze River estuary display different levels of ecological vulnerability. These two species also exhibit distinct responses to environmental factors such as temperature and chlorophyll concentration.

Conclusion The study's findings indicate that climate change will accelerate the population differentiation of *C. lucidus* and the habitat loss of *C. niveatus*. These results underscore the importance of prioritizing the southern Yellow Sea in future research and emphasize the necessity of developing adaptive conservation strategies for both species.

Keywords Habitat suitability, Environmental change, Population differentiation, Marine ecology, Local adaptation, *Collichthys lucidus*, *Collichthys niveatus*

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Background

Since the Industrial Revolution, greenhouse gas emissions from human activities have led to a significant rise in global temperatures, causing extreme weather events, including ocean heatwaves and the La Niña phenomenon [1, 2]. Uneven heat distribution causes changes in the global wind field, disrupting ocean circulation [3]. Additionally, the dissolution of excess carbon dioxide in the oceans leads to seawater acidification, altering the original environmental conditions [4]. These climate changes are reducing biodiversity and ecosystem stability in marine ecosystems [5]. An increasing number of studies have demonstrated that climate change poses significant survival challenges to marine fish by accelerating habitat loss and migration [6].

Fish are extensively involved in nutrient cycling in the oceans and have indispensable ecological significance and great economic value for fisheries [7]. Most fish species demonstrate an adaptive capacity to respond to habitat shifts induced by climate change through migration to deeper ocean waters or higher latitudes [8, 9]. These migrations not only reflect the flexibility of fish, but also emphasize the significant impact of climate change on marine biodiversity. Fish responses to climate change depend on their unique evolutionary traits. The study showed that Indo-Pacific fishes with shorter life are more sensitive to temperature changes [10]. Even within a species, different populations may respond to climate change differently due to local adaptations [11]. These responses may emphasize the importance of incorporating a phylogenetic perspective into biodiversity conservation under changing climatic conditions.

Species Distribution Models (SDMs), also known as ecological niche models, are statistical models that establish the relationship between species occurrence data and environmental factors in their habitats [12]. They have been widely used in the study of species' response to climate change [13]. SDMs are based on the hypothesis of ecological niche conservatism, which assumes that species tend to persist and spread in their original or similar habitats [14]. By analyzing the relationship between geographic and environmental data, SDMs can identify the ecological niches of species and analyze their habitat preferences. Projecting such ecological niches into current or future climate scenarios can help assess the habitat suitability and ecological vulnerability of species under future conditions [15, 16]. For example, Shin et al. used SDMs to predict significant habitat loss and range shifts for the Korean clawed salamander due to climate change, highlighting the model's role in guiding conservation strategies [17]. In addition, SDMs are widely used in assessing ecological vulnerability because they quantify the changes in habitat suitability caused by various environmental stressors [18]. Analyzing ecological vulnerability can improve our understanding of the mechanisms by which species respond to future climate change. However, species-level SDMs are insufficient to capture habitat-specific adaptive traits and the climate vulnerability of populations within a species [19]. Bayliss et al. demonstrated that incorporating genetic structure into modeling enables population-level SDMs to provide a more detailed understanding of population distribution changes [20]. This approach aids in identifying the coping strategies of populations within a species in response to climate change. It also enhances understanding of the relationships between species and their environments [21]. This leads to more accurate predictions of suitable habitats and aids in identifying climate-sensitive areas [22].

The genus *Collichthys* consists of two sibling species [23], *Collichthys lucidus* and *Collichthys niveatus.* About 5 million years ago, the two species began to diverge, but still have similar morphological characteristics [24], suggesting potential similarities and differences in their ecological niches and environmental adaptations. Their natural distributions are different: *C. niveatus* is only found in the Yellow and Bohai Seas, while *C. lucidus* is widely distributed in the Yellow and Bohai Seas, the East China Sea and the South China Sea [25]. Serving as bait for many commercially important fish species, *Collichthys* plays a crucial role in the marine ecosystem's food chain [26]. Ecological niche divergence arises from a complex interplay of factors, including differences in resource allocation, competitive pressures, species interactions, and environmental gradients [27]. Together, these factors drive species to occupy different ecological niches in ecosystems, thus contributing to ecosystem diversity and stability. By comparing their ecological niche differentiation, this analysis enhances our understanding of the evolutionary processes and interspecific relationships of these two species. In addition, *C. lucidus*, widely distributed across three climatic zones—tropical, subtropical, and temperate—exhibits significant genetic differences between northern and southern populations, as identified through various molecular markers by Song et al. [28]. This means that significant differences in environmental factors between the northern and southern seas have led to the formation of adaptive evolutionary patterns in different geographic populations of *C. lucidus*. Understanding the differences in distribution patterns and population differentiation is important for further understanding the habitat adaptation and ecological vulnerability of various populations in the face of future climate change. This knowledge enables the implementation of more accurate conservation and development measures.

In this study, the climatic risks faced by two offshore fish species were assessed, and potential adaptations to changing environmental conditions were explored. Initially, ecological niche differences between the two species, as well as between the northern and southern populations of *C. lucidus*, were compared, along with an analysis of the climatic factors contributing to these differences. Next, the effects of climatic and environmental factors on habitat suitability and ecological vulnerability were examined. Finally, areas where both species are expected to experience significant changes in habitat suitability and ecological vulnerability under future climate scenarios were identified, leading to the proposal of targeted conservation strategies.

Methods

Data collection and processing

Occurrence and environmental data for the modeling were obtained from publicly available databases. Occurrence data for both species were collected from the Global Biodiversity Information Facility (GBIF), Ocean Biodiversity Information System (OBIS), and other literature (Table S1). To ensure data accuracy, the occurrence data were cleaned to remove errors, duplicates, and missing records. Secondly, the R package *spThin*(v0.2.0) was used to ensure only one record in each 5×5 arc-minute grid (~ 9.2 km × 9.2 km) to reduce the risk of overfitting caused by occurrence data. Finally, the study area was defined based on the analysis of the thinned occurrence data for both species. Population differences were not observed in *C. niveatus* (CN). However, existing evidence suggests that *C. lucidus* (CL) is differentiated into two populations [29]. Therefore, *C. lucidus* was divided into two populations based on the vicinity of Wenzhou (about 28°N): the northern population (CLN) and the southern population (CLS), for subsequent analysis.

Current and future environmental data for the two fishes were obtained from bio-ORACLE (V2.2) and GMED, including 16 candidate environmental variables potentially affecting their distribution (Table S2). For future projections, we considered two time periods: 2040–2050 (denoted as 2050) and 2090–2100 (denoted as 2100), under two climate scenarios: RCP2.6 and RCP8.5. These scenarios represent greenhouse gas concentrations ranging from low (optimistic emission levels) to high (pessimistic emission levels) [30]. Environmental variables were rasterized, cropped to the latitudinal and longitudinal ranges of corrected occurrence data and resampled to a 5×5 arcminutes resolution using the bilinear interpolation method. To minimize potential bias caused by high covariance between variables, the values of the corresponding environmental variables were extracted using the latitude and longitude of the occurrence data. Pearson correlation coefficients were calculated for each pair of variables [31]. If the correlation coefficient between two variables exceeded |0.7|, the less important one was excluded. In this study, water depth and distance from shore were assumed to remain constant over time. Ultimately, the filtered environmental variables were used for subsequent ecological niche comparison and modeling analysis.

Ecological niche comparison

Using filtered environmental variables and corrected occurrence data, we compared the ecological niches of two fish species and the two populations of CL. The corresponding values for each selected environmental variable were extracted based on the latitude and longitude of the occurrence data, resulting in three sets of seven-dimensional variables (with each environmental factor representing one dimension). We then employed principal component analysis (PCA) to reduce the dimensionality of the environmental variables and analyze the ecological niches. To capture the most important information from the multidimensional environmental data, we calculated the cumulative variance of the seven components and retained the first few that explained more than 80% of the total variance [32]. Subsequently, hypervolumes were constructed for each group using the R package *hypervolume* to measure the size of the ecological niche in multidimensional space [33]. Ecological niche differentiation within the two groups was assessed using the R package *BAT* [34]. Niche differentiation (βtotal) consists of two components: niche shift and niche contraction/expansion, with values ranging from 0 to 1, representing complete overlap to complete separation. The proportion of each component in βtotal indicates its contribution to niche differentiation. The shift refers to the change in the position occupied by a species in an ecological space. While contraction/expansion emphasizes changes in the extent of ecological niches, indicating that the niches of a species become narrower or wider in certain dimensions [35]. Additionally, the composition of the first four principal components was analyzed to explore the specific environmental variables affecting ecological niche differentiation.

Species distribution modeling

The R package *Biomod2* (v3.5.1) was employed to construct SDMs [36]. Only individual models with superior performance were used to construct the ensemble model. The remaining models were used to build the ensemble model. In the modeling process, the presence-absence matrix and seven environmental variables were used to construct ensemble models for CN, CLS, and CLN, and map them onto current and future climate scenarios. In the study area, 10,000 pseudo-absence points were randomly generated to better capture the potential distribution and environmental response of fish species. A presence-absence matrix was obtained by combining these data with the corrected occurrence data, which served as the occurrence data used in the modeling. Based on this matrix and the selected environmental variables, ten algorithms from *Biomod2* were individually applied to construct SDMs, with each algorithm repeated ten times to minimize the effects of chance. Model performance was tested using the 5-fold cross-validation method, where the data were split into a calibration (80%) and a validation (20%) dataset [37]. The True Skill Statistic (TSS) and Area Under the Curve (AUC) were used as metrics for evaluating individual and ensemble models [38]. Models were considered to have satisfactory performance with TSS > 0.7 and AUC > 0.8, which were the criteria for constructing the ensemble model. To reduce bias from varying model performances, a weighted average algorithm was employed to build the ensemble model. Additionally, the Continuous Boyce Index (CBI) was used as a complementary performance indicator for the ensemble model. The CBI is a threshold-independent indicator that ranges from −1 to 1, with higher values indicating better consistency between model predictions and the test dataset distribution [39]. After constructing the ensemble models, the relative importance of environmental variables was assessed by randomization. As part of the integrative ecological analysis, response curves for the four most important environmental variables were examined to explore the specific ecological niche requirements of species and populations in greater detail.

Habitat suitability and ecological vulnerability

Three ensemble models (CN, CLN, CLS) were mapped to current and future (2050 and 2100) climate scenarios to visualize their habitat suitability and ecological vulnerability under long-term climate change. To reduce climate model bias, variables were averaged across four climate models: the ESM4 model (Geophysical Fluid Dynamics Laboratory), CSEM2-WACCM model (National Center for Atmospheric Research), NorESM2-LM model (Norwegian Climate Consortium), and ESM1-2-HR model (Max Planck Institute). The maximum suitability change for the two fish species under future climate change was examined at both species and population levels. Additionally, two climate scenarios, RCP2.6 and RCP8.5, were used to represent the most optimistic and pessimistic outcomes, respectively. Habitat suitability and ecological vulnerability of the two *C. lucidus* populations in their respective regions (separated at 28°N) were calculated separately to achieve a population-level evaluation. To assess potential overlap between the two populations under future climate scenarios, we overlaid their binary distributions (presence/absence). The methods used to calculate ecological vulnerability were consistent with those employed by Rémi Tournebize et al. [22]:

$$\mathrm{V}_E = S_{\text{present}} - S_{\text{fiture}}$$

Where $S_{present}$ and S_{future} represent suitability under current and future climate scenarios, respectively. When the V_E value is positive, it indicates that habitat suitability will decrease in the future. Conversely, when V_E is negative, it indicates that habitat suitability will increase in the future, and that the species is likely to experience better survival in this region.

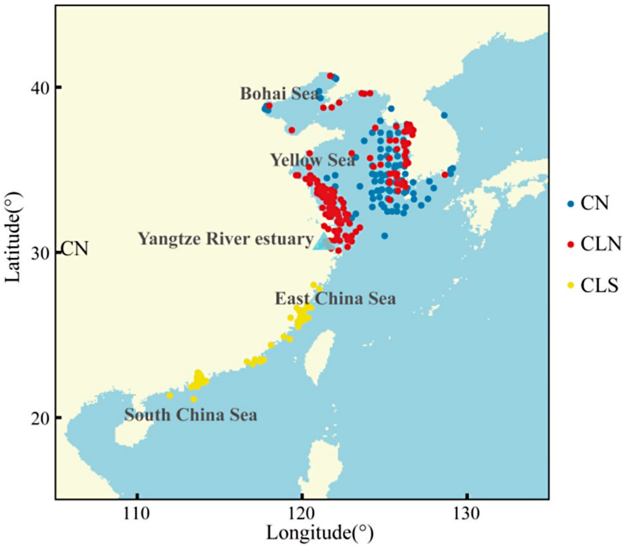

Fig. 1 The occurrence records of *C. niveatus* (CN) and two population of *C. lucidus*(CLS, CLN). The triangle represents the location of Yangtze River estuary

Results

Ecological niches comparison

We compared the fundamental ecological niche differences among CN, CL, and CLN, CLS. For their corrected occurrence data in the study area (105 ° E-135 ° E and 15 ° N-45 ° N), 125, 126, and 58 true occurrence records were obtained, respectively (Fig. 1). Seven environmental variables for ecological niches comparison and modeling were ultimately selected: mean temperature, depth, mean chlorophyll concentration, mean salinity, offshore distance, minimum dissolved oxygen concentration, and mean flow velocity (Fig. S1). The first four principal components explained 90.3% of the variation in ecological niche comparisons for CL and CN, and 87% for CLS and CLN (Fig. S2). The four-dimensional hypervolume of CL (2150.24) was significantly larger than that of CN (569.05), implying that the ecological niche of CL is larger and essentially encompasses that of CN (Fig. 2a). The ecological niche difference between them was primarily caused by the contraction/expansion of their ecological niches, contributing 96.40% to βtotal (Table S3). The difference in center of mass position between the two hypervolumes was mainly along PC1, which consisted

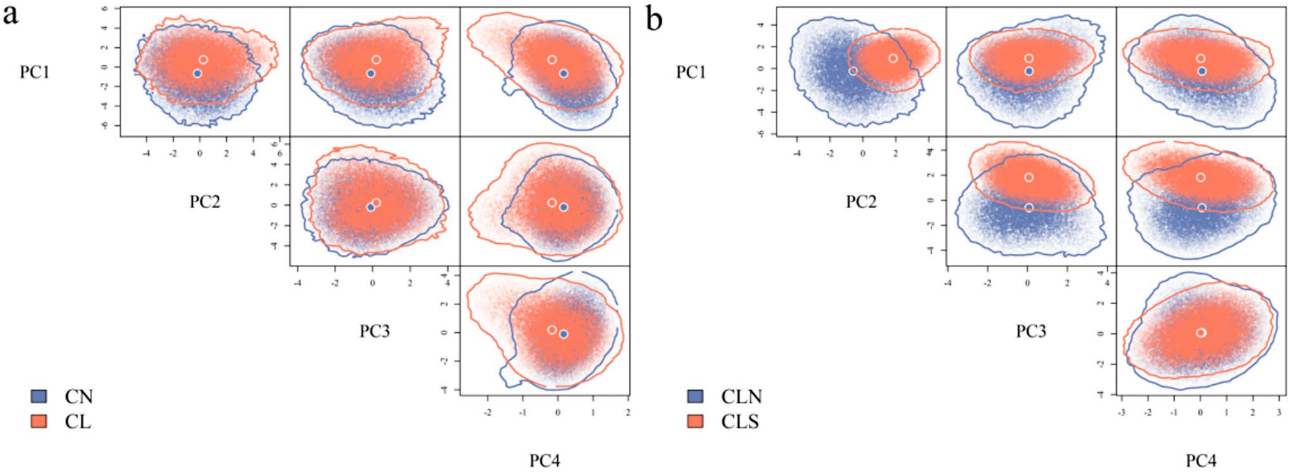

Fig. 2 Ecological niche comparisons. (**a**) The niches of CL and CN, (**b**) the niches of *C. lucidus* within CLS and CLN

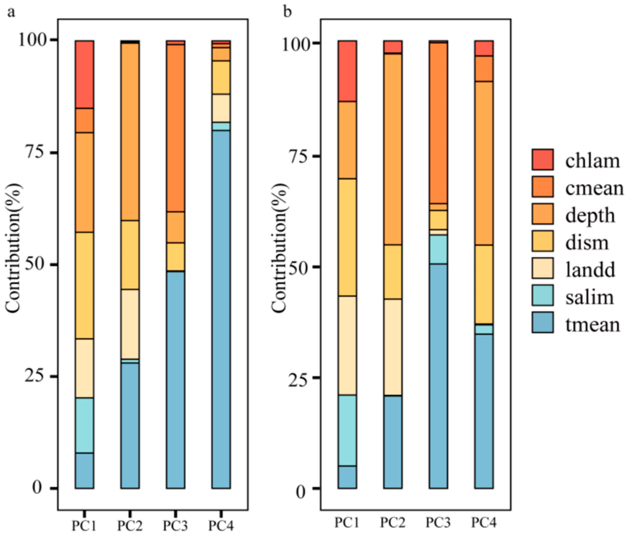

Fig. 3 Environmental factors contributing to the first four principal components (PC1-PC4) in PCA: (**a**) for CL and CN; (**b**) for CLS and CLN, and colors represent different factors

mainly of mean temperature, mean chlorophyll concentration, and minimum dissolved oxygen. For the two CL populations, the ecological niche of CLN (711.93) was larger than that of CLS (374.11), and the centers of mass of the hypervolumes also indicated a significant difference in their ecological niches. This difference between the two populations was not only due to the contraction/expansion of the ecological niches (55.53%), but also due to shift (44.47%). The distance between the centers of mass of their ecological niches was mainly attributed to PC2, which is composed mainly of depth, offshore distance, and mean temperature and minimum dissolved oxygen (Fig. 3b).

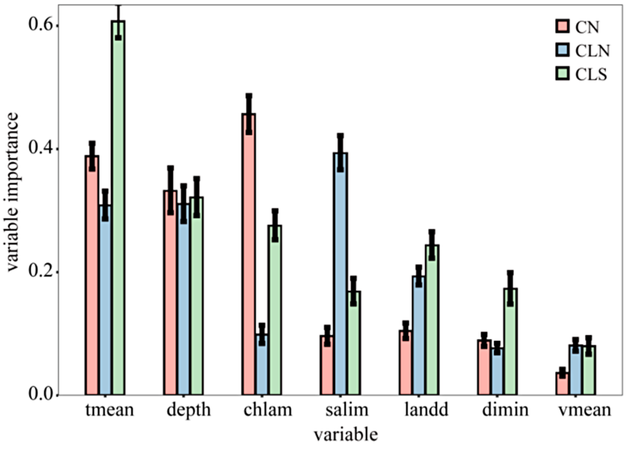

Fig. 4 The relative importance of seven environmental variables for SDMs of CLN, CLS and CN

SDMs prediction and climate response

The Surface Range Envelope (SRE) and Maximum Entropy (MaxEnt) models were excluded, and the remaining algorithms were used to build the ensemble model (Fig. S3). The ensemble models had high TSS (CN: 0.949, CLS: 0.951, CLN: 0.962) and CBI values (CN: 0.992, CLN: 0.981, and CLS: 0.987), which indicated that the three ensemble models had good performance.

We also obtained the relative importance of the seven variables from ensemble models. These results indicated that mean temperature and depth were highly important for these models. Additionally, mean chlorophyll concentration was more important for CLS and CN than for CLN. In contrast, mean salinity was more crucial for CN (Fig. 4). We also plotted climate response curves for the first four important environmental variables (mean temperature, depth, mean chlorophyll concentration, and mean salinity) (Fig. 5). Compared to CLS, CLN and CN were more adapted to the temperature range of 0 to 5 °C but they were less adapted to high temperatures (20

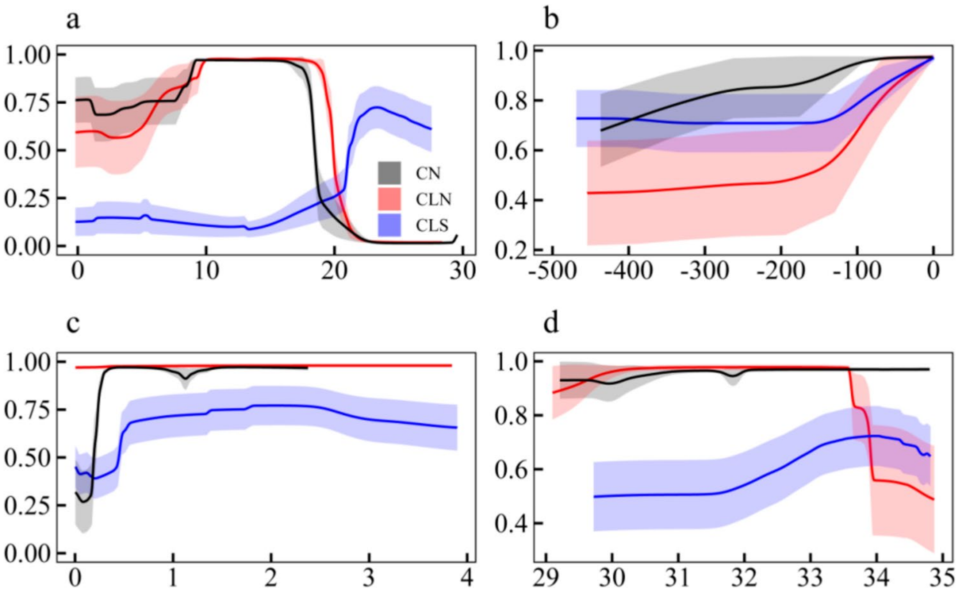

Fig. 5 Response curves for environmental factors of CN, CLN and CLS: (**a**) mean temperature(℃); (**b**) depth(m); (**c**) mean concentration of chlorophyll(mmol/m^3); and (**d**) mean salinity(PSS). The Y-axis represents the probability of species' occurrence under specific environmental conditions

to 30 °C) (Fig. 5a). They all showed a strong preference for habitats with water depths ranging from 0 to 100 m (Fig. 5b). CLN and CN clearly preferred environments with higher chlorophyll concentrations (Fig. 5c). CN, in contrast, was less sensitive to changes in mean salinity than the two CL populations (Fig. 5d).

Habitat suitability and ecological vulnerability

Ensemble modeling showed that the two species differed significantly in their potential ranges, with CN concentrated in the Bohai Sea, Yellow Sea, and southern Korean waters, while CL was widely distributed in the Bohai Sea, Yellow Sea, and the East and South China Sea (Figs. 6a and 7a). Both species showed different degrees of decreased suitability under different future climate scenarios; CN's habitat was reduced by 10.7–36.1% and its distribution area in the Yellow Sea would gradually contract from south to north. Its habitat in the Bohai Sea tended to fragment and its future habitat would be further reduced (Fig. 6b-e), especially under the RCP8.5 scenario in 2100 (36.1% reduction).

The results of the ensemble model also indicated that CLN and CLS do not overlap in their binary distribution (Fig. S4). Therefore, the habitat suitability and ecological vulnerability of both populations under the same scenario are presented in the same plot (Fig. 7a-i). Compared to CN, the change in habitat suitability of CL showed the same trend, but the change was relatively slight (1.2–13.1% reduction). Only the 2100 RCP8.5 scenario showed a more significant reduction (13.1% reduction). They showed strong adaptations (except for 2100 RCP8.5) in their main distribution areas, e.g., the Yellow Sea and the coastal waters of the East China Sea. We also found that both species showed high ecological vulnerability in the southern Yellow Sea (Figs. 6 and 7f-i). In specific areas, such as the Yangtze River estuary, the two species showed large differences in habitat suitability and climate vulnerability, with CL showing an increase in the 2050RCP2.6, 2050RCP8.5, and 2100RCP8.5 scenarios (Fig. 6f-i), while CN showed a decrease in all of them. Within CL, the northern and southern populations showed opposite adaptive changes and ecological vulnerability in the Yangtze estuary.

Discussion

Interspecific differences

The two species may have become reproductively isolated about 5.5 million years ago [28], but they still show similarities in their basic ecological niches. Joint studies of these two fishes can provide a comprehensive understanding of their different responses to future climate change and provide a theoretical basis for the sustainable development and conservation of fishery resources from a phylogenetic perspective.

Since they mainly inhabit near-shore and estuarine waters, their habitat is particularly affected by changes in water level caused by tidal fluctuations [40], and all seven environmental variables contribute to PC1 to varying degrees. Among these factors, chlorophyll concentration may influence the ecological niche by affecting the availability of food sources. Since food availability is likely a significant factor shaping the fundamental niche of species, it could in turn influence their distribution, survival, and reproduction, as well as energy balance, interspecies

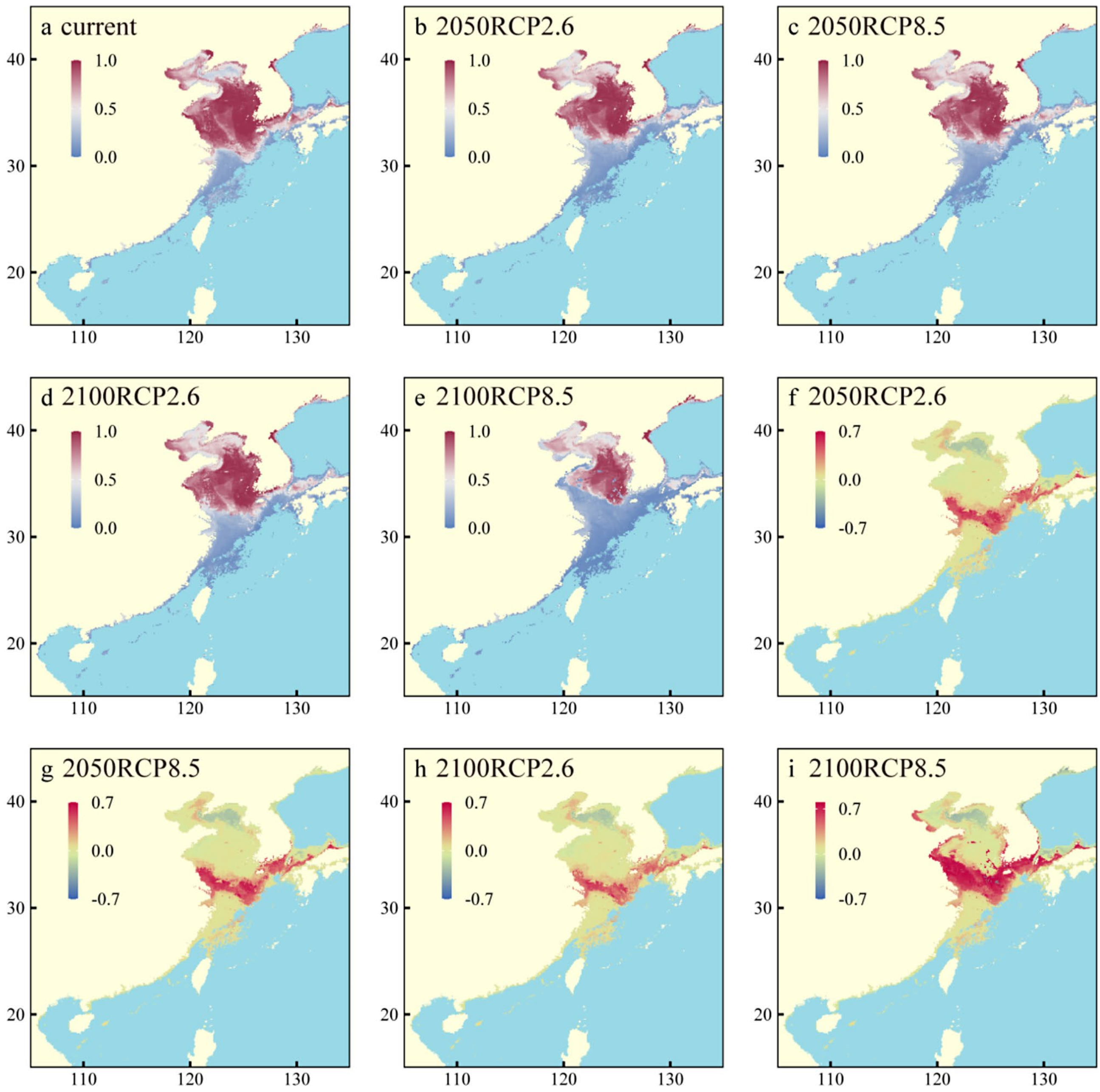

Fig. 6 Spatial analysis for the potential distribution and ecological vulnerability of *C. niveatus* under present and future climates, the current distribution(**a**); (**b**-**e**) for the distribution of future climate scenarios; (**f**-**i**) for ecological vulnerability of future climate scenarios

interactions, and adaptive behaviors within the ecosystem. As two species of secondary consumers feeding on small aquatic animals such as copepods [41], a wider ecological niche facilitates CL's access to more food, giving it an advantage in the interspecific competition with CN.

By comparing the ecological niches and distribution ranges of the two species, we tentatively concluded that the main reason for the difference in their ecological niches after differentiation was the contraction of CN's ecological niche. The spatial overlap between two species in the Bohai and Yellow Seas is mainly caused by CLN, which is widely distributed throughout the Bohai and Yellow Seas, whereas CLN is mainly distributed closer to land, reducing the intensity of interspecific competition to some extent. This difference in distribution causes CLN and CN to exhibit different patterns in their responses to environmental factors. The lower mean salinity and greater day-night temperature fluctuations in nearshore waters allow CLN to exhibit not only higher sensitivity to salinity changes, but also a broader range of temperature suitability. Compared to CN, CLN's greater temperature suitability facilitates its adaptation to

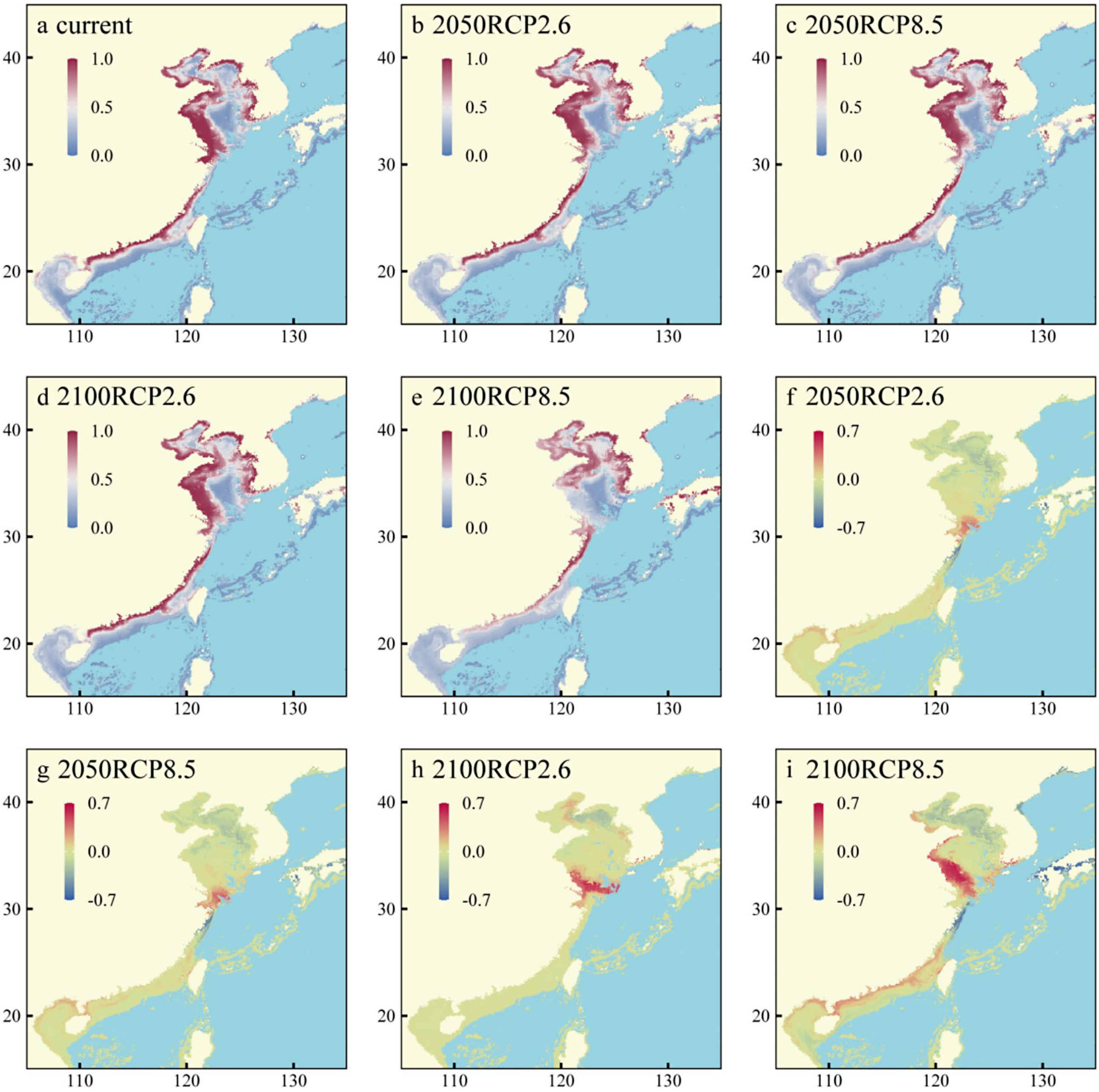

Fig. 7 Spatial analysis for the potential distribution and ecological vulnerability of *C. lucidus* under present and future climates, the current distribution (**a**); (**b**-**e**) for the distribution of future climate scenarios; (**f**-**i**) for ecological vulnerability of future climate scenarios

future climate scenarios, resulting in lower habitat suitability change and higher ecological vulnerability. It is worth noting, however, that this does not mean that habitat adaptation of CLN in the future can be overlooked. Under the 2100 RCP8.5 scenario, CLN similarly experienced greater habitat loss and higher climate vulnerability. This implies that habitat adaptations of both species require long-term attention under high-intensity climate change. In addition, the trend of population differentiation in CL will become more pronounced with climate change. This suggests that the species' distribution range should be considered when studying the effects of climate change. A wider distribution range can lead to potential population differentiation and local adaptation, which may improve the suitability of species in response to climate change. For CN, concentrated distribution range and future habitat adaptation suggest that significant population differentiation may not occur.

Despite the significance of SDMs in conservation and management studies, their limitations should be acknowledged. Due to the lack of additional occurrence data, the ensemble models may not fully capture the associations with habitat environments, potentially leading to discrepancies between the model predictions and the actual future distributions of the two fish species. Therefore, it is essential to interpret the results of SDMs with caution, and to fully consider other information and methods when developing conservation and management strategies. As demonstrated by Anna Tigano et al. (2023) [42], predictions of vulnerability to future climate change at the population or species level can be improved by combining species distribution models with genomic data. The same research approach can be applied to CL and CN to clarify how climate change affects habitat adaptation by influencing the frequency of adaptive genetic loci. This method not only allows the prediction of potential impacts of future environmental changes on these species but also provides a scientific basis for developing responses to the challenges posed by climate change [43]. Although it was hypothesized that both fish species would migrate to deeper oceans to adapt to future climate change, a hypothesis that was confirmed by Fuchs et al. in their study of larval migration in benthic species [44]. Uncertainty remains due to the lack of depth information in the occurrence data, preventing certainty about two species' migration to more appropriate depths.

Intraspecific variation of *C. lucidus*

Species-level SDMs consider species as a whole and, for widely distributed species, can only provide information on their approximate adaptive ranges. They overlook much detailed information about their local environmental adaptations. Considering that, they do not fully reflect the various population dynamics. Using RAD-seq, it was demonstrated that two well-identified population divisions exist in CL [45]. Comparison results show that the significant niche differences between these two CL populations are caused by niche contraction/expansion and migration. The Chinese offshore was drastically affected by climate change during the Quaternary Ice Age, when the sea level drop during the glacial maximum made the continental shelves of the Bohai, Yellow and East China Seas almost entirely land [46]. The divergence of the two populations was accelerated during this period (19,000 to 26,000 years ago), shaping the present-day distribution pattern [29]. The potential distribution of CLS is closer to the shore(Fig. S5). Compared to deeper waters, the environmental conditions near the shore, such as salinity and temperature, fluctuate more dramatically [47]. Since the potential distribution of CLS is mainly located in these areas, it exhibits better adaptability to environmental changes, leading to lower ecological vulnerability in the face of future climate change.

In addition, the distribution of CLS and CLN will migrate northward in response to the changes in marine environment caused by climate change. However, the differing ecological vulnerability of two CL populations in the waters north of the Yangtze River and south of the Yellow Sea demonstrates their different responses to climate change. CLS was able to acquire new habitats to offset habitat loss in the South China Sea in response to future climatic changes due to its good adaptation to high temperatures, whereas the CLN faced extensive habitat loss in this area. Such differences should be further investigated in conjunction with genotype-environment association analysis (GEA) to identify genes associated with climate adaptation. Gene flows associated with the northward migration of CLS may enhance the future climate adaptation of CLN, but the northward migration of CLN may create barriers to it, and we believe that populations in this region should be monitored in future studies. This will not only provide valuable insights for studying ecosystem changes and assessing biological resources in the waters near the Yangtze River estuary, but also further explore the potential for mutual rescue among populations in different distribution areas under climate change.

Fisheries resource management and development

The two species of *Collichthys* are not only small economically important fish, but also serve as important baits for many large marine species, and have important ecological and economic value [48]. Fish resources in the Yangtze River estuary are currently being overexploited [49]. Additionally, our study identified potential habitat loss for these two species in the southern waters of the Yellow Sea under future climate scenarios. These findings emphasize the urgency of implementing priority conservation measures in this area. We recommend that the fishing ban in this area be extended appropriately in response to their declining suitability under climate change. Furthermore, the Bohai and Yellow Seas are important habitats for these two species, but they have been severely impacted by anthropogenic factors such as pollution and overfishing activities [50]. The differences in ecological vulnerability between the two CL populations in the Yangtze River estuary make this region a hotspot for studying its population dynamics. We believe that further investigation into population structure, gene flow, and genetic vulnerability is necessary to assess the adaptation of different populations to future climate conditions, in order to develop targeted management measures. This will provide a scientific basis for further ex-situ breeding and reintroduction, enhancing the habitat adaptability of different populations. Of course, in order to prevent the potential biological invasions and impact on the ecological structure caused by those measures, it is also necessary to study the feeding habits and life history traits of different populations.

Conclusion

In summary, this study represents the first consideration of two *Collichthys* species together to assess the potential impact of climate on their distribution. The findings revealed that population-level SDMs offer more detailed insights into population dynamics for widely distributed species, highlighting the importance of using different levels of SDMs for species with varying distribution ranges in predicting outcomes. The comparison of prediction results for the two fish species demonstrated significant similarity in their ecological niches, indicating a common trend of habitat adaptation in the southern Yellow Sea. Furthermore, the population-level analysis of CL indicated that the Yangtze River estuary waters should receive more attention in the study of inter-population gene flows and rescue potential. Therefore, specific conservation and management strategies are recommended to protect areas with elevated climate vulnerability, ensuring the sustainable use of both fish species.

Abbreviations

SDMs	Species Distribution Models
GBIF	Global Biodiversity Information Facility
OBIS	Ocean Biodiversity Information System
CN	Collichthys lucidus
CL	Collichthys niveatus
CLN	the northern population of C. lucidus
CLS	the southern population of C. lucidus
TSS	True Skill Statistic values
AUC	Area Under the Curve
CBI	Continuous Boyce Index
PCA	Principal component analysis
chalm	mean chlorophyll concentration
cmean	mean current velocity
depth	the depth of ocean
dism	the mean dissolved oxygen concentration
landd	the offshore distance
salim	the mean salinity
tmean	the mean water temperature

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12862-024-02339-7.

Supplementary Material 1: Supplementary Figure 1 The figure illustrates the correlation coefficients for each pair of 16 environmental variables, employing '***X***' to mark cases where the p-value surpasses 0.05, indicating the absence of statistically significant associations. If the correlation coefficient between two variables exceeded |0.7|, the less important one was excluded. Supplementary Figure 2 Principal Component Analysis (PCA) of seven selected predictive factors, illustrating the explained variance percentages and cumulative variance percentages for each principal component: (**a**) for CL and CN; (**b**) for CLS and CLN.. Supplementary Figure 3 Predictive performance of ten algorithms for CN, CLN and CLS: (**a**) True Skill Statistics (TSS); (**b**) Area Under the Curve (AUC). The red dashed line indicates the ensemble model cut-off. Suplementary Table 1 The source of occurrence records for CN and CL. Suplementary Table 2 Environment variables for preliminary model analysis.

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Author contributions

K.L. conceived and designed the research method, data collection, and wrote the manuscript; and conducted the analyses.Y.T., W.H. and B.W. provided significant input through many reviews on the manuscript preparation, R packages installation and processing. S.L.,B.C. and M.Z. contributed significant input into the manuscript by supervising the study. L.Z. reviewed drafts of the paper supervised experiment, reviewed and edited the paper. All authors have read and contributed to the writing of the manuscript.

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Data availability

The dataset supporting the findings of this research is available upon request.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

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References

1. Monastersky R. Global carbon dioxide levels near worrisome milestone. Nature. 2013;497(7447):13–4.
2. Smith KE, Burrows MT, Hobday AJ, Sen Gupta A, Moore PJ, Thomsen M, Wernberg T, Smale DA. Socioeconomic impacts of marine heatwaves: Global issues and opportunities. Science. 2021;374(6566):419–25.
3. Yang H, Lohmann G, Krebs-Kanzow U, Ionita M, Shi XX, Sidorenko D, Gong X, Chen XE, Gowan EJ. Poleward Shift of the Major Ocean Gyres Detected in a Warming Climate. Geophys Res Lett 2020, 47(5).
4. Noor NM, Das SK. Effects of Elevated Carbon Dioxide on Marine Ecosystem and Associated Fishes. Thalassas. 2019;35(2):421–29.
5. Sun J, Lin M, Chen M, Xu K. Marine biodiversity under global climate change. Biodivers Sci. 2016;24(7):737–38.
6. Hollowed AB, Barange M, Beamish RJ, Brander K, Cochrane K, Drinkwater K, Foreman MGG, Hare JA, Holt J, Ito S, et al. Projected impacts of climate change on marine fish and fisheries. Ices ICES J Mar Sci. 2013;70(5):1023–37.
7. Olden JD, Vitule JRS, Cucherousset J, Kennard MJ. There's more to Fish than Just Food: Exploring the Diverse Ways that Fish Contribute to Human Society. Am. Fish. Soc. Symp. 2020; 45(9):453 – 64.
8. Freitas C, Villegas-Ríos D, Moland E, Olsen EM. Sea temperature effects on depth use and habitat selection in a marine fish community. J Anim Ecol. 2021;90(7):1787–800.
9. Campana SE, Stefánsdóttir RB, Jakobsdóttir K, Sólmundsson J. Shifting fish distributions in warming sub-Arctic oceans. Sci Rep. 2020, 10(1).
10. Wang HY, Shen SF, Chen YS, Kiang YK, Heino M. Life histories determine divergent population trends for fishes under climate warming. Nat Commun 2020, 11(1).
11. Li LJ, Zhao LL, Fu JB, Sun B, Liu CD. Predicting the habitat suitability for populations of Pacific cod under different climate change scenarios considering intraspecific genetic variation. Ecol Indic. 2022;142:48.
12. Araújo MB, Anderson RP, Barbosa AM, Beale CM, Dormann CF, Early R, Garcia RA, Guisan A, Maiorano L, Naimi B et al. Standards for distribution models in biodiversity assessments. Sci Adv 2019, 5(1).

13. Booth TH, Nix HA, Busby JR, Hutchinson MF. BIOCLIM: the first species distribution modelling package, its early applications and relevance to most current MAXENT studies. Divers Distrib. 2014;20(1):1–9.
14. Peterson AT, Soberón J, Sánchez-Cordero V. Conservatism of ecological niches in evolutionary time. Science. 1999;285(5431):1265–67.
15. Newbold T. Future effects of climate and land-use change on terrestrial vertebrate community diversity under different scenarios. Proc. Royal Soc. B. 2018; 285(1881).
16. Thuiller W, Lavergne S, Roquet C, Boulangeat I, Lafourcade B, Araujo MB. Consequences of climate change on the tree of life in Europe. Nature. 2011;470(7335):531–34.
17. Shin Y, Min MS, Borzée A. Driven to the edge. Species distribution modeling of a Clawed Salamander (Hynobiidae: *Onychodactylus koreanus*) predicts range shifts and drastic decrease of suitable habitats in response to climate change. Ecol Evol. 2021;11(21):14669–88.
18. Isaac NJB, Jarzyna MA, Keil P, Dambly LI, Boersch-Supan PH, Browning E, Freeman SN, Golding N, Guillera-Arroita G, Henrys PA, et al. Data Integration for Large-Scale Models of Species Distributions. Trends Ecol Evol. 2020;35(1):56–67.
19. Collart F, Hedenäs L, Broennimann O, Guisan A, Vanderpoorten A. Intraspecific differentiation: Implications for niche and distribution modelling. J Biogeogr. 2021;48(2):415–26.
20. Bayliss SLJ, Schweitzer JA, Bailey JK. Aggregate population-level models informed by genetics predict more suitable habitat than traditional species-level model across the range of a widespread riparian tree. PLoS ONE. 2022, 17(9).
21. Dawson TP. Beyond predictions: Biodiversity conservation in a changing climate. Science. 2011;332(6030):664–67.
22. Tournebize R, Borner L, Manel S, Meynard CN, Vigouroux Y, Crouzillat D, Fournier C, Kassam M, Descombes P, Tranchant-Dubreuil C, et al. Ecological and genomic vulnerability to climate change across native populations of Robusta coffee (*Coffea canephora*). Global Change Biol. 2022;28(13):4124–42.
23. Zhang S, Li M, Zhu JF, Xu SN, Chen ZZ. An Integrated Approach to Determine the Stock Structure of Spinyhead Croaker *Collichthys lucidus* (*Sciaenidae*) in Chinese Coastal Waters. Front Mar Sci 2021, 8.
24. Zhao L. Genetic diversity of two marine fishes and mitochondrial genome-based phylogeny of the family Sciaenidae. Ocean University of China: Ocean University of China;; 2016.
25. Ma G, Gao T, Sun R. Genetic differentiation of two *Collichthys* based on 16S rRNA and Cyt b genetic sequence. Nanfang Shuichan Kexue. 2010, 6(02):13–20.
26. Lai L, Zhang S, Lu L, Lin K, Lyu S, Zeng J, Chen h, Wang X. Population characteristics of Collichthys lucidus in the Pearl River Estuary during 2017 and 2020 (in Chinese). Pestic Environ. 2022;33:1413–19.
27. Székely D, Cogalniceanu D, Székely P, Denoël M. Adult-Juvenile interactions and temporal niche partitioning between life-stages in a tropical amphibian. PLoS ONE. 2020, 15(9).
28. Yin L, Gao T, Song N. Structural analysis and population genetics of the control region of *Collichthys lucidus*. J. Oceanol. Limnol. 137 – 45.
29. Song N, Ma GQ, Zhang XM, Gao TX, Sun DR. Genetic structure and historical demography of *Collichthys lucidus* inferred from mtDNA sequence analysis. Environ Biol Fishes. 2014;97(1):69–77.
30. Moss RH, Edmonds JA, Hibbard KA, Manning MR, Rose SK, et al. The next generation of scenarios for climate change research and assessment. Nature. 2010;463(7282):747–56.
31. Johnston R, Jones K, Manley D. Confounding and collinearity in regression analysis: a cautionary tale and an alternative procedure, illustrated by studies of British voting behaviour. Qual Quant. 2018;52(4):1957–76.
32. Blonder B, Morrow CB, Maitner B, Harris DJ, Lamanna C, Violle C, Enquist BJ, Kerkhoff AJ. New approaches for delineating *n*-dimensional hypervolumes. Methods Ecol Evol. 2018;9(2):305–19.
33. Blonder B. Do Hypervolumes Have Holes? Am Nat. 2016;187(4):E93–105.
34. Cardoso P, Rigal F, Carvalho JC. BAT Biodiversity Assessment Tools, an R package for the measurement and estimation of alpha and beta taxon, phylogenetic and functional diversity. Methods Ecol Evol. 2015;6(2):232–36.
35. Carvalho JC, Cardoso P. Decomposing the Causes for Niche Differentiation Between Species Using Hypervolumes. Front Ecol Evol. 2020, 8.
36. Thuiller W, Georges D, Gueguen M, Engler R, Breiner F, Lafourcade B, Patin R, Blancheteau H. (2024). biomod2: Ensemble Platform for Species Distribution Modeling. https://biomodhub.github.io/biomod2/
37. Fushiki T. Estimation of prediction error by using K-fold cross-validation. Stat Compt. 2011;21(2):137–46.
38. Swets JA. Measuring the accuracy of diagnostic systems. Science. 1988;240(4857):1285–93.
39. Shatz AJ, Rogan J, Sangermano F, Ogneva-Himmelberger Y, Chen H. Characterizing the potential distribution of the invasive Asian longhorned beetle (*Anoplophora glabripennis*) in Worcester County. Mass Appl Geogr. 2013;45:259–68.
40. Khojasteh D, Hottinger S, Felder S, De Cesare G, Heimhuber V, Hanslow DJ, Glamore W. Estuarine tidal response to sea level rise. The significance of entrance restriction. Estuarine, Coastal Shelf Sci. 2020; 244.
41. Ma G, Gao T, Sun D. Discussion of relationship between *Collichthys lucidus* and *C. niveatus* based on16S rRNA and *Cytb* gene sequences. South China Fisheries Sci. 2010;7:13–20.
42. Tigano A, Weir T, Ward HGM, Gale MK, Wong CM, Eliason EJ, Miller KM, Hinch SG, Russello MA. Genomic vulnerability of a freshwater salmonid under climate change. Evol Appl 2024, 17(2).
43. Theissinger K, Fernandes C, Formenti G, Bista I, Berg PR, Bleidorn C, Bombarely A, et al. How genomics can help biodiversity conservation. Trends Genet. 2023;39(7):545–59.
44. Kendall MS, Poti M, Karnauskas KB. Climate change and larval transport in the ocean: fractional effects from physical and physiological factors. Global Change Biol. 2016;22(4):1532–47.
45. Zhao LL, Qu FY, Song N, Han ZQ, Gao TX, Zhang ZH. Population genomics provides insights into the population structure and temperature-driven adaptation of *Collichthys lucidus*. BMC Genomics. 2021, 22(1).
46. Wang Y, Long H, Yi L, Yang LH, Ye XY, Shen J. OSL chronology of a sedimentary sequence from the inner-shelf of the East China Sea and its implication on post-glacial deposition history. Quat Geochronol. 2015;30:282–87.
47. Dossa AN, Alory G, da Silva AC, Dahunsi AM, Bertrand A. Global Analysis of Coastal Gradients of Sea Surface Salinity. Remote Sens. 2021, 13(13).
48. Sun R, Sun P, Yu H, Ju P, Ma S, Liang Z, Heino M, Shin Y-J, Barrier N, Tian Y. Exploring fishing impacts on the structure and functioning of the Yellow Sea ecosystem using an individual-based modeling approach. J Mar Sys. 2024;242:103946.
49. Chen DQ, Xiong F, Wang K, Chang YH. Status of research on Yangtze fish biology and fisheries. Environ Biol Fishes. 2009;85(4):337–57.
50. Zhang Z, Yang W, Ding J, Sun T, Liu H, Liu C. Identifying changes in China's Bohai and Yellow Sea fisheries resources using a causality-based indicator framework, convergent cross-mapping, and structural equation modeling. Environ Sustain Ind. 2022;14:100171.

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