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Widespread freshwater non-native fishes exhibit synchronized population dynamics with functionally similar natives

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Invasive non-native fish species can profoundly disrupt ecosystems. In invasion ecology, using the functional similarity with native species to help predict demographic rates of non-native species and infer the ecological processes underlying it remains largely unexplored. Utilizing a comprehensive analysis of 2,903 species pairs across 153 sampling sites in rivers distributed in different continents, we evaluated interspecific synchrony patterns among populations of native and non-native fish species and explored their relationship with functional and phylogenetic dissimilarities using a linear mixed model. Our results indicate that non-native fish exhibit higher synchrony with native species that share similar ecological and morphological traits. This finding corroborates our hypothesis that co-occurring non-native and native species that are more functionally similar are more synchronized and emphasizes the importance of environmental filtering significantly shaping population dynamics between native communities and coexisting non-native species. We highlight the potential of widespread non-native species in increasing synchronous patterns and consequently decreasing community stability. By elucidating which type of dissimilarities (ecological, life history, morphological, and phylogenetic) can predict synchrony and which ecological mechanisms facilitate the coexistence of native and non-native species, this research underscores the ecological implications of invasion dynamics in the long term and helps to guide conservation efforts.

Keywords Invasive species, Trait similarity, Population dynamics, Freshwater, Long-term trends, Co-occurrence, Pair of species

Non-native species are one of the major threats to biodiversity[1]. They can affect ecosystems in various ways, such as extirpating native species, altering community structure[2–4], and disrupting important functions and services in invaded ecosystems[5,6]. Invasion ecology studies have commonly used functional similarity with native species to help predict different stages of invasion, i.e., the establishment and dispersion/impact of non-natives[7–10]. Various invasion hypotheses are indeed being tested within the framework of this trait-based approach[11]. However, using the functional similarity with native species to help predict demographic rates of non-native species and infer the ecological processes underlying it remains largely unexplored[12]. More specifically, little is known about the extent to which the temporal population dynamics of native and non-native species are similar when they coexist or how these similarities in dynamics relate to functional differences between species. Investigating these aspects could provide insights into the mechanisms that drive long-term coexistence within invaded communities, an essential aspect in invasion dynamics[13,14]. Also, analyzing long-term patterns at the population level is critical for understanding invasion dynamics and forecasting the potential impacts of non-native species[15–17]. Therefore, addressing these questions offers valuable insights into invasion ecology from the population level, a poorly explored perspective, which has been recognized as having the ability to capture the variability and complexity of invasion dynamics more effectively than species-level approaches[18,19].

When assessing temporal population dynamics, the abundances of pairs of co-existing species can vary synchronously through time (e.g., the abundance of native species increases/decreases when the abundance of non-native species increases/decreases or vice-versa), show compensatory dynamics (e.g., the abundance of

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native species decreases when the abundance of non-native species increases or vice-versa), or vary independently of each other. This degree of interspecific synchrony can depend on similarities in their responses to variations in environmental conditions and species interactions. For example, synchronous dynamics can arise from species responding similarly to environmental variation[20,21] or due to positive interactions between them[22,23]. On the other hand, compensatory dynamics between populations are thought to arise from competition[24–26] but also from different responses to environmental variation[27–29]. Finally, idiosyncratic responses to the environment and neutral mechanisms (i.e., stochasticity) can ultimately generate independent dynamics between populations[27,30,31]. Since functionally similar species are thought to respond similarly to environmental changes (i.e., environmental filtering hypothesis) or to compete for available resources (i.e., limiting similarity principle[32]), the relationship between species functional similarity and interspecific synchrony patterns can help to draw inferences about the ecological mechanisms driving coexistence between native and non-native species. If functionally similar native and non-native species vary synchronously with each other, then it is likely that they respond similarly to environmental change[22,33], backing up the environmental filtering hypothesis. In opposite, if functionally similar pairs of native and non-native species have compensatory dynamics, competitive interactions (the limiting similarity principle) may contribute more to determine their coexistence in the community[22,34]. Despite the valuable ecological insights provided by combining functional similarity and interspecific synchrony approaches, this method has yet to be tested, to the best of our knowledge, with a focus on non-native species.

In general, previous studies examining native and non-native species functional traits through a comparative approach have revealed a lack of consensus regarding the role of ecological processes driving invasion dynamics. For instance, some studies suggested that non-native species with traits closely aligned with those of the native community establish or spread more[20,33,35–37]. This is because their invasion success relies on possessing specific traits that enable survival in the environmental conditions of the recipient ecosystems. This pattern highlights the importance of the environmental filtering process in driving invasion dynamics[8]. Other studies showed a contrasting view, suggesting that species with dissimilar traits are more successful in the invasion process because they experience less biotic resistance exerted by competition and predation pressure from the native community[9,38,39]. The variability in outcomes regarding the mechanisms underlying the success of non-native invasions and their coexistence with natives in communities has been reported to depend on the specific traits considered in the study[8,35].

Studies assessing species functional distance commonly use traits categorized into different types[33,37,38,40,41]. For example, life-history traits involve characteristics related to species growth, reproduction, and survival. Ecological traits relate to species' interactions with their environment, including feeding habits and preferred food sources[42,43]. Morphological traits, on the other hand, encompass the observable physical or structural characteristics of the organism, e.g., body size and shape[44]. Finally, researchers have also used phylogenetic relatedness as a surrogate for functional similarities between species[45,46], because this type of information (i.e., the evolutionary story) can be a surrogate for various phenotypic, genetic, and behavioral features of species[47,48]. All of these traits are assumed to capture resource partitioning within resident communities or non-native ecological preferences and tolerances to environmental conditions. However, it is crucial to compare and understand the contribution of these different trait types when assessing the relationship between functional similarity and synchrony level between native and non-native species.

Moreover, when considering common and widespread non-native species, specific characteristics are reported to make them more successful in persisting in a new ecosystem[49,50]. For fishes, these species are reported as having (among other attributes) a larger body size than natives[51,52] and/or exhibit diet plasticity (i.e., omnivores), or still consume a wide variety of food from specific trophic guilds (i.e., piscivores; Tonella et al.[53]). These characteristics are linked to lower chances of being predated and higher competitive advantage when considering more specialist native species[54,55]. Therefore, non-native fishes are expected to be less affected by local ecological processes, such as biotic resistance, due to competition for available resources and predation interactions[56]. On the other hand, non-native species tend to strongly respond to changes in environmental conditions[57]. In general, due to their opportunistic characteristics, these species tend to positively respond (e.g., higher growth and fecundity) to the environment when it offers suitable conditions[58]. Conversely, these species negatively respond to more stressful conditions (e.g., instability in hydrological conditions or severe climatic events)[59,60]. This happens when non-native species are not well adapted to the environmental conditions of the recipient habitat[61,62]. Despite previous studies showing the importance of environmental filtering driving non-native communities within ecosystems[56], this relation between the environment and temporal dynamics of non-native species was poorly explored at the population level, and little has been done for comparing these dynamics with patterns observed in native species.

Therefore, considering these aspects, here we evaluated interspecific synchrony patterns among populations of native and non-native species within communities and explored their relationship with functional and phylogenetic similarities. For this, we used an extensive database containing temporal data on riverine fish communities, the RivFishTime[63]. In this dataset, some sampled points are inhabited by some widespread non-native fish species. We expect to answer whether the functional and phylogenetic relatedness of coexisting native and non-native fishes are good predictors of synchrony patterns in their population dynamics. In addition, we investigated if sets of traits (life-history, ecological, and morphological) or phylogenetic information can predict the similarity in their population dynamics, and if outcomes are consistent across the different trait types. Because successful non-native species tend to possess more generalists traits that reduce the competition by available resources[55,64], we do not expect compensatory dynamics (i.e., negative covariation between populations) due to limiting similarity to be the main mechanism driving the coexistence of populations of non-native fish species with native ones. Therefore, we hypothesize that co-occurring non-native and native species that are more functionally similar are more synchronized, suggesting that environmental filtering is the primary mechanism driving non-native and native species coexistence.

Methods

Fish database

We obtained fish occurrence and abundance data from the 'RivFishTIME' database[63]. This is a global database of long-term riverine fish surveys from 46 regional and national monitoring programs and individual academic research efforts, encompassing the period between 1951 and 2019. It includes 11,386 time series of riverine fish community catch data, with abundance records, geographical location, and sampling methodology information for each time series. The spatial range of the database includes 19 countries, five biogeographical realms, and 402 hydrographical basins worldwide[63].

Data selection

To ensure the quality and consistency of our data for statistical analysis, we filtered the time series depending on the sampling methods and the species sampled. Regarding the sampling methods, we considered the time series length (at least 10 years;[57]), sampling periodicity (annual), and sampling unit (abundance - number of individuals and CPUE). Concerning the sampled species, we selected species that occurred in at least 60% of the time series to exclude rare and infrequent species[22]. Additionally, for non-native species, we filtered out those occurring in less than ten sampling sites. We determined the species status (native and non-native) related to where the species was sampled using literature information[42,65–67]. Native species are those fish that naturally occur in a particular watershed, while non-native species are those that have been introduced to regions outside their native ranges[46]. According to these criteria, eight non-native species and 129 native species were selected for this study. The non-native fish species were *Ameiurus melas*, *Ctenopharyngodon idella*, *Cyprinus carpio*, *Gambusia holbrooki*, *Hypophthalmichthys molitrix*, *Lepomis gibbosus*, *Pseudorasbora parva*, and *Xiphophorus hellerii*. Finally, according to these criteria, 153 time series, i.e., sampling sites, were selected for the present study. The selected time series were sampled in countries from different geographic regions (continents), including Australia (Oceania), Canada and the United States (North America), France, Hungary, and Spain (Europe) (Figure S1; Table S1).

Functional and phylogenetic distances

We collected 17 functional traits of each species from specific literature[68,69], see Table S2. All selected traits are commonly used in studies about fish invasion ecology and are reported as representing niche similarity with native community or non-native ecological preferences and tolerances to environmental conditions[33,37,38,40,41]. They were classified into three trait groups: ecological, life history, and morphological (Table S2;[42,70]). We calculated the functional distance between each pair of native and non-native species co-occurring at the same sampling site. We obtained the functional distance for each trait group, resulting in three functional distance values for each species pair. For ecological and life-history traits, we used an adaptation of the Gower distance using the function *gawdis* from the "gawdis" package[71]. For the morphological traits (all continuous), we used the Euclidean distance to represent morphological distances. To obtain phylogenetic information on the fish species, we used the *FishPhyloMaker* function from the "FishPhyloMaker" package[72]. This function constructs a synthetic phylogenetic tree for a subset of species, based on the backbone phylogeny of ray-finned fishes from[73] and rules for taxa insertion based on cladistic hierarchy and species taxonomic information[72]. After obtaining the phylogeny for our subset of species, we measured phylogenetic distances between each species pairs using the *cophenetic* function from the "ape" package[74].

Data analyses

In each site, interspecific synchrony was calculated between each native and non-native species pair. To do so, we first removed long-term trends in the abundance time series of each species[75] by applying a linear regression between abundance and time and using the residuals of this model in the following steps. Then, we used Spearman's rank correlation coefficient between the detrended abundance time series (residuals) of each species pair. After, to assess if the functional and phylogenetic distances between native and non-native species are good predictors of interspecific synchrony patterns, we performed a Linear Mixed Model (LMM) using the synchrony values between species pairs as the response variable. As predictor variables (fixed terms), we included the functional distances (i.e., ecological, life history, and morphological), the phylogenetic distances, and the number of sampling years of each time series.

The environmental context is a crucial aspect to take into account when assessing functional similarity patterns, especially when considering an invasion process[76]. Therefore, we also included the air temperature (°C) information for each location, a surrogate to water temperature, as a fixed covariable. Water temperature is related to resource availability and is an important environmental constraint for ectothermic organisms such as fish[77,78]. For this, we extracted the mean annual air temperature recorded at the height of 2 m above the Earth's surface at each location from NASA's POWER database (Prediction of Worldwide Energy Resource), utilizing the package "nasapower"[79]. In addition, the species pair ID, the non-native species ID, and the sampling site ID were included as random terms. The interactions between functional distances and temperature were not included in the final model as they were not statistically significant.

We ran the LMM using the *lmer* function from the "lme4" package[80]. Multicollinearity was assessed using the 'check_collinearity' function from the 'performance' package[81], and VIF values < 1.5 indicated no significant issues. To evaluate the model's assumptions, we employed the *testResiduals* function from the "DHARMa" package[82]. The assessment of model goodness-of-fit involved the computation of marginal (R^2m) and conditional (R^2c) coefficients of determination[83]. For this, we used the *r.squaredGLMM* function from the "MuMIn"

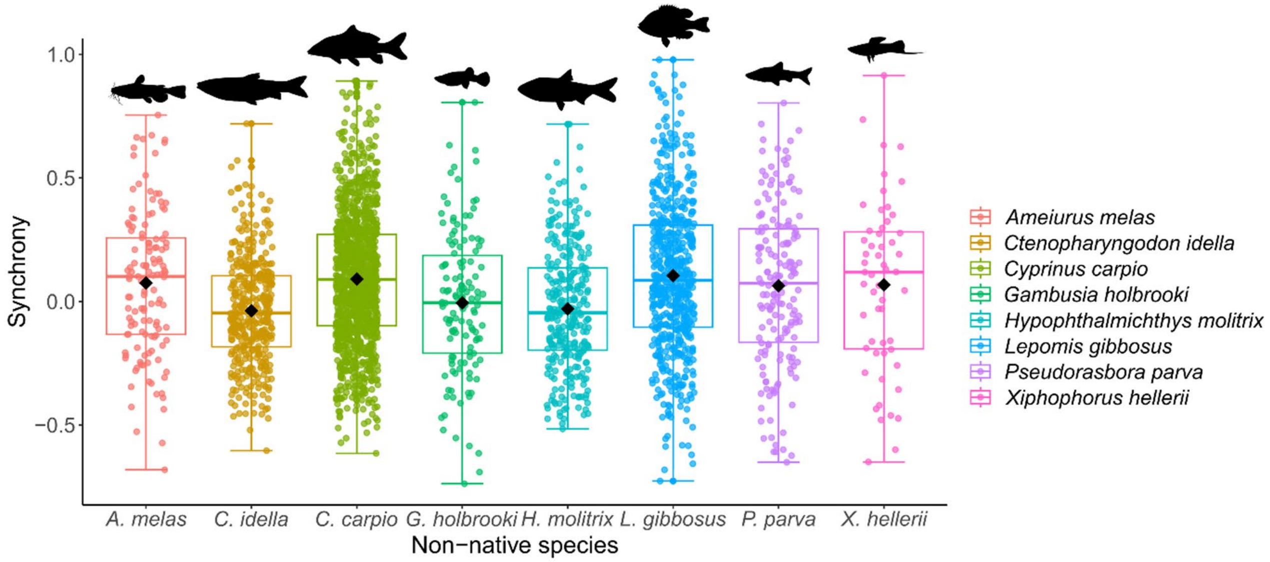

Fig. 1. Synchrony values (pairwise Spearman's correlations) of non-native species with co-occurring native species. Black diamonds represent mean values.

RFT code	Species pair	Continent	IS	MD	ED
Highly synchronous species pairs (positive synchrony)					
G1033	***Cyprinus carpio***/*Ictiobus bubalus*	North America	0.880	8.040	0.393
G1033	***Cyprinus carpio***/*Ictiobus cyprinellus*	North America	0.869	3.026	0.081
G1073	***Cyprinus carpio***/*Aplodinotus grunniens*	North America	0.893	25.013	0.288
G259	***Xiphophorus hellerii***/*Gobiomorphus australis*	Oceania	0.915	2.372	0.446
G118	***Lepomis gibbosus***/*Alburnus alburnus*	Europe	0.882	15.157	0.165
G7615	***Lepomis gibbosus***/*Perca fluviatilis*	Europe	0.855	33.226	0.569
G7644	***Lepomis gibbosus***/*Scardinius erythrophthalmus*	Europe	0.852	21.728	0.108
G8000	***Lepomis gibbosus***/*Squalius cephalus*	Europe	0.859	33.232	0.156
G8000	***Lepomis gibbosus***/*Perca fluviatilis*	Europe	0.877	33.226	0.569
G8148	***Lepomis gibbosus***/*Rhodeus sericeus*	Europe	0.918	29.007	0.341
G8148	***Lepomis gibbosus***/*Rhodeus amarus*	Europe	0.918	28.803	0.090
G8718	***Lepomis gibbosus***/*Tinca tinca*	Europe	0.979	45.411	0.404
Pairs with strong compensatory dynamics (negative synchrony)					
G221	***Gambusia holbrooki***/*Leiopotherapon unicolor*	Oceania	− 0.738	29.831	0.581
G7626	***Lepomis gibbosus***/*Perca fluviatilis*	Europe	− 0.727	33.226	0.569

Table 1. Species pairs with the highest (positive, > 0.85) and lowest (negative, < -0.70) interspecific synchrony values in each continent. RFT code = rivfishtime site code. IS = Interspecific synchrony values (i.e., pairwise Spearman's correlations). MD = Morphological distance. ED = Ecological distance. The non-native species in each species pair is highlighted in bold.

package[84] and the *tab_model* function from the "sjPlot package"[85]. All statistical analyses were conducted in the R environment[86].

Results

In total, we analyzed 2,903 pairs of species distributed in 153 sampling sites, with 290 unique pairs of species encompassing eight non-native and 129 native species. Time series length ranged from 10 to 31 years. The number of native and non-native species analyzed per sampling site ranged, respectively, from one to 37 and from one to three (Table S1).

Among the non-native species (Fig. 1), *Lepomis gibbosus* presented the highest mean synchrony with co-occurring native species (mean $\rho = 0.104 \pm 0.31$), followed by *Cyprinus carpio* (mean $\rho = 0.090 \pm 0.26$). *Lepomis gibbosus* also showed the highest synchrony value (maximum $\rho = 0.979$). On the other hand, *Gambusia holbrooki* showed the strongest compensatory dynamics (minimum ρ = -0.738, Table S3). In Europe, the non-native species *Lepomis gibbosus* presented the highest synchrony values with native species (Table 1) but also high compensatory dynamics (ρ< -0.70) with the native species *Perca fluviatilis* (Fig. 2). In North America, *Cyprinus carpio* was greatly synchronous with native species of the genus *Ictiobus* (Fig. 2) and *Aplodinotus grunniens* (Table 1). In Oceania, *Xiphophorus hellerii* was highly synchronized with *Gobiomorphus australis* (Table 1).

Morphological and ecological distances between species were significantly related to interspecific synchrony (Table 2). Synchrony between pairs of native and non-native species decreased as morphological and ecological distances increased (Fig. 3). Life history and phylogenetic distances did not explain significant variation in pairwise synchrony between native and non-native species.

Discussion

We evaluated the interspecific synchrony patterns among native and widespread non-native fishes, exploring their relationship with functional and phylogenetic similarities. Pairs of native and non-native species showed a range of dynamics, from highly synchronous (i.e., both species abundances increasing and decreasing at the same time) to compensatory dynamics (i.e., increases in abundance of one species while the other decreases in abundance, *sensu*[31]. We found that the similarity between native and non-native fish species can predict their level of synchrony. Specifically, we showed that non-native species tend to be more synchronized with native ones with more similar ecological and morphological characteristics. On the other hand, similarities in life-history traits and phylogenetic relatedness were not related to synchrony in abundance between species. Finally, the observed relationship between interspecific synchrony and trait similarity may suggest that similar responses to environmental variation drive the similarity in population dynamics of the studied native and non-native species[20,22,87].

We found that non-native fish populations exhibit greater synchrony with native species that share similar functional traits. This finding suggests that, in general, non-native fish respond to changes in environmental conditions similarly to native species that are morphologically and ecologically similar. Consequently, environmental filtering appears to be the primary mechanism driving the temporal dynamics of non-native species and long-term coexistence with native communities. This aligns with the recent study by[46], which demonstrated the significance of environmental filtering in shaping spatial co-occurrence patterns between functionally similar native and non-native riverine fish species. Thus, our hypothesis that co-occurring native and non-native species that are more functionally similar are more temporally synchronized was supported. In contrast, compensatory dynamics (i.e., negative covariation between populations) arising from the limiting similarity process do not seem to rule the coexistence of native and non-native fish populations with similar traits. This is likely because successful non-native species often exhibit more generalist preferences and higher trait plasticity in invaded environments. These features may allow them to adapt more readily to resource availability and avoid competitive interactions with similar native species, or, in some cases, outcompete them, sometimes leading to their extirpation[55,64]. This finding underscores the importance of considering the role

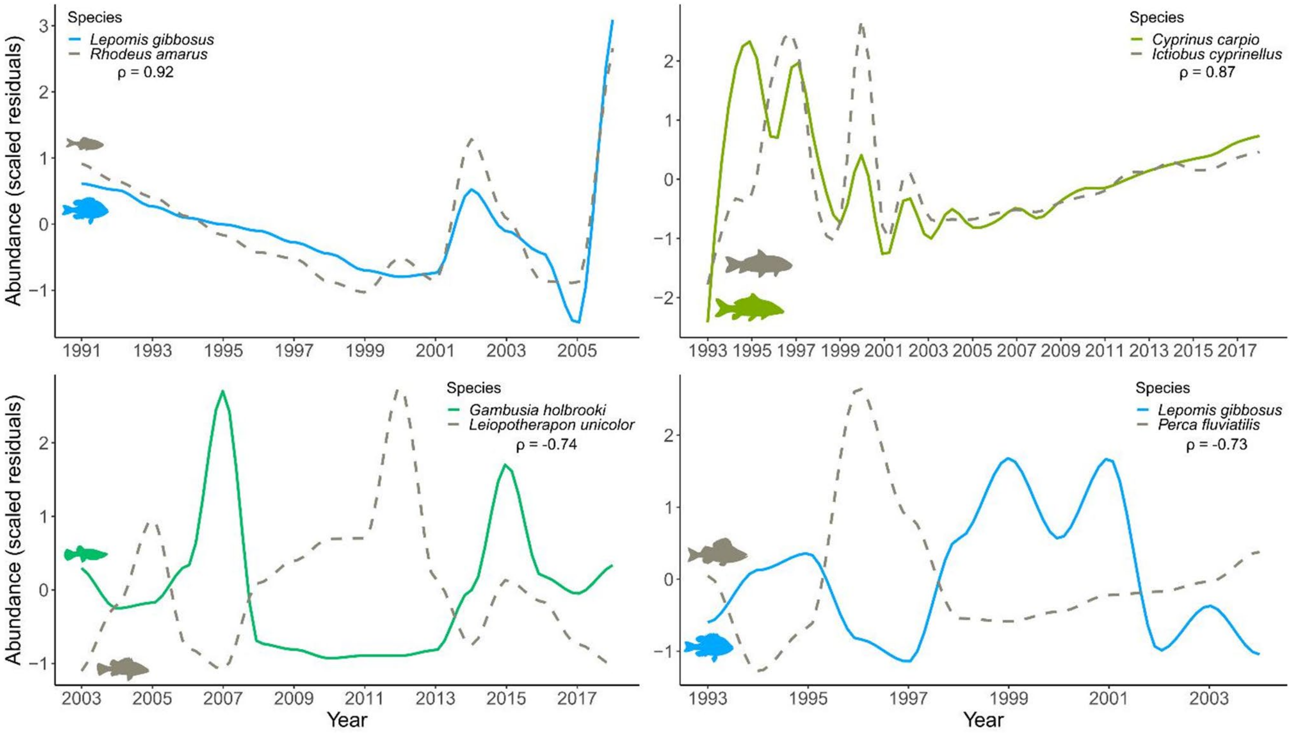

Fig. 2. Temporal dynamics of the abundance and the Spearman's correlation coefficients (ρ) of species pairs in this study. The species in the top panels present synchronous dynamics. The species in the bottom panel present compensatory dynamics.

	Interspecific synchrony			
Predictors	**Estimates**	**Std.error**	**CI**	**P**
(Intercept)	0.028	0.020	− 0.010 to 0.066	0.153
Morphological distance (log)	**− 0.022**	0.008	− 0.038 to − 0.007	**0.004**
Life history distance	− 0.017	0.010	− 0.037 to 0.003	0.104
Ecological distance	**− 0.026**	0.008	− 0.043 to − 0.010	**0.001**
Phylogenetic distance	0.006	0.007	− 0.008 to 0.021	0.393
Number of years	− 0.012	0.011	− 0.033 to 0.010	0.282
Mean annual temperature	0.003	0.010	− 0.018 to 0.023	0.799
Random effects				
σ^2	0.06			
$\tau_{00\ sp\_pair\ ID}$	0.00			
$\tau_{00\ sampling\ sites\ ID}$	0.01			
$\tau_{00\ non-native\_sp\ ID}$	0.00			
ICC	0.16			
N_{sp_pair}	290			
$N_{non-native\_sp}$	8			
$N_{sampling\ sites}$	153			
Observations	2903			
Marginal R^2/conditional R^2	0.026/0.182			

Table 2. Summary of the mixed effect model of pairwise interspecific synchrony between native and non-native species, as a function of functional distances (log-transformed morphological, life-history and ecological) and phylogenetic distances. The number of sampled years in each time series and the mean water temperature of each sampling site were used as covariates. The random effects were the identity (ID) of the species pair, the sampling sites ID, and the non-native species ID.

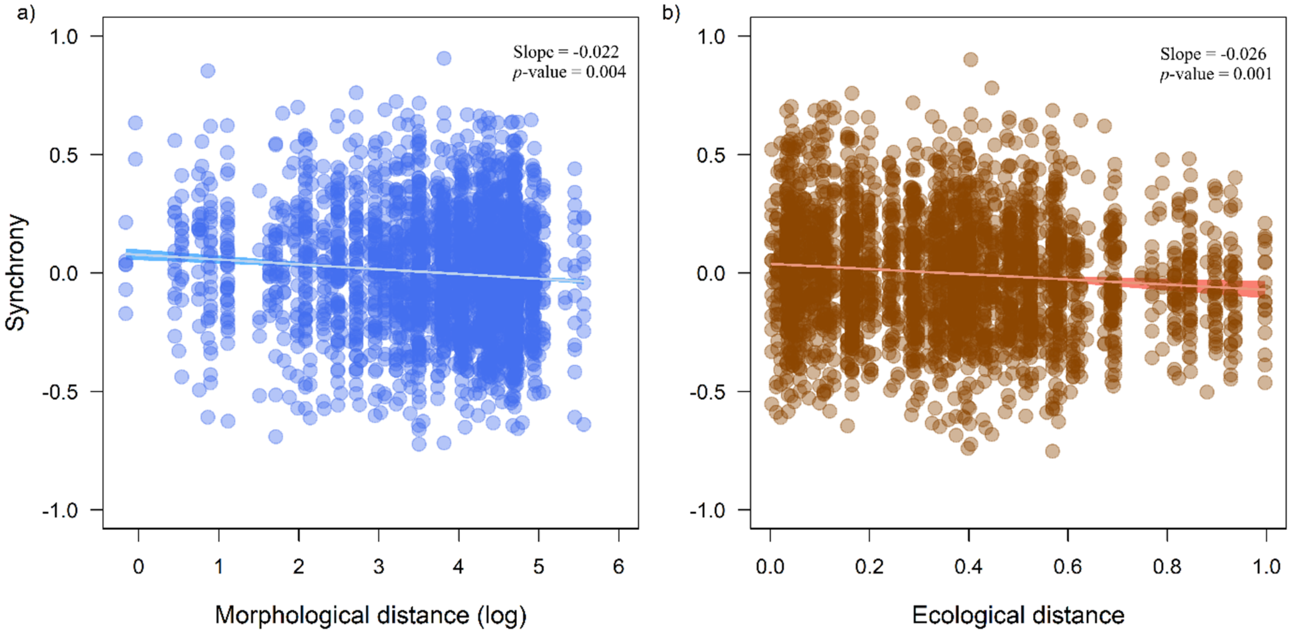

Fig. 3. Relationships between interspecific synchrony (pairwise Spearman's correlations) and functional distances between species pairs (native x non-native species). (**a**) Morphological distances (traits related to body morphology - see Table S2) and (**b**) Ecological distances (trophic level and type of habitat), $n = 2903$.

of non-native species in community dynamics when assessing levels of synchrony. Finally, our results suggest that non-native species that are functionally like native communities may enhance synchronous patterns within communities, potentially reducing ecosystem stability in the face of future disturbances. Future research should explore how non-native species affect the stability of communities over time (e.g.[57,88]).

Ecological and morphological functional distances have proven to be effective in predicting synchrony in population fluctuations between native and non-native fishes. This finding is consistent with prior research assessing the relationship between interspecific synchrony and similarities in ecological or morphological traits of terrestrial[87,89] and aquatic groups[20,90,91]. For example[33], related levels of interspecific synchrony of phytoplankton with ecological traits such as motility and silica use. For freshwater fish, ecological traits such as diet and habitat preference are crucial for assessing the ecological mechanisms driving communities and populations, directly influencing how species utilize available resources and respond to changes in abiotic conditions[92,93]. Additionally[90], found that body size, a morphological trait, predicted synchrony among fish species (including non-native ones) experiencing severe drought in a tropical reservoir. The significant contribution of morphological distance explaining the variance in similarities of population dynamics reinforces their role as a good surrogate of fish features (e.g., ecological or reproductive) directly related to species fitness[94]. Such a finding highlights functional trait similarity with native communities as a valuable approach to understanding population dynamics when assessing the invasion process. On the other hand, the lack of congruence in results for the other trait distances (i.e., life history and phylogenetic) emphasizes the necessity for careful trait selection when comparing population dynamics between native and non-native species, indicating the need for considering different traits to ensure robust comparisons.

Regarding patterns of each non-native species, *Lepomis gibbosus* (pumpkinseed) and *Cyprinus carpio* (common carp) presented synchronous dynamics with a variety of native species in the invaded area. As these species are generalists and have high abundance and a wide distribution in the non-native area, they likely dwell in diverse environmental conditions and habitat types[95,96]. Thus, their responses to environmental variation probably coincide with the responses of many native species in the invaded areas, generating synchrony between their populations. On the other hand, *Gambusia holbrooki* (eastern mosquitofish) presented a high frequency of compensatory dynamics with native species in the invaded areas. Like the other non-native species in this study, this small-sized fish with a fast life-cycle also dwells in a variety of environmental conditions[97], but presented a contrasting population dynamics with native species. Therefore, a likely explanation for this pattern is negative interactions. This includes competition and aggressiveness, as this species has high competitive potential and niche overlap with native species and shows fin-nipping behavior[97–99]. Additionally, predation on the eggs and larvae of native species by this non-native fish may further elucidate the contrasting patterns observed in their populations[100]. Finally, similar species can still respond differently to environmental changes if there is temporal differentiation in their niches[14]. This could lead to a pattern of compensatory dynamics in their abundance in the absence of negative interactions.

Regarding patterns in different geographic regions, some non-native species, such as *L. gibbosus* in Europe, presented both highly synchronous and strong compensatory dynamics with native species, depending on the sampling site (e.g., water body and/or country). The similarity in ecological and morphological traits can partially explain this variation in dynamics. For example, *L. gibbosus* and *Rhodeus amarus* ($\rho = 0.91$) are ecologically similar, as both species prefer to inhabit vegetated areas in still or slow-flowing waters[69,101]. On the other hand, *L. gibbosus* had compensatory dynamics with *Perca fluviatilis* (ρ = -0.73), as they differ largely in habitat preferences and trophic level (mainly because of the larger prey size consumed by *P. fluviatilis*). However, it is important to note that the pair *Lepomis gibbosus/Perca fluviatilis* also presented high synchrony in some locations (see Table 1), therefore it is likely that local abiotic and biotic conditions can also influence their population dynamics. Further research could investigate the drivers of spatial variation in interspecific synchrony between pairs of native and non-native species.

It is well known that the environmental context is an important aspect to consider when analyzing patterns in invasion ecology[102] and when using a trait similarity approach with native species[12]. Selected sites were located in geographic regions placed in temperate zones (even in Australia), where temporal data is more readily available. Therefore, future studies should consider extrapolating these questions to different environments, such as tropical habitats and those with varying levels of disturbance, to understand better how these conditions might influence the importance of selected traits and the ecological mechanisms driving invasion dynamics. Also, it is crucial to replicate or adapt this study for different ecosystems (e.g., terrestrial and other aquatic environments). Another limitation of our study is that we were not able to determine the exact invasion stage of the non-native species analyzed (e.g., recently introduced or naturalized and spread) at each site despite all locations being sampled over an extended period. However, our results provide a general understanding of the main patterns involved in the long-term coexistence of native and non-native species in freshwater ecosystems.

Conclusion

In conclusion, we highlight that functional traits have proven to be valuable tools for inferring the temporal population dynamics of common non-native fish species and their synchrony with native communities. Also, we identified the primary mechanistic explanation (environmental filtering) that helps to drive the long-term coexistence between native and non-native fish species. This knowledge is essential for advancing our understanding of invasion ecology and informing conservation efforts. Firstly, we showed that trait similarity with native communities can help to understand the invasion process and the ecological mechanisms underlying temporal dynamics within populations in invaded ecosystems, using an approach that relies on interspecific synchrony - a relatively unexplored method. Secondly, it enhances our ability to forecast the temporal dynamics of widespread non-native species populations. This aspect can be a powerful strategy for policymakers and management decision-makers in developing effective prevention and management strategies for ecosystems threatened by widespread non-native species, one of the main concerns in ecology.

Data availability

The data used in this study are publicly available and were originally published in Comte et al. (2021). The dataset can be accessed at https://idata.idiv.de/ddm/Data/ShowData/1873?version=12.

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Author contributions

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Declarations

Competing interests

The authors declare no competing interests.

Additional information

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