PRIMARY RESEARCH PAPER

Tributaries create habitat heterogeneity and enhance fish assemblage variation in one of the largest reservoirs **in the world**

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Abstract The Three Gorges Reservoir is one of the largest reservoirs in the world. Previous studies uncovered longitudinal changes in fsh assemblages among riverine, transitional, and lacustrine zones, but whether they vary at small-scale habitats and how tributaries contribute to fsh conservation is poorly understood. We selected three neighboring tributaries with diferent habitat characteristics within and among tributaries and hypothesized that

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the small-scale habitat heterogeneity within or among tributaries could shape spatial and temporal variation in fsh assemblages. We analyzed spatial (among tributaries, pelagic versus benthic, lower versus upper reach) and seasonal patterns of fsh assemblage and their relationship with the environment. Piscivorous, limnophilic, and mid-pelagic species dominated the fish assemblage in different habitats. Fish assemblage structure varied spatially between lower and upper reaches and among tributaries. Fish assemblages also varied seasonally, mainly related to environmental variability (i.e., water depth, water temperature, pH, specifc conductivity, riparian slope, and vegetation coverage). Catch per unit effort was similar between

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L. Fang Jiujiang Academy of Agricultural Sciences, Jiujiang 332005, Jiangxi, People's Republic of China pelagic and benthic habitats but exhibited horizontal and seasonal changes. The most infuential environmental variables were water depth, water temperature, dissolved oxygen, and pH. Our results supported the hypothesis, and indicated that we should protect tributaries that provide important areas for fsh diversity in large reservoirs.

Keywords Small-scale habitat heterogeneity · Habitat protection · Fish diversity · Large reservoir

Introduction

Habitat heterogeneity involves the spatial and temporal complexity of natural habitats at diferent scales, and it is critical to maintaining biodiversity (Mac-Arthur & MacArthur, [1961;](#page-14-0) Kovalenko et al., [2012](#page-13-0); Spurgeon et al., [2018;](#page-14-1) Heidrich et al., [2020](#page-13-1)). Evaluating the multidimensionality of the relationship between habitat heterogeneity and biological communities remains a priority in ecological research (Alberti & Wang, [2022](#page-12-0); Miao et al., [2022](#page-14-2)), particularly in the face of global climate change, habitat loss, and biodiversity decline (Eddy et al., [2021\)](#page-13-2). For fish fauna, habitat heterogeneity can influence fish diversity and assemblage structure at multiple temporal and spatial dimensions (López-Delgado et al., [2020\)](#page-13-3), where habitat heterogeneity can be derived from channel geomorphology (e.g., lake area, river width, sediment particle size, shoreline development, and vegetation coverage; Eadie & Keast, [1984](#page-13-4)), hydrology (e.g., water depth, flow velocity; Smith & Mather, [2013\)](#page-14-3), water quality, and food availability (Ye et al., [2007;](#page-15-0) Spurgeon et al., [2018\)](#page-14-1). However, artifcial hydrological change alters habitat heterogeneity in freshwater ecosystems, leading to habitat homogenization and potentially diminishing fsh diversity (Zeng et al., [2017\)](#page-15-1).

At present, 57,985 large dams (height>15 m or height 5–15 m and impounding > 3 million m³) have been built in the world, and dam building is still growing at an annual growth rate of 2%–3% (ICOLD, [2019\)](#page-13-5). How habitat changes after dam construction afect fsh assemblages is a major concern for freshwater ecologists. Fish undergo diferent life history stages, from spawning, hatching, larvae, juvenile, to reproductive and senescent adult (Chen & Liu, [2022\)](#page-12-1). Each stage requires particular environmental

conditions (e.g., water velocity, water temperature, dissolved oxygen, vegetation coverage, and food availability) and fsh at all stages are susceptible to damming (Toussaint et al., [2016\)](#page-15-2). Dams block the migratory pathways of fshes and disrupt the hydrological conditions required for ovulation and fertilization and development of eggs, larvae, and young (Pelicice et al., [2015](#page-14-4); Arantes et al., [2019\)](#page-12-2). These combined efects on life history traits afect population persistence. Impoundment reduces fow rate and the abundance of rheophilic fsh (Sá-Oliveira et al., [2015\)](#page-14-5). Dam-induced changes in food availability often increase the abundance and dominance of generalist fsh species (Turgeon et al., [2019\)](#page-15-3). Lastly, as the riverine habitat is replaced by large areas of lentic habitat after dam regulation, the resulting habitat homogeneity can simplify fsh assemblages and lead to fsh diversity decline (Perônico et al., [2020\)](#page-14-6). These combined impacts afect fsh assemblages at a large scale, and the detrimental effect on fish biodiversity is exacerbated by the fact that the areas with greater hydropower development are generally located in river reaches with the most diverse habitat heterogeneity (e.g., headwaters, rapids) (Cheng et al., [2015](#page-12-3)).

From a metacommunity perspective, tributaries constitute an important source contributing to the maintenance of fsh diversity in dammed systems (Vasconcelos et al., [2021\)](#page-15-4). In large reservoirs, tributaries provide essential refuges to migratory and riverine species and also act as a natural stocking source (Da Silva et al., [2015;](#page-13-6) Vitorino Junior et al., [2016;](#page-15-5) Marques et al., [2018](#page-14-7); Azevedo-Santos et al., [2021;](#page-12-4) Vasconcelos et al., [2021\)](#page-15-4). After impoundment, tributaries retain diferent habitats at the local scale. In turn, fish assemblage structure is influenced by local conditions, including water depth (Mattos et al., [2014\)](#page-14-8), fow regime (Yan et al., [2011](#page-15-6)), water temperature (Togaki et al., [2023\)](#page-15-7), transparency (Mattos et al., [2014\)](#page-14-8), dissolved oxygen (Ostrand & Wilde, [2001](#page-14-9)), substrate size (Wang et al., [2013\)](#page-15-8), shelter (Mattos et al., [2014\)](#page-14-8), and riparian vegetation coverage (Montag et al., [2019](#page-14-10)). The variation in these environmental variables creates small-scaled habitat heterogeneity within and among tributaries after dam regulation which support fish assemblages by providing spawning, feeding, and refuge (Szalóky et al., [2021](#page-14-11)).

The upper reach of the Yangtze River and its tributaries have diverse fow regimes and complex habitats and harbor the highest fsh species richness in China (Liu & Cao, [1992\)](#page-13-7). The impoundment of the Three Gorges Dam formed an enormous reservoir with a total length of 667 km and a total area of 1080 km^2 , which dramatically impacted aquatic habitats and fshes therein (Liao et al., [2018a\)](#page-13-8). The average fow velocity of the mainstream decreased by 90% after the impoundment, and the lotic areas were greatly reduced (Yang et al., [2012\)](#page-15-9), which generated a longitudinal gradient of riverine, transitional, and lacustrine habitats from the upper to lower sections of the mainstem that forms the reservoir, and from the upstream to downstream of reservoir tributaries. In addition, the artifcially regulated water level altered the natural hydrological regime of the river, and diminished the hydrological heterogeneity in the reservoir (Liao et al., [2019\)](#page-13-9). Based on these habitat changes, previous studies investigated alterations to the structure of fsh assemblages in the TGR at large scales, including spatial comparisons among diferent reservoir sections (upper, middle, and lower; Liao et al., [2018a](#page-13-8)), and temporal comparisons between pre- and post-impoundment, and among diferent impoundment stages, from the perspectives of species richness (Gao et al., [2010;](#page-13-10) Yang et al., [2012](#page-15-9); Liao et al., [2018a\)](#page-13-8), assemblage structure (Wu et al., [2007;](#page-15-10) Gao et al., [2010;](#page-13-10) Yang et al., [2012](#page-15-9); Zhao et al., [2015\)](#page-15-11), and life history (Perera et al., [2014](#page-14-12); Liao et al., [2018b,](#page-13-11) [2019\)](#page-13-9). These studies found that habitat homogeneity simplifed fsh assemblages in the TGR; however, they also revealed a relatively high fish diversity in the whole reservoir due to the remaining lotic stretches at the upper section of the reservoir. Additionally to the lotic upper stretch of the TGR,>10 tributaries fowing into the TGR create relatively high heterogeneity at a local scale (Xu et al., [2012\)](#page-15-12). Nevertheless, how local habitat conditions infuence fsh assemblages in the TGR is still poorly understood.

To fll up this knowledge gap, our study selected three neighboring tributaries fowing into the lower section of the TGR as a model system to evaluate the infuence of reservoir tributaries on fsh diversity in large reservoirs. Specifcally, the three tributaries constitute heterogeneous habitat characterized by variable water quality and physical characteristics within and among tributaries and relative to the reservoir. These tributaries' lower and upper reaches are afected by the TGR during the high water season (175 m, winter), while the upper reaches can partly recover riverine state during the low water period (145 m, summer). We investigated spatial and seasonal patterns in fish assemblage structure among the three tributaries and evaluated the relationship between assemblage structure and habitat characteristics. We hypothesized that the small-scale habitat heterogeneity within (gradients, habitats) or among tributaries (identity) could shape spatial and temporal variation in fsh assemblages. Specifcally, we aimed to: (1) test whether fsh assemblage structure difered among tributaries, reaches within tributaries, and seasons; (2) identify the potentially environmental variables driving spatial and temporal changes in fsh assemblage structure.

Materials and methods

Sampling sites

The TGR is located in the upper reach of the Yangtze River with a high fsh species richness and contains numerous tributaries distributed in diferent reservoir sections. The Xiangxi River (X), Yuanshui River (Y), and Qinggan River (Q) are three neighboring tributaries located on the lower section of the TGR and, together with the mainstem, form a dendritic river network. The reservoir has partly impounded the three tributaries, yet diferent local-scale habitats with various water quality and physical characteristics remain within and between tributaries. At each tributary, we selected the lower (X-Lower, Y-Lower, and Q-Lower) and upper (X-Upper, Y-Upper, and Q-Upper) reaches to sample (Fig. [1\)](#page-3-0). The X-Upper, Y-Upper, and Q-Upper reaches are about 21 km, 15 km, and 18 km from the mainstem of the TGR, while the X-Lower, Y-Lower, and Q-Lower reaches are about 0.8 km from the mainstem, and these areas are free of dams. Summary information on sampling reaches is included in Table [1.](#page-4-0)

Fish sampling

We seasonally sampled fshes at the lower and upper reaches per tributary during the summer (July), autumn (October), winter (January), and spring (April) seasons between July 2020 and January 2022 (*N*=36 sampling events per season; i.e., 3 rivers * 2 reaches * 3 sites * 2 repeated days). We sampled benthic and pelagic fshes using benthic and **Fig. 1** Three Gorges Reservoir in the Yangtze River (upper right corner map) and the location of the lower and upper reaches of three reservoir tributaries flowing into the lentic section of the reservoir (center map). Abbreviations: Xiangxi River (X-Lower, X-Upper), Qinggan River (Q-Lower, Q-Upper), and Yuanshui River (Y-Lower, Y-Upper). Dotted arrows represent the flow direction
of the Yangtze River

pelagic experimental multi-panel gillnets, respectively. The two gillnet types have diferent heights (2 and 5 m, benthic and pelagic, respectively) but have the same length (30 m) and mesh-size structure. Each gillnet consisted of 12 panels (2.5 m each) of diferent mesh sizes (10, 16, 20, 25, 31, 39, 48, 58, 70, 86, 110, 125 mm, stretched mesh sizes). These multimesh gillnets are comparable to CEN 2015 standard (CEN, [2015\)](#page-12-5). We randomly selected three sites (\approx 500 m apart) at each sampling reach, covering diferent habitats, and we tied together three benthic gillnets $(3*30 \text{ m} = 90 \text{ m}$ total length) and three pelagic gillnets $(3*30 \text{ m} = 90 \text{ m}$ total length) and deployed them for 12 h (18:00–19:00 to 6:00–7:00) per site. We repeated our sampling at each sampling site the next day to increase capture (24 h total). The pelagic and benthic gillnets have diferent headropes with foats and footrope with sinkers, and we always ensured that the pelagic and benthic gillnets sampled the surface and bottom water, respectively. We deployed gillnets from the littoral to the pelagic areas with the aid of a boat driving in reverse. We estimated the depth of the benthic areas sampled by benthic gillnets based on their total length $(3*30 \text{ m} = 90 \text{ m})$ and the maximum riparian slope of sampling sites (85° angle); the benthic gillnets can sample the maximum water depth of 89.7 m.

We identifed all caught fshes to species level (Ding, [1994\)](#page-13-12) and measured their total length (TL), standard length (SL), and body weight (BW) to 0.1 mm, 0.1 mm, and 0.01 g, precision, respectively. We categorized each fsh species based on their dietary guild (Herbivorous, detritivores, planktivorous, omnivorous, invertivores, and piscivorous; Ding, [1994\)](#page-13-12), water layer (pelagic, mid-pelagic, mid-benthic, and benthic; Ding, [1994\)](#page-13-12), fow guild (eurytopic, rheophilic, and limnophilic; Xiao et al., [2015](#page-15-13)), and native status (Ding, [1994](#page-13-12); Ba & Chen, [2012](#page-12-6); Online Resource 1). Among these, we classifed fshes with superior, sub-superior, sub-inferior, and inferior mouth position as pelagic, mid-pelagic, mid-benthic, and benthic dwellers, respectively (Ding, [1994](#page-13-12); Lund et al., [2010\)](#page-14-13). We calculated catch per unit effort per sampling unit (i.e., sampling location) based on fsh biomass (BPUE, g/ $m²$ of gillnets per night) and abundance (NPUE, individuals/ $m²$ of gillnets per night), respectively. We also calculated relative abundance or relative

Values for substrate and natural zone represent mean percentages among transects

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biomass per fsh species per site (e.g., abundance per species/total abundance per site).

Habitat characterization

The highest water level at the TGR occurs from autumn to winter (from November to January), whereas the lowest occurs during summer (June and July). During the high water level season, the TGR creates a backwater efect in the tributaries, which equalizes their water level with that of the TGR. We, therefore, investigated the physical habitat characteristics of tributaries during the lowest water level period (i.e., summer, July). We established ten random transects at each sampling reach, separated by 100 m from each other. At each transect, we measured maximum water depth (MWD, m) with a Speedtech sounder, and visually defned water-levelfuctuation zones (water-land transition zone formed by fuctuating water level at an elevation ranging between 145 and 175 m above sea level; Chen et al., [2020\)](#page-12-7) as natural (no artifcial transformation) and artifcial conditions (artifcial transformation by hardening of shorelines with riprap or concrete; Lapointe et al., [2014](#page-13-13)), and estimated the vegetation cover in the riparian zone (Zhu et al., [2020\)](#page-15-14). We categorized the substratum of water-level-fuctuation zones as rock, riprap, pebble, sand, and mud, recorded their respective proportions, and then grouped them into rock and sand-mud to facilitate the analysis (Eitzmann & Paukert, [2010\)](#page-13-14), and we classifed artifcial riprap and concrete as rock substratum. We also estimated the riparian slope of each transect and calculated the average slope (degree) of each reach (Table [1](#page-4-0)). Due to the steep slopes, the substratum and vegetation coverage values are aerial proportions. We seasonally measured water transparency (WTR, m) with a Secchi disk, and quality parameters of surface water, including pH, water temperature (WTE), dissolved oxygen (DO), and specifc conductivity (Con) with an YSI Pro Plus multiparameter water quality analyzer at fve random transects. We also measured the vertical profle of dissolved oxygen with two-second intervals at about 0.4 m depth intervals, to a maximum depth of 94 m using an optical sensor installed on an YSI EXO2 multiparameter water quality sonde.

Data analysis

We calculated species richness, relative abundance, and relative biomass for each sampling reach by pooling data from multiple sampling sites. We measured taxonomic beta-diversity among sampling reaches based on our "reach \times species" dataset using Jaccard's dissimilarity index. We used permutated multivariate analyses of variance (PERMANOVA) to assess diferences in assemblage structure between pelagic and benthic habitats among the three tributaries, the lower and upper reaches, and four seasons. We also used the PERMANOVA to analyze spatial diferences in fsh assemblage structure, categorized by dietary guild, water layer, and flow guild, among six sampling reaches (identifed by its tributary: X-Lower, Y-Lower, Q-Lower, X-Upper, Y-Upper, and Q-Upper). We then used Non-metric multidimensional scaling (NMDS) with Bray–Curtis similarity to visualize spatial and seasonal variation in fsh assemblage structure. Similarity percentages (SIMPER) tests were used to assess the contribution of fsh species to the spatial and seasonal diferences.

We also examined relationships between spatial and seasonal variation in fsh assemblages and environmental variables using canonical correspondence analysis (CCA). The CCA selects a linear combination of environmental variables and maximizes the dispersion of the species scores (Abdel-Dayem et al., [2021\)](#page-12-8). The ordination output shows patterns directly related to the environmental conditions being examined. We used the variance infation factor (VIF) value to test collinearity among environmental variables and excluded collinear variables with VIF>10 (Gladyshev et al., [2018\)](#page-13-15); in the CCA model, we included seasonal water quality variables (i.e., MWD, WTE, DO, pH, WTR, and Con) and physical variables which are expected to be equal year round (i.e., rock substratum, slope, and vegetation coverage). We used the Monte Carlo permutation test (1000 permutations) to analyze the signifcance of the CCA model and its canonical axes. We calculated correlation coefficients for explanatory variables representing the importance of each variable on each axis. We excluded 14 fish species occurring at only one reach from the PERMANOVA, NMDS, SIMPER, and CCA analyses to reduce the infuence of rare species (Legendre & Legendre, [1998](#page-13-16)).

We implemented linear mixed-effects model (LMM) to compare the BPUE or NPUE between pelagic and benthic assemblages (i.e., the two gillnet types) and included reach (identifed by its tributary: X-Lower, Y-Lower, Q-Lower, X-Upper, Y-Upper, and Q-Upper) as a random factor to account for the lack of independence between multiple sampling events conducted in the same area (i.e., *N*=237 sampling events total; 3 tributaries * 2 reaches * 2 net types * 7 seasons * 2–3 sampling sites) (Bates et al., [2015](#page-12-9)). Given the lack of diference between gillnet types, we pooled pelagic and benthic gillnets yield per sampling event and evaluated spatial and temporal diferences in abundance. Specifcally, we modeled BPUE or NPUE as a function of reach (identifed by its tributary), season, and their interaction using a general linear model (GLM). We also modeled the BPUE or CPUE against environmental predictor variables (including MWD, WTE, DO, pH, WTR, and Con) and added reach (identifed by its tributary) as random factor using a LMM. Prior to analyses, we transformed the BPUE and NPUE data by log- and logit transformations, respectively.

We conducted all statistical analyses in R (v.4.0.2, R Foundation for Statistical Computing, Vienna, Austria). We calculated the taxonomic beta-diversity using the betapart package (Baselga & Orme, [2012](#page-12-10)). We performed the regression model, main effects estimation (Type III Wald's X^2 test), model fit plots and tests, and post hoc comparisons through the lme4 (Bates et al. [2015\)](#page-12-9), car (Fox & Weisberg, [2011\)](#page-13-17), and emmeans packages (Lenth et al., [2022\)](#page-13-18), respectively. We implemented the NMDS, CCA, PERMANOVA, and Simper analyses using the vegan package (Oksanen et al., [2020\)](#page-14-14). We considered statistically signifcant diferences at an alpha level of 0.05.

Results

We collected a total of 10,373 individuals weighing 579.9 kg and identifed a total of 55 fsh species at the upper and lower reaches of the three tributaries (averaged TL=181.3±1.0 mm; BW=55.9±4.2 g $(mean \pm S.E.).$). Of these, the order Cypriniformes with three families and 38 species dominated, followed by Perciformes (three families, six species) and Siluriformes (two families, six species). The family Cyprinidae had the highest species richness (34 species), followed by Bagridae (four species), Cobitidae (three species), and Serranidae (three species). Among these, 49.1% of species inhabited benthic habitats; 60% were limnophilic species; 25.5%, 29.1%, and 21.8% were piscivorous, invertivorous, and omnivorous species, respectively; 9.1% of species (fve) were non-native species (Online Resource 1). The species richness per reach ranged from 32–44 (X-Lower=44, X-Upper=41, Y-Lower=32, $Y-Upper = 35$, $Q-Lower = 34$, and $Q-Upper = 33$, respectively).

Spatial and temporal patterns of fish assemblage structure

We observed an overarching pattern, where a few fish species accounted for most of the biomass and abundance in reservoir tributaries. Specifcally, 15 species accounted for 91.2% of the biomass and 12 species made up 90.2% of the abundance. *Coilia brachygnathus* Kreyenberg & Pappenheim, 1908 was the most abundant species, which accounted 20.2% of the biomass and 34.6% of the abundance (Online Resource 1). The averaged value of taxonomic beta-diversity was higher when comparing reaches among tributaries (0.41 ± 0.11) ; lower vs. lower: 0.39 ± 0.27 ; upper vs. upper: 0.42 ± 0.28 ; lower vs. upper: 0.43 ± 0.19 ; mean \pm SE) than when the comparisons were made between the lower and upper reaches within tributaries $(0.32 \pm 0.22;$ X-Lower vs. X-Upper, 0.31; Y-Lower vs. Y-Upper, 0.33; Q-Lower vs. Q-Upper, 0.33). Fish assemblage structure varied between the pelagic and benthic habitat (PERMANOVA,

 $F = 5.39$, $P < 0.001$), among the three tributaries (*F*=2.66, *P*=0.001; X–Y, *P*=0.01; Q-X, *P*=0.02; Q-Y, *P*=0.55; Fig. [2](#page-6-0)a), between the lower and upper reaches $(F = 2.98, P = 0.004; Fig. 2b)$ $(F = 2.98, P = 0.004; Fig. 2b)$ $(F = 2.98, P = 0.004; Fig. 2b)$, and among four seasons $(F=3.15, P=0.001;$ all pairwise comparisons *P*<0.01, except for autumn vs. winter, spring vs. summer; Fig. [2](#page-6-0)c). *Coilia brachygnathus* (Simper test, 26.5%), *Hemiculter bleekeri* Warpachowski, 1888 (11.1%), *Pseudobrama simony* (Bleeker, 1864) (8.7%), *Culter alburnus* Basilewsky, 1855 (6.5%), *Hemiculter leucisculus* (Basilewsky, 1855) (6.5%), *Pelteobagrus nitidus* (Sauvage & Dabry de Thiersant, 1874) (5.8%), *Pseudolaubuca sinensis* Bleeker, 1864 (4.6%), *Pelteobagrus vachelli* (Richardson, 1846) (4.3%), *Squalidus argentatus* (Sauvage & Dabry de Thiersant, 1874) (4.4%), and *Saurogobio dabryi* Bleeker, 1871 (3.8%) principally contributed to both spatial and temporal diferences (Simper test, 82.2% in total; Fig. [2](#page-6-0)). When fish species were categorized based on their dietary guild, water layer, and flow guild, assemblage structure also varied within and among tributaries (PERMANOVA, Dietary guild: *F*=0.48, *P*=0.03; Water layer: *F*=0.55, *P*=0.01; Flow guild: *F*=0.57, *P*=0.01). Overall, Overall, mid-pelagic (73.4%), and limnophilic (50.9%) groups dominated the biomass, irrespective of tributaries. The Yuangshui and Qinggan have less abundance in piscivorous fsh than the Xiangxi, but have more abundance in planktivorous fsh. From the upper to lower reaches of the tributaries, the abundance of mid-pelagic fsh decreased but that of rheophilic fsh increased (Table [2](#page-7-0)).

Fig. 2 Non-metric multidimensional scaling (NMDS) based on abundance showing changes in fsh assemblage structure among tributaries (**a**), reaches within tributaries (**b**), and seasons (**c**). Species abbreviations: Ps_si, *Pseudolaubuca sinen-*

sis; Sp_si, *Spinibarbus sinensis*; Co_br, *Coilia brachygnathus*; Cu_da, *Culter dabryi*; Pe_va, *Pelteobagrus vachelli*; Ac_ch, *Acheilognathus chankaensis*

Type	Functional group	X-Lower	X-Upper	Y-Lower	Y-Upper	O-Lower	Q-Upper	PERMANOVA
Diet	Herbivorous	4.3	1.2	7.8	15.6	5.0	0.7	$F = 0.48, P = 0.03$
	Detritivores	3.9	3.8	3.4	1.9	2.6	3.7	
	Planktivorous	17.2	18.1	17.6	55.2	58.9	50.9	
	Omnivorous	1.6	1.5	9.1	1.9	0.6	5.7	
	Invertivores	15.4	10.2	13.2	4.6	16.1	8.3	
	Piscivorous	57.6	65.2	48.9	20.8	16.8	30.9	
Water layer	Pelagic	0.1	0.01	$\mathbf{0}$	$\mathbf{0}$	0.1	0.03	$F = 0.55, P = 0.01$
	Mid-pelagic	68.1	81.1	59.6	75.3	75.6	80.6	
	Mid-benthic	8.7	5.0	15.0	18.1	9.1	4.1	
	Benthic	23.0	14.0	25.4	6.57	15.3	15.2	
Flow	Eurytopic	20.9	22.6	21.1	57.2	62.8	58.2	$F = 0.57, P = 0.01$
	Rheophilic	11.2	6.1	13.8	3.5	14.7	2.2	
	Limnophilic	67.9	71.3	65.1	39.3	22.5	39.6	

Table 2 Spatial patterns of relative biomass (%) of fsh functional groups inhabiting three tributaries of the Three Gorges Reservoir assessed by PERMANOVA

X Xiangxi River, *Y* Yuanshui River, *Q* Qinggan River, *Lower* lower reach, *upper* upper reach

The evaluated environmental factors explained 59.1% of the total variation associated with the frst and second axes of the CCA (Permutation test, $F = 2.29$, $P < 0.01$; adjusted $R^2 = 0.35$). The MWD, WTE, pH, Con, slope, and vegetation coverage signifcantly afected fsh assemblage structure (Permutation test, all $P < 0.05$). The first axis summarized 38.2% of the variance $(F=7.87, P<0.01)$ and was positively correlated with Con (correlation coefficient=0.71) and WTE (0.63) , influencing the abundance of *C. brachygnathus* and *H. bleekeri*; in contrast, it was negatively correlated with pH (-0.43) and vegetation coverage (-0.57) , influencing the abundance of *Parabramis pekinensis* (Basilewsky, 1855) and *Ctenopharyngodon idella* (Valenciennes, 1844). The second axis summarized 20.9% of the variance $(F = 4.31, P < 0.01)$ and was positively correlated with pH (0.47) and vegetation coverage (0.38), infuencing the abundance of *P. pekinensis*, *Pelteobagrus fulvidraco* (Richardson, 1846), and *P. nitidus*; in contrast, it was negatively correlated with MWD (-0.83) and slope (-0.33) , infuencing the abundance of *Leiocassis longirostris* (Bleeker, 1864), *Rhinogobio cylindricus* Günther, 1888, *Coreius heterodon* (Bleeker, 1864), *Acheilognathus macropterus* (Bleeker, 1871), and *Silurus meridionalis* Chen, 1977 (Fig. [3](#page-8-0)).

Spatial and temporal comparison of CPUE

The overall BPUE was 8.96 ± 0.77 g/m²/night (mean \pm SE, *N*=237), which was similar between pelagic gillnets $(9.31 \pm 1.15 \text{ g/m}^2/\text{night}, N=121)$ and benthic gillnets $(8.6 \pm 0.94 \text{ g/m}^2/\text{night}, N = 116;$ LMM, $X^2 = 2 \times 10^{-4}$, $P = 0.99$). The pooled average of the BPUEs changed spatially and temporally, as indicated by a signifcant interaction efect between reach and season (GLM, $F=2.42$, $P=0.003$), and the significant effect of reach $(F=9.62, P<0.001)$ and season $(F = 15.65, P < 0.001;$ Online Resource 2). The averaged BPUE was the lowest at Y-Lower in winter $(1.92 \pm 0.29 \text{ g/m}^2/\text{night})$, and the highest at Y-Upper during spring $(35.33 \pm 8.11 \text{ g/m}^2/\text{night})$; Fig. [4](#page-9-0)).

The overall NPUE was 0.19 ± 0.02 ind./m²/night (mean \pm SE, *N*=237), which was similar between the two gillnet types (benthic: 0.22 ± 0.03 ind./m²/ night, pelagic: 0.16 ± 0.02 ind./m²/night; $X^2 = 3.22$, $P=0.07$). The pooled average of the NPUEs also changed spatially and temporally, but the spatial variation appears to be mediated by season (reach×season: *F*=2.19, *P*=0.01; reach: *F*=2.08, *P*=0.07; season: *F*=33.6, *P*<0.001; Online Resource 2). The lowest averaged NPUE was observed at the X-Upper in winter $(0.05 \pm 0.01 \text{ ind.})$

Fig. 3 Results of canonical correspondence analysis (CCA) showing the relationship between environmental variables and fish assemblage structure in the lower and upper reaches of the Xiangxi River, Qinggan River, and Yuanshui River. Variables abbreviations: DO, dissolved oxygen; WTR, water transparency; WTE, water temperature; Con, specific conductivity; MWD, maximum water depth. Species abbreviations: Pa_pe, *Paralramis pekenensis*; Pe_fu, *Pelteobagrus fulvidraco*; Pe_ni, *Pelteobagrus nitidus*; Cu_al, *Culter alburnus*; Pe_va, *Pelteoba-*

macropterus; Le_lo, *Leiocassis longirostris*; Rh_cy, *Rhinogobio cylindricus*; Co_he, *Coreius heterodon*; Cy_ca, *Cyprinus carpio*; Ar_no, *Aristichthys nobilis*; Cu_er, *Cultrichthys erythropterus*; Pr_ch, *Protosalanx chinensis*

m2 /night), and the highest at the X-Lower in summer $(0.51 \pm 0.11 \text{ ind./m}^2/\text{night}; \text{Fig. 4}).$

Both the BPUE and NPUE decreased with water level (MWD; LMM, BPUE: $X^2 = 30.57$, $P < 0.001$; NPUE: $X^2 = 10.10$, $P = 0.001$) and dissolved oxygen (DO, BPUE: $X^2 = 4.02$, $P = 0.04$; NPUE: $X^2 = 5.73$, $P=0.02$). Meanwhile, the BPUE increased with pH $(X^2 = 9.71, P = 0.002)$, and NPUE increased with water temperature (WTE, $X^2 = 10.08$, $P = 0.002$; Fig. [5\)](#page-9-1).

Discussion

Classical and contemporary studies demonstrate that habitat heterogeneity infuences the species assemblage structure of various animal taxa (MacArthur & MacArthur, [1961;](#page-14-0) Alberti & Wang, [2022](#page-12-0); Meerhoff & González-Sagrario, [2022\)](#page-14-15). Previous studies at the TGR demonstrated the role of large-scale habitat heterogeneity on fsh assemblage structure (e.g., Liao et al., [2018a;](#page-13-8) Yang et al., [2021](#page-15-15)). The present study

grus vachelli; Ps_sim, *Pseudobrama simony*; Co_br, *Coilia brachygnathus*; Cu_da, *Culter dabryi*; Cl_id, *Ctenopharyngodon idella*; Ps_si, *Pseudolaubuca sinensis*; He_le, *Hemiculter leucisculus*; Sq_ar, *Squalidus argentatus*; He_bl, *Hemiculter bleekeri*; Si_me, *Silurus meridionalis*; Ac_ma, *Acheilognathus*

Fig. 4 Spatial and seasonal changes of the averaged (i.e., two net types) catch per unit effort based on fish biomass (BPUE) and abundance (NPUE) in the lower and upper reaches of the Xiangxi River (X-Lower, X-Upper), Qinggan River (Q-Lower,

Q-Upper), and Yuanshui River (Y-Lower, Y-Upper). Values with diferent lowercase letters above the bar are signifcantly diferent at alpha 0.05

Fig. 5 The efect of key environmental variables on fsh biomass (BPUE) and abundance (NPUE) in the three tributaries. The gray band represents the 95% confdence interval. *MWD* maximum water depth, *DO* dissolved oxygen, *WTE* water temperature

goes a step further to investigate whether fsh assemblage structure is infuenced by small-scale habitat heterogeneity and to explore how reservoir tributaries contribute to the conservation of fish diversity in large reservoirs. Our results supported the hypothesis that fsh assemblage structure difered among tributaries, reaches within tributaries, and seasons. The most infuential environmental variables were water depth, water temperature, dissolved oxygen, and pH, which constituted the components of habitat heterogeneity driving spatial and temporal changes in fsh assemblage structure.

The Xiangxi, Qinggan, and Yuanshui are three neighboring tributaries connected with the TGR mainstem; after impoundment, flow in their lower reach is year-round static, while in the upper reach, flow is temporally static during the high water level due to a backwater effect. We found that fish assemblage structure exhibited spatial heterogeneity among the three tributaries and upper and lower reaches within tributaries and showed temporal heterogeneity among four seasons. We also found that averaged beta-diversity among tributaries was higher than that within tributaries. These fndings indicate that reservoir tributaries form small-scale habitat heterogeneity through spatial variation and temporal transformation of habitat characteristics. Due to habitat heterogeneity, reservoir tributaries constitute important refuges for diferent fsh categories. Spatial turnover across tributaries also create diferences in species compo-sition (Vitorino Junior et al., [2016\)](#page-15-5), thereby maintaining diverse fsh assemblages in large reservoirs. Previous studies found similar phenomena (Li et al., [2016;](#page-13-19) Pfauserová et al., [2022](#page-14-16)) and argued for protecting tributary habitats and constructing artifcial habitats to improve habitat heterogeneity in reservoirs (Lin et al., [2014](#page-13-20); Marques et al., [2018](#page-14-7)). Small-scale habitat heterogeneity among reservoir tributaries and between reaches within tributaries, together with longitudinal habitat heterogeneity among the lentic, transitional, and lotic sections (Liao et al., [2018a\)](#page-13-8), likely contributes to maintaining the high fish diversity observed at the regional scale. Species richness in the surveyed reservoir tributaries accounts for 88.7% (55 out of 62 species) of the total richness in the lower section of the TGR (Liao et al., [2018a\)](#page-13-8).

Understanding which environmental factors contribute to the aforementioned small-scale heterogeneity and how they interact to support biodiversity is crucial for freshwater fsh conservation. In this study, a mix of water quality and physical stream attributes, chiefy water depth, water temperature, pH, specifc conductivity, riparian slope, and vegetation coverage, were found to be drivers of fsh assemblage variation. First, we found that fshes producing sinking eggs (e.g., *Pelteobagrus* spp.; Ding, [1994\)](#page-13-12) or grassattached eggs (e.g., *Cyprinus carpio* Linnaeus, 1758,

Paralramis pekenensis (Basilewsky, 1855), *C. alburnus*, and *Culter dabryi* (Bleeker, 1871); Ding, [1994\)](#page-13-12) preferred habitats in the upper reaches. The upper reaches recover to a riverine state with decreased water levels during spring and summer, and at the same time, terrestrial plants also recover rapidly at the water-level-fuctuation zones, except for the Xiangxi. This consistency suggests that the upper reaches provide important spawning structure for these fsh groups (Hladík & Kubecka, [2004;](#page-13-21) Marshall et al., [2015\)](#page-14-17). Second, our results also revealed that fshes producing rock-attached eggs (e.g., *L. longirostris*, *S. meridionalis*) and drifting eggs (e.g., *P. sinensis*, *H. bleekeri*, and *S. argentatus*) were more abundant in the lower reaches, which is likely because the lower reaches have deeper water and contain mixed substratum with abundant rocks, providing important reproduction and nursery grounds for these fsh groups (Probst et al., [2009](#page-14-18); Szalóky et al., [2021\)](#page-14-11).

The TGR has water-level-fuctuation zones with a total shoreline length of 5426 km and an area afected by drawdown events of 350 km^2 , which are mainly covered with herbaceous plants such as Bermuda grass, *Cynodon dactylon* (Linnaeus) Persoon, and annual species like *Xanthium sibiricum* Patrin ex Widder (Dou et al., [2023](#page-13-22)). The upper reaches of the tributaries have shallower water depth and higher vegetation coverage in the water-level-fuctuation zones; these areas attracted more herbivorous species such as *C. idella* and *P. pekenensis*, suggesting that vegetation provided a food subsidy to these fshes (Felden et al., [2021](#page-13-23)) and enhanced structural complexity with increasing water level (Norris et al., [2020\)](#page-14-19). A previous study revealed a similar phenomenon, i.e., riparian plants and fooded vegetation were important food sources for fshes in the Daning River, a tributary of the TGR (Deng et al., [2018](#page-13-24)). In addition, some lotic fsh species (e.g., *R. cylindricus*, *C. heterodon*), that only spawn in the riverine mainstem upstream of the TGR, were commonly sampled at the lower reaches, suggesting that the confuence areas of tributaries with the reservoir provide important feeding and nursery ground for lotic fsh species (Moreira et al., [2022](#page-14-20)). The water temperature mainly afected the abundance of common small-bodied fsh populations (e.g., *C. brachygnathus* and *H. bleekeri*), which preferred warmer habitat in the upper reaches during summer. These species are zooplanktivorous fsh, and in turn, zooplankton biomass was higher during spring and summer (spring: 1.40 ± 0.34 mg/L; summer: 0.65 ± 0.13 ; autumn: 0.22 ± 0.09 ; winter: 0.04 ± 0.01 ; C. Liao, unpublished information) and in the upper reaches (upper: 0.98 ± 0.26 ; lower: 0.42 ± 0.09 mg/L; C. Liao, unpublished information) of the three tributaries. These lines of evidence suggest that upstream summer migration may be related with behavioral traits of fish seeking optimal thermal conditions for spawning and feeding (Togaki et al., [2023\)](#page-15-7).

We also found that fsh abundance exhibited spatial and seasonal variation. Gillnets are commonly used to estimate fsh resources, yet capture can be infuenced by factors such as mesh size (Loisl et al., [2014\)](#page-13-25) and diel variation in fsh activity (Wegscheider et al., 2020). In this study, we sampled fish using multimesh gillnets comparable to CEN 2015 standard (CEN, [2015\)](#page-12-5), and standardized the sampling time (night) and duration to ensure comparability across reaches and seasons. To the best of our knowledge, it is the frst time that such comparable multimesh gillnet sampling approach was used to survey fsh assemblages in the TGR, rather than studying fish assem-blages based on fisher's catches (Gao et al., [2010](#page-13-10); Yang et al., [2012](#page-15-9); Wei et al., [2021\)](#page-15-17). Interestingly, we obtained similar averaged CPUEs between pelagic and benthic gillnets, suggesting that the benthic and pelagic habitats have similar fsh abundance in the three tributaries. This can be explained by several reasons. The benthic dissolved oxygen often afects benthic fsh abundance (Prchalová et al., [2008](#page-14-21)); commonly, in deep reservoirs, dissolved oxygen is relatively low below the thermocline and leads to a low benthic fsh abundance compared to the pelagic layer (Järvalt et al., [2005](#page-13-26); Prchalová et al., [2008](#page-14-21)). In these reservoir tributaries, the dissolved oxygen $was > 6$ mg/L all the way down to a depth of 50 m (unpublished information), which may stem from high water transparency and rapid water exchange rate (>10 times per year) therein (Lu & Yang, [2020](#page-13-27)). Regardless of the mechanisms originating high dissolved oxygen, this dissolved oxygen concentration is sufficient to sustain benthic fishes year-round (Wen et al., [2022\)](#page-15-18), Meanwhile, the benthic fsh faunas were dominated by omnivorous and invertivores fshes (e.g., *S. dabryi*, *S. argentatus*, *P. vachelli*, and *P. nitidus*), and the abundant detritus, zoobenthos, and shrimps therein can provide abundant food resources to maintain relatively high benthic fsh abundance (Liao et al., [2019](#page-13-9)).

Spatial (e.g., horizontal and vertical, upper and lower reaches) and temporal (e.g., seasonal, diel) variation in fsh abundance is common in reservoirs, which may be induced by matching environmental change, as well as by fsh morphological adaptations and behavior (i.e., littoral vs. pelagic) (Riha et al., [2022](#page-14-22)). We found that the averaged fsh BPUE and NPUE exhibited seasonal and spatial changes in the three reservoir tributaries, among which the main infuencing environmental variables were water depth, water temperature, dissolved oxygen, and pH. First, water depth decreases from the lower to the upper reach; in turn, we found that BPUE and NPUE tended to increase from the lower to the upper reaches of the tributaries, and the shallowest Y-Upper reach yielded the highest BPUE (averaged 20.53 $g/m^2/night$) during our study. Other studies found similar spatial patterns and attributed such fndings to abundant food resources and suitable habitats for feeding and spawning activities in shallow areas (Prchalová et al., [2008,](#page-14-21) [2009](#page-14-23)). The spatial diferences in phytoplankton (lower: 3.63 ± 1.21 mg/L; upper: 12.37 ± 4.12 mg/L; C. Liao, unpublished information) and zooplankton biomass (lower: 0.42 ± 0.09 mg/L; upper: 0.98 ± 0.26 ; C. Liao, unpublished information) in our study supported this assumption; shallower habitats support greater autochthonous primary productivity and therefore, greater consumer fsh biomass. The second factor, water temperature, changed along with seasonal fuctuations in water depth at the TGR, where water level declines from winter (175 m) to summer (145 m). During spring and summer, water temperature increased (Liao et al., [2018a](#page-13-8)), and most fsh species increased their feeding activity and swimming speed, which increased the BPUE and NPUE specially in the upper reaches (Specziár et al., 2013). Dissolved oxygen and pH also are considered to be important factors infuencing fsh abundance (Matthews et al., [2004](#page-14-25); Khalsa et al., [2021](#page-13-28)). In our study, dissolved oxygen and pH were at a suitable range for fshes; thus, the observed gradients in water depth, water temperature, and other factors most likely infuenced fsh abundances. Meanwhile, we acknowledge some shortcomings during our fsh sampling; we should have measured the deployed depth of each benthic gillnet, and deployed other gillnets in the water layers between those sampled by the pelagic and benthic gillnets. These strategies would allow future studies investigate changes in fsh assemblages at diferent depths.

Conclusion

In conclusion, the present study demonstrated that fish assemblage structure differed among tributaries, reaches within tributaries, and seasons due to the heterogeneity in water quality and physical stream attributes. The fndings from this study revealed that reservoir tributaries in the TGR have abundant fsh both in pelagic and benthic habitats, and fsh abundance varied spatially and temporally driven by water quality and physical variables at a small scale. Our results also improve scientifc understanding of how smallscale habitat heterogeneity enhances spatial and temporal variation of fsh assemblage structure. Based on our fndings, local habitat heterogeneity is critical for conserving fsh diversity in large reservoirs coupled with large-scale heterogeneity among the lotic, transitional, and lentic zones.

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Data availability The datasets analyzed during the current study are available from the corresponding author on reasonable request.

Code availability The codes used in this study are available from the corresponding author on reasonable request.

Declarations

Confict of interest The authors have no conficts of interest to declare that are relevant to this article.

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