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Increasing drying changes the relationship between biodiversity and ecosystem multifunctionality

Chaoran Li[1], Jun Hou[1], Ming Kong[2], Yu Yao[3], Tanveer M. Adyel[4], Jun Wu[1], Guoxiang You[1], Yue Yu[5], Songqi Liu[6], Zijun Yang[1] & Lingzhan Miao[1] ✉

Increased drying of rivers under global climate change is leading to biodiversity loss. However, it is not clear whether biodiversity loss affects river functions. In this study, we investigated the changes in biofilm community diversity and functions in an artificial stream after different drying durations. A critical drying duration of around 60 days was found in the microbial composition and functions. Therefore, different drying durations can be divided into short-term drying (~0–20 days) and long-term drying (~60–130 days) to analyse the effect of biodiversity in terms of ecosystem functions. In summary, the dominant relationship of biodiversity on community stability got uncoupled after long-term drying. Community assembly became dominant in maintaining multifunctionality with increasing drying duration rather than biodiversity as traditionally perceived. This study reveals the importance of community assembly, extending theoretical knowledge of the relationship between biodiversity and ecosystem multifunctionality.

Extreme events (e.g. drying) induced by climate warming and human activities significantly affected river ecosystems and caused degradation of ecosystem functions[1,2]. River disconnection and drying are becoming more frequent and severe under the influence of extreme drying, such as intermittent rivers and ephemeral streams (IRES) which experience intermittent dryings, and this alteration in river hydrology and resource availability significantly affects the entire benthic ecosystem[3,4]. As a crucial ecological indicator in river ecosystems, benthic biofilm is paramount in unravelling the biodiversity and ecosystem functions[5]. In recently, Maestre, et al. [6] found that plant function was positively and significantly related to species richness in drylands, and this relationship became progressively stronger and more positive as environmental stress increased[7]. However, Alvarez, et al.[8] observed a decoupling of α-diversity from ecosystem function after environmental disturbances in a river ecosystem, possibly due to the community instability caused by rapid biotic turnover during the recovery period. So β-diversity and microbial network structure should be considered to completely analyse biodiversity, which may provide deeper insights than focusing on a single alpha diversity in isolation[9,10]. Therefore, in response to various environmental pressures, exploring the relationship between biodiversity and ecosystem function (BEF) has become a priority for ecologists[11–13].

In addition, actual ecological communities are undoubtedly governed by rules such as niche-based theory and the neutral theory, and different community assembly mechanisms were demonstrated to also significantly affect ecosystem functions[14,15]. Based on the niche-based theory and the neutral theory[16,17], ecologists broadly accepted that both stochastic ('neutral') and deterministic processes influence community assembly simultaneously[18], which includes five driving mechanisms: homogeneous selection, homogenising dispersal, undominated, dispersal limitation, and heterogeneous selection[19,20]. Consequently, exploring the determinism and stochasticity in the community assembly process is critical to comprehending the effect of community assembly to ecosystem functions[12,21]. Ecosystems are highly valued for supporting various ecological functions, yet most research focuses on single processes in isolation. Therefore, the relationship between biodiversity and ecosystem multifunctionality (B-EMf) deserves more research attention[22–24]. Further to this, microbial community stability should be focus on since the

[1]Key Laboratory of Integrated Regulation and Resources Development on Shallow Lakes, Ministry of Education, College of Environment, Hohai University, Nanjing, 210098, People's Republic of China. [2]Nanjing Institute of Environmental Sciences, Ministry of Ecology and Environment, Nanjing, 210042, People's Republic of China. [3]School of Environment, Nanjing Normal University, Nanjing, 210023, China. [4]Centre for Nature Positive Solutions, School of Science, RMIT University, Melbourne, VIC, 3000, Australia. [5]Department of Civil, Environmental, and Geomatic Engineering, ETH Zürich, Zürich, 8092, Switzerland. [6]School of Environmental Science and Engineering, Suzhou University of Science and Technology, Suzhou, 215009, People's Republic of China. ✉e-mail: lzmiao@hhu.edu.cn; mlz1988@126.com

sustainability of both the multifunctionality and biodiversity rendered by the benthic ecosystem are dependent on a relatively stable microbiome[25].

The state of ecosystems during rewetting is more important for investigating the ecological effects of intermittent rivers than focusing on the state during drying. Considering that complex interactions of biofilm communities and multifunctionality can be clearly analysed in controlled environments, experiments were carried out using artificially modified rivers which rewetting after different drying durations. Metabolic functions related to elements such as carbon, nitrogen and phosphorus were considered in the calculation of biofilm multifunctionality, based on their necessity for ecosystem maintenance and energy flow[10,11]. The partial least squares path models (PLS-PM) were used to analyse the main factors affecting ecosystem multifunctionality after different drying duration, whether biodiversity or community assembly, and whether community stability plays an important role in maintaining multifunctionality.

Results

The responses of biofilm functions during rewetting after different drying duration

The biofilm multifunctionality index increased with increasing drying duration up to 60 days, while no further increase in the index was observed beyond this duration (Supplementary Fig. 1a). Similar responses were also observed in the nitrogen metabolic index (Supplementary Fig. 1b), carbon metabolic index (Supplementary Fig. 1c), and phosphorus metabolic index (Supplementary Fig. 1d). The cluster analysis between groups after z-score standardisation with different biofilm functions showed that the longer the duration of drying, the stronger the functional difference with control, with a critical drying period of 60 days (Fig. 1a). Specifically, the biofilm metabolic activities of BGLU, NADH, NOS, AMO, LAP, NAR and ACP peaked after 60 days of drying and then decreased following prolonged drying (Fig. 1a), while the responses of ecosystem metabolism were exactly the opposite, with decreases after 60 days of drying followed by an increases (Fig. 1a). Additionally, there was a significant difference between the biofilm multifunctionality after moderate drying duration (control, 20 days, and 60 days) and after prolonged drying duration (100 days and 130 days) (Fig. 1b, Supplementary Table 4, PERMANOVA, $p < 0.05$). Meanwhile, the same difference was also found in the biofilm carbon cycle and the nitrogen cycle after different drying duration (Fig. 1b, Supplementary Table 4, PERMANOVA, $p < 0.05$); and the gradually increased difference with increasing drying between the control with each experimental group was found in phosphorus cycle (Fig. 1b, Supplementary Table 4, PERMANOVA, $p < 0.05$).

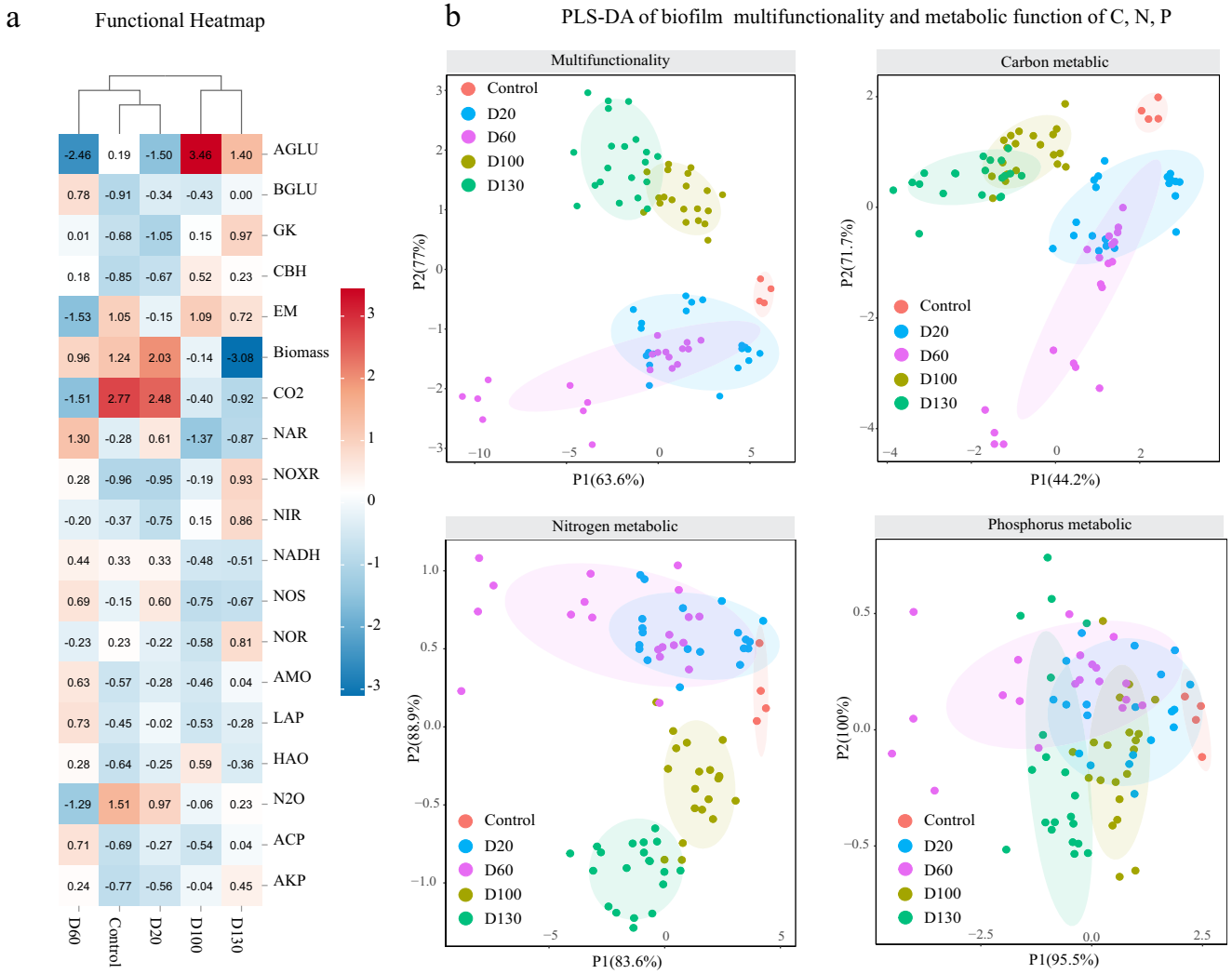

Fig. 1 | The responses of biofilm functions during rewetting after different droughtdrying duration. a Heatmap of all ecosystem functions related to the cycling and storage of carbon, nitrogen, and phosphorus. The values on the colour blocks means the index after z-score standardisation. The cluster tree was constructed based on PERMANOVA. **b** PLS-DA of biofilm multifunctionality and elemental metabolism (carbon metabolic, nitrogen metabolic and phosphorus metabolic) after different drying duration.

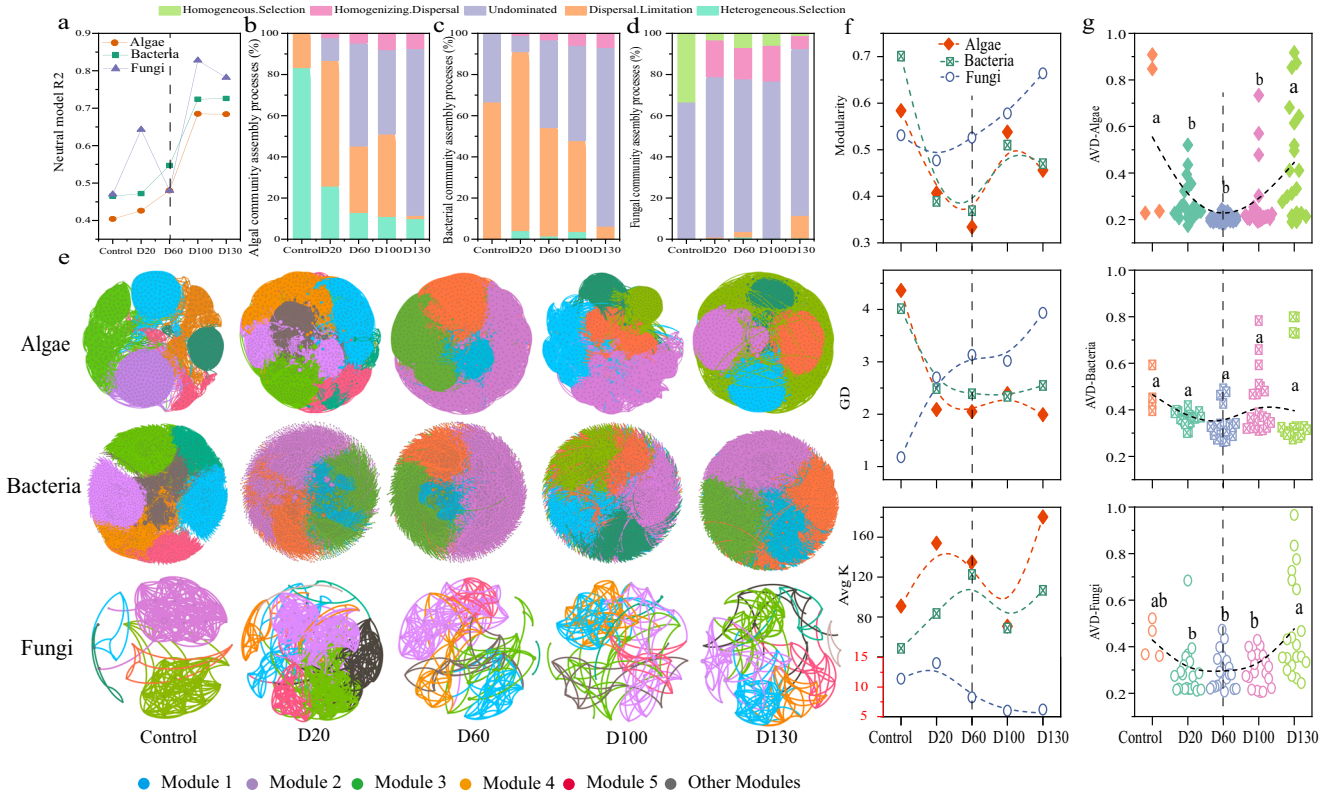

Fig. 2 | The changes of microbial network and community assembly mechanisms. **a** The fitting results of biofilm neutral community model (R^2); (**b**-**d**). Biofilm community assembly. Deterministic processes include homogeneous and variable selection, and stochastic processes include dispersal limitation, homogenising dispersal, and undominated; (**e**). Network revealing the modular associations among biofilm OTUs; (**f**). Topological nature of the network structure (modality, Avg K and GD); and (**g**). Biofilm community stability (AVD) of different components after different drying duration. The black dashed line (f and g) marks the 'drying inflection point'. D20 is rewetting after 20 days of drying. Different letters (**g**) indicate significant differences within the biofilm community stability (ANOVA, $p < 0.05$) across different drying duration.

The changes of microbial network and community assembly mechanisms

All samples approached saturation in rarefaction curves analysis, indicating that the sequencing effort was sufficient to estimate the responses of these biofilm microbial communities to drying and rewetting alternation (Supplementary Figs. 2, 3). Neutral community model fits (R^2) showed that the effects of stochasticity gradually dominated in the biofilm community assembly, especially after 60 days of drying (Fig. 2a and Supplementary Figs. 7–9). Meanwhile, the findings of the null model showed that undominated processes and dispersal limitation were the significant drivers of algal and bacterial community assembly, and the undominated processes always dominated the fungal community assembly (Fig. 2b–d). The network modularity of the different biofilm fractions responded consistently to the different drying duration, which decreased and then increased with drying duration, with a significant inflexion point at around 60 days of drying. At the same time, the fungal network were more sensitive with a considerable inflexion point occurring after 20 days (Fig. 2e, f). However, the networks, AvgK and GD of the bacteria and algae were precisely the opposite of the fungal network, as AvgK of the fungal network gradually decreased, and GD gradually increased with increasing drying (Fig. 2f). Nevertheless, they both showed a significant inflexion point at around 20 days of drying (Fig. 2f). In addition, the eukaryotic community stability decreased and then increased significantly with increasing drying, while the stability of bacteria showed no significant change, indicating that eukaryotic microorganisms were significantly affected by drying and unable to recover rapidly during the rewetting period (Fig. 2g).

The effects of different drying duration on the relationship between biodiversity and multifunctionality

Based on the critical drying period of 60 days in the changes in biofilm functions and biodiversity with increasing drying duration, especially the clustering results of biofilm multifunctionality (Fig. 2b), a short-term drying group (control and D20) and a long-term drying group (D60, D100, and D130) can be classified (Fig. 4). Prolonged drying had a significant effect on the BEF relationship and the relationship of the community assembly mechanism with ecosystem functions (Fig. 3a, b, PLS-PM). After long-term drying, biodiversity decoupled with ecosystem functions, and instead community assembly contributes more to functions (Fig. 3a, b), especially to phosphorus cycle (Fig. 3a, b).

The PLS-PM results showed that the increasing drying duration had a significant effect on the relationship of biofilm multifunctionality with community assembly (from −0.289 to 0.446) and biodiversity (from −0.28 to 0.191) during rewetting (Fig. 3c, d). The most important predictor for biofilm multifunctionality was community assembly rather than biodiversity (Fig. 3c, d). In addition, the relationship of multifunctionality with community stability similarly changed from a negative to a positive effect (Fig. 3c, d). With drying increasing, the significant impact of biofilm biodiversity on community stability during rewetting was weakened (Fig. 3c, d).

Discussion

For investigating the mechanism of climate change aggravated river drought on river ecological functions, this study analysed the main factors affecting ecological multifunctionality after different drying durations by the PLS-PM model with biofilm as the object. The research seeks to determine whether the factor is biodiversity or community assembly and if community stability

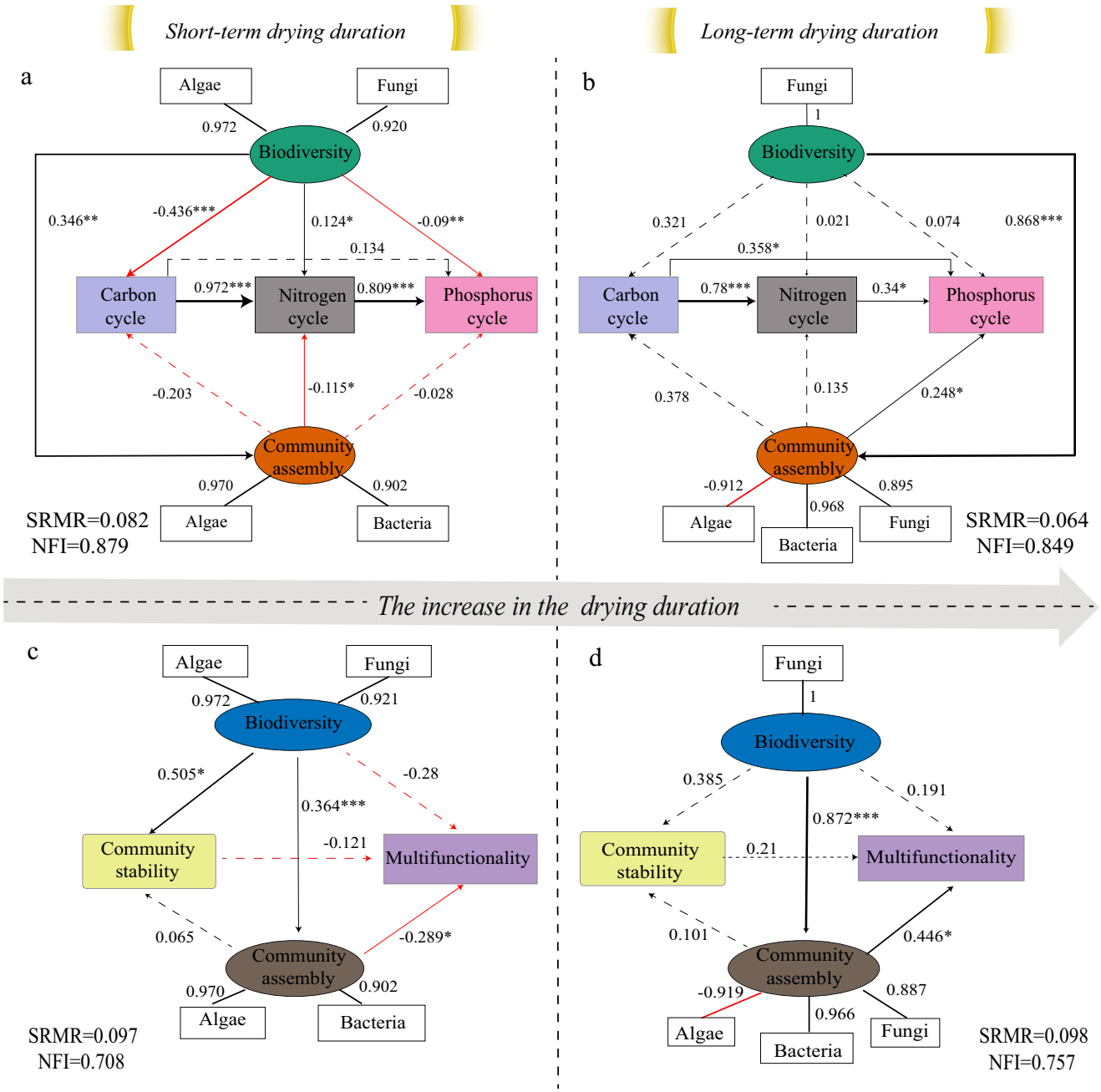

Fig. 3 | The effects of different drought timesdrying duration on the relationship between biodiversity and multifunctionality. The relationship between biodiversity and community assembly and the cycling function of different elements during rewetting of different drying durations (**a**, **b**) and the relationship with multifunctionality and community stability (**c**, **d**). The red and black lines represent negative and positive correlations, respectively, and the asterisks represent significant effects. Arrow width is proportional to the strength of the relationship (Supplementary Table 6). Insignificant biofilm functional and structural parameters were excluded based on their outer loadings by employing SmartPLS software (Version 3, Boenningstedt, Germany).

plays an important role in maintaining multifunctionality. The results provide evidence regarding the importance of community assembly on multifunctionality in intermittent streams, considering the effect of the drying period during rewetting.

The critical drying duration for biofilm biodiversity and functions

The phosphorus cycle of biofilm showed higher drying resistance than the carbon and nitrogen cycles (Fig. 1b), reflecting the importance of phosphorus to generate energy for microbial metabolism during rewetting[26,27]. In contrast, the carbon and nitrogen cycles of the biofilm could not maintain the same state with control after a prolonged drying duration (Fig. 1b). This is because after a prolonged drying there are not enough carbon and nitrogen sources within the biofilm for microbial growth, and it can only use phosphorus to generate energy for survival[5]. Based on the correlative nature of the individual functions[28], biofilm multifunctionality was more sensitive to increasing drying than single functions (Fig. 1), reflecting the similar underlying processes to increasing drying[29].

The same critical time point of river drying was also observed in the fitting result of the neutral community model (Fig. 3a), and the increasing dominance of stochasticity resulted from the stimulation from the hydrological change perturbations to stochastic factors[30,31]. Biofilm communities

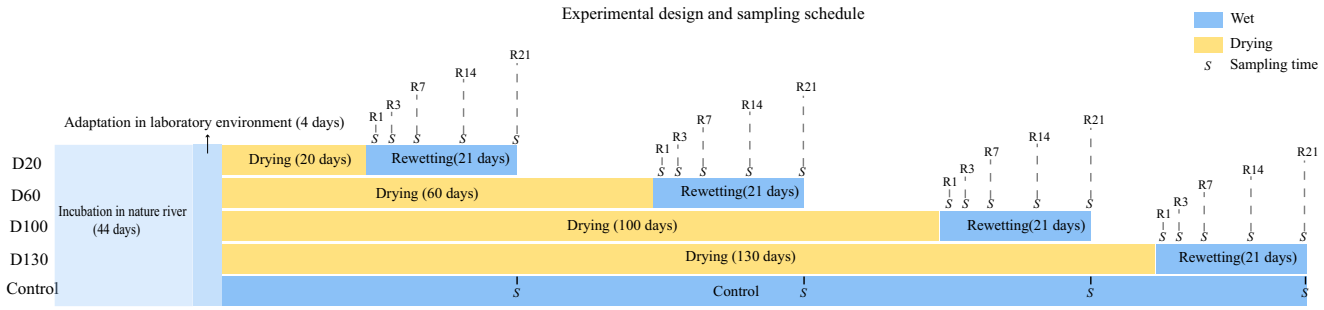

Fig. 4 | The alternation of drying and rewetting experimental design and sampling time axis. D20 is the experimental group that rewetting after 20 days of drying. R1 means the first day after rewetting.

are more susceptible to stochasticity with decreasing diversity[32,33] (Supplementary Fig. 8). Of the stochastic influence, undominated as the major factor for community assembly mechanisms of all components of biofilms (Fig. 3b–d), and it was especially significant for fungi. This might be due to microorganisms reduce interspecies competition by changing their resource utilisation strategies to increase individual independence with limited habitat resources after a prolonged drought, which may exert a more substantial influence in a low heterogeneous environment and beta diversity (Supplementary Table 5)[34–36]. The varied influence of dispersal limitation on different components of biofilms may be related to their different survival strategies, as the relative abundance of the microbial community could be the major factor influencing dispersal limitation[37–39]. Prolonged drying reduce microbial heterogeneity, diminishing ecosystem resilience by rendering microbial communities less equipped to face environmental adversities[40]. This homogenisation disrupts the efficient cycling of key nutrients such as carbon, nitrogen, and phosphorus—elements critical for ecosystem productivity and health. Such disruptions may impair vital ecosystem services, including soil fertility, water purification, and greenhouse gas regulation[41,42].

The growing theoretical and empirical evidence suggests that the mechanisms driving spatial variation in diversity to the in-depth study of the BEF relationship are of high theoretical importance[43]. Apart from the decreased microbial alpha diversity with increasing drought (Supplementary Figs. 4–6), the reduction in beta-diversity (Bray–Curtis dissimilarity between groups) with prolonged drying durations indicated that extended drying periods contributed to decreased microbial community heterogeneity (Supplementary Table 5), which could substantially impact biofilm functions through the "insurance effects" (microorganisms maintain their functions in variable environments by increasing beta diversity)[44].

Furthermore, the consistent response of the biofilm network modularity of the different components indicated different microbial communities rescaled to form a complex network of interactions following drying disturbance[45]. In this study, the bacterial and algal network's response mechanism to increasing drying stress reflected a tight and complex network structure[46], with a critical period of 60 days for rivers to dry up. The response of the fungal network was the opposite (Fig. 3e, f), which might be due to the higher environmental adaptation for fungi under extreme conditions[47], especially under the more impaired conditions of bacterial and algal communities[48,49]. There was also a critical time point of river drying at 60 days for eukaryotic (fungi and algae) community stability, corresponding to biofilm functions and confirming the community stability's critical effect on biofilm function[25]. Meanwhile, bacteria were more resistant to increasing drying, likely due to its most complex network or resistant phenotypes[50]. Consistent with the cluster analysis of biofilm functions and the result of the PLS-DA from multifunctionality, there was a critical drying period for rivers at around 60 days for biofilm biodiversity (Figs. 1–3). So, a short-term drying group (control and D20) and a long-term drying group (D60, D100, and D130) were classified based on the result.

The relationship between biodiversity and ecosystem functions decoupled after long-term drying

Two possible explanations exist for the decoupling between biodiversity and ecosystem functions after prolonged drying (Fig. 3). The first facet to consider is functional plasticity, defined as the ability of microbial communities to adapt to environmental fluctuations by fine-tuning their performance[49]. For example, BGLU, NOS, LAP, AMO and NAR tended to adapt to environmental changes (increase followed by decrease or a decrease followed by the rise with increasing drying duration) (Fig. 1a). While analysed from the perspective of elemental metabolic cycling, the elemental metabolic cycling functions of the biofilm differed significantly before and after the critical period for rivers to dry up (60 days of drying) (Fig. 1b). This was especially true for the carbon and nitrogen element metabolic functions (Fig. 1b), indicating that functional plasticity is not the only explanation for this decoupling. Hence, functional redundancy might also contribute to the results that some metabolic functions of biofilms could be maintained at a certain level when the biofilm diversity had been irreversibly affected by a prolonged drying, even though they may have behaved differently for a single function[51]. In addition, the explanatory power of biodiversity was always vital for community assembly(Fig. 3), since microbial species adapt to environmental change by generating a trade-off between environmental filtering and disposal limitation[52].

Community assembly is more important for ecosystem multifunctionality than biodiversity after long-term drying

The environment selects microbial functional traits rather than species to maintain essential ecosystem functions[53], which is why community assembly contributed more to biofilm ecosystem functions than biodiversity after long-term drying (Figs. 3, 4). The significant effect of community assembly on biofilm ecosystem functions shifted to the phosphorus cycle from the nitrogen cycle, which could be because the phosphorus cycle was more susceptible to being filtered by environmental conditions[54] (Fig. 3). Notably, the relationship between biofilm multifunctionality and different factors changed from a negative to a positive correlation following prolonged drying (Fig. 4), indicating that coexisting species, following niche partitioning based on various resources, could positively interact and further improve community functional performance[14]. There was a relatively significant positive effect between biofilm biodiversity and community stability (Fig. 4), while after long-term drying, the narrow distribution of community functional groups and the depleting redundancy of biofilm functions may have weakened the relationship between biofilm biodiversity and community stability[55].

Limitations and environmental implications

A critical period for rivers to dry up of around 60 days significantly altered the biodiversity and multifunctionality of biofilm communities. This shift emphasises the resilience of microbial communities to short-term drying conditions, where biodiversity significantly influences multiple ecosystem processes. However, the dependence of ecosystem multifunctionality on community assembly became more pronounced under long-term drying

conditions, suggesting that the structural dynamics of microbial communities play a key role in maintaining ecosystem multifunctionality under environmental stress. Furthermore, this study highlights the importance of stochastic processes in community assembly, especially under prolonged drying conditions, which may lead to reconfiguration of interactions between community assembly and ecosystem multifunctionality.

Understanding the relationship between community assembly and microbial functions is at the forefront of current ecological research[56,57]. Yet, this paradigm has not been broadly studied in river ecosystems. In this study, we examined the impact of different drying duration on the effect of biodiversity and community assembly on biofilm multifunctionality through indoor simulation experiments. Nevertheless, it is essential to acknowledge that the controlled experimental environment might potentially restrict the extensive extrapolation of our findings, considering the heterogeneous environmental composition in natural IRES. For example, the dynamics of critical variables, including light, temperature, and organic matter within natural river ecosystems, might coincide with dry-to-wet transitions and affect the extent and nature of biofilm responses[58]. More rigorous tests and further field experiments on the generality of this result in different ecosystems are needed for consideration as a fundamental principle of microbial ecology.

Based on this study, increasingly refined insights have been gained into the critical period for rivers to dry up of biofilm multifunctionality and the vital contribution of community assembly in driving it. Addressing the identified research gaps will progressively enhance the future policy relevance of critical periods for rivers to dry up. Implementing timely rewetting replenishment before reaching the critical period for rivers to dry up is likely the most essential and effective strategy. Additionally, biodiversity decoupled from ecosystem functions after long-term drying disturbances, meaning further work to identify the main drivers of ecosystem functions will be critical for ultimately predicting the response of community functions to environmental changes. More importantly, the increasing prominence of stochastic processes becomes more pronounced with longer drying durations, and community assembly is more important for ecosystem multifunctionality than biodiversity.

This study suggests an inaugural demonstration of the dominant role of stochastic assembly in shaping community structure and ecosystem multifunctionality. Elucidating the intricate connections among community assembly, biodiversity, and ecosystem functioning is critical for preserving biodiversity and effectively managing ecosystems.

Methods

Biofilm colonisation and laboratory experiment

Cobbles (2–3 cm in diameter) were colonised in Qin Huai River (32°03 36.2 N; 118°44 38.1 E) in May 2023 (mean temperatures is 16–24 °C), and the colonisation and water quality parameters are detailed in the Supporting Information (Supplementary Table 1). After 44 days, these cobbles with biofilm were translocated to acclimatised to the artificial streams(160 cm long, 20 cm wide, and 30 cm high) in a greenhouse at 18 ± 2 °C for four additional days under constant water quality through the addition of a nutrient solution per week (Supplementary Table 2)[59–62]. The channels were equipped with a pump (BT100-1L, Longer Precision Pump Co., Ltd., Baoding, China) to ensure water recycling and that the velocity of 0.14 m/s was maintained (consistent with the velocity of the Qin Huai River)[63].

In order to study the effect of drying duration on river ecosystems, we set up four experimental groups (after 20, 60, 100, and 130 days of drying duration, with measurements of biofilm community compostion and ecological functions during the 21 days of rewetting), and a control group without drying[64,65]. Samples were collected from experimental groups at five different times (after rewetting 1, 3, 7, 14 days and 21 days) and four replicates per time by randomly selecting specific amounts of cobbles from the channels. And sampled from the control group when experimental groups finish rewetting 21 days everytime (Fig. 4). More details are provided in the Supporting Information (Supplementary Note 1).

DNA sequencing and analyses

Four biofilm replicates were collected at five different times from four experimental groups during the rewetting and sampled from the control group at four different rewetting periods (Fig. 4). Detailed descriptions of the DNA extraction, eukaryotic (algal and fungal) 18S and bacterial 16S amplifications, and MiSeq sequencing are available in the Supporting Information and Supplementary Note 2[46]. The MagaBio Soil/Fecal Genomic DNA Purification kit (Bioer, Hangzhou, China) was used to extract the total DNA. The primer pair 515 F (5'-GTGCCAGCMGCCGCGGTAA-3') and 806 R (5'-GGACTACHVGGGTWTCTAAT-3')[66,67] was chosen to amplify the V4 hypervariable regions of the 16S rRNA gene for bacteria. For eukaryotes, we used 528 F (5' GCGGTAATTCCAGCTCCAA) and 706 R (5' AATCCRAGAATTTCACCTCT) primer sequences to amplify the V4 region of the 18S rRNA gene[46]. Meanwhile, the fungus and algae were distinguished from each other at the kingdom level for analyse; then the number of effective tags (no. of seqs) and the operational taxonomic units (OTUs) synthesis information table (OTU_table) were obtained for the subsequent analysis.

Microbial community beta diversity (community heterogeneity) was calculated through the dissimilarity between experimental communities based on the Bray–Curtis index[31]. Network analyses of different biofilm components (bacteria, fungi, and algae) were conducted on species abundance data at the OTU level[68], with Pearson's correlation p-value ≤ 0.05 and $|cor| > 0.5$. Additionally, biofilm microbial community stability was evaluated in terms of average variation degree, which was calculated using the deviation degree from the mean of the normally distributed OTU relative abundance[69]. We analysed the biofilm community assembly based on the null model using the iCAMP v1.5.12 package[70] and the neutral community model[18]. The R^2 value indicates the goodness of fit to the neutral community model, which means that the community assembly is fully consistent with stochastic processes when R^2 is close to 1[71]. The Supporting Information provides the detailed experimental determination, including statistical analyses of sequencing data (Supplementary Note 2).

Biofilm multifunctionality

In order to comprehensively assess functional changes in river ecosystems, we calculated z-scores for all ecosystem functions related to the cycling of carbon, nitrogen, and phosphorus. More detailed experimental determinations are provided in the Supporting Information (Supplementary Note 3 and Supplementary Table 3). At first, we averaged the standardised scores[13] of all individual ecosystem functions and calculated z-scores of all functions evaluated[72] as in Eqs. 1–2. Based on related functions, carbon metabolic, nitrogen metabolic and phosphorus metabolic also be calculated in the same way. The multifunctionality index was the average z-score for all functions measured.

$$x_{z-score} = \frac{x_i - \mu}{\sigma} \quad (1)$$

$$MF = \sum_{1}^{n} X_{z-scorei} \quad (2)$$

Where x_i is each biofilm function, μ refers to the mean of the x_i and σ refers to the standard deviation of the x_i. $X_{z-scorei}$ is the z-score of each biofilm function, and n is n is the number of all ecological functions monitored.

Partial least squares path models

The PLS-PM was constructed to calculate the relationship of BEF, as well as the impact of community assembly amd biodiversity on multifunctionality. We analysed the biodiversity of different biofilm components (algae, bacteria, and fungi) by computing z-scores of their alpha (richness), beta (community heterogeneity), and network diversity (AvgK, AvgCC, GD, and modularity) as in Eqs. 1–2[72]. We took the biofilm biodiversity, carbon cycle index, nitrogen cycle index, phosphorus cycle index, community stability and community assembly of different microbial components (fungi, algae,

and bacteria) as different potential variables in PLS-PM[73,74]. During the model fitting process, insignificant biofilm functional and structural parameters were excluded based on their outer loadings by employing SmartPLS software (Version 3, Boenningstedt, Germany), with the validity of the fitting results (Model_Fit, Path Coefficients, *p*-values for both direct and indirect effects, and other indicators). D_ULS, D_G and Rms Theta in the model fit indices are all such that smaller values indicate a better fit, while the model is only acceptable when SRMR is <0.1 and NFI is >0.7[46]. The dashed and solid lines are used to distinguish direct and indirect effects between the factors, allowing to focus only on the direct effects when performing impact analyses.

Statistical analyses

The significant differences in biofilm functions and biodiversity among groups was performed by a one-way ANOVA analysis ($n = 4$) after ensuring that all assumptions of ANOVA were met. This included verifying the independence of samples, testing for normality using the Shapiro-Wilk test, and confirming homogeneity of variances with Levene's test. The data will be appropriately transformed (e.g., log-transformed) where necessary to meet these assumptions. The results were considered statistically significant at $p < 0.05$. Partial Least-Squares Discriminant Analysis (PLS-DA) was used to distinguish the biofilm multifunctionalities of different groups based on PERMANOVA (Adonis) analyses (Anderson, 2001), as well as analysed the differences in elemental metabolic (carbon metabolic, nitrogen metabolic and phosphorus metabolic). To study the influence of the biodiversity of different biofilm components (algae, bacteria, and fungi) on biofilm functions, the mantel test was conducted based on Pearson's correlation using the ggcor package in R[75].

Data availability

The 16S and 18S sequence data that support the findings of this study are available in the NCBI repository (accession code: PRJNA1014953). The remaining data supporting the findings of this study are available within the article and source data file.

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Author contributions

Conceptualisation: J.H., M.K. Methodology: Y.Y., J.W., G.Y. Investigation: S.L., Z.Y., T.M.A. Visualisation: Y.Y., C.L. Supervision: J.H., L.M. Writing—original draft: C.L. Writing—review & editing: C.L., J.H., L.M.

Competing interests

The authors declare no competing interests.

Additional information

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Correspondence and requests for materials should be addressed to Lingzhan Miao.