Article

# Multidimensional β-diversity responses to global change: a meta-analysis highlighting divergent effects on plant communities

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In the Anthropocene, global change is reshaping biological communities, potentially leading to widespread biotic homogenization—a worrying erosion of biological distinctiveness. However, the extent to which human activities have homogenized plant communities worldwide remains a pivotal unresolved question. To address this gap, we conduct a global meta-analysis of 1604 experimental and observational comparisons from 256 studies to assess the impacts of major global change drivers on plant β-diversity across its taxonomic, functional, and phylogenetic dimensions. The findings indicate no significant net change in plant β-diversity globally, with responses varying markedly across global change factor types, biogeographic regions, ecosystems, and plant life forms. Specifically, climate change and biological invasions are consistently associated with reduced β-diversity, while land management (e.g., ecological restoration, reduced grazing, and controlled burning) is associated with increased β-diversity. The effects of land-use change (e.g., urbanization, habitat fragmentation, and infrastructure development) and multiple interacting factors are variable. Crucially, impacts differ across biodiversity dimensions. For instance, climate change is associated with reduced taxonomic and functional β-diversity but is associated with increased phylogenetic β-diversity. Our study calls for a shift in conservation focus from solely preventing species extinctions to addressing compositional changes in communities. It emphasizes the importance of functional and phylogenetic processes and the need to integrate all three biodiversity dimensions into monitoring and planning to maintain ecosystem resilience and evolutionary potential.

Human-induced global change factors (GCFs)—such as climate change, land-use intensification and expansion, and overexploitation of biological resources—are driving a global biodiversity crisis, as widely acknowledged in recent assessments[1,2]. While species extinction linked to those pressures is well documented[3], whether α- and β-diversity are also undergoing systematic declines, particularly at large spatial scales, remains contested[4,5]. Using a global dataset of biodiversity time series spanning 150 years and encompassing both marine and terrestrial systems, Dornelas et al.[6] found no consistent temporal trend in plant α-diversity. This finding has spurred growing interest in the hypothesis

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that biological homogenization—manifested as a decline in β-diversity—may be a more pervasive signature of the Anthropocene biodiversity crisis than species loss alone.

Biotic homogenization is typically marked by the loss of native species and the spread of generalists[7,8]. Emerging evidence suggests that anthropogenic disturbances can impose specific environmental filters[9,10], which may selectively eliminate rare species or promote the establishment of non-native species[11,12], ultimately reducing β-diversity. Conversely, biotic differentiation—reflecting increased dissimilarity among communities—has also been frequently observed in human-modified landscapes due to enhanced habitat heterogeneity[13,14]. These contrasting patterns raise a key question: is biotic homogenization of plant communities a universal outcome of the Anthropocene?

Global patterns of β-diversity have attracted growing attention in recent years. Blowes et al.[4], analyzing from 461 metacommunities surveyed over 10 to 91 years and 64 species checklists spanning 13 to more than 500 years, found that despite evidence of both homogenization and differentiation, the most common outcome was no net change in β-diversity. Similarly, Keck et al.[15] examined β-diversity across major taxonomic groups, habitat types, and five dominant human pressures, but also reported no consistent global trend toward biotic homogenization. While both studies included plants in their datasets, they did not explicitly present or interpret plant-specific patterns. Blowes et al.[4] aggregated results across taxa without disaggregating or discussing patterns for individual groups. Keck et al.[15], although differentiating taxonomic groups in their figures, did not provide a detailed analysis or interpretation of plant β-diversity, and did not comprehensively account for the multiple factors that influence effect size. Consequently, it remains unclear whether plant β-diversity follows similar global trends or whether specific GCFs and environmental contexts lead to divergent trajectories in plant communities.

Existing reviews of plant β-diversity dynamics have largely been limited to specific regions (e.g., tropical and subtropical forests[16]), individual GCFs (e.g., biological invasions[17]), or particular mechanisms of biotic homogenization[18,19]. Comprehensive global-scale assessments remain scarce. Moreover, β-diversity extends beyond taxonomic turnover (i.e., species replacement) to include phylogenetic and functional dimensions, which reflect differences in evolutionary histories and ecological strategies across communities[20]. Increasing evidence

shows that these dimensions often respond divergently to global change[10,21,22] and focusing on a single dimension or two of them at a time can obscure key biodiversity trends[23,24]. These limitations hinder a comprehensive understanding of how global change is reshaping plant community composition at multiple dimensions of biodiversity.

To address these knowledge gaps and evaluate the impacts of GCFs on plant β-diversity, this study synthesizes data from 256 studies encompassing 1604 paired comparisons between human-impacted and reference sites. Human impacts are classified into five types of GCFs: climate change (CC), biological invasion (BI), land use change (LUC), land management (LM), and multiple factors (MF). To account for the high heterogeneity observed across studies, a two-level sub-group analysis is performed to disentangle the effects of different GCFs across three dimensions of β-diversity. Furthermore, this study applies random forest models and meta-regression to assess how geographic, environmental, biological, and methodological factors modulate these responses. It provides a comprehensive quantitative synthesis of GCF effects on taxonomic (TB), functional (FB), and phylogenetic (PB) β-diversity and identifies key predictors of variation. Specifically, we address three questions: (1) Is there a global trend toward biotic homogenization of plant communities under GCFs? (2) How do biogeography, environmental context, focal taxa, and study design shape the direction and strength of GCF effects on plant β-diversity? (3) Are the impacts of different GCF types consistent across the three dimensions of plant β-diversity?

## Results
### General literature patterns
Our compiled dataset reveals that plant β-diversity responds to GCFs primarily through homogenization or differentiation across TB, FB, and PB, with few cases showing no change (Fig. 1). CC, LUC, and BI more frequently resulted in homogenization (191, 144, and 78 cases, respectively) than differentiation (150, 130, and 44 cases), while LM and MF showed the opposite trend, with more instances of differentiation (400 and 46) than homogenization (352 and 37). These patterns underscore the context-dependent and multidimensional nature of GCF effects on plant community composition.
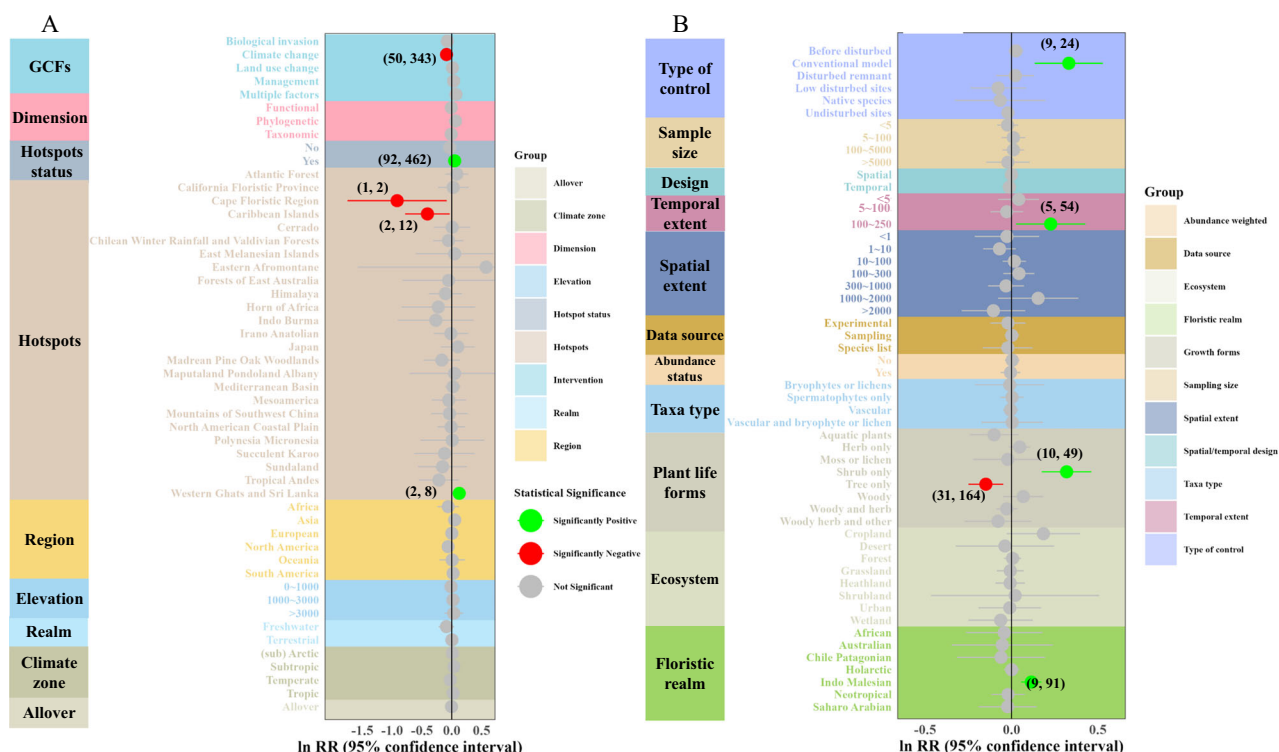
### Effects of GCFs on plant β-diversity
Our global meta-analysis indicated that anthropogenic global change factors (GCFs) did not significantly alter plant β-diversity, as evidenced
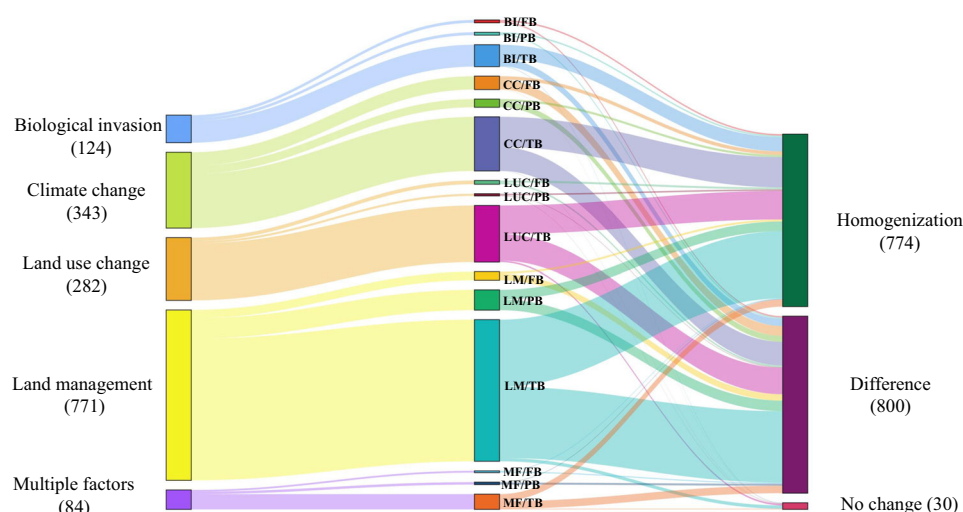


**Fig. 1 | Sankey diagram demonstrating the effect of five intervention types on the three dimensions of plant β-diversity.** The thickness of the lines is proportional to the number of tests corresponding to each combination of intervention type and diversity dimension. Colors are used to differentiate each combination type. TB taxonomic β-diversity, FB functional β-diversity, PB phylogenetic β-diversity, BI biological invasion, CC climate change, LUC land use change, LM land management, MF multiple factors. Source data are provided as a Source Data file.

**Fig. 2 | Context-dependent effects of GCFs on plant β-diversity.** The effect size (ln RR) of GCFs on plant β-diversity varies across different GCFs, dimensions, hotspot status, hotspots, regions, elevations, realms, and climate zones (**A**), as well as across ecosystems, florinal realms, plant life forms, taxa types, abundance status, data sources, and study design aspects such as temporal extent and spatial extent (**B**). Data are presented as mean ± 95% CIs of the estimated effect sizes. The numbers in parentheses indicate the number of studies and the number of observations, respectively. Source data are provided as a Source Data file.

by the confidence interval of the obtained response ratio (ln RR = −0.0031, 95% CI: −0.0406 to 0.0344), which overlapped with zero (Fig. 2A, Allover). However, results from different GCFs revealed a significant negative impact of climate change (CC) on plant β-diversity (ln RR = −0.088, 95% CI: −0.1599 to −0.0161) (Fig. 2A, GCFs).

In addition, there were significant positive impacts of GCFs on plant β-diversity (ln RR = 0.0491, 95% CI: 0.045 to 0.0936; $p < 0.05$) within biodiversity hotspots, compared to areas outside biodiversity hotspots (Fig. 2A, Hotspots status). GCFs reduced the β-diversity of trees by 13.93% (ln RR = −0.15, 95% CI: −0.0936 to −0.0045; $p < 0.05$) (Fig. 2B, Plant life forms). In contrast, GCFs increased the β-diversity of shrubs by 37.58% (ln RR = 0.319, 95% CI: 0.1751 to 0.4628), with significant effects ($p < 0.05$).

Furthermore, studies examining temporal spans between 100 and 250 years showed that GCFs significantly increased plant β-diversity by 25.50% (ln RR = 0.2271, 95% CI: 0.0265 to 0.4277; $p < 0.05$) (Fig. 2B, Temporal extent). Studies using the "conventional model versus novel model" design showed a significant increase in plant β-diversity by 39.33% (ln RR = 0.3317, 95% CI: 0.1348 to 0.5286; $p < 0.05$) (Fig. 2B, Type of control). Additionally, GCFs increased plant β-diversity in the Indo-Malesian region by 12.13% (ln RR = 0.1145, 95% CI: 0.056 to 0.1731; $p < 0.05$) (Fig. 2B, Floristic realm).

**The impacts of five GCF types on three dimensions of β-diversity**
In the subgroup analysis of the three dimensions of diversity−taxonomic β-diversity (TB) ($Q_t = 252995.9$, $p < 0.0001$, $I^2 = 99.48\%$), functional β-diversity (FB) ($Q_t = 17944.9891$, $p < 0.0001$, $I^2 = 99.25\%$), and phylogenetic β-diversity (PB) ($Q_t = 2119.5555$, $p < 0.0001$, $I^2 = 92.36\%$))− no significant overall effects of GCFs on plant β-diversity were detected (Supplementary Fig. 3).

Moreover, when the effects of different GCF types were analyzed, BI was found that significantly reduced plant β-diversity by 7.79% (ln RR = 0.0754, 95% confidence interval, 2.25–12.84%) ($Q_t = 1518.18$,

$p < 0.0001$, $I^2 = 91.90\%$) and exhibited no positive effects under any specific study conditions. In contrast, other GCFs did not show significant impacts on overall plant β-diversity (CC: ln RR = −0.0225, −0.0921 to 0.047, $Q_t = 27415.24$, $p < 0.0001$, $I^2 = 98.75\%$; LUC: ln RR = 0.0063, −0.0665 to 0.0792, $Q_t = 145459.98$, $p < 0.0001$, $I^2 = 99.81\%$; LM: ln RR = −0.1358, −0.3698 to 0.0982, $Q_t = 94999.7749$, $p < 0.0001$, $I^2 = 99.19\%$; MF: ln RR = −0.0119, −0.0699 to 0.0461, $Q_t = 2976.73$, $p < 0.0001$, $I^2 = 97.08\%$) (Supplementary Fig. 4). Egger's regression test indicated potential publication bias for LUC ($p < 0.05$) and LM ($p < 0.05$) (Supplementary Tables 2 and 3). For these cases, the bias-corrected effect sizes estimated using the trim-and-fill method deviated from the original values and did not fully retain the direction of effect (Supplementary Tables 2 and 3). This, combined with the high heterogeneity observed in initial subgroup analyses, prompted two-level subgroup analyses.

Secondary subgroup analysis was conducted to explore the interaction between the dimensions of diversity and GCF types (Supplementary Fig. 5). The results indicated that BI led to significant decrease of TB in the Himalayan region (ln RR = −0.1025, 95% CI: −0.1593 to −0.0456) and aquatic plant communities (ln RR = −0.2369, 95% CI: −0.4304 to −0.0435) (Supplementary Fig. 5). CC significantly reduced both TB by 7.74% (ln RR = −0.0831, 95% CI: −0.157 to −0.0091) and FB by 28.14% (ln RR = −0.3305, 95% CI: −0.5726 to −0.0884), with this effect being most prominent in vascular plants from the temperate climate zone and the Holarctic floristic realm (Supplementary Fig. 5). At the same time, CC led to a significant increase in PB by 18.55% (ln RR = 0.1702, 95% CI: 0.0238 to 0.3166), particularly in grassland ecosystems (Supplementary Fig. 5).

The impact of LUC on TB was only significant at larger spatial extents exceeding 2000 m (ln RR = −0.1369, 95% CI: −0.231 to −0.0427) ($p < 0.05$). Although LM had a significant negative effect on PB (ln RR = −0.2385, 95% CI: −0.438 to −0.0389), it also exhibited positive effects on both TB and FB under certain research designs and environmental
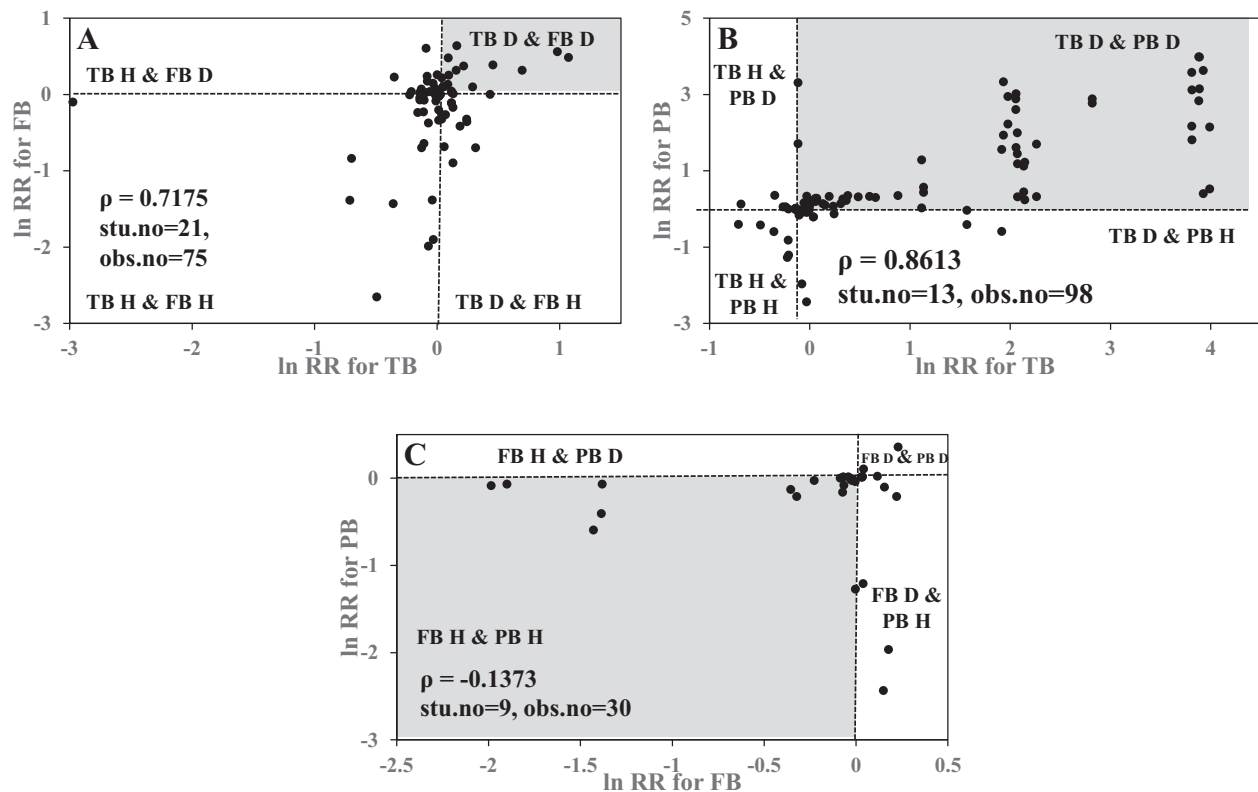
**Fig. 3 | Bivariate meta-analysis of log-response ratios (ln RR) illustrating the impact of GCFs on plant β-diversity. A** TB versus FB ln RR, **B** TB versus PB ln RR, and **C** FB versus PB ln RR. The quadrants delineate the patterns of homogenization (H) or differentiation (D) for TB, FB, and PB. The gray shaded areas highlight the predominant trends. The correlation coefficients (ρ) is the result of a bivariate meta-analysis and represents the strength of the relationship between the variables in each panel. The points in the figure represent ln RR of different diversity dimensions from the same study. The sample size is indicated by the number of studies (stu.no) and observations (obs.no). Source data are provided as a Source Data file.

conditions. Moreover, when multiple GCFs were present simultaneously, there was limited research involving the PB effect, and the responses of TB and FB tended to become statistically weaker (Supplementary Fig. 5). These results highlight that the type of GCF is an important moderator of biodiversity change.

The bivariate meta-analysis conducted on studies that included two or more biodiversity dimensions simultaneously revealed a strong positive correlation between TB and PB ($\rho = 0.861$, Fig. 3B), with 21 out of 75 paired observations showing a simultaneous increase in both TB and PB under the influence of GCFs. A moderate positive correlation was also found between TB and FB ($\rho = 0.7175$, Fig. 3A), with 53 out of 98 paired observations indicating that both TB and FB increased together. However, a weak negative correlation was observed between PB and FB ($\rho = -0.1373$, Fig. 3C), despite 15 out of 30 observations showing a simultaneous decrease in both dimensions. When combined with the results of our subgroup analyses, these findings underscore that each diversity dimension exhibits distinct ecological response thresholds and stability under GCFs.

### Factors influencing the effects of GCFs

Random forest analyses identified biogeographic context, study design, and ecological and climate context as the most influential moderators shaping the effect sizes of GCFs on plant β-diversity (Supplementary Fig. 6). Additionally, the study subject significantly modulated the effects of both overall GCFs (29.17%) and CC (19.96%). Notably, the GCF type explained a greater proportion of variance in effect sizes than the diversity dimension. Nevertheless, the diversity dimension remained an important predictor across all moderator groups, with the exception of BI, where its contribution was minimal.

Although our model did not fully meet the assumptions of normality and homoscedasticity (as indicated by diagnostic tests) (Supplementary Fig. 7), we addressed these potential violations by applying multilevel meta-regression models with cluster-robust standard errors. This approach improves the reliability of standard error estimates, allowing us to interpret the general trends in effect sizes with respect to moderator variables. While $p$-values are reported, we emphasize the interpretation of effect size direction, magnitude, and confidence intervals, rather than relying solely on significance testing. The meta-regression results indicate that the negative effects of CC became more pronounced over time, whereas the positive effects of LM increased correspondingly (Supplementary Fig. 8H). In contrast, the negative effects of BI did not exhibit clear changes with increasing values of continuous moderators (Supplementary Fig. 8).

### Discussion

Our global meta-analysis showed that, on average, GCFs had no statistically significant effect on plant β-diversity (Fig. 2A). This apparent stability likely reflects a near-equal split in opposing trends: among 1604 observations from 256 studies, 49.88% showed increases in β-diversity, while 48.25% reported decreases—effectively canceling each other out. Notably, only 1.87% of cases reported no change, indicating that shifts in community composition are common but bidirectional. This finding aligns with Keck et al.[15], who synthesized data across all major taxonomic groups and concluded that, although human pressures strongly affect community composition, there is no consistent global trend toward biotic homogenization. In contrast, Blowes et al.[4] found that "no change" was the most common outcome across 461 metacommunities and 64 species checklists. In their study, "no change" represented a true absence of directional trends, unlike the

averaged opposing effects observed in our analysis. This discrepancy may be due to differences in study scope and temporal resolution: Blowes et al.[4] synthesized long-term, often decadal datasets that smooth out short-term fluctuations, and included a wider array of ecosystems and taxa, potentially diluting strong but localized signals of biotic change.

Similarly, a global synthesis of plant α-diversity found no consistent trend, with positive and negative changes occurring at equal frequencies[6]. Although based on long-term, standardized datasets spanning multiple taxa, including plants, the study—like ours on β-diversity—captured highly heterogeneous responses rather than a unidirectional pattern. Taken together, these results suggest that biodiversity responses to GCFs are rarely uniform, even across large spatial or temporal scales. Instead of focusing on average trends, it may be more informative to identify the specific environmental conditions and GCFs type associated with increases or declines in diversity. Such an approach can clarify where and under what conditions diversity increases or declines.

Random forest analyses identified GCF type, biodiversity dimension, life form, ecosystem, and region as the most influential moderators shaping the effects of GCFs on plant β-diversity (Supplementary Fig. 6). These findings partially align with those of Keck et al.[15], who reported biome, pressure type, organism group, and spatial scale as key drivers of biodiversity change. This convergence underscores the multifactorial and context-dependent nature of biodiversity responses to global change. Two-level subgroup analyses further revealed that these moderators not only have independent effects but may also interact to jointly influence biodiversity outcomes (Supplementary Figs. 3–5). Notably, the effects of GCFs on plant β-diversity varied with GCF type and biodiversity dimension, and were also contingent upon ecological context and study design. These patterns indicate that the effects of GCFs are shaped not only by individual moderators such as GCF type or biodiversity dimension, but also by their interactions with ecological context and focal taxa. Although some moderators included in the random forest models, such as life form, taxa type, and realm, exhibited moderate correlations, the random forest is generally robust to multicollinearity. Nevertheless, we acknowledge that multicollinearity may influence the relative importance rankings by distributing explanatory power among correlated variables. Readers should therefore interpret variable importance rankings with this consideration in mind.

When evaluating the effects of individual GCFs, our analysis revealed that climate change (CC) significantly reduced overall plant β-diversity at the global scale (Fig. 2A and Supplementary Fig. 3). This decline was most pronounced in tree species, while shrub β-diversity showed a significant increase. These contrasting trends likely reflect differences in adaptive strategies across plant life forms. Trees are generally more vulnerable to climate-related stress, such as drought and temperature extremes, as documented in previous studies[25,26]. In contrast, many shrub species possess traits that enable persistence and regeneration in disturbed or fluctuating environments, which may buffer them against climatic pressures[27,28]. These divergent responses highlight the importance of accounting for functional group identity when assessing biodiversity responses to global anthropogenic change.

Importantly, the effects of CC also varied across different biodiversity dimensions. We found that CC selectively filters species in terms of taxonomic β-diversity (TB), primarily based on functional traits (FB), favoring those better adapted to shifting environmental conditions. This result is consistent with previous studies demonstrating the role of traits in mediating species' responses to environmental stressors[29,30]. In contrast, we observed no comparable filtering effect on phylogenetic β-diversity (PB), suggesting that PB may be less sensitive to climatic pressures or buffered by evolutionary history. Thus, although no single dimension of diversity fully captures species identity[4], integrating taxonomic, functional, and phylogenetic

perspectives provides a more complete yet tractable framework for understanding biodiversity dynamics under global change.

As anticipated, biological invasion (BI) consistently led to biotic homogenization of plant communities (Supplementary Fig. 4). This finding aligns with Daru et al.[18], who documented widespread declines in plant β-diversity across temporal scales and spatial resolutions using a dataset of more than 200,000 plant species. However, Petsch et al.[17] reported that the effects of non-native species on β-diversity varied by study design, spatial scale, and diversity dimension, without identifying ecosystem-specific differences. Our results diverge from this pattern by revealing pronounced ecosystem-level variation: homogenization was substantially stronger in freshwater ecosystems, particularly among aquatic plants (Supplementary Figs. 4–5). These findings emphasize the need to explicitly consider the vulnerability of freshwater ecosystems to biological invasions when developing biodiversity conservation strategies.

In contrast to the effects of CC and BI, our study found that land management (LM) practices significantly enhanced plant β-diversity (Supplementary Fig. 5). Through the reintroduction of generalists and the creation of heterogeneous habitats, LM interventions promote the assembly of diverse plant communities and contribute to increased ecosystem complexity[31,32]. As a result, LM practices elevated TB—particularly in the Asia and Holarctic floristic realms—and expanded FB within forest ecosystems. These findings are consistent with previous researches emphasizing the positive role of ecological restoration in enhancing biodiversity[32,33].

However, our analysis also revealed a contrasting pattern: while LM practices led to increases in both TB and FB, they were simultaneously associated with a decline in PB. This divergence suggests that current restoration efforts, despite promoting taxonomic and functional diversity, may overlook evolutionary distinctiveness. A likely explanation is the frequent reliance on a limited set of broadly adaptable or commercially available generalists, which, though taxonomically and functionally diverse, are often phylogenetically clustered. As a result, the evolutionary breadth of restored communities remains constrained. These findings underscore the importance of broadening species selection in restoration projects to include lineages representing deeper evolutionary histories. The Kunming–Montreal Global Biodiversity Framework, adopted in 2022, sets ambitious targets for inclusive conservation[34]. Our results lend strong support to its emphasis on integrating multiple facets of biodiversity. In particular, the observed reduction in PB highlights the urgent need to incorporate phylogenetic perspectives into restoration planning to achieve more holistic and effective biodiversity outcomes.

In summary, our key finding is that, at the global scale, plant diversity has experienced no net change, primarily due to the offsetting effects of local gains and losses. The ongoing biodiversity crisis is reflected more in the extinction of specific species or populations than in a consistent decline in either α- or β-diversity. Observed shifts in community composition are likely driven by multiple interacting factors. Anthropogenic drivers—particularly climate change and biological invasions—have led to declines in plant β-diversity in many parts of the world, notably among trees, freshwater ecosystems, and in North America (Fig. 2 and Supplementary Fig. 4). In contrast, ecological restoration efforts, such as afforestation, generally enhance β-diversity and contribute to its maintenance. These findings highlight the importance of restoration as an effective biodiversity conservation strategy and highlight its potential role in advancing the goals of the Kunming–Montreal Global Biodiversity Framework. Future analyses of human impacts on plant communities should incorporate all three dimensions of diversity. A narrow focus on diversity metrics or species composition alone can obscure the identity of species being lost or gained. In contrast, integrating taxonomic, functional, and phylogenetic dimensions offers a more comprehensive assessment and helps mitigate this limitation.
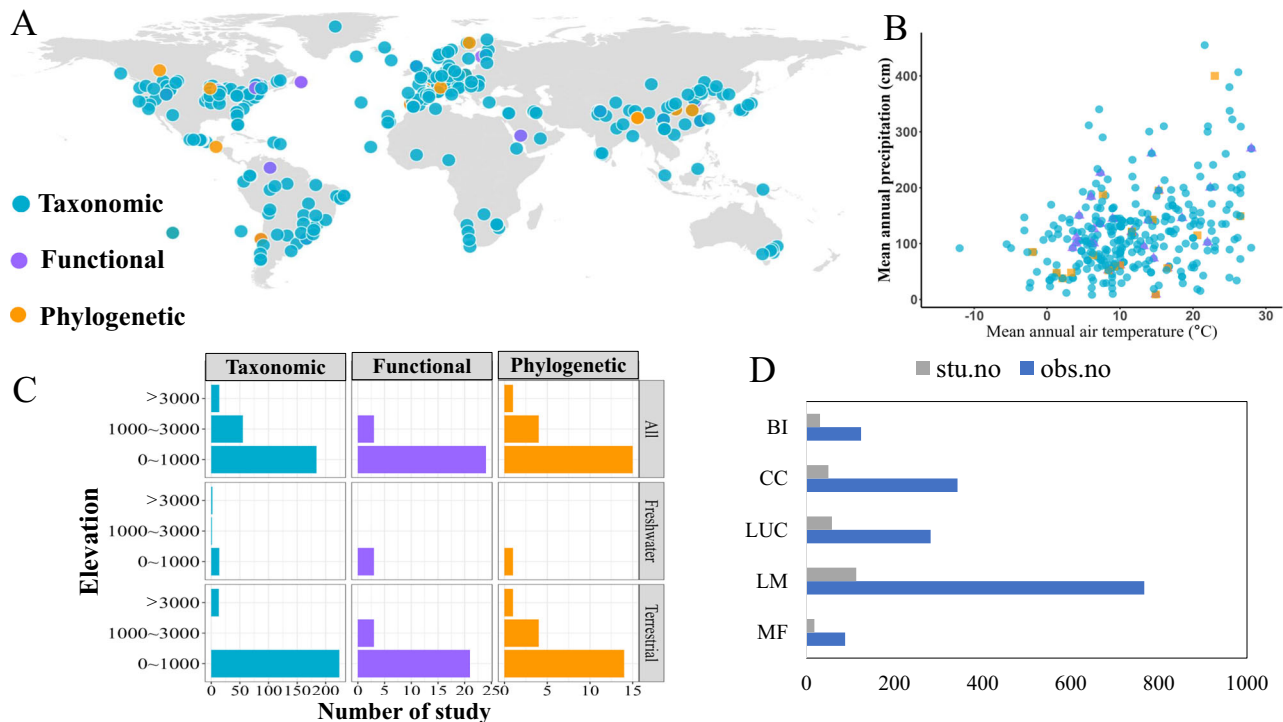
**Fig. 4 | Global distribution of the survey sites included in our analysis.**
**A** Distribution of sampling sites in studies investigating taxonomic, functional, and phylogenetic dimensions of plant β-diversity. The insets show the distribution of sampling sites along the latitudinal and longitudinal gradients (excluding Antarctica). **B** Distribution of sampling sites in the global climate space defined by mean annual temperature and mean annual precipitation. Beta-diversity dimensions are distinguished by both color and shape: TB is shown as circles, FB as triangles, and PB as squares. **C** Number of sampling sites in different biomes (terrestrial and freshwater) and at different elevation ranges (0-1000, 1000–3000 and >3000 m a.s.l.). **D** Number of studies focusing on different types of GCF. The sample size is indicated by the number of studies (stu.no) and observations (obs.no).

We applied Egger's regression and the trim-and-fill method to account for potential publication bias; however, inherent limitations remain, as the available studies are unevenly distributed across geographic regions, taxonomic groups, biodiversity dimensions, and study designs. For example, regions such as Australia and Africa are less studied, which may constrain the generality of the global inferences (Fig. 4A); and although we integrated taxonomic, functional, and phylogenetic dimensions of β-diversity, the existing data were biased toward taxonomic measures (Fig. 1). This imbalance may limit comparability across dimensions and highlights the need for more traits and phylogenetic based monitoring. Finally, to better capture the interactions among global change drivers, more studies using multifactorial designs are needed. Addressing these shortcomings and gaps are critical to better identify the global patterns of GCF effects on plant β-diversity.

## Methods
### Literature search
We conducted a literature search in Web of Science, Google Scholar, and the China Knowledge Resource Integrated (CNKI) between 29 March and 31 November 2023. The search strategies for each database were as follows:

- **Web of Science:** We used the following search query in the Topic field (TS = ): TS= (beta diversity OR β diversity) AND (biotic homogen* OR biotic differentiat* OR biotic heterogen* OR biological homogen* OR biological differentiat* OR biological heterogen*).
- **Google Scholar:** The same keyword combination was entered directly into the general search bar: (beta diversity OR β diversity) AND (biotic homogen* OR biotic differentiat* OR biotic heterogen* OR biological homogen* OR biological differentiat* OR biological heterogen*).

- **CNKI:** We searched in the Topic field using the Chinese equivalents of the above terms, including the phrases corresponding to beta diversity OR β diversity OR biotic homogenization OR biotic heterogenization.

Across the three databases, our search initially retrieved 35,206 records after deduplication within each database (see Supplementary Fig. 1). Since some studies appeared in multiple databases, we subsequently merged the datasets and conducted cross-database deduplication to eliminate overlapping records. In addition, we manually reviewed the reference lists of key review papers and relevant studies that cited them[16,17,19,35–37], which yielded 229 additional studies. After combining the database records with these citation-tracked studies, we performed a final round of deduplication across all sources. This process resulted in a total of 14,977 unique studies for screening. Only published, peer-reviewed articles were retained for the final analysis.

### Literature screening and exclusion criteria
First, all studies were independently screened by two researchers (HLL and YH) based on titles, keywords, and abstracts to identify studies that might focus on the effects of human-induced global change on plant β-diversity, excluding 4766 papers. Then, two researchers (HLL and MN) independently conducted a full-text review of the remaining 1779 articles. Unsuitable publications were excluded based on the following criteria: (1) no consideration of specified GCFs, (2) review papers and studies lacking quantitative analysis, (3) articles predicting changes related to homogenization or differentiation in plant communities composition based on changes in plant α-diversity but not directly analyzing the impact of GCFs on plant β-diversity, (4) articles lacking statistical comparisons between the effects of GCFs and control groups, and (5) articles focusing on intraspecific variation caused by GCFs. (6) To reduce the potential biases in the results, the

observations with sample sizes smaller than 3 were also excluded. Any uncertainties or disagreements were resolved through discussion with a third reviewer (PL). The PRISMA flowchart (Supplementary Fig. 1) illustrates the procedures we used to select the studies suitable for analysis.

Finally, our search yielded 1604 test results from 256 studies (Supplementary Data 1) across all continents except Antarctica (Fig. 4A, D). This dataset included information pertaining to TB (1,305 tests from 246 studies), FB (136 tests from 28 studies), and PB (163 tests from 20 studies). The tests conducted in these studies spanned terrestrial and freshwater biomes across six vegetated continents, covering elevations from less than 5 to 4715 m (Fig. 4C) and wide temperature and precipitation gradients (Fig. 4B).

## Critical appraisal

To assess the quality of studies included in this review, we applied an adapted version of the framework proposed by Mupepele et al.[38], which was specifically designed to evaluate the strength of evidence in studies related to ecosystem services and biodiversity conservation. This framework considers aspects such as study design, data collection, analytical methods, and reporting quality (Supplementary Table 1). In selecting and adapting the specific criteria for our study, we also referred to the approaches used by Huynh et al.[39] and Su et al.[40].

Each included study was critically appraised using this framework, and assigned a quality score. Based on the total score, studies were categorized into four levels of evidence: very strong (>75%), strong (50–74%), moderate (25–49%), and weak (<24%). All studies included in the meta-analysis were rated as 'very strong' evidence (quality score >75%) based on our appraisal framework (see Supplementary Data 2 for details).

## Data extraction

We independently extracted measures of central tendency (mean and median), dispersion (standard deviations, standard error, confidence intervals, and amplitude), and sample sizes for both the control (sites not exposed to GCFs) and statistical treatment (sites affected by GCFs) groups in the selected studies by two groups (HLL and WWX combined as group one, and YC and YH combined as group two). In cases where studies did not report outcomes correctly or lacked sufficient original data, they were excluded from our analysis. In the case of studies that did not provide means and standard deviations, we estimated these values from medians and interquartile range values and amplitudes based on Hozo et al.[41] and Wan et al.[42] or from standard errors and confidence intervals as described in Lajeunesse[43]. We used Web-PlotDigitizer (v.4.7) (https://apps.automeris.io/wpd/index.zh_CN.html) to extract values from the graphs in the selected studies. If a study involved more than two levels of GCFs, we extracted data for as many levels as possible.

We also collected data from each study for the following seven categories: (1) GCF types, which included biological invasion (BI), climate change (CC), land use change (LUC), land management (LM), and multiple factors (MF); (2) biodiversity dimension, encompassing TB, FB, and PB; (3) biogeographic context, including latitude, longitude, region, realm, elevation, and whether the study site was within a biodiversity hotspot; (4) ecological and climatic context, covering climatic zone, ecosystem, flora realm, mean annual precipitation (MAP, mm), and mean annual temperature (MAT, °C); (5) study design and sampling framework, specifying whether the study focused on temporal or spatial design, sample size, control sample type, temporal extent, and spatial extent; (6) data structure, including data sources and whether the data were abundance-weighted; and (7) focal taxa and functional groups, which included the examined plant taxa, plant life forms, data sources, and whether the data were abundance-weighted. If the referenced study did not report the latitude and longitude for the study area, the approximate coordinates were derived by geocoding

the site name in Google Earth 7.0 (free version). If the referenced study did not report MAT, MAP, or elevation, the values were derived from WorldClim using the site's geographic location (i.e., latitude and longitude). Because some studies covered wide areas (e.g., entire countries or even the entire globe) and did not include specific latitude and longitude coordinates, they were not assigned environmental metrics using the above-mentioned methods, accounting for 6% of the total.

In our classification, "CC" encompassed events such as wildfires, temperature increases, and broader climatic shifts; "LUC" referred to the effects of fragmentation, urbanization, habitat loss, road construction, the erection of wind towers, and mining activities; "LM" pertained to a range of human actions including controlled burning, ecological restoration, logging operations, grazing practices, plantations, comprehensive forest management, and agricultural activities; and finally, "MF" denoted instances where more than two human activities were simultaneously present. In this study, all these factors were referred to as GCFs.

## Effect size calculation

Beta diversity is broadly characterized as the ratio (or difference) between gamma diversity and alpha diversity, or the variation (or dissimilarity) in composition among assemblages within a defined spatial area[19]. Correspondingly, the methods used for the calculation of β-diversity can be categorized into three main groups: multiplication ($\beta = \gamma / \bar{a}$), addition ($\beta = \gamma - \bar{a}$), and dissimilarity measures (such as the Jaccard or Sørensen index for presence/absence data, or percentage difference, such as the Bray–Curtis index of dissimilarity for variations in the relative abundances of species).

We estimated the log-response ratio (ln RR) as a measure of effect size. This parameter is the natural logarithm of the ratio of mean β-diversity measured during statistical treatment (numerator) to that of the control (denominator)[44]. To minimize bias in effect size estimation and variance calculation, we adopted the multivariate Delta method proposed by Lajeunesse[45], which addresses the small-sample bias associated with conventional log response ratio (ln RR) estimators. Specifically, we used a second-order Taylor series expansion to adjust both the mean (Eq. 3) and sampling variance (Eq. 4) of ln RR, enhancing the robustness and accuracy of effect size estimates, particularly under the small-sample conditions common in ecological research. Negative and positive effect sizes indicated that GCFs decreased and increased β-diversity, respectively (denoting biotic homogenization and biotic differentiation, respectively). Equations are defined as follows:

$$\text{lnRR} = \ln\left(\frac{\overline{X_t}}{\overline{X_c}}\right) \tag{1}$$

$$v_i = \frac{S_t^2}{n_t \bar{X}_t^2} + \frac{S_c^2}{n_c \bar{X}_c^2} \tag{2}$$

$$\text{RR}^\triangle = \text{lnRR} + \frac{1}{2}\left[\frac{(\text{SD}_T)^2}{n_T \bar{X}_T^2} - \frac{(\text{SD}_C)^2}{n_C \bar{X}_C^2}\right] \tag{3}$$

$$\text{var}(\text{RR}^\triangle) = \text{var}(v_i) + \frac{1}{2}\left[\frac{(\text{SD}_T)^4}{n_T^2 \bar{X}_T^4} + \frac{(\text{SD}_C)^4}{n_C^2 \bar{X}_C^4}\right] \tag{4}$$

where Xt and Xc represent the mean plant diversity under GCFs and in the control, respectively.

Furthermore, ordination analysis, which includes principal component analysis, redundancy analysis, correspondence analysis, principal coordinate analysis, and nonmetric multidimensional scaling, serves as a pivotal method for analyzing ecological community data[46].

In our dataset, there are 47 studies that used ordination plots to visually display the effects of human activities on β-diversity. To include the data from these 47 studies in our meta-analysis, we followed the method described by Zhou et al.[47] to convert the community data from two-dimensional ordination plots to one-dimensional data in order to extract the raw data from these articles. Initially, we extracted the sample positions on the first two ordination axes. Then, we computed the Euclidean distances among different samples using the packages *vegan*[48] v.2.6.8 in R, obtaining the distances within the control (Dc) and treatment (Dt) groups, and calculated the means, standard deviations, and sample sizes of both groups. Finally, we determined the RR of β-diversity (RR_Beta) using Eq. (5) as follow:

$$\ln RR_{Beta} = \ln(\frac{\overline{D_t}}{\overline{D_c}}) \qquad (5)$$

where $\overline{Dc}$ and $\overline{Dt}$ are the means for the Dc and Dt groups, respectively. Their corresponding variances were calculated as Eq. (5). Overall, ln RR_Beta values < 0 indicated that GCFs decreased β-diversity, while values > 0 indicated that they increased this parameter. Its variances ($v$) were calculated as:

$$v = \frac{S_t^2}{n_t \bar{D}_t^2} + \frac{S_c^2}{n_t \bar{D}_c^2} \qquad (6)$$

where $n_t$ and $n_c$ are the sample sizes of the variable in the treatment and control, respectively; $s_t$ and $s_c$ are the standard deviations of the variable in the treatment and control, respectively. The percentage change in plant β-diversity induced by GCFs was calculated using the equation $(e^{\ln RR} - 1) \times 100\%$.

According to the test results, the response of plant β-diversity to GCFs did not differ significantly between studies that used different computational methods (Supplementary Fig. 2), suggesting that studies that adopt such methodological approach can be used to assess the response of plant β-diversity to GCFs.

### Statistical analysis

**Testing the overall impact of GCFs on plant β-diversity.** To evaluate whether GCFs generally drive biotic homogenization in plant communities, we tested the overall direction of plant β-diversity responses to GCFs using a mixed-effects model with restricted maximum likelihood (REML) estimation to compute the weighted mean of ln RR, implemented via the rma.mv() function in the *metafor*[49] package (v.4.6.0). Since some studies contributed more than one effect size and there were cases where multiple datasets shared a single control group, we conducted a hierarchical meta-analysis to account for the non-independence of our data. Specifically, we treated Control ID (nested within Study ID) as a random effect to control for the potential correlation of effect sizes within the same study or control group. The random effect of Study ID accounted for potential autocorrelation arising from regional environmental conditions, study-specific methodologies, and biases. The model is as follows:

$$\text{Effect Size}_{i,j} = \beta_0 + (1|\text{Study ID}) + (1|\text{Study ID} : \text{Control ID}) + \epsilon_{i,j} \qquad (7)$$

Where Effect Size$_{ij}$ represents the effect size for the i-th observation within the j-th study. $\beta_0$ is the fixed effect (the total effect of GCF on plant beta diversity). (1|Study ID) accounts for variation between studies. (1|Study ID: Control ID) accounts for variation due to control groups nested within each study. $\epsilon_{i,j}$ is the residual error term.

We computed the overall mean effect size across all studies included in the meta-analysis. To assess heterogeneity among effect sizes, we reported both the total Q statistic ($Q_t$) and the $I^2$ statistic. The $Q_t$ statistic evaluates whether the variability in observed effect sizes exceeds that expected by chance alone, with a significant result

indicating the presence of true heterogeneity. The $I^2$ statistic quantifies the proportion of total variation attributable to true heterogeneity rather than sampling error, with values of 25%, 50%, and 75% commonly interpreted as low, moderate, and high heterogeneity, respectively[50]. The overall model showed a high total heterogeneity ($Q_t = 308760$, $p < 0.0001$, $I^2 = 99.93\%$), indicating that nearly all differences in the observed effect were attributable to between-study differences in intervention outcomes.

### Consistency analysis of GCFs effects on TB, FB, and PB

To assess the effects of specific GCFs on the three dimensions of plant β-diversity, we performed a two-level subgroup analysis. At the first level, we categorized the data by diversity dimension (taxonomic, functional, and phylogenetic) and GCF type (biological invasion, climate change, land-use change, land management, and multiple factors), resulting in eight subgroups. The second level further combined these categories, yielding 15 unique subgroups to evaluate the interactive effects of GCF type and diversity dimension.

To further explore the consistency of responses in TB, FB, and PB to GCFs, we conducted multilevel bivariate meta-analyses. These analyses focused on studies that included two or more biodiversity dimensions simultaneously. The model accounted for the nested structure of the data by incorporating random effects for observation identity (-1|Obser_ID) and study-level variation across dimensions (-Dimension|Study_ID), using an unstructured variance-covariance matrix.

### Identifying drivers of variation in β-diversity responses

To evaluate the relative contribution of potential moderators—including GCF type, biodiversity dimension, geographic location, environmental conditions, data characteristics, research subject, and study design—we employed a random forest approach. Prior to model fitting, we assessed the extent of missing data across moderator variables. The variable "temporal extent" was excluded due to >50% missingness. The remaining variables were imputed using the *missForest*[51] package (v1.5), a non-parametric random forest-based imputation method. Imputation accuracy was high (NRMSE = 0.1192; PFC = 0), and similarly acceptable across all GCF-specific subsets (BI: 0.1557; CC: 0.0013; LUC: 0.1369; LM: 0.1112; MF: 0.1187; all PFC = 0), satisfying the recommended thresholds (NRMSE < 0.2, PFC < 0.1[51,52]).

Random forest models were fitted using the randomForest() function from the *randomForest*[53] package (v4.7-1.2) in R. To identify the most influential moderators and assess statistical significance, we applied two-sided permutation-based significance testing using the *rfPermute*[54] package (v2.5.2) with 1,000 iterations. This method evaluates the importance of each predictor by assessing its contribution to model accuracy through random permutations, with false discovery rate (FDR) correction applied for multiple comparisons. Model performance was evaluated on the independent test set using $R^2$ (calculated as 1 - SS_residual/SS_total) and RMSE.

To further investigate the influence of continuous moderators on effect sizes, we conducted additional meta-regression analyses using the rma.mv() function from the *metafor*[49] package (v4.6.0). The models were specified with a nested random-effects structure (Study_ID/Control_ID) and fitted using restricted maximum likelihood (REML). To account for potential violations of model assumptions, we applied cluster-robust standard errors with CR2 adjustment—an approach recommended for enhancing the reliability of meta-regression results under conditions where standard assumptions may not be fully met[55,56].

### Publication bias

To assess potential publication bias, we conducted Egger's regression test[57] to detect funnel plot asymmetry and applied the trim-and-fill method[58] to estimate and adjust for potentially missing studies. Although small publication bias was observed for some variables, the

corrected effect sizes were largely consistent with the original values and retained the same direction of effect (Supplementary Tables 2 and 3). However, there were exceptions in the global-scale effects of LUC and LM, as well as the response of TB to GCFs. This, along with the high heterogeneity observed in the initial subgroup analysis, prompted us to conduct a two-level subgroup analysis, which showed that our results were not influenced by publication bias (Supplementary Tables 2 and 3).

All statistical analyses were conducted in R v.4.4.1[59].

### Reporting summary

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

## Data availability

The data supporting the findings of this study are available within the Supplementary Information. The following datasets are provided: Supplementary Data 1 (Reference list of included studies), Supplementary Data 2 (Study quality assessment). Source data are provided with this paper.

## Code availability

The R code used to generate the results and analyses in this study has been deposited in the Figshare repository at https://doi.org/10.6084/m9.figshare.30304906[60].

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## Author contributions
H.L.L. conceived the study, performed the data analysis and visualization, and led the writing of the manuscript. She also contributed to the literature review, data extraction, and data management. P.L. provided critical revisions to the manuscript. H.Y. contributed to data management. Y.C., M.N., Y.H., and W.X. contributed to the literature review and data extraction.

## Competing interests
The authors declare no competing interests.

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