

Land use change consistently reduces α -but not β - and γ -diversity of bees

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Published Version

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Available at <https://centaur.reading.ac.uk/120190/>

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To link to this article DOI: <http://dx.doi.org/10.1111/gcb.70006>

Publisher: Wiley

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Land Use Change Consistently Reduces α - But Not β - and γ -Diversity of Bees

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Received: 27 February 2024 | **Revised:** 21 November 2024 | **Accepted:** 22 November 2024

Funding: Toby P.N. Tsang was supported by the Hong Kong General Research Fund (17115119) and the University of Toronto Scarborough Postdoctoral Fellowship Program. The Hong Kong General Research Fund was awarded to Lauren C. Ponisio and Timothy C. Bonebrake. Lauren C. Ponisio was also funded by the NSF (Award ID: 2009075). A. A. Amado De Santis was partly supported by the National Research Council of Argentina (CONICET), SIGMA Xi Foundation, a PIUNT project from the National University of Tucumán, Argentina (UNT), and PUE 023 project from the National Research Council of Argentina (CONICET). Adrian González-Chaves was funded by a grant from the Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP; Interface Project, No. 2013/23457-6). Alexandra-Maria Klein was supported by the German Science Foundation (DFG),

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Grant Number KL 1849/4-1, and the Alexander-von-Humboldt Foundation. Alyssa B. Stewart was partly supported by funding from Mahidol University (Strategic Research Fund) and the Thailand Research Fund (Grant MRG6080124). András Báldi was partly funded by the European Union's Horizon 2020 project "Safeguard" (Grant Agreement ID: 101003476). Andrea Holzschuh was supported by the European Union's Horizon 2020 project "Safeguard" (Grant Agreement No. 101003476) and the Federal Ministry of Food and Agriculture (BMEL) via the Federal Office for Agriculture and Food (BLE) (Grant No. 2821ABS002). Anson Main was supported by the Missouri Department of Conservation. Antonio Diego de Melo Bezerra was supported by CAPES (Coordination of Superior Level Staff Improvement). Annika Hass, Catrin Westphal, and Svenja Bänisch were supported by the LEGATO project that was funded by the BMBF (German Federal Ministry of Education and Research) Framework Programme Research for Sustainable Development (FONA, FKZ: 01LL0917A, 01LL0917D). Drissa Coulibaly and Katharina Stein were funded by the German Federal Ministry of Education and Research (BMBF) within the project WASCAL (West African Science Service Centre on Climate Change and Adapted Land Use). Svenja Bänisch was also supported by the DAAD (Germany Academic Exchange Service) scholarship. Benoît Geslin and Isabelle Dajoz were funded by the Region Ile-de-France through the DIM Astréa and the R2DS program. Blandina Felipe Viana and Juliana Hipólito were supported by the Brazilian National Council for Scientific and Technological Development (CNPq) through the following projects: codes INCT IN-TREE (465767/2014-1) and PVE—Science Without Borders (407152/2013-0); Juliana Hipólito was supported by CAPES scholarships; and Blandina Felipe Viana was supported by CNPq for the grant (PQ code: 305470/2013-2). Breno M. Freitas was funded by CNPq through the project code Universal 14/2011 (#473454/2011-4) and Breno M. Freitas was supported by a CNPq Research Grant (#302934/2010-3). Bruno Ferreira Marques was supported by CNPq for a Research Productivity Fellowship (#308358/2019-8). Luísa G. Carvalheiro was funded by CNPq (#307625/2021-4). Mariana Beal-Neves was supported by CAPES (Coordination of Superior Level Staff Improvement). Ana Carolina Pereira Machado was supported by CNPq (#141736/2020-8) and CAPES (#COOPBRASS: 88887.947041/2024-00). André Rodrigo Rech was supported by FAPEMIG (#APQ-00932-21, #APQ-03100-21, #APQ-01152-22, #APQ-01151-23, #APQ-03262-23, and #RED-00039-23), CNPq (#311665/2022-5 and #423939/2021-1), and CAPES (#88887.837988/2023-00 and #88887.368784/2019-00). Catalina Gutiérrez-Chacón was supported by the Colombian Department of Science, Technology and Innovation—Colciencias (call 529). Caleb Wilson and Mary A. Jamieson were supported by the Foundation for Food and Agricultural Research New Innovator Award (FFAR Award No. 430876) (<https://foundationfar.org/>) and the Oakland University Provost Graduate Student Research Award (Oakland.edu). David Kleijn and Jeroen Scheper were supported by the European Community's Seventh Framework Programme (FP7/2007–2013) under Grant Agreement No 244090, STEP Project (Status and Trends of European Pollinators, www.step-project.net). Jeroen Scheper and David Kleijn were also supported by the Dutch Ministry of Economic Affairs (BO-11-011.01-011 and KB-14-003-006). Eileen F. Power and Jane C. Stout were supported by the Irish Department of Agriculture, Fisheries and Food Research Stimulus Fund (RSF), funded under the National Development Plan (2007–2013). Elsa Youngsteadt was supported by the USDA National Institute of Food and Agriculture Award Number 2020-67013-31916 and USDA National Institute of Food and Agriculture Hatch Project 1018689. Eunice Enriquez was supported by Organization for Women in the Developing World (OWSD), and the Secretaria nacional de Ciencia y Tecnología del gobierno de Guatemala (SENACYT). Frédéric McCune and Valérie Fournier were funded by the Natural Science and Engineering Research Council of Canada (NSERC) Discovery Grant Program and the Fonds de Recherche Nature et Technologies Québec (FRQNT). Gideon Pisanty and Yael Mandelik were partially funded by the Israel Ministry of Agriculture Research Grant No. 824-0112-08 and the Israel Science Foundation Research Grant No. 919/09. Jose L. Gonzalez-Andujar, Jordi Izquierdo, and Jane Morrison were supported by FEDER (European Regional Development Funds) and the Spanish Ministry of Economy and Competitiveness grants (Project Numbers AGL2012-33736 and AGL2015-64130-R). The Natural Sciences and Engineering Research Council of Canada (NSERC) provided Jane Morrison with a doctoral scholarship. Katherine J. Turo was supported by USDA-NIFA Postdoctoral Fellowship 2021-67012-35153 and the National Science Foundation, Grant/Award Numbers: CAREER 1253197 and DGE-1343012. Keng-Lou James Hung was supported by UC San Diego Academic Senate Bridge Fund Grant BIO088B, NSF Doctoral Dissertation Improvement Grant DEB-1501566, National Geographic Society Young Explorer Grant 9014-11, a Mildred E. Mathias Graduate Student Research Grant from the University of California Natural Reserve System, the Jeanne Marie Messier Memorial Endowed Fund, Sigma Xi Grant in Aid of Research G20111015158245, and NSF Biological Research Collection Grant DBI-0956388. Montserrat Plascencia, Robyn D. Quistberg, and Stacy Philpott were funded by the USDA National Institute of Food and Agriculture, Grant/Award Number: 2016-67019-25185, and USDA National Institute of Food and Agriculture, Grant/Award Number: 2016-67032-24987. Kristoffer Hylander and Ulrika Samnegård were supported by the Swedish research councils: The Swedish International Development Coordination Agency (SIDA) (SWE-2009-134, awarded to Kristoffer Hylander) and Formas (229-2009-991, awarded to Kristoffer Hylander). K. Ballare was supported in part by the Graduate Program in Ecology, Evolution and Behavior at The University of Texas at Austin, Texas Department of Parks and Wildlife, and the USDA Forest Service. Laura A. Burkle was supported by Washington University in St. Louis, Tyson Research Center, Montana State University, National Science Foundation (DEB 0934376, 20133168225, and 1256788), and Western Sustainable Agriculture Research and Education (SW13-043). Natalia Escobedo-Kenefic and Patricia Landaverde-González were supported by Dirección General de Investigación de la Universidad de San Carlos de Guatemala (Digi-USAC) through the research grant 4.8.63.2.272012. Natapot Warrit and Pakorn Nalinrachatakan were supported by BIFA: Biodiversity Fund for Asia (BIFA5_005 and BIFA6_009) via GBIF and the National Science and Technology Development Agency (NSTDA), Thailand. Pornpimon Tangtorwongsakul was funded by The National Science and Technology Development Agency (NSTDA) under the project "Effect of urbanisation on species richness and abundance of indicator species inhabiting Thailand's most important wetland." Yunhui Liu was supported by the National Natural Science Foundation of China (No. 41871186). Yves Basset was funded by the Czech Science Foundation (GAČR 20-31295S). The Missouri Cooperative Fish and Wildlife Research Unit is jointly sponsored by the Missouri Department of Conservation, the University of Missouri, the US Fish and Wildlife Service, the US Geological Survey, and the Wildlife Management Institute. Use of trade, product, or firm names is for descriptive purposes only and does not imply US Government endorsement.

Keywords: agriculture | bees | biodiversity decline | land uses | pollinators | urban

ABSTRACT

Land use change threatens global biodiversity and compromises ecosystem functions, including pollination and food production. Reduced taxonomic α -diversity is often reported under land use change, yet the impacts could be different at larger spatial scales (i.e., γ -diversity), either due to reduced β -diversity amplifying diversity loss or increased β -diversity dampening diversity loss. Additionally, studies often focus on taxonomic diversity, while other important biodiversity components, including phylogenetic diversity, can exhibit differential responses. Here, we evaluated how agricultural and urban land use alters the taxonomic and phylogenetic α -, β -, and γ -diversity of an important pollinator taxon—bees. Using a multicontinental dataset of 3117 bee assemblages from 157 studies, we found that taxonomic α -diversity was reduced by 16%–18% in both agricultural and urban habitats relative to natural habitats. Phylogenetic α -diversity was decreased by 11%–12% in agricultural and urban habitats. Compared

with natural habitats, taxonomic and phylogenetic β -diversity increased by 11% and 6% in urban habitats, respectively, but exhibited no systematic change in agricultural habitats. We detected a 22% decline in taxonomic γ -diversity and a 17% decline in phylogenetic γ -diversity in agricultural habitats, but γ -diversity of urban habitats was not significantly different from natural habitats. These findings highlight the threat of agricultural expansions to large-scale bee diversity due to systematic γ -diversity decline. In addition, while both urbanization and agriculture lead to consistent declines in α -diversity, their impacts on β - or γ -diversity vary, highlighting the need to study the effects of land use change at multiple scales.

1 | Introduction

Human activities have transformed global terrestrial environments for anthropogenic land uses, mainly agriculture and urban development (Ellis et al. 2010). These processes reduce biodiversity by creating environments with unsuitable biotic and abiotic conditions and enhancing competitive exclusion (Mayfield et al. 2010), ultimately threatening ecosystem functions (van der Plas 2019). A common approach in evaluating the ecological impacts of land use change is to compare the number of taxa within assemblages (taxonomic α -diversity) between natural habitats and anthropogenic habitats (Purvis and Hector 2000). Previous studies have found that taxonomic α -diversity in different taxa can be reduced by 19%–40% in agricultural habitats and 4%–50% in urban habitats on average (Newbold et al. 2015).

However, taxonomic α -diversity analyses could fail to capture the potential effects of land use change on homogenizing assemblages, thus underestimating γ -diversity loss (i.e., diversity at larger spatial scales) (Socolar et al. 2016). Taxonomic β -diversity, relatively understudied compared with taxonomic α -diversity, captures compositional variations between assemblages and can determine how α -diversity loss upscales to γ -diversity (Mori, Isbell, and Seidl 2018; Socolar et al. 2016). Specifically, reduced and increased β -diversity can result in higher and lower γ -diversity loss relative to what would be expected based on α -diversity losses alone (Socolar et al. 2016). While land use change is expected to homogenize assemblages and reduce β -diversity, empirical studies have shown mixed results (Newbold et al. 2016).

Regardless of the spatial scale at which it is measured, a limitation of taxonomic diversity is its inability to effectively reflect ecological differences between species, such as morphology, physiology, and phenology (Purvis and Hector 2000; Tucker et al. 2017). Recent studies have increasingly emphasized analyzing phylogenetic diversity alongside taxonomic diversity (Cadotte and Tucker 2018; Tucker et al. 2017). As evolution shapes species traits, phylogenetic approaches can efficiently capture high-dimensional ecological differences, reducing the risks of omitting important traits (Tucker et al. 2017, 2018). Additionally, phylogenetic diversity has exhibited similar or even better performance than taxonomic diversity in explaining ecosystem functions or services across sites (Tucker et al. 2019; van der Plas 2019).

While not always the case, responses of phylogenetic diversity to land use change should largely follow taxonomic diversity change (Tucker and Cadotte 2013). However, land use could also lead to more phylogenetic diversity loss than would be expected based on the taxonomic diversity loss. This is because land use change can strengthen phylogenetic habitat filtering (Grab et al. 2019; Nowakowski et al. 2018), causing only a subset of

phylogenetically similar species to persist under anthropogenic land uses due to conserved traits (Duarte 2011). Interestingly, the filtering effects on α - and β -diversity can vary, again demonstrating the importance of analyzing both α - and β -diversity to better understand net impacts at larger spatial scales (i.e., γ -diversity) (Nowakowski et al. 2018).

To understand how land use change affects taxonomic and phylogenetic diversity, we focused on a well-studied and ecologically important taxon, bees. Pollination services by bees can be greater in sites with high bee taxonomic and phylogenetic α -diversity and landscapes with high taxonomic β -diversity between sites (Grab et al. 2019; Weekers et al. 2022; Winfree et al. 2018) compared to lower diversity sites and landscapes. Ongoing global land use change is known to reduce bee diversity generally (Cariveau and Winfree 2015; De Palma et al. 2016; Winfree, Bartomeus, and Cariveau 2011). However, the exact effects can vary with land use types, with some studies reporting increased bee diversity under land use change (Cariveau and Winfree 2015; Prendergast, Dixon, and Bateman 2022; Winfree, Bartomeus, and Cariveau 2011). Furthermore, the impacts of anthropogenic land uses are often evaluated using taxonomic α -diversity, even though other biodiversity metrics could exhibit different patterns (De Palma et al. 2017; Harrison, Gibbs, and Winfree 2018). Importantly, some bee lineages are especially sensitive to land use change, which could lead to a more substantial decline in phylogenetic diversity relative to taxonomic diversity (Grab et al. 2019; Harrison, Gibbs, and Winfree 2018).

We examined the ecological impacts of land use change on global bee diversity using bee assemblage data from agricultural, urban, and natural habitats across all continents except Antarctica, where bees are absent. Our objectives were to (1) compare taxonomic and phylogenetic α -, β -, and γ -diversity among natural, agricultural, and urban habitats; (2) investigate whether land use change leads to stronger phylogenetic habitat filtering; and (3) identify the genera particularly affected by the agricultural and urban habitats. For Objective 1, we expected that natural habitats would contain greater taxonomic and phylogenetic α -, β -, and γ -diversity. For Objective 2, we predicted declines in phylogenetic diversity in urban and agricultural habitats, even after controlling for taxonomic diversity, due to increased phylogenetic habitat filtering.

2 | Materials and Methods

2.1 | Data Collection, Cleaning, and Filtering

Bee data were collected from various sources, including the PREDICTS database (Hudson et al. 2014), a

previous meta-analysis on bee diversity in agricultural systems (Kennedy et al. 2013), literature searches, and expert recommendations (see Section S1 for details and the limitations of our dataset). We corrected species synonyms using a bee species guide and world checklist (Ascher and Pickering 2022). Missing taxa were further reviewed by a taxonomist coauthor (John S. Ascher). For 1% of 2257 species-level identifications, no matches were found; these were treated as morphospecies instead of species. For morphospecies or genus-level data, we checked the validity of the genus in the checklist and corrected them when necessary.

Datasets were divided into different studies (see Table S1 for details of each study) according to their sampling strategies, which were broadly classified as (1) “flower visitors,” if the study sampled flower-visiting bees within an area; (2) “targeted plants,” if the study sampled flower-visiting bees of targeted plant species; and (3) “all bees” for any other method, such as pan traps, hand netting, and vane traps. Thus, if a dataset provided bee data based on different sampling strategies, such as pan traps and hand-netting bees from targeted plant species, the data would be separated into different studies. For each site within each study, we aggregated bee species abundance data across sampling dates (hereafter referred to as assemblage). We excluded *Apis mellifera* from all assemblages, as they were often from managed colonies.

We only included assemblages in our analyses if the following criteria had been met: (1) The sampling strategy had a broad taxonomic focus rather than only focusing on certain groups of bees (e.g., *Bombus* spp., solitary bees). (2) Spatial coordinates were recorded. (3) The number of individuals observed was recorded. (4) At least 10 individuals were identified to at least the genus level to ensure reliable rarefaction results (see below). We did not use a threshold higher than 10 individuals because this might bias the analyses against impoverished assemblages. The threshold is also consistent with or higher than that used in previous studies based on rarefaction (Blowes et al. 2022; van Klink et al. 2024). (5) The assemblages had sampling completeness of $\geq 50\%$ to ensure the reliability of diversity estimates. Sampling completeness was calculated using the R package iNEXT3D (Chao et al. 2021). (6) The assemblage had at least 95% of observed individuals identified to at least the genus level to ensure reliable estimations of phylogenetic diversity. We did not set a minimum number of assemblages to include in a study for subsequent analyses.

2.2 | Definition of Land Uses

We classified the land use of each assemblage based on the predominant environment within the sampling area. Natural habitats were defined as areas primarily covered by vegetation resulting from natural succession or restoration (i.e., active attempts to bring the site to a more natural state). Agricultural habitats were defined as sites managed for growing resources, including food and animal products. Urban habitats included green spaces covered by planted vegetation (not natural succession) managed for amenity or recreation (e.g., lawns and gardens). See Section S2 for details of the land use classification.

2.3 | Phylogeny

We used a global genus-level phylogeny to quantify the phylogenetic diversity of each assemblage (Hedtke, Patiny, and Danforth 2013). Tip names on the phylogenetic tree were corrected using Ascher and Pickering (2022) and further reviewed by a taxonomist coauthor (John S. Ascher). We converted the tree to ultrametric using a non-negative least square (Turley et al. 2022). The strong cophenetic correlation (Pearson's $r = 0.93$) indicated that the tree's structure was largely conserved. Our data contained taxa from 355 genera, of which 32 were missing from the tree and were added to the closest sister genus available (Table S2). We randomly selected one species in the tree from each genus, then attached all species from each study as polytomies at the midpoint of its corresponding genus branch, as this approach has been demonstrated to capture phylogenetic diversity well when a species-level phylogeny is unavailable (Qian and Jin 2021). While the use of a genus-level phylogeny might not fully capture phylogenetic patterns of assemblages, previous bee studies have used the same phylogeny and detected phylogenetic diversity changes and phylogenetic habitat filtering (De Palma et al. 2017; Harrison, Gibbs, and Winfree 2018; Hendrix, Forbes, and MacDougall 2018). We quantified the phylogenetic α -diversity of each assemblage by generating 10 phylogenetic trees and found that the values of phylogenetic α -diversity were highly correlated (Pearson's $r > 0.99$). Thus, we only used the first phylogenetic tree for subsequent analyses.

2.4 | α - and γ -Diversity Estimates

In our analyses, α - and γ -diversity always represent within- and across-sample diversity, respectively, within the same land use type. Thus, comparing α - and γ -diversity across habitats allows for assessing whether diversity loss is exacerbated at larger spatial scales by land use change (Chase et al. 2019; Socolar et al. 2016). To estimate taxonomic and phylogenetic α - and γ -diversity, we estimated both metrics with the Hill number equal to 1, as it considers the relative abundance of species within assemblages and is less prone to undersampling than lower Hill numbers (Roswell, Dushoff, and Winfree 2021).

We estimated α -diversity for all assemblages, while γ -diversity was estimated only for studies with at least five assemblages from at least one land use. Additionally, γ -diversity was only estimated for studies that indicated sampling effort for each assemblage. We pooled species abundance data across assemblages of the same land uses within each study before conducting the γ -diversity rarefaction analyses. To control for differences in sampling completeness between assemblages across studies, we extrapolated all α - and γ -diversities to their asymptotes (i.e., when sampling completeness equals 1). Each assemblage's taxonomic and phylogenetic diversity was estimated using iNEXT3D (Chao et al. 2021).

2.5 | β -Diversity Estimates

For each land use in each study, we used multiplicative partitioning ($\beta = \gamma / \text{mean } \alpha$) to obtain their β -diversity (Jost 2007). This method is especially suitable to understand the spatial scaling of diversity loss, as it represents the scaling factor relating

α - and γ -diversity (Baselga 2013; Socolar et al. 2016). The metric also reflects the contribution of β -diversity to γ -diversity (contribution of $\beta = (1 - \alpha/\gamma) \times 100\% = (1 - 1/\beta) \times 100\%$).

The corresponding γ - and α -diversities were taken from rarefaction analyses. As more abundant assemblages should more heavily influence γ -diversity estimates, mean α -diversity was weighted according to the total abundance of each assemblage (Crist et al. 2003). Consistent with the γ -diversity analyses, our analyses included only studies with at least five assemblages in at least one land use.

2.6 | Climatic and Methodological Variables

We collected a variety of climatic and methodological variables to control for their effects on bee diversity and to better quantify any effect of land use change (Table 1). For climatic variables, we collected mean annual temperature and annual precipitation, as well as the seasonality of each assemblage from the public database CHELSA v1.2 (Karger et al. 2017). Annual precipitation was square root transformed to reduce the effects of outliers. All data were at 30-arc-second (~1 km) resolution.

For the β - and γ -diversity analyses, we additionally included methodological variables in the models that might affect both diversity metrics, namely, (1) study extent, (2) standard deviations in sampling efforts across assemblages, (3) the number of assemblages, (4) standard deviations in sampling completeness

across assemblages, and (5) log-transformed mean sampling completeness across assemblages (Table 1; see Section S3 for details and rationales to include these variables).

Preliminary analyses found high collinearity (Pearson's $r > 0.7$) among climatic variables and among the mean and standard deviations in sampling completeness across assemblages. Thus, we conducted robust PCA separately for all climatic variables and the two methodological variables. We included climatic PC1 and PC2 for subsequent analyses, which captured >81% of the climatic variations within our dataset (Table S3). Increasing PC1 scores primarily reflect colder sites with high seasonality in temperature but low seasonality in precipitation, while increasing PC2 scores reflect warmer and wetter sites with lower temperature seasonality and lower precipitation seasonality.

For the two methodological variables, we extracted the PCA1 score to represent them, as it captured 93.1% variations across assemblages. A higher sampling effort PCA1 score indicates lower mean sampling completeness with higher variation across assemblages (Table S3). Robust PCA was conducted using R-package rrcov (Todorov and Filzmoser 2009).

2.7 | General Modeling Strategy

We used mixed models to identify the effects of land use while controlling for methodological and climatic covariates, as well as

TABLE 1 | Predictors for the models related to each objective. Objectives 1a, 1b, and 1c are to compare α -, β -, and γ -diversities across three land uses, respectively. Objectives 2a, 2b, and 2c are to assess whether agricultural and urban habitats exhibited stronger phylogenetic habitat filtering in α -, β -, and γ -diversities, respectively. Objective 3 is to identify genera with altered abundance in agricultural and urban habitats relative to natural habitats. The rationales including different variables and their transformations have been described in the main text.

Variable name	Description	Objectives
Land use	A factor with three levels: Natural/agricultural/urban	1–3
Sampling method	A factor with three levels: All bees/floral visitor only/floral visitor of targeted plants	1–3
Climate PCA1	PCA1 score based on mean annual temperature, annual precipitation, as well as temperature and precipitation seasonality of each assemblage	1–3
Climate PCA2	PCA2 score based on the aforementioned climatic variables	1–3
log(Number of assemblages)	Number of assemblages of each land use within a study	1b–1c 2b–2c
Sampling effort SD	The standard deviation of sampling efforts between assemblages of the same land use within a study	1b–1c 2b–2c
Sampling completeness PCA1	PCA1 score based on the mean and standard deviation of sampling completeness between assemblages of the same land use within a study	1b–1c 2b–2c
log(Sampling extent)	Maximum distance between assemblages of the same land use within a study	1b–1c 2b–2c
log(Taxonomic diversity)	The taxonomic counterpart of phylogenetic α -, β -, and γ -diversities	2
Study identity	Added as random effects to account for other differences between studies	1–3
Spatial autocorrelation term	Controlling for spatial autocorrelation within each study based on the latitude and longitude of each assemblage	1a, 2a, 3a

other unaccounted-for study differences using random effects. Study-level variation can lead to varying estimates of land use effects. For example, the effects may be stronger in warmer landscapes with fewer natural habitats in the surrounding environments (Ganuza et al. 2022; Kennedy et al. 2013). Methodological factors such as sampling area (Azaele et al. 2015) and methods (Lee and Guénard 2019) can also alter estimates of land use effects. Here, we focused on the general trend across studies rather than examining how land use change interacts with other environmental or methodological variables. Therefore, apart from a few climatic and methodological covariates, we used study identity as a random effect to control for such study-level variations.

This statistical framework has been used in previous quantitative syntheses assessing land use effects on diversity or abundance by comparing data from studies conducted in different regions based on different methods. It also allows for studies with data on one land use only (De Palma et al. 2016; Millard et al. 2021; Newbold et al. 2015). A summary of how mixed models work is provided in Section S4. Additionally, we provide a simple simulation (Section S5) to justify our approach of including study-level land use effects, despite some studies only providing bee data for a single land use. We emphasize here that mixed models do not estimate study-level land use effects (or, in general, any random slope) through modeling its relationship in each study individually. Rather, the calculations involve calculating the fixed effects and the variance-covariance matrix, which uses data from all studies (Raudenbush and Bryk 2002). Below we provided a brief description of the models. For mathematical expressions, please refer to Table S4.

2.8 | Objective 1a: α -Diversity

To examine how taxonomic and phylogenetic α -diversity varied across land uses, we built linear mixed models with Gaussian distributions using log-transformed α -diversity. We specified log-transformed α -diversity as the response to improve normality. For predictors, we included sampling method (three levels: all bees/flower visitors/targeted plants) and land use (three levels: natural/agricultural/urban) of each site. Climatic PC1 and PC2 scores were also added as predictors to control for the effects of regional climate on bee α -diversity. Our analyses included nominal variables, so we set the intercepts as natural habitats sampled with methods targeting all bees. We further used sampling completeness as a weight in the regression, such that poorly sampled sites (and, therefore, those with higher uncertainty in diversity estimates) had lower weights in the analyses (Carvalho et al. 2013).

For random effects, study identity was added as a random intercept, with land use effects added as random slopes, so the estimates of land use effects could vary across studies. The random slopes were never correlated with random intercepts to facilitate model convergence (Matuschek et al. 2017).

Additionally, to control for spatial autocorrelation, we added an assemblage-level random intercept based on the spatial coordinates of each site. The Matérn correlation model was used to construct the correlation matrix and estimate the spatial random effect. All spatial random effects were study specific,

indicating that spatial autocorrelations were modeled within but not across studies, as they had very different methodologies. Indeed, we detected substantial spatial autocorrelation between sites within the same study but not between sites across different studies (Section S6). We compared models with and without spatial random effects and found that the model including spatial autocorrelation had a significantly improved model fit, as indicated by a reduction of >490 in the conditional Akaike information criterion.

We built the linear mixed model using R package spaMM, which allows including spatial random effects (Rousset and Ferdy 2014). We then conducted an omnibus test for differences across land uses based on F tests using R package lmerTest (Kuznetsova, Brockhoff, and Christensen 2017). If the effect of land use was significant, we further conducted pairwise comparisons across the three land uses, with the p -value adjusted by false discovery rate corrections.

2.9 | Objective 1b and 1c: β - and γ -Diversity

The β - and γ -diversity analyses were conducted at the study level (i.e., each land use from a study contributes 1 data point). In the models, log-transformed multiplicative β -diversity (to improve normality) and untransformed γ -diversity were the responses. Land uses, sampling methods, climatic PC1 and PC2 scores, number of sampling sites, standard deviations of sampling efforts, PC1 scores based on sampling completeness, and study extent were added as predictors. Climatic PC1 and PC2 scores were averaged across assemblages of the same land use in each study. Study extent and number of sampling sites were log-transformed, as their effects tend to be nonlinear (Beck, Holloway, and Schwanghart 2013; Marcon, Zhang, and Hérault 2014; Marion, Fordyce, and Fitzpatrick 2017; Soininen, McDonald, and Hillebrand 2007). We added sampling completeness of γ -diversity as weights in the models to account for some pooled assemblages being more unreliable in diversity estimations due to low completeness. Study identity was added as a random intercept.

We started with a model that included the interaction between land use and study extent due to potential differences in distance-decay relationship across land uses. However, the interaction term was nonsignificant. Therefore, we included no interaction term in the final model. Again, an omnibus test was conducted for the effect of land use, and if significant, pairwise comparisons were conducted across land use. Linear mixed models were built with R package lme4 (Bates et al. 2015) and p -values were obtained from lmerTest (Kuznetsova, Brockhoff, and Christensen 2017). Pairwise comparisons were conducted in emmeans (Lenth 2024), with the p -values adjusted by false discovery rate corrections.

2.10 | Objective 2: Phylogenetic Habitat Filtering in Natural, Agricultural, and Urban Habitats

If agricultural and urban land uses increase phylogenetic habitat filtering, their negative effect on phylogenetic diversity should still be significant after adding taxonomic diversity as

a covariate. Previous studies have used this approach to assess whether environments have lower phylogenetic diversity than expected based on taxonomic diversity (Barreto, Graham, and Rangel 2019; Sol et al. 2017). We did not use null model analyses because some of the studies in our meta-data set included studies with single land use, which did not capture species that fail to persist in different land uses (Lessard et al. 2012).

We added taxonomic diversity as an additional predictor to the phylogenetic diversity models described in Objective 1a-c. For α - and γ -diversity, the relationship between phylogenetic and taxonomic diversity is a decelerating relationship, but for β -diversity, it is largely linear (Figure S1). Thus, we added log-transformed taxonomic diversity into each model. Note that for α - and β -diversity models, the responses were also log-transformed. This effectively models a power law relationship, which can range from linear to nonlinear. We only conducted pairwise comparisons between land uses if the omnibus test revealed a significant effect.

2.11 | Objective 3: Genus Abundance Across Land Uses

To facilitate interpretations of diversity patterns, we further identified genera that have reduced abundance in agricultural and urban habitats relative to natural habitats. We conducted the analyses at the genus rather than species level, as the latter would lead to strong temperate region biases, given that more tropical studies relied on morphospecies or genus-level identifications. For this objective, we selected 51 genera that were frequently detected across studies, and thus, the effects of land use can be reliably quantified (see Section S7 for details).

Our analyses included genera with different geographical distributions, such as the cosmopolitan genus *Megachile* and the Neotropical genus *Partamona* (Michener 2007). Thus, different trends across genera could be driven by their varying sensitivity to land use changes and regional differences in the extent of environmental changes and management intensity. Quantifying the contributions of each mechanism would require additional life-history and environmental data. Nevertheless, our results can identify the genera more systematically affected by different land use drivers regardless of the underlying mechanisms.

We built a model for each genus with their abundance in each assemblage as the response and land use, sampling method, and climatic PC1 and PC2 scores as predictors. Random effects were identical with the α -diversity models (Objective 1a), with study identity as a random intercept and land use as a random slope to control for between-study differences. Again, a spatial term based on Matérn correlation nested within studies was added to control for spatial autocorrelation. We used negative binomial mixed models to analyze abundance changes across land uses (Warton 2005). An offset-capturing log-transformed sampling effort of each assemblage was also added.

For one genus (*Dasypoda*), abundance data based on sampling flower visitors of all or targeted plant species were not available. Thus, we dropped sampling method from the model. For

31 genera, the effects of land use were only compared between agricultural and natural habitats, as there was a lack of urban studies containing abundance data of these genera. When three land uses were analyzed, we conducted pairwise comparisons if a significant result was obtained from the omnibus test. As we analyzed multiple genera, results might be affected by multiple comparisons. We further adjusted pairwise comparison p -values using false discovery rate corrections.

We extracted the predicted abundance for each model for each land use while holding climatic PC1 and PC2 at their mean values, as well as holding the sampling strategy at “All bees.” We then calculated the ratio of predicted abundance between agricultural (or urban) and natural habitats (agricultural or urban/natural). We further log-transformed these ratios to convert them into arithmetic scales (Agresti 2007). We then used the package *phytools* (Revell 2012) to assess if there were phylogenetic signals in the log-transformed ratio based on Pagel's λ .

Briefly, Pagel's λ assesses whether any biological characteristics follow Brownian motion, a standard evolutionary model that assumes the differences in the characteristics accumulate through a random walk over evolutionary time scales (Pagel 1999). λ Equals 1 when the characteristics are consistent with Brownian motion expectations. Alternatively, λ can be as low as 0 when the characteristics deviate from the evolutionary model. While other metrics to measure evolutionary signals exist, Pagel's λ is known to be the most robust metric according to simulation studies (Münkemüller et al. 2012).

3 | Results

Our analyses included bee assemblage data from 3117 assemblages and 437,091 individuals of 4002 taxonomic units from 157 studies. The majority of the data (2574 assemblages from 120 studies) were in temperate regions (i.e., absolute latitude $> 23.4^\circ$), mainly North America and Europe, while 543 assemblages from 37 studies were in the tropics (Figure 1a). All studies identified specimens to species-level or morphospecies-level whenever possible, except two studies, which identified specimens to genus level. Sampling methods of individual studies range from point-based sampling (e.g., single vane trap) to aggregating samples within an area as large as 10 ha. In general, most studies were conducted along transects < 100 m or within plots < 1 ha (Table S1). Forty-two studies (27%) provided data on bee assemblages in more than one land use. All diversity models had high conditional R^2 (0.63–0.91, Tables S5–S8).

3.1 | Objective 1a: α -Diversity

Taxonomic α -diversity declined by an average of 15.8% in agricultural ($p = 0.006$; 95% CI: 1.9%, 27.6%) and 19.6% in urban habitats ($p = 0.006$; 95% CI: 3.1%, 33.2%) compared with natural habitats after controlling for climatic and sampling differences (linear mixed models; Figure 1b, Table S5). Using the genus-level phylogeny of bees (Hedtke, Patiny, and Danforth 2013), we found that phylogenetic α -diversity declined by an average of

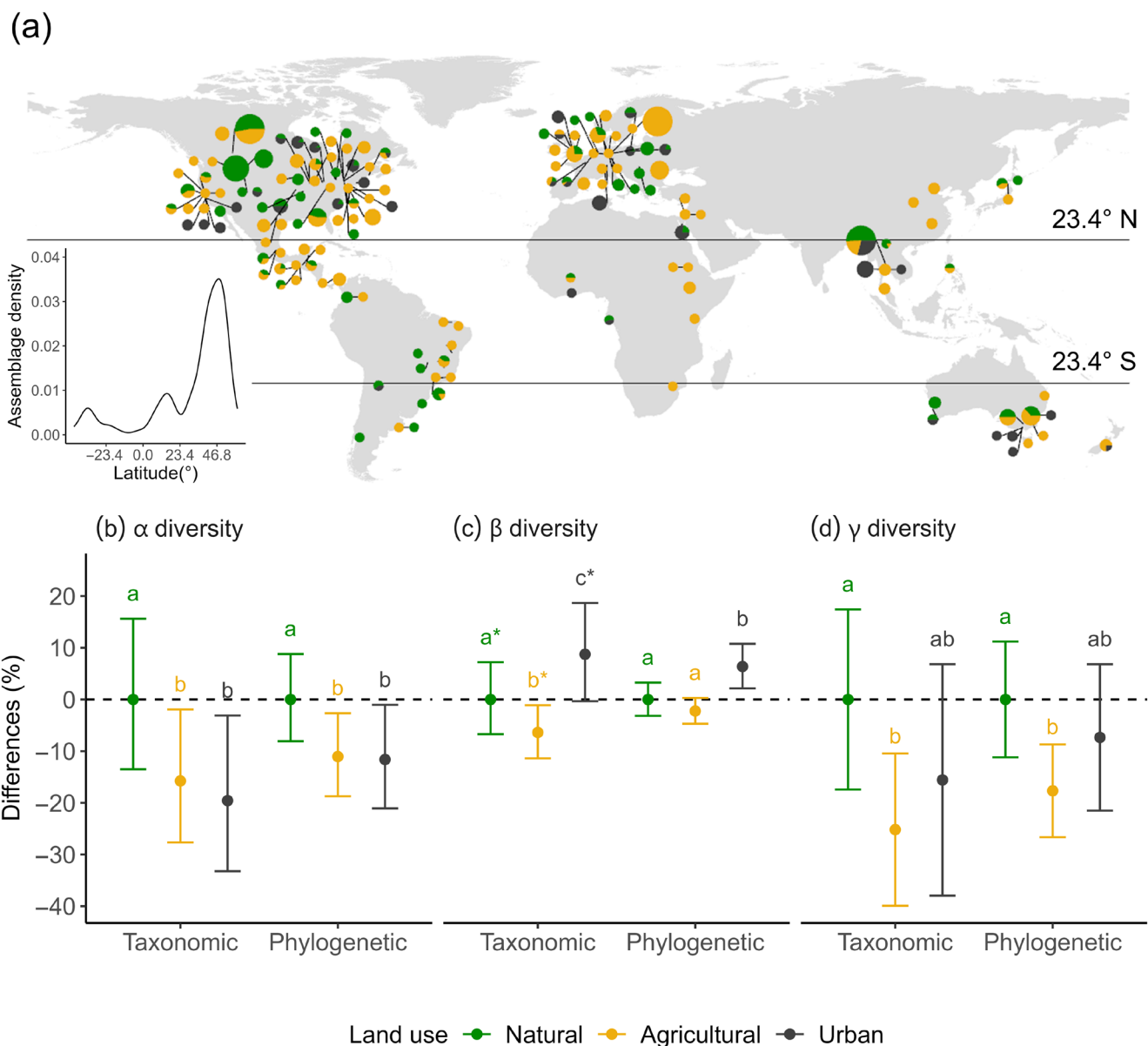


FIGURE 1 | (a) Map showing locations of 157 studies included, and the proportion of natural, agricultural, and urban habitats sampled within the study. Pie size is proportional to the number of sampled sites in each study, ranging from 1 to 368. The density plot indicates the distribution of the studied assemblages ($n = 3117$) along the latitudinal gradient. (b–d) Diversity changes relative to values of natural habitats, with each panel showing responses of one diversity metric: (b) α -, (c) β -, and (d) γ -diversity. Point estimates represent model predictions of each land use based on fixed effects only, while error bars are 95% confidence intervals. The estimations of α -diversity were obtained by holding other covariates at the mean or mode values. For β - and γ -diversity, the estimation reflects a standardized sampling study with all assemblages having 100% sampling completeness, and other covariates at the mean or mode values. Small letters above error bars indicate results from pairwise comparisons, with different letters representing different groups. *Indicates that the pairwise comparisons included marginally nonsignificant results ($p = 0.06$).

11.0% in agricultural habitats ($p = 0.005$; 95% CI: 2.7%, 18.7%) and 11.6% ($p = 0.017$; 95% CI: 1.0%, 21.1%) in urban habitats relative to natural habitats (Figure 1c, Table S5). Pairwise comparisons between agricultural and urban habitats were nonsignificant for both diversity metrics.

3.2 | Objective 1b: β -Diversity

The average taxonomic β -diversity was 1.75 (95% CI=1.66, 1.83), making up 42.7% of the taxonomic γ -diversity. Using linear mixed models, we observed a 6.4% decline in taxonomic

β -diversity in agricultural habitats relative to natural habitats, although the results were marginally nonsignificant ($p = 0.06$; 95% CI=1.1%, 11.4%; Figure 1c, Table S6). Pairwise comparisons also revealed marginally nonsignificant differences between urban and natural habitats, with 8.8% higher taxonomic β -diversity in urban habitats ($p = 0.06$; 95% CI=−0.4%, 18.7%; Figure 1c, Table S6). However, we detected 16.2% higher taxonomic β -diversity in urban compared to agricultural habitats ($p = 0.004$; 95% CI= 6.5%, 26.8%).

Across studies, phylogenetic β -diversity averaged at 1.20 (95% CI=1.17, 1.22), equivalent to 16.7% contribution of phylogenetic

γ -diversity. Phylogenetic β -diversity was highest in urban habitats—6.4% higher than natural habitats ($p=0.004$; 95% CI= 2.2%, 10.7%; Figure 1c, Table S5) and 8.8% higher than agricultural habitats ($p<0.001$; 95% CI: 4.5%, 13.3%). However, we found minimal evidence of differences between agricultural and natural habitats.

3.3 | Objective 1c: γ -Diversity

Taxonomic γ -diversity was, on average, 25.2% lower in agricultural than in natural habitats ($p=0.008$; 95% CI: 10.5%, 39.9%; Figure 1d, Table S7). A 15.6% decline was also observed in urban habitats relative to natural habitats, but the difference was not statistically significant. Differences between urban and agricultural habitats were also nonsignificant.

Similarly, we found that phylogenetic γ -diversity declined by 17.8% ($p=0.006$; 95% CI: 8.7%, 26.7%) in agricultural habitats relative to natural habitats (Figure 1d, Table S7). The pairwise comparison between natural and urban habitats, as well as between agricultural and urban habitats, was nonsignificant.

3.4 | Objective 2: Phylogenetic Habitat Filtering in Natural, Agricultural, and Urban Habitats

After controlling for their taxonomic counterparts using linear mixed models, phylogenetic α - and γ -diversity metrics exhibited

minimal differences across land uses (Figure 2a,c, Table S8). However, we found that phylogenetic β -diversity was highest in urban habitats, while agricultural and natural habitats exhibited similar values (Figure 2b, Table S8). Specifically, phylogenetic β -diversity in urban habitats was 3.9% higher than in natural habitats ($p=0.03$; 95% CI: 0.44%, 7.5%) and 4.5% higher than in agricultural habitats ($p=0.03$; 95% CI: 0.84%, 7.97%).

3.5 | Objective 3: Genus Abundance Across Land Uses

Compared with their average abundance in natural habitats, 73% and 61% of common genera exhibited reduced average abundance in agricultural and urban habitats, respectively, echoing the results of diversity analyses (Table S9, Figure S2). Eight genera showed significantly lower abundance in agricultural habitats, four belonging to the family Megachilidae (*Osmia*, *Hoplitis*, *Megachile*, and *Anthidium*). Only *Protandrena* (mining bees and ground nesters) had increased abundance in agricultural habitats relative to natural habitats. For urban habitats, only *Osmia* (mason bees, primarily cavity nesters) exhibited a significant response to land use, with reduced abundance in urban relative to natural habitats. We detected some phylogenetic signals in the responses to agricultural (Pagel's $\lambda=0.38$, $p=0.08$) and minimal signals in the responses to urban habitats (Pagel's $\lambda<0.001$, $p=1$) (Figure 3). After controlling phylogeny, responses of bee genera to urban

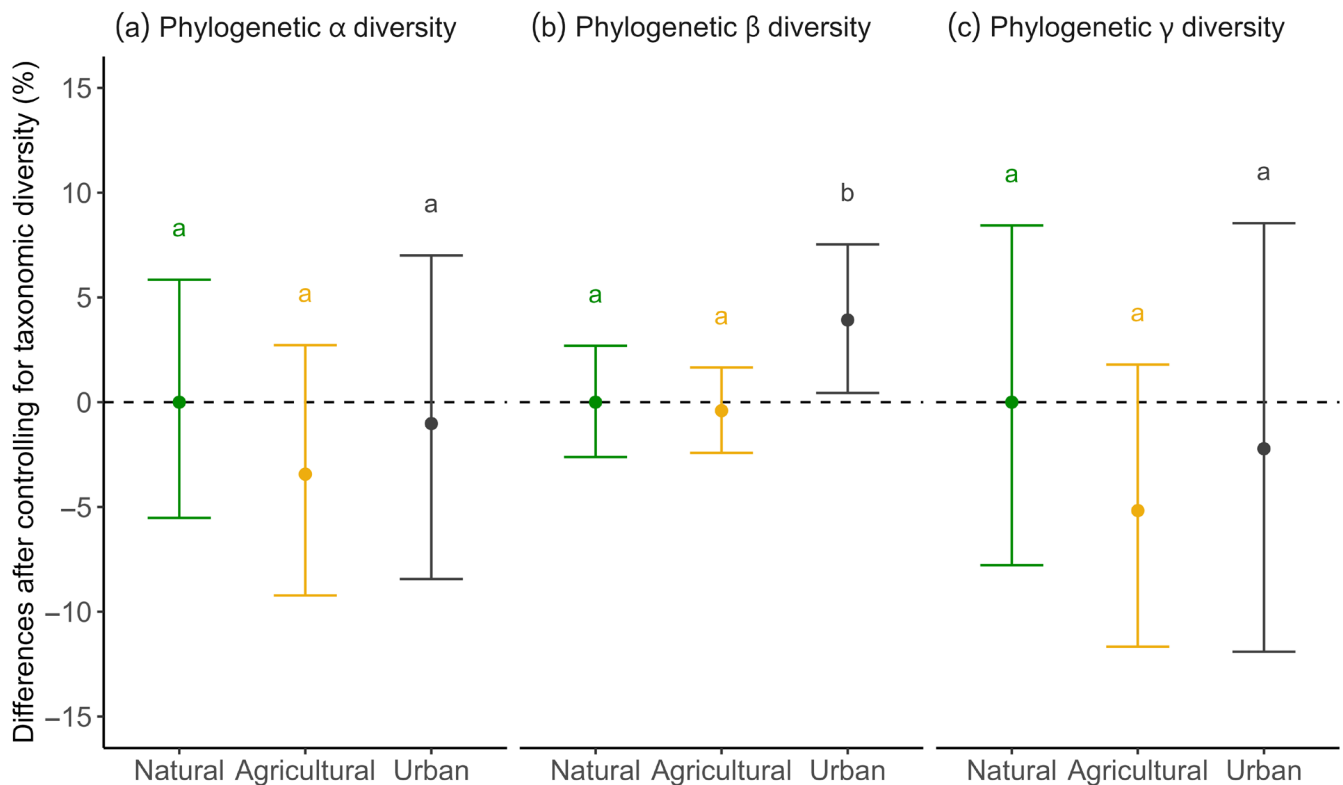


FIGURE 2 | Percent differences in phylogenetic (a) α -, (b) β -, and (c) γ -diversity metrics after controlling for their taxonomic counterparts, using natural habitats as the baseline. Error bars represent 95% confidence intervals, while point estimates present model predictions based on fixed effects only. The estimated α -diversity was based on holding all other covariates at the mean or mode values. The estimated β - and γ -diversities were based on assuming studies with standardized sampling and all assemblages with 100% sampling completeness, while other covariates were at the mean or mode values. Small letters above error groups indicate different grouping based on pairwise comparisons.

FIGURE 3 | Phylogenetic relationships of all genera examined and their responses to agricultural (a) and urban land uses (b) in terms of abundance. When the ratio equals 1, genus abundance in agricultural or urban habitats is the same as in natural habitats. Genera in red and blue are significantly more and less abundant in anthropogenic land uses, respectively. See Figure S2 for bar plots representing how individual genera respond to agricultural and urban land uses differently.

and agricultural habitats were weakly correlated (Pearson's $r=0.09$) (Figure S2).

4 | Discussion

Biodiversity loss observed at local scales (α -diversity) can be dampened or amplified at larger spatial scales (γ -diversity), depending on changes in the scaling factor (β -diversity) (Socolar et al. 2016). We synthesized the trends in how two major land use drivers, namely, agriculturalization and urbanization, affect bee taxonomic and phylogenetic α -, β -, and γ -diversity. We found that the trends in α -, β -, and γ -diversity are largely consistent between taxonomic and phylogenetic metrics when responding to the same land use driver. The α -diversity declines under the different anthropogenic land uses are consistent with our expectations and previous studies based on other taxa (Millard et al. 2021; Newbold et al. 2015). These results provide additional evidence of the threats of agricultural and urban expansion (Dicks et al. 2021) by demonstrating their negative impacts on phylogenetic α -diversity in addition to taxonomic α -diversity. The responses of β -diversity to land uses are more variable, as urban habitats exhibited higher β -diversity than natural habitats, which is in contrast with the general expectation that urbanization drives biotic homogenization (Socolar et al. 2016). At the same time, we found some support for agricultural habitats having reduced taxonomic β - but not phylogenetic β -diversity. These ultimately lead to reduced taxonomic and phylogenetic γ -diversity in agricultural habitats, but not urban habitats, where we failed to detect significant γ -diversity loss compared to natural habitats. The β - and γ -diversity results highlight the threat of agricultural expansions to large-scale bee diversity due to systematic γ -diversity decline. Broadly, our results provide empirical evidence showing that, although α -diversity responses may be similar across land use drivers, β -diversity responses vary, resulting in different γ -diversity consequences.

The differing responses of β -diversity to urban and agricultural land use may be a result of differing environmental heterogeneity within these land use categories. In our dataset, most studies compared assemblages within a single city or landscape, with the mean and 95% percentile of the study extent being 38 and 478 km, respectively. At these scales, different management practices within cities, such as varying ornamental plants or mowing frequencies due to owner preferences (Aronson et al. 2017; Lerman et al. 2018; Prendergast, Dixon, and Bateman 2022), can increase environmental heterogeneity and, therefore, result in higher β -diversity than natural habitats (Alberti 2016). Conversely, β -diversity exhibited varying trends or marginal declines in agricultural habitats across studies. While agricultural activities reduce environmental heterogeneity, particularly in monocultural croplands (Leong et al. 2016), the effects can be more variable in subsistence agriculture systems (Landaverde-González et al. 2017), potentially explaining the marginal results. This ultimately led to detectable declines in γ -diversity in

agricultural habitats but not urban habitats. Thus, our results indicate that while land use impacts are usually reported to affect α -diversity negatively across terrestrial taxa, these conclusions do not necessarily extend to γ -diversity, particularly with urbanization (Fenoglio, Rossetti, and Videla 2020; Liang et al. 2023; Newbold et al. 2015; Sol et al. 2017).

We found no evidence that land use change systematically strengthens phylogenetic habitat filtering, and in fact, we found relaxed filtering in urban habitats for β -diversity of bees. Previous bee studies have found variable phylogenetic habitat filtering effects across different types of agricultural and urban environments (Bartomeus et al. 2018; Odanaka and Rehan 2019; Ramírez et al. 2015; Villalta et al. 2022), potentially leading to no generalizable patterns when coarse land use classification is used. Studies of phylogenetic habitat filtering for β -diversity are rare. The weakly relaxed phylogenetic habitat filtering in urban habitats detected can again be explained by increased environmental heterogeneity in cities compared with natural and agricultural habitats (Alberti 2016; Aronson et al. 2017). For example, given the strong co-evolutionary history between bees and plants (Brown and Cunningham 2022), different planting preferences across urban green spaces can attract varying bee lineages, leading to higher phylogenetic β -diversity than expected based on taxonomic β -diversity. Nevertheless, the weakly relaxed phylogenetic filtering for phylogenetic β -diversity did not propagate to γ -diversity of bees in urban habitats, as phylogenetic β -diversity only contributed to 16.7% of γ -diversity across studies.

Apart from their varying impacts on bee diversity, another difference between the two land uses is that the genus-level abundance changes exhibited an intermediate phylogenetic signal in agricultural habitats but minimal signal in urban habitats. The small number of genera in our analyses (≤ 51) limited our statistical power (Münkemüller et al. 2012), while genus-level analyses can underestimate phylogenetic signals (Rabosky 2015). Species-level analyses, including rare species, are needed to determine the true extent of phylogeny in governing bees' responses to the two land uses. Nevertheless, the stronger phylogenetic signals in agricultural habitats suggest a higher importance of evolutionarily conserved traits, such as nesting biology and lecty (Odanaka and Rehan 2019), in determining species abundance in these environments (Grab et al. 2019). Alternatively, species responses to urban habitats may be more driven by stochasticity (Sattler et al. 2010) or evolutionarily labile traits, such as thermal tolerances (Hamblin et al. 2017).

As phylogenetic and taxonomic diversity respond similarly to agricultural and urban land uses, conservation measures that increase taxonomic diversity in agricultural and urban habitats are expected to increase their phylogenetic counterparts. These findings can facilitate decision-making in management targeting multiple diversity metrics, as the responses of phylogenetic diversity to different environmental drivers are less

understood than those of taxonomic diversity (Cadotte and Tucker 2018). For α -diversity, measures such as organic farming, crop diversification, establishing flower strips, and planting gardens have been found to increase pollinator taxonomic α -diversity in meta-analyses or quantitative syntheses (Kennedy et al. 2013; Lichtenberg et al. 2017; Majewska and Altizer 2020; Scheper et al. 2013). Studies have also evaluated the effectiveness of conservation measures in enhancing taxonomic β -diversity (Ponisio, M'Gonigle, and Kremen 2016), although they are relatively rare compared with studies focusing on taxonomic α -diversity. The same environmental drivers could increase taxonomic α -diversity but reduce taxonomic β -diversity in bees (Steinert et al. 2020), meaning that associated conservation measures can simultaneously mitigate and exacerbate the impacts of land use change, leading to unclear net effects on γ -diversity. Thus, we emphasize the importance of conducting additional taxonomic β - and γ -diversity assessments on the effectiveness of conservation measures to better understand their contributions to mitigating land use impacts.

Many large-scale conservation assessments focusing on the impacts of land uses are based on projecting α -diversity models to different land use scenarios (Chaudhary et al. 2015; De Palma et al. 2017; Newbold et al. 2015). While α -diversity patterns are helpful for conservation planning, they might not apply to biodiversity at larger spatial scales (e.g., national-, regional-, or landscape-level biodiversity), which might have exacerbated/weakened diversity loss depending on β -diversity changes (Socolar et al. 2016). Our findings demonstrate that qualitative conclusions about land use impacts can differ between α - and γ -diversity analyses. Based on our results, while taxonomic and phylogenetic α -diversity of bees might exhibit similar changes in agriculturalization and urbanization hotspots, the consequences for γ -diversity can be very different, with more substantial impacts at larger scales expected in agriculturalization hotspots such as West Africa and Southeast Asia (Williams et al. 2021). Given the need to conserve biodiversity and its associated ecosystem functions at multiple scales (Socolar et al. 2016; Winfree et al. 2018), our study confirms the threat of agricultural expansions to global bee diversity. It also highlights the need to understand processes determining β - and γ -diversity changes and integrate these diversity metrics into conservation assessments.

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Acknowledgments

Toby P.N. Tsang was supported by the Hong Kong General Research Fund (17115119) and the University of Toronto Scarborough Postdoctoral Fellowship Program. The Hong Kong General Research Fund was awarded to Lauren C. Ponisio and Timothy C. Bonebrake. Lauren C. Ponisio was also funded by the NSF (Award ID: 2009075). A. A. Amado De Santis was partly supported by the National Research Council of Argentina (CONICET), SIGMA Xi Foundation, a PIUNT project from the National University of Tucumán, Argentina (UNT), and PUE 023 project from the National Research Council of Argentina (CONICET). Adrian González-Chaves was funded by a grant from the Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP; Interface Project, No. 2013/23457-6). Alexandra-Maria Klein was supported by the German Science Foundation (DFG), Grant Number KL 1849/4-1, and the Alexander-von-Humboldt Foundation. Alyssa B. Stewart was partly

supported by funding from Mahidol University (Strategic Research Fund) and the Thailand Research Fund (Grant MRG6080124). András Báldi was partly funded by the European Union's Horizon 2020 project "Safeguard" (Grant Agreement ID: 101003476). Andrea Holzschuh was supported by the European Union's Horizon 2020 project "Safeguard" (Grant Agreement No. 101003476) and the Federal Ministry of Food and Agriculture (BMEL) via the Federal Office for Agriculture and Food (BLE) (Grant No. 2821ABS002). Anson Main was supported by the Missouri Department of Conservation. Antonio Diego de Melo Bezerra was supported by CAPES (Coordination of Superior Level Staff Improvement). Annika Hass, Catrin Westphal, and Svenja Bänisch were supported by the LEGATO project that was funded by the BMBF (German Federal Ministry of Education and Research) Framework Programme Research for Sustainable Development (FONA, FKZ: 01LL0917A, 01LL0917D). Drissa Coulibaly and Katharina Stein were funded by the German Federal Ministry of Education and Research (BMBF) within the project WASCAL (West African Science Service Centre on Climate Change and Adapted Land Use). Svenja Bänisch was also supported by the DAAD (Germany Academic Exchange Service) scholarship. Benoît Geslin and Isabelle Dajoz were funded by the Region Ile-de-France through the DIM Astréa and the R2DS program. Blandina Felipe Viana and Juliana Hipólito were supported by the Brazilian National Council for Scientific and Technological Development (CNPq) through the following projects: codes INCT IN-TREE (465767/2014-1) and PVE—Science Without Borders (407152/2013-0); Juliana Hipólito was supported by CAPES scholarships; and Blandina Felipe Viana was supported by CNPq for the grant (PQ code: 305470/2013-2). Breno M. Freitas was funded by CNPq through the project code Universal 14/2011 (#473454/2011-4) and Breno M. Freitas was supported by a CNPq Research Grant (#302934/2010-3). Bruno Ferreira Marques was supported by CNPq for a Research Productivity Fellowship (#308358/2019-8). Luisa G. Carvalheiro was funded by CNPq (#307625/2021-4). Mariana Beal-Neves was supported by CAPES (Coordination of Superior Level Staff Improvement). Ana Carolina Pereira Machado was supported by CNPq (#141736/2020-8) and CAPES (#COOPBRASS: 88887.947041/2024-00). André Rodrigo Rech was supported by FAPEMIG (#APQ-00932-21, #APQ-03100-21, #APQ-01152-22, #APQ-01151-23, #APQ-03262-23, and #RED-00039-23), CNPq (#311665/2022-5 and #423939/2021-1), and CAPES (#88887.837988/2023-00 and #88887.368784/2019-00). Catalina Gutiérrez-Chacón was supported by the Colombian Department of Science, Technology and Innovation—Colciencias (call 529). Caleb Wilson and Mary A. Jamieson were supported by the Foundation for Food and Agricultural Research New Innovator Award (FFAR Award No. 430876) (<https://foundationfar.org/>) and the Oakland University Provost Graduate Student Research Award (Oakland.edu). David Kleijn and Jeroen Scheper were supported by the European Community's Seventh Framework Programme (FP7/2007–2013) under Grant Agreement No 244090, STEP Project (Status and Trends of European Pollinators, www.step-project.net). Jeroen Scheper and David Kleijn were also supported by the Dutch Ministry of Economic Affairs (BO-11-011.01-011 and KB-14-003-006). Eileen F. Power and Jane C. Stout were supported by the Irish Department of Agriculture, Fisheries and Food Research Stimulus Fund (RSF), funded under the National Development Plan (2007–2013). Elsa Youngsteadt was supported by the USDA National Institute of Food and Agriculture Award Number 2020-67013-31916 and USDA National Institute of Food and Agriculture Hatch Project 1018689. Eunice Enríquez was supported by Organization for Women in Science for the Developing World (OWSD), and the Secretaría nacional de Ciencia y Tecnología del gobierno de Guatemala (SENACYT). Frédéric McCune and Valérie Fournier were funded by the Natural Science and Engineering Research Council of Canada (NSERC) Discovery Grant Program and the Fonds de Recherche Nature et Technologies Québec (FRQNT). Gideon Pisanty and Yael Mandelik were partially funded by the Israel Ministry of Agriculture Research Grant No. 824-0112-08 and the Israel Science Foundation Research Grant No. 919/09. Jose L. Gonzalez-Andujar, Jordi Izquierdo, and Jane Morrison were supported by FEDER (European Regional Development Funds) and the Spanish Ministry of Economy and Competitiveness grants (Project Numbers AGL2012-33736 and AGL2015-64130-R). The

Natural Sciences and Engineering Research Council of Canada (NSERC) provided Jane Morrison with a doctoral scholarship. Katherine J. Turo was supported by USDA-NIFA Postdoctoral Fellowship 2021-67012-35153 and the National Science Foundation, Grant/Award Numbers: CAREER 1253197 and DGE-1343012. Keng-Lou James Hung was supported by UC San Diego Academic Senate Bridge Fund Grant BIO088B, NSF Doctoral Dissertation Improvement Grant DEB-1501566, National Geographic Society Young Explorer Grant 9014-11, a Mildred E. Mathias Graduate Student Research Grant from the University of California Natural Reserve System, the Jeanne Marie Messier Memorial Endowed Fund, Sigma Xi Grant in Aid of Research G20111015158245, and NSF Biological Research Collection Grant DBI-0956388. Montserrat Plascencia, Robyn D. Quistberg, and Stacy Philpott were funded by the USDA National Institute of Food and Agriculture, Grant/Award Number: 2016-67019-25185, and USDA National Institute of Food and Agriculture, Grant/Award Number: 2016-67032-24987. Kristoffer Hylander and Ulrika Samnegård were supported by the Swedish research councils: The Swedish International Development Cooperation Agency (SIDA) (SWE-2009-134, awarded to Kristoffer Hylander) and Formas (229-2009-991, awarded to Kristoffer Hylander). K. Ballare was supported in part by the Graduate Program in Ecology, Evolution and Behavior at The University of Texas at Austin, Texas Department of Parks and Wildlife, and the USDA Forest Service. Laura A. Burkle was supported by Washington University in St. Louis, Tyson Research Center, Montana State University, National Science Foundation (DEB 0934376, 20133168225, and 1256788), and Western Sustainable Agriculture Research and Education (SW13-043). Natalia Escobedo-Kenefic and Patricia Landaverde-González were supported by Dirección General de Investigación de la Universidad de San Carlos de Guatemala (Digi-USAC) through the research grant 4.8.63.2.27.2012. Natapot Warrit and Pakorn Nalinrachatakan were supported by BIFA: Biodiversity Fund for Asia (BIFA5_005 and BIFA6_009) via GBIF and the National Science and Technology Development Agency (NSTDA), Thailand. Pornpimon Tangtorwongsakul was funded by The National Science and Technology Development Agency (NSTDA) under the project "Effect of urbanisation on species richness and abundance of indicator species inhabiting Thailand's most important wetland." Yunhui Liu was supported by the National Natural Science Foundation of China (No. 41871186). Yves Basset was funded by the Czech Science Foundation (GAČR 20-31295S). The Missouri Cooperative Fish and Wildlife Research Unit is jointly sponsored by the Missouri Department of Conservation, the University of Missouri, the US Fish and Wildlife Service, the US Geological Survey, and the Wildlife Management Institute. Use of trade, product, or firm names is for descriptive purposes only and does not imply US Government endorsement. We thank Faye Benjamin, Virginie Boreux, Dan Cariveau, Bryan N. Danforth, Brianne Du Clos, Elizabeth Elle, Rufus Isaacs, Florian Kohler, Claire Kremen, Greg Loeb, Jessamyn S. Manson, Jon Marshall, Doreen Mengel, Lisa Neame, Gesine Pufal, Romina Rader, Taylor Ricketts, Agustin Saez, Christof Schüepp, Felipe Deodato da Silva e Silva, Rebecca Tonietto, Julianna Wilson, Jort Verhulst, and Rachel Winfree for providing data. We also thank individuals who participated in collecting and collating these data. The findings and conclusions in this publication are those of the authors and should not be construed to represent any official USDA or US Government determination or policy but to represent the views of the US Geological Survey.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The data and R-scripts supporting the findings of the study are openly available in Zenodo at <https://doi.org/10.5281/zenodo.14302883> and on GitHub at <https://github.com/tpaknok/BeeLandUse>. Climate data from CHELSA v1.2 are available at <https://doi.org/10.16904/envdat.228.v2.1>. The PREDICTS database is available at <https://doi.org/10.5519/0066354>.

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Supporting Information

Additional supporting information can be found online in the Supporting Information section.