GENETIC DIVERSITY AFFECTS ECOSYSTEM FUNCTIONS ACROSS TROPHIC LEVELS AS MUCH AS SPECIES DIVERSITY, BUT IN AN OPPOSITE DIRECTION

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ABSTRACT

Understanding the relationships between biodiversity and ecosystem functioning stands as a cornerstone in ecological research. Extensive evidence now underscores the profound impact of species loss on the stability and dynamics of ecosystem functions. However, it remains unclear whether the loss of genetic diversity within key species yield similar consequences. Here, we delve into the intricate relationship between species diversity, genetic diversity, and ecosystem functions across three trophic levels —primary producers, primary consumers, and secondary consumers— in natural aquatic ecosystems. Our investigation involves estimating species diversity and genome-wide diversity -gauged within three pivotal species- within each trophic level, evaluating seven key ecosystem functions, and analyzing the strength of the relationships between biodiversity and ecosystem functions (BEFs). We found that, overall, the absolute effect size of genetic diversity on ecosystem functions mirrors that of species diversity in natural ecosystems. We nonetheless unveil a striking dichotomy: while genetic diversity was positively correlated with various ecosystem functions, species diversity displays a negative correlation with these functions. These intriguing antagonist effects of species and genetic diversity persists across the three trophic levels (underscoring its systemic nature), but were apparent only when BEFs were assessed within trophic levels rather than across them. This study reveals the complexity of predicting the consequences of genetic and species diversity loss under natural conditions, and emphasizes the need for further mechanistic models integrating these two facets of biodiversity.

Introduction

Diversity *within* and *among* species are both important to ensure and stabilize ecosystem functions (Cardinale *et al.* 2012; Raffard *et al.* 2019). Studies on the links between biodiversity and ecosystem functioning (BEFs) have primarily focused on the interspecific (species) facet of biodiversity (Balvanera *et al.* 2006; Hooper *et al.* 2005). However, the intraspecific (genetic) facet of biodiversity has also recently been shown to have substantial effects on ecosystem functions (Crutsinger *et al.* 2006; Hughes & Stachowicz 2004; Reusch *et al.* 2005). Recent meta-analyses have shown that genetic diversity of plant and animal populations affect ecosystem functions, and that the strength (and shape) of intraspecific BEFs is similar to that of species diversity (Raffard *et al.* 2019; Wan *et al.* 2022).

Although natural assemblages encompass both intra- and interspecific diversity, most studies investigating BEFs are considering each biodiversity facet separately (but see, Fridley & Grime 2010; Prieto *et al.* 2015). This makes it difficult to differentiate the relative role of genetic and species diversity in ecosystem functions, impeding general predictions regarding the consequences of biodiversity loss as a whole on ecosystem functions (Blanchet *et al.* 2023). For instance, we are currently unaware whether genetic diversity may functionally compensate for a species loss in an (species-poor) ecosystem, whether the loss of genetic diversity within a few species in an assemblage is as detrimental for ecosystem functions as a species loss, or whether the combined loss of genetic and species diversity may have non-additive consequences for ecosystem dynamics. Although these biodiversity loss scenarios are realistic, our knowledge on the relative role of genetic *vs*. species diversity in ecosystem functions are still too scarce to provide reliable predictions.

The few studies investigating the combined effects of genetic and species diversity on ecosystem functions were all conducted experimentally by manipulating the genetic and species diversity of assemblages under controlled conditions (Fridley & Grime 2010; Hargrave *et al.* 2011; Prieto *et al.* 2015). Our understanding of genetic (intraspecific) and species (interspecific) BEFs therefore relies on simplified ecosystems that often lack variation in other factors (including spatial scales, abiotic factors…), and in which feedbacks between ecosystem functions and biodiversity are limited (Duffy *et al.* 2017; Prunier *et al.* 2023). However, knowledge acquired from BEFs at the interspecific level reveals that environmental variation can either reduce or enhance the effects of biodiversity on ecosystem functions, hence generating large variance in the magnitude and direction of BEFs measured in the wild (Hagan *et al.* 2021; Van Der Plas 2019). To our knowledge, the question of whether environmental variation decreases or enhances the relative influence of genetic and species diversity on ecosystem functions has never been tackled. Therefore, we

need further realistic field studies of BEFs, embracing the whole diversity of life forms (from genes to species) to generate insightful knowledge for future mechanistic models.

BEF studies often consider a single trophic level, despite accumulating evidence that biodiversity at a given trophic level can propagate across trophic levels, generating "multi-trophic BEFs" (Lefcheck *et al.* 2015; Soliveres *et al.* 2016). For instance, studies testing the joint effects of genetic and species diversity on ecosystem functions have mostly considered the effect of primary producer diversity on their own productivity ("*within-trophic level BEFs*", e.g., Hargrave *et al.* 2011; Prieto *et al.* 2015). However, genetic and species diversity within a given trophic level may have propagating effects on the ecosystem at other trophic levels (hereafter, "*between-trophic level BEFs*"). For instance, a genetically-diverse predator population shares their resources more efficiently than a genetically-poor predator population, which might permit a higher prey species coexistence and hence a larger prey biomass (*between-trophic level* BEFs due to genetic diversity, e.g., Raffard *et al.* 2021). Alternatively, a species-rich community of primary producers likely exhibits higher primary production, as organisms in species-rich communities share basal resources more efficiently than in species-poor communities (*within-trophic level BEFs due to species diversity,* Balvanera *et al.* 2006; Hooper *et al.* 2005). Similarly, the relative impact of genetic and species diversity should likely be inconsistent across trophic levels. For instance, the relative impact of genetic diversity on ecosystem functions should increase with increasing trophic levels, because the higher the trophic level, the lower the species richness and the higher the chance for genetic diversity to have strong effects on functions (Blanchet *et al.* 2020). Studies considering genetic and species BEFs under a realistic multitrophic scenario may thus provide insightful information that has so far been rarely revealed.

Here, we conducted a field study to test the relative importance of genetic and species diversity for ecosystem functions across multiple trophic levels in a natural landscape. We focused on three trophic levels from river ecosystems; riparian trees (primary producers), macroinvertebrate shredders (primary consumers) and fish (secondary consumers). For each trophic level, we quantified the species diversity of each community, as well as the genetic diversity of a single target and dominant species (*Alnus glutinosa*, *Gammarus* sp. and *Phoxinus dragarum* respectively). We further estimated several ecosystem functions, including leave decomposition of riparian trees, biomass (as productivity estimates) of each target species and total biomass of each community within each trophic level. We relied on causal analyses, taking into account the direct and indirect effects of the environment (through biodiversity) on ecosystem functions (Duffy *et al.* 2016) to test i) whether BEFs measured at the genetic level (*genetic* BEFs) are similar in magnitude and direction to BEFs measured at the species level (*species* BEFs); and ii)

whether *within-trophic level* BEFs are similar in magnitude than *between-trophic level* BEFs. We also tested whether the relative effects of species and genetic diversity on ecosystem functions (within or between trophic levels) are consistent across the three trophic levels (primary producers, primary consumers and secondary consumers), in order to generalize findings along the trophic chain.

Materials and methods

Sampling sites and trophic chain

We sampled 52 sites in Southern France from the Adour-Garonne watershed, and distributed along an east-west gradient in the Pyrenees Mountains (**Figure 1a**). We acquired data on species diversity, genetic diversity and ecosystem functions at three trophic levels (primary producers, primary consumers and secondary consumers) (**Figure 1b**). Riparian trees (57 species in the sampled area) provide organic matter in the form of fallen leaves as a food source for decomposers. We selected the common alder *Alnus glutinosa* for acquisition of genetic data due to its dominance at most sites and its functional relevance, as its roots serve as shelters for many aquatic species and are involved in nitrogen fixation. Macroinvertebrate shredders (101 genera in the sampled area) are primary consumers using leaves as resources, and converting them into accessible organic matter for other species. We focused on the most abundant Gammarid (Crustacean) species for genetic data acquisition, referred to as *Gammarus* sp. This species has not yet been formally named although it is phylogenetically distinct from its closest relative, *Gammarus fossarum* (Carnevali 2022; Piscart, unpublished data). This species is particularly efficient at decomposing tree leaves, in particular those from *Alnus* (Macneil *et al.* 1997). Fish (20 species in the sampled area) are secondary consumers feeding on invertebrates (amongst others). We used the minnow *Phoxinus dragarum* as the fish target species as it is an abundant and important predator strongly impacting invertebrate communities (Raffard *et al.* 2021).

Biodiversity estimates

Species datasets. At each site, we collected data on the abundance of all species within each trophic level, at one occasion for trees (July-August 2021) and two occasions for invertebrates (July and November 2020) and fishes (mid-July to mid-August 2020 and 2021), to obtain accurate biodiversity estimates. We identified tree species along a 200m transect of each river bank, excluding trees with trunk smaller than 2cm in diameter and more than

one meter away from the bank. The abundances of trees were estimated as the total number of individuals per species and per site. For invertebrates, we identified shredders to the genus level (or to the family level for some groups such as chironomids) sampled from two types of standardized traps installed in four micro-habitats per site: natural coconut brushes (15*5.5 cm, bristles length 7.5 cm) recovered after 1.5 month of colonization, and litter bags (15*11 cm, 0.8 cm mesh size) filled with senescent *Alnus* leaves from each site and recovered after nine days of colonization (see below). We calculated abundances of each genus by summing the number of individuals per genus found in the coco brushes and the litter bags, and we averaged the abundances over the two sampling occasions to get a single estimate per genus per site. For fish, we collected all specimens during single-pass electric fishing sessions over a mean area of ~ 469.9 m^2 (± 174 m^2) per site. We anesthetized, identified and counted individuals at the species level. We calculated fish abundances as the number of individuals per species and per m^2, and we averaged the abundances over the two sampling occasions as for invertebrates.

Genetic datasets. At each site, we collected tissue from up to 32 individuals of each of the three target species. We collected fresh leaves of *A. glutinosa* in May 2020, specimens of *Gammarus* sp. in February 2020, and a piece of pelvic fin from *P. dragarum* individuals in summer 2020. The DNA of these samples was extracted using commercial kits for *Alnus* and *Gammarus sp.* and a salt-extraction protocol for *P. dragarum* (see Fargeot *et al.* 2023 for details). For each specimen, DNA concentrations were measured using Qubit 3.0 fluorometer (Life Technologies®, USA). Sequencing was performed based on equimolar pools of DNA ("pool-seq" approach, Schlötterer *et al.* 2014) from each population and each species. For *Gammarus sp*., we also obtained a ~600 bp mitochondrial sequence from the COI mitochondrial gene from each individual to ensure identification and avoid mixing individuals from different species. *Gammarus* sp. was found allopatric in most sites, but for a few sites from the eastern part of the area in which two species were identified (Carnevali 2022). In this latter case, we conserve only the target species for creating the DNA pools. We created one DNA pool per site per species (52 pools for *A. glutinosa*, 47 pools for *Gammarus* sp. and 44 pools for *P. dragarum*) and performed double-digest restriction-site associated DNA sequencing (ddRAD-seq) for *A. Glutinosa* and *Gammarus* sp. (respectively, PstI/MseI and Pst/HindIII enzymes) and normalized Genotyping-by-Sequencing (nGBS) for *P. dragarum* (MsII enzyme). Library preparation and pool-sequencing were executed by LGC Genomics (Biosearch Technologies®, Germany) on an Illumina NovaSeq® (2x150 pb). Data processing was performed following De Kort *et al.* (2018), except that read mapping was performed on reference genomes. The genome of *A. glutinosa* was already available (Griesmann *et al.* 2018), and we assembled reference genomes from Illumina short-read

sequencing and PacBio long-read sequencing for *Gammarus. sp.* (available upon request) and *P. dragarum* (accession number on DDBJ/ENA/GenBank: JARPMJ000000000), respectively. SNP calling was performed with (i) filtering of raw sequencing files; (ii) indexing of reference genomes; (iii) mapping reads to the reference; (iv) filtering for unpaired and badly/non-mapped reads; (v) assembling all read information in a single file per population and per species and (vi) calculating SNP allelic frequencies (De Kort *et al.* 2018). The total numbers of SNPs retrieved were 583 862 for *A. glutinosa*, 331 728 for *Gammarus* sp. and 414 213 for *P. dragarum* (see Fargeot *et al.* 2023 for details).

Species and genetic diversity estimates. We calculated □- diversity per site using the Shannon entropy from the "hillR" R package for both species and genetic diversity. The Shannon entropy is a metric of evenness that takes into account the distribution of allele or species abundances within each site (Chao *et al.* 2014) by weighting each species/allele by its proportional abundance (q = 1). Results were similar when using the Simpson's diversity index (q = 2, results not shown).

Ecosystem function measurements

At each site, we measured seven ecosystem functions. We collected biomass data of all species at each trophic level (hereafter "total biomass") and the biomass of each target species as estimates of productivity, as well as the decomposition rate of *Alnus* leaves. For riparian tree biomass, we used the trunk diameter of each single tree as a proxy of individual tree biomass, and we summed the trunk diameters of all trees found along the transect (divided by the length of the transect) to estimate the total tree biomass per site and per meter of bank. The same approach was used to estimate *A. glutinosa* biomass. For macroinvertebrate shredders, we estimated the total invertebrate biomass by drying all individuals for 24h at 60°C before weighing them (10^{-4}g precision). The same procedure was used to estimate the biomass of *Gammarus* sp. For both estimates, we averaged biomasses over the two sampling sessions. For fish, (fresh) total fish biomass was estimated as the total weight of all individuals (0.01g precision) per site, whereas *P. dragarum* biomass was the mass of all *P. dragarum* specimens per site. Fish biomasses were averaged over the two sampling sessions.

For the decomposition rate, we quantified leaf mass loss in litter bags placed in four micro-habitats per site twice (July and November 2020). We gathered and dried senescent leaves during fall 2019 from five *Alnus* trees per site to limit individual-specific effects on decomposition. Litter bags were 15cm x 11cm pockets of plastic-wire mesh (mesh size; 8 mm to allow invertebrates colonization) in which we introduced 4g of dried leaves before

closing the bags with staples. We installed three bags per micro-habitat (12 per site) that we removed sequentially after ~9 days, ~18 days and ~27 days respectively to estimate decomposition rates. Bags were brought back to the laboratory, the remaining leaves were cleaned, dried and weighed. Decomposition rate was estimated as the slope of leaf mass loss over time (obtained from a linear model) that we averaged across replicates and temporal sessions (Raffard *et al.* 2021).

Environmental data

A major challenge for inferring BEFs from empirical data is to take into account the direct and indirect (through biodiversity) effects of environmental factors on ecosystem functions (Duffy *et al.* 2016, 2017). Failing to do this may result in overestimated and/or artefactual BEFs, especially if the same environmental factor simultaneously affects biodiversity and ecosystem processes (Grace *et al.* 2016). For each site, we measured thirteen variables related to river topography and physico-chemical characteristics that likely influence biodiversity and ecosystem processes (Altermatt 2013). *River bed width* (m) was averaged from five measurements per site. *Connectivity* was calculated as the "closeness centrality", *i.e.,* the inverse of the sum of the distances of a node to all other nodes along the shortest paths possible (Altermatt 2013), using QGIS and the "RiverDist" R package. *Altitude* (m), *distance from the outlet* (m) and *east-west gradient* (longitudinal position along the Pyrenees chain) were measured using QGIS; *oxygen concentration* ($mg.L^{-1}$), *oxygen saturation* (%), *water temperature* (°C), *specific conductivity* (µS/cm) and *pH* were measured (and averaged) in summers 2020 and 2021 using a multi-parameter probe (Aqua TROLL 500, In-Situ Inc.). Concentration of NO_{3-}, NO_{2-}, NH_4^+ and PO_4^{3-} were estimated (and averaged) during summers 2020 and 2021 from a filtered water volume (100mL) using the Alpkem Flow Solution Iv Autoanalyzer (OI Analytical®).

A Principal Component Analysis combining all thirteen variables was performed using the R package "ade4" (Dray & Dufour 2007), and coordinates of each site on the two first axes (38.03% of the total variance, see **Table 1**) were used as two synthetic environmental variables for further analyses. We kept only these two first axes to avoid collinearity and over-parameterization of subsequent models. The first axis is defined by a strong contribution of (in decreasing order) oxygen concentration and altitude (**Table 1**). The second axis is defined by a strong contribution of east-west gradient and connectivity (**Table 1**).

Statistical analyses

BEF relationships. To quantify the strength of association between biodiversity estimates and ecosystem functions (BEFs), we performed piecewise Structural Path Models (pSEM, "piecewiseSEM" package, Lefcheck 2016). pSEM allows modelling direct and indirect causal relationships among a set of response variables and predictors (Shipley 2009). Further, pSEM uses local estimates of each linear structural equation separately (*i.e.*, parameters are estimated from a series of independent models forming a general causal graph), which allows the inclusion of a large number of parameters despite modest sample sizes (Shipley 2009). We ran a pSEM for each ecosystem function separately (*i.e.*, seven pSEMs, see an example in **Figure 2**). In each pSEM, the ecosystem function was the dependent variable whereas the six biodiversity estimates (species and genetic diversity estimated for each trophic level) and the two synthetic environmental variables were the predictors. In each model, environmental predictors were allowed to explain each biodiversity estimate (indirect effects of environmental variables through their influence on biodiversity, see **Figure 2**). For some functions (in particular those associated with plant biomass), irrelevant biodiversity-functions links were not included (e.g., the impact of fish diversity on tree biomasses).

For each function, we retrieved the local parameter associated with the direct effect of each biodiversity estimate (six per function, but for some functions for which ecology-irrelevant BEFs were excluded) on the function (coloured arrows in **Figure 2**), which provides both the magnitude and the direction of each BEF. To smoothen comparison, we calculated a standardized effect size for each BEF by applying the Fisher's Z transformation (*Zr*) to the local parameters. Our seven measures of ecosystem functions were not correlated one to each other (all $r_{pearson}<|0.39|$).

Direction and magnitude of all types of BEFs. We used a linear model to test (i) whether the magnitude and direction of *genetic* BEFs are similar to those of *species* BEFs, and (ii) whether *within-trophic level* BEFs are similar in effect size to *between-trophic level* BEFs. In this model, *Zr* (providing the direction and magnitude of each BEF, n=34) was the dependent variable, and the predictors were the diversity facets used to measure biodiversity (genetic or species diversity) and the type of BEF (*within-trophic* or *between trophic* levels, triangles vs. dots in **Figure 2**). We included the two-term interaction between diversity facet and type of BEF to test whether the magnitude and direction of *genetic* and *species* BEFs are consistent across *within-trophic level* and *between-trophic level* BEFs.

We ran an additional linear model similar to the previous one, except that we added as a fixed effect the trophic level at which biodiversity was measured to estimate BEFs (primary producers, primary consumers or secondary consumers) as well as all interaction

terms. Interaction terms allow testing the consistency of major conclusions across trophic levels, thereby determining the extent to which our findings can be generalized along the trophic chain. Models were run using the R base lm function and significance of fixed effects was determined using type III ANOVA (function Anova from the "car" R package, α=0.05).

Results

We found a significant interaction between the facet at which biodiversity is measured (genetic or species diversity), and the type of BEF that was measured (within- or between trophic levels; **Table 2**). This indicates (i) that -overall- *within-trophic level* BEFs were negative when considering species diversity ($Zr_{Within*Species}$ = -0.185, 95% CI [-0.343, -0.027]), whereas *within-trophic level* BEFs were positive when considering genetic diversity ($Zr_{Within*Genetic}$ = 0.168, 95% CI [0.010, 0.326], see **Figure 3a**), and (ii) that this pattern was not observed for *between-trophic levels* BEFs, where no particular trend was observed (**Figure 3a**). This finding indicates that species and genetic diversity have opposite effects on ecosystem functions when considering *within-trophic level* BEFs; species diversity is negatively associated, whereas genetic diversity is positively associated with ecosystem functions, but only when the influence of biodiversity on ecosystem functions is measured within the same trophic level. Noteworthily, the range of effect sizes found for *species* and *genetic* BEFs strongly overlaps, with values ranging from strongly negative to strongly positive (**Figure 3a**). The same conclusions were obtained when all possible links between biodiversity and ecosystem functions (i.e., including ecologically-irrelevant BEFs, see above) were considered (interaction term between biodiversity facet and type of BEFs, p=0.006), and when a mixed model including the ecosystem function identity as a random term was ran (interaction term between biodiversity facet and type of BEFs, p<0.018).

When including the trophic level at which biodiversity is measured, we found no significant interaction terms between trophic levels and other fixed effects nor any additive effect of trophic levels (see **Table S1**). This indicates that our main findings were consistent across trophic levels, *i.e.*, the respective negative and positive effects on ecosystem functions of species and genetic diversity hold statistically true across all trophic levels (**Figure 3b**).

Discussion

We provide empirical evidence that, in natural ecosystems, the effect sizes of genetic and species diversity on multi-trophic ecosystem functions are of similar magnitude, but operate in opposite directions. Indeed, for BEFs measured at the same trophic level, the

effects of species diversity on ecological functions were moderately negative on average, whereas the effects of genetic diversity were moderately positive. This suggests an antagonistic effect between the genetic and the species components of biodiversity in the modulation of ecosystem functions within one trophic level. This antagonistic effect was not identified for BEFs measured across trophic levels, since in these cases the influence of both genetic diversity and species diversity on ecosystem functions was generally not different from zero. These conclusions hold true across three trophic levels (plants, invertebrates and fish), indicating that the relative effects of genetic and species diversity on ecosystem functions are not limited to a specific trophic level.

Our results confirm a previous meta-analysis demonstrating that genetic and species diversity modulates ecosystem functions with a similar magnitude (Raffard *et al.* 2019), and results from few experimental studies that manipulated both the genetic and species components of biodiversity under controlled conditions (e.g., Jiang *et al.* 2022; Prieto *et al.* 2015). Indeed, within trophic levels, the absolute effect size of genetic and species diversity on ecosystem functions were of the same magnitude ($|Zr| = 0.168$ and 0.185 for genetic and species diversity effects respectively), and slightly greater than the effect sizes reported under controlled conditions ($|lnRR| = 0.132$ and 0.134 for genetic and species diversity effects respectively, Raffard *et al.* 2019) and those more generally reported for *species* BEFs ($|Zr| = 0.101$, Balvanera *et al.* 2006). The range of variation in effect size estimates was also the same for *genetic*- and *species* BEFs, ranging from low (null) values to high ($|Zr| > 0.4$) absolute values, as it is expected for BEFs measured under natural conditions (Hagan *et al.* 2021; Van Der Plas 2019). This demonstrates for the first time that under natural conditions, the effects of genetic and species components of biodiversity on ecosystem functions are comparable. However, our study goes two steps further as (i) it extends the conclusion made by Raffard *et al.* (2019) to multiple trophic levels and (ii) it demonstrates that the effects of genetic and species BEFs can actually operate in opposite directions.

As pointed out by Raffard *et al.* (2019), the vast majority (91% of 23 reviewed studies by 2019, see also Wan *et al.* 2022) of studies investigating the effects of genetic diversity on ecosystem functions have focused on primary producers, and all of them were based on experiments, which is also the case for most studies manipulating both genetic and species diversity. These trends strongly hamper any generalization. On the contrary, our findings provide a strong support for broadening the conclusion that both genetic and species diversity can influence ecosystem functions in the wild. More strikingly, our results demonstrate that, although the absolute effect sizes of genetic and species BEFs are of similar magnitude, for *within-trophic level* BEFs, the direction of their effects are opposite; species diversity (in general) reduces the rate of ecosystem functions, whereas genetic

diversity enhances the same functions. For instance, all other things being equal, higher fish species diversity is associated with a lower productivity (biomass) in *P. dragarum*, whereas its own genetic diversity is associated with a higher productivity (**Table S2**). As genetic and species diversity have been found to be uncorrelated spatially in this landscape (Fargeot *et al.* 2023), covariation among diversity estimates cannot explain these patterns. These antagonistic effects of genetic and species diversity on ecosystem functions parallel previous experimental findings on plants (Hazard *et al.* 2017; Tang *et al.* 2022). It is now essential to understand the mechanisms sustaining these antagonistic effects as a step forward.

S*pecies* BEFs were on average negative (see **Table S2** for individual estimates), which contrasts with the general view that species biodiversity favours ecosystem functions, although it is not that surprising (Dee *et al.* 2023; Hagan *et al.* 2021). Indeed, the net effect of species biodiversity on ecosystem functions results from the combined effects of both negative factors, arising from antagonistic interactions such as negative complementarity or negative selection effect, and positive factors, arising from beneficial interactions such as niche complementarity or facilitation (Loreau & Hector 2001). It is likely that, in our case, the net effect of interspecific interactions mostly results from negative complementarity among species (or strong negative selection effect), whereas the net effect of intraspecific interactions may result from facilitative interactions and/or improved niche complementarity with increased genetic diversity. Intraspecific competition is generally stronger than interspecific competition (Connell 1983), and intraspecific interactions could be expected to lead more frequently to negative complementarity (and hence negative *genetic* BEFs) than interspecific interactions. Since we observe the opposite, we can hypothesize that genetic diversity is essential to increase niche complementarity within species (Bolnick *et al.* 2003) and hence to reduce the pervasive effects of intraspecific interactions (Hughes *et al.* 2008; Prunier *et al.* 2023). Given the empirical nature of our study, it is hard to tease apart underlying mechanisms. Theoretical approaches, modelling simultaneously the genetic and species components of biodiversity, would be extremely useful to reveal the mechanisms sustaining opposite effects of intra- and interspecific diversity on ecosystem functions.

These antagonistic effects were observed only for BEFs measured *within* trophic levels, not for those measured *between* trophic levels. An overall *between-trophic level* BEF not different from zero suggests that biodiversity at a trophic level has only limited impact on ecosystem functions at another trophic level. For example, the biomass of *P. dragarum* was primarily influenced by genetic and species diversity in fishes, rather than the diversity of their preys (**Figures S2**). However, for both genetic and species estimates of biodiversity, there was a substantial variation in effect sizes for *between-trophic level* BEFs that ranged from negative to positive BEFs (**Figure 3**). This suggests that biodiversity effects across

trophic levels may be more variable in their direction than within-trophic level BEFs, which appear as more constrained. Variability in the magnitude and direction of effect sizes for *between-trophic level* BEFs likely blur a more general trend, but this variation is actually expected under natural conditions in which interactions involve multiple prey and predator species, fostering co-adaptation among communities from different trophic levels (Aubree *et al.* 2020; Poisot *et al.* 2013). In these cases, trophic complementarity between two trophic levels (i.e., the originality of a species based on the identity of the species it interacts with) might be a stronger determinant of ecosystem functions than complementarity measured at either one of the two trophic levels (Poisot *et al.* 2013). Quantifying trophic complementarity among our three target species (and communities) using stable isotope or gut content analyses for instance would be extremely valuable to assess whether this complexity can better explain BEFs between trophic levels than diversity measured at one of the trophic level (Aubree *et al.* 2020).

The empirical patterns we revealed here were all extremely consistent across the three trophic levels, hence allowing generalization. BEFs were not particularly stronger at any specific trophic level (**Figures S2**) and the relative effects of genetic and species diversity were not dependent on the trophic level at which the function was estimated. We may have expected a stronger top-down regulation (i.e., biodiversity of predators has more effects than biodiversity of preys) of ecosystem functions since previous studies showed that biodiversity loss should have greater consequences for multi-functionality when it occurs at higher trophic levels (Lefcheck *et al.* 2015). For instance, increased genetic diversity within a predatory fish species has experimentally been shown to indirectly increase the rate of litter decomposition by increasing the diversity of shredders (Raffard *et al.* 2021). Similarly, the relative effects of genetic and species diversity on functions may have varied among trophic levels, and in particular the relative importance of genetic diversity may have been higher for species-poor trophic levels (i.e., fish community) because of a “compensatory effect”. We found no evidence for these potential trophic-level dependencies, but instead found extremely consistent patterns, which, from a broader perspective, reveal the importance of integrating both multi-trophic and multi-faceted approaches in predicting the overall consequences of biodiversity loss on ecosystem functioning.

To conclude, we found that the genetic (intraspecific) and species (interspecific) facets of biodiversity are both important drivers of ecosystem functions in a natural and multi-trophic context. In the wild, these two facets of biodiversity can, as expected, generate low to moderately high impacts on ecosystem functions measured across three trophic levels, and they can operate in opposite directions. This demonstrates the importance for managers to develop integrative conservation plans spanning the entire diversity of life (from

genes to species). For instance, genetic diversity loss often precedes species loss, and our results suggest that -in mountain streams- losing genes may actually be particularly detrimental for the performance of ecosystem functions. As such, it appears essential to maintain populations with high levels of genetic diversity in these ecosystems. Future studies should (i) extend these findings to other ecosystems and by quantifying natural genetic variation in more than a single species per trophic level, (ii) generate theoretical predictions regarding the mechanisms sustaining the antagonistic effects of genetic and species diversity on functions we revealed, and (iii) use a broader integrative approach for estimating biodiversity across facets (*inclusive* biodiversity) by using either a trait-based approach or a genetic-based approach as recently proposed by Blanchet *et al.* (2023) and Loreau *et al.* (2023).

AUTHOR CONTRIBUTION

Laura Fargeot: Conceptualization (Supporting); Methodology (Equal); Software (Equal); Validation (Equal); Formal analysis (Lead); Investigation (Lead); Data curation (Lead); Writing - original draft (Lead); Writing - review & editing (Equal); Visualization (Lead); Supervision (Equal); Project administration (Lead). **Camille Poesy:** Methodology (Equal); Validation (Equal); Investigation (Lead); Data curation (Supporting); Supervision (Equal); Project administration (Supporting). **Maxim Lefort:** Methodology (Supporting); Investigation (Lead); Data curation (Supporting); Supervision (Equal); Project administration (Supporting). **Jérôme G. Prunier:** Methodology (Supporting); Software (Equal); Formal analysis (Supporting); Investigation (Supporting); Resources (Equal); Data curation (Supporting); Writing - original draft (Supporting); Writing - review & editing (Supporting). **Madoka Krick:** Methodology (Supporting); Investigation (Equal). **Rik Verdonck**: Methodology (Supporting); Software (Equal); Investigation (Supporting); Writing - review & editing (Supporting). **Charlotte Veyssière:** Methodology (Supporting); Investigation (Equal). **Murielle Richard:** Methodology (Supporting); Investigation (Supporting); Writing - review & editing (Supporting). **Delphine Legrand:** Validation (Equal); Writing - review & editing (Equal); Visualization (Supporting). **Géraldine Loot:** Validation (Equal); Investigation (Supporting); Writing - review & editing (Supporting); Visualization (Supporting). **Simon Blanchet:** Conceptualization (Lead); Methodology (Lead); Software (Supporting); Validation (Equal); Formal analysis (Supporting); Investigation (Lead); Resources (Equal); Data curation (Supporting); Writing - original draft (Supporting); Writing - review & editing (Lead); Visualization (Lead); Supervision (Lead); Project administration (Lead); Funding acquisition (Lead).

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Table 1. Characteristics of the two first principal components identified by the Principal Component Analysis (PCA) ran on the thirteen environmental variables. The part of the total environmental variance (%) and the contribution of each variable on each component are shown. The variables that contributed significantly to the axis are highlighted in bold.

	Component 1	Component 2
Part of total Variance (%)	21.66	16.37
River width	0.596	0.320
Connectivity	-0.155	**0.646**
Altitude	**0.648**	-0.385
Distance from outlet	0.528	-0.331
East-west gradient	0.105	**-0.795**
Oxygen concentration	**0.738**	0.343
Oxygen saturation	0.266	-0.509
Water temperature	-0.594	-0.012
Specific conductivity	-0.463	-0.045
pH	0.573	0.398
Concentration in $NO_3^+NO_2$	-0.369	-0.286
Concentration in NH_4+	-0.019	-0.207
Concentration in PO_4^{3-}	-0.279	0.236
Global characteristic	Low altitude, poorly oxygenated site - High altitude, highly oxygenated sites	Poorly connected east site - Highly connected west site

Table 2. ANOVA table for the linear model testing the effects of the biodiversity facet (species or genetic diversity) and the type of BEF (*within-* or *between-trophic levels*) on the magnitude and direction of the relationships between biodiversity and ecosystem functions measured in a riverine trophic chain.

	D.f.	F-value	P-value
(Intercept)	1, 30	0.326	0.572
Biodiversity facet	1, 30	0.220	0.642
Type of BEF	1, 30	5.246	**0.029**
Biodiversity facet*Type of BEF	1, 30	5.274	**0.028**

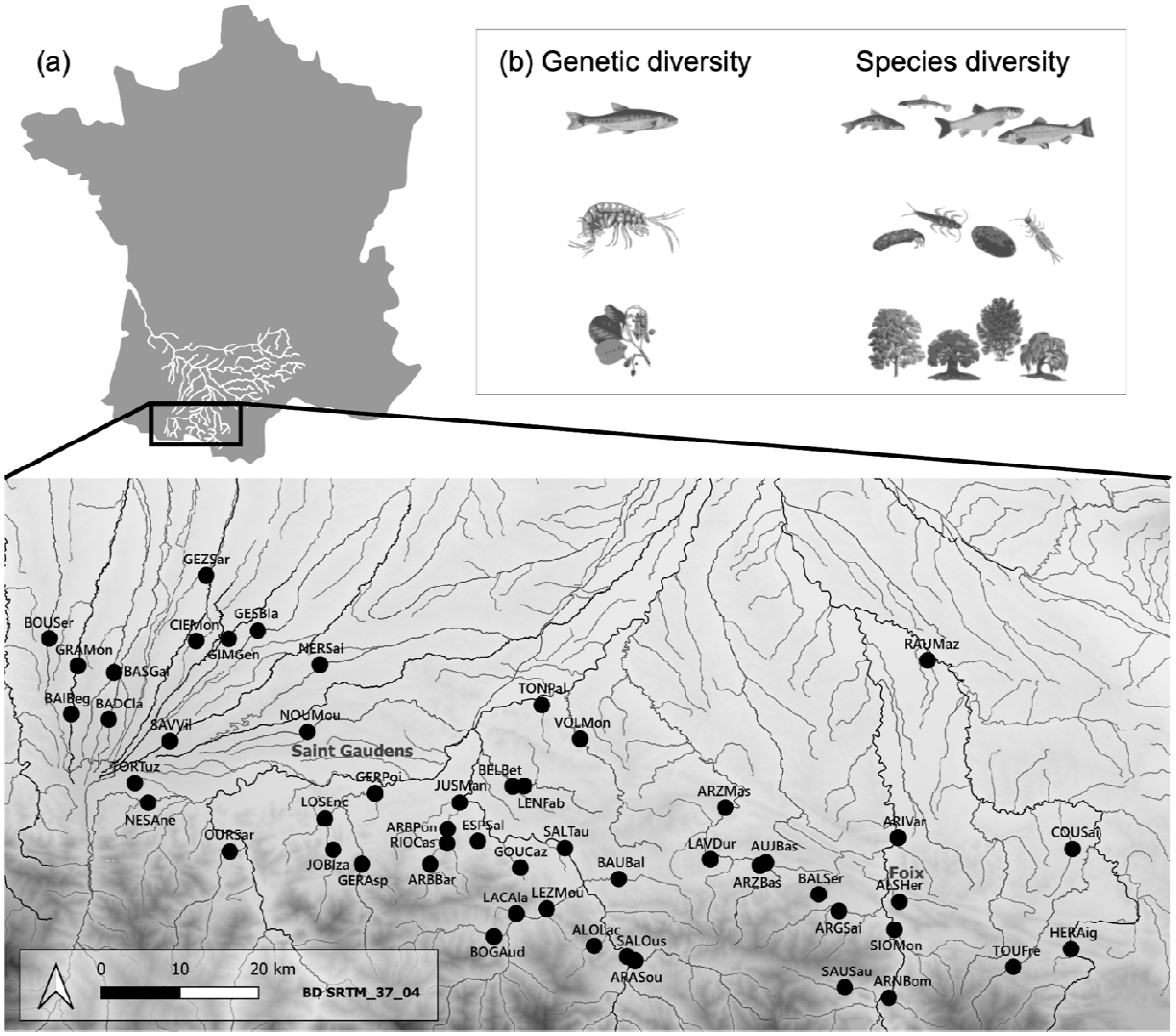
Figure captions

Figure 1. Location of sampling sites and illustration of the trophic chain. **(a)** Distribution of the 52 sampling sites (black dots) spanning a East-West gradient at the foothills of the Pyrenees Mountains (France). Each site is denoted by a six-letter code, with the three first letters indicating the river name and the three last letters indicating the closest city or village. **(b)** Our study focused on a tri-trophic food chain commonly found in mountain rivers, consisting of riparian trees, macroinvertebrate shredders and fishes (from bottom to top). Within each trophic level, we measured two facets of biodiversity: genetic diversity in a single target species within each trophic level (specifically *Phoxinus dragarum*, *Gammarus* sp. and *Alnus glutinosa*), and species diversity from communities.

Figure 2. Example of one of the seven causal models used to quantify the relationships between (species and genetic) diversity and ecosystem functions. We focused on seven ecosystem functions associated with genetic and species diversity at three trophic levels (green for primary producer, orange for primary consumer and blue for secondary consumer). Each relationship between biodiversity and ecosystem functions (n = 6 values per function, but for some functions for which irrelevant links were not considered, see the text, n = 32 values in total) was measured at the same trophic level (triangles) or at another trophic level (dots).

Figure 3. Magnitude and direction of the relationships between biodiversity and ecosystem functions (BEFs) measured in a riverine trophic chain. (a) The magnitude and direction of BEFs are expressed as effect sizes (*Zr*) and are displayed according to the facet used to measured biodiversity (genetic or species diversity, light grey and white boxplots respectively) and to the type of BEFs (*within-trophic level* BEFs or *between-trophic level* BEFs, triangles and dots respectively). Red colour and stars indicate global effect sizes that are significantly different from zero (p-value <0.01). Large symbols are mean ± 95%IC. (b) Same representation as (a) but with details at each trophic level (mean ± 95%IC, green for primary producer, orange for primary consumer and blue for secondary consumer). The trophic level at which BEFs are measured is coherent across all trophic levels.

Figure 1


(a)
(b) Genetic diversity
Species diversity
GEZSar
BOUSer
GRAMon
BASGal
BAIBeg
BADCla
SAVVil
CIEMon
GESBla
GIMGen
NERSai
NOUMou
Saint Gaudens
TORTuz
NESAne
GERPoi
LOSEnc
OURSar
JUSMan
BELBet
LENFab
ARBPom
RIOCas
ESPSal
SALTau
GOUCaz
JOBIza
GERAsp
ARBBar
BAUBal
LACAla
LEZMou
ALOLac
SALOus
BOGAud
ARASou
TONPal
VOLMon
ARZMas
LAVDur
AUJBas
ARZBas
BALSer
ARGSai
SAUSau
ARNBom
SIOMon
ALSHer
Foix
ARIVan
RAUMaz
COUSai
TOUFre
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0
10
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BD SRTM_37_04

Figure 2

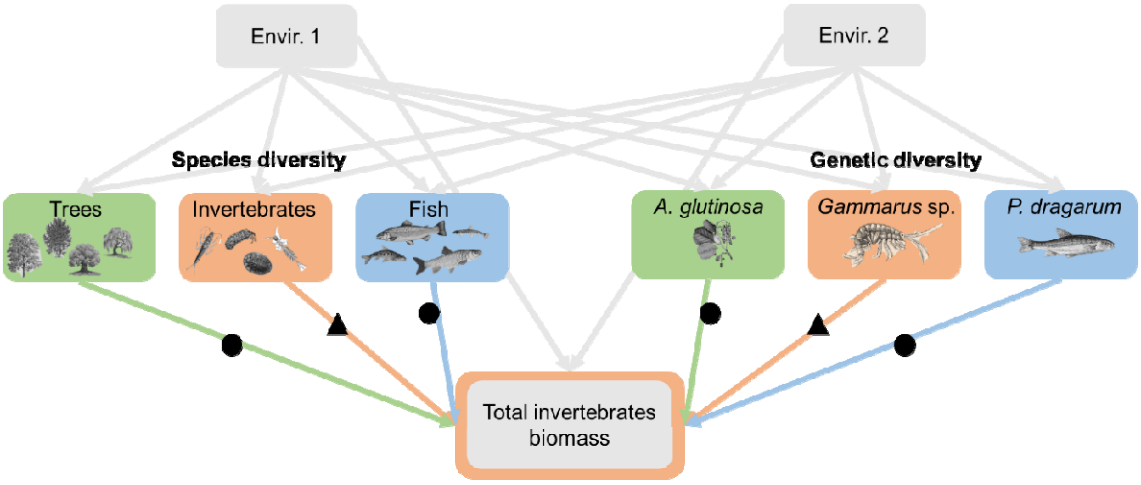
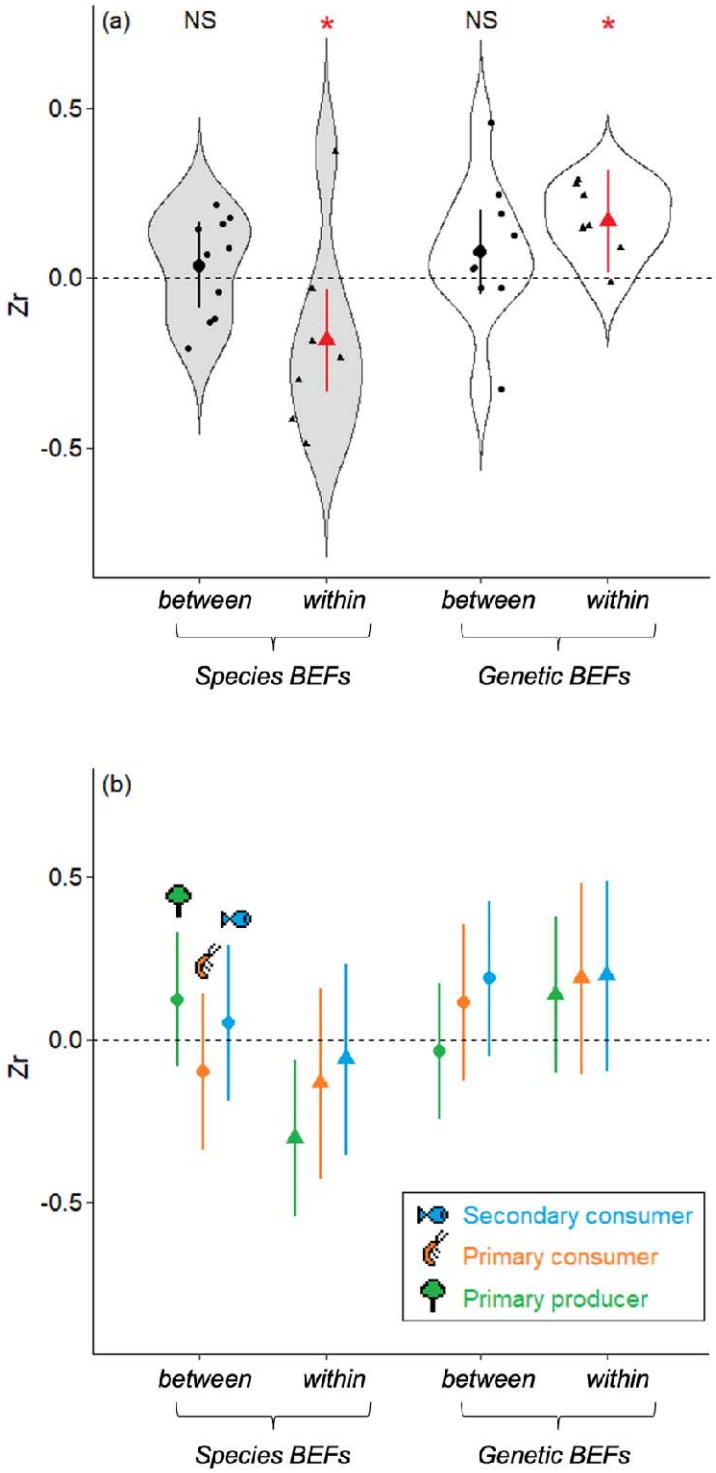

Envir. 1
Envir. 2
Species diversity
Genetic diversity
Trees
Invertebrates
Fish
A. glutinosa
Gammarus sp.
P. dragarum
Total invertebrates biomass

Figure 3


(a)
NS
*
NS
*
0.5
0.0
-0.5
Zr
between
within
between
within
Species BEFs
Genetic BEFs
(b)
0.5
0.0
-0.5
Zr
Secondary consumer
Primary consumer
Primary producer
between
within
between
within
Species BEFs
Genetic BEFs

SUPPLEMENTARY MATERIALS

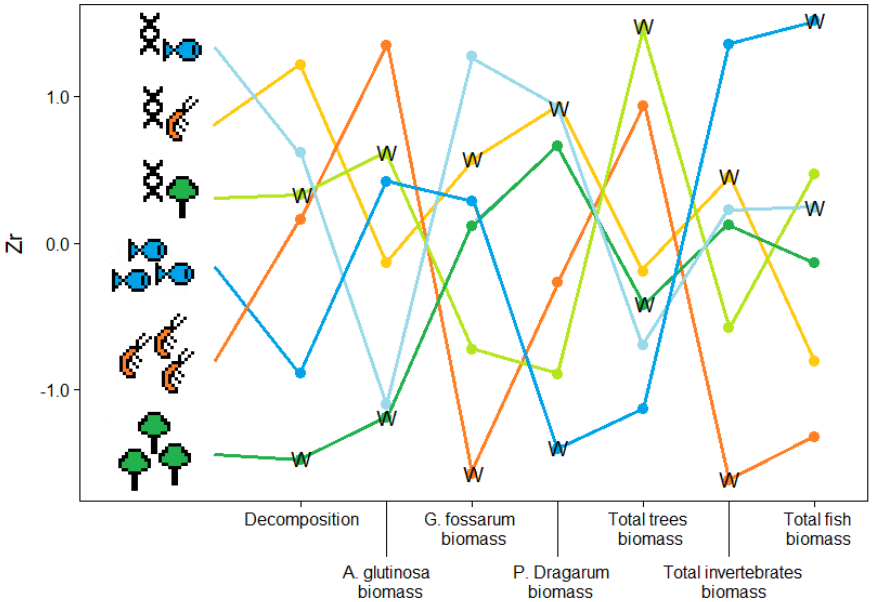


Figure S1. The six biodiversity estimates (genetic and species diversity at the three trophic levels) have idiosyncratic effects on ecosystem functions. They include (from top to bottom) genetic diversity in *Phoxinus dragarum*, *Gammarus* sp., and *Alnus glutinosa*, as well as species biodiversity in fish, macroinvertebrates shredder, and riparian tree communities. *Within-trophic* level BEFs (marked as 'W') display a bimodal distribution with strong positive and negative BEFs. Positive BEFs are more pronounced with light colours (light green, orange, and blue, representing genetic biodiversity), while dark colours (dark green, orange, and blue, representing species biodiversity) show a stronger negative relationship. Other relationships occur between different trophic levels and exhibit a general trend of idiosyncrasy. Note that all possible BEFs are displayed in this graph (n=42), although only 34 of them (those that are relevant biologically) are included into analyses.

Table S1. ANOVA table for the linear model testing the effects of the biodiversity facet (species or genetic diversity), the type of BEF (*within-* or *between-trophic levels*) and the trophic level at which BEFs are estimated (primary producers, primary consumers or secondary consumers) on the magnitude and direction of the relationships between biodiversity and ecosystem functions measured in a riverine trophic chain.

	D.f.	F-value	P-value
(Intercept)	1, 24	0.440	0.513
Biodiversity facet	1, 24	0.092	0.764
Type of BEF	1, 24	4.711	**0.040**
Trophic level	2, 24	0.565	0.575
Biodiversity facet*Trophic level	2, 24	0.501	0.612
Trophic level*Type of BEF	2, 24	0.362	0.699
Biodiversity facet*Type of BEF	1, 24	4.930	**0.036**

Table S2. Estimates of individual effect sizes (Zr) for *within-trophic* level BEFs. Estimates are shown for the genetic (intraspecific Zr) and species (interspecific Zr) components of biodiversity measured at each trophic level (riparian trees, macroinvertebrate shredders and fish). 95% confidence intervals are provided together with the estimate of each BEF.

Ecosystem function	Intraspecific Zr	95% CI	Interspecific Zr	95% CI
Decomposition	-0.012	[-0.394, 0.370]	-0.293	[-0.630, 0.060]
A. glutinosa biomass	0.128	[-0.179, 0.433]	-0.447	[-0.695, -0.143]
G. sp biomass	0.292	[-0.120, 0.688]	-0.273	[-0.661, 0.128]
P. dragarum biomass	0.244	[-0.064, 0.542]	-0.529	[-0.803, -0.166]
Riparian tree biomass	0.280	[-0.062, 0.609]	-0.183	[-0.485, 0.122]
Macroinvertebrate shredders biomass	0.097	[-0.242, 0.435]	-0.051	[-0.381, 0.279]
Fish biomass	0.159	[-0.260, 0.575]	0.326	[-0.123, 0.753]