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Biodiversity recovery following delta-wide measures for flood risk reduction

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Biodiversity declined markedly over the past 150 years, with the biodiversity loss in fluvial ecosystems exceeding the global average. River restoration now aims at flood safety while enhancing biodiversity and has had success locally. However, at the scale of large river distributaries, the recovery remained elusive. We quantify changes in biodiversity of protected and endangered species over 15 years of river restoration in the embanked floodplains of an entire river delta. We distinguish seven taxonomic groups and four functional groups in more than 2 million field observations of species presence. Of all 179 fluvial floodplain sections examined, 137 showed an increase in biodiversity, particularly for fast-spreading species. Birds and mammals showed the largest increase, that is, +13 and +3 percentage point saturation of their potential based on habitat. This shows that flood risk interventions were successfully combined with enhancement of biodiversity, whereas flood stage decreased (~24 cm).

INTRODUCTION

Global biodiversity decreased over the past centuries at similar rates as during previous mass extinctions in Earth’s history (1). Paradoxically, the systematic analysis of local assemblages over the past 40 years showed a large change in species composition, but no consistent loss (2), which led to the explicit inclusion of spatial scale in biodiversity trends (3). The trends in composition may be driven by the introduction of alien species, habitat degradation, and climate change. These changes do not take away the risk of local extinction for many threatened native species, and societal norms on the preferred species composition have been translated in many countries into laws and regulations that protect vulnerable and endangered species. As a subset of the global ecosystem, the fluvial ecosystems showed extinction rates of freshwater fauna that are five times higher than for terrestrial fauna (4). River corridors and deltas potentially maintain high species richness because the periodic flooding links the main channel to the floodplains, and because the river supplies the water and nutrients to sustain life (5, 6). However, especially in Europe and North America, land use change and population increase contributed to floodplain degradation and the decline in freshwater biodiversity. This degradation is still ongoing in Southeast Asia and Sahelian Africa (5). Currently, habitats associated with 65% of the river discharge are classified as moderately to highly threatened (7), showing that the valuable ecosystems in the world’s deltas are severely stressed (8, 9). At a global scale, river impairment will continue in the near future (10), although the number of efforts to restore rivers at the scale of entire deltas is increasing worldwide (11). Costly river restoration projects aim at combining multiple objectives including flood safety, biodiversity, navigation, water supply, and recreation (11, 12). The large investments in these projects justify the question whether these efforts are successful. Although pioneer vegetation rapidly restores the “naturalness” perceived by a casual observer, it remains unclear how successful these restoration measures are for biodiversity in general and for threatened species in particular. The effects of river restoration on flood hazards are routinely evaluated using calibrated hydrodynamic models. In contrast, biodiversity recovery has been evaluated with a very limited set of species (13, 14), or it is evaluated with partial spatial coverage, with inconsistent data, and for a limited number of intervention types. Recently, meta-analyses of restoration success suggested that river restoration positively influenced fish, macroinvertebrates, and aquatic plants, but only few assessments were based on consistent data sets (15). Long-term species observation data are key to determining restoration success over large areas (16), but inadequate monitoring of restoration success is still pervasive (17).

Unique to our study on the Rhine River is the systematic spatio-temporal assessment of biodiversity changes following river restoration covering an entire active river delta and a relatively long time span. River restoration led to changes in land cover due to cyclic rejuvenation of floodplain vegetation, side channel construction, and adaptive management of meadows that allows extensive grazing, to which we will refer jointly as “measures” (18, 19). The measures carried out in the Rhine distributaries (Fig. 1A) (20) led to a mean reduction in the predicted water level of 24 cm during the design discharge, which is specified by national law as a flood event with an average return period of 1250 years (Fig. 1B). We assessed biodiversity changes (i) for all protected and endangered species together, (ii) for four functional groups in each of seven taxonomic groups, and (iii) as a result of implemented measures. We take advantage of the most detailed species observation data set known to us: the National Database Flora and Fauna (NDFD) of the Netherlands, comprising long-term distribution data of higher plants and animals in the entire river Rhine delta. Within the embanked floodplains of the Rhine distributaries (Fig. 1A), more than 2 million observations of species presence (1993–2014) were collected, validated, and stored in a database (see the Supplementary Materials). These observations bracket the starting year of 1997 for data availability on detailed land cover.

RESULTS

Mapping biodiversity changes
A large number of biodiversity indices exist depending on the type of diversity and the spatial scale (3). Here, we computed specific biodiversity indices for valuation of protected and endangered species

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at the taxonomic level of order or higher for all species that are characteristic of river-floodplain systems. In addition, species were only selected if they were protected and/or regarded as endangered according to formal policy documents and legislation. These indices are referred to as “biodiversity” for brevity, although they include a subset of endangered species that are characteristic of fluvial systems and exclude nonprotected, nonthreatened, and invasive alien species. We chose this subset of protected and endangered species to exclude common native species that do not contribute to the signal of recovery.

We used the BIOSAFE (Spreadsheet Application for Evaluation of BIOdiversity) model (21, 22), which was adapted for automated mapping. BIOSAFE links 614 protected species in seven taxonomic groups (higher plants, dragonflies plus damselflies, butterflies, herpetofauna, fish, birds, and mammals) to 82 ecotope classes. Ecotopes are defined as “spatial landscape units that are homogeneous as to vegetation structure, succession stage, and the main abiotic factors that are relevant to plant growth” (23). The vector-based ecotope files were gridded to a 20-m spatial resolution for computational efficiency. To understand the effects of landscape changes on functional biodiversity, we classified the species according to their dispersal rate and specificity of habitat requirements, leading to four functional groups per taxonomic group: “slow-spreading generalist,” “fast-spreading generalist,” “slow-spreading specialist,” and “fast-spreading specialist.” We ran BIOSAFE for all 179 freshwater floodplain sections in the Rhine River distributaries (Fig. 1D) with ecotope maps of 1997, 2005, 2008, and 2012, as well as species presence data from the NDFF (24). We distinguish “best-case” results that are based on all NDFF observations and “worst-case” results that are based on subsampled observations to rigorously compensate for the possible increase in sampling effort. For data reduction, we calculated the following indices per floodplain section: $PotTax$ and $ActTax$, the potential and actual biodiversity of protected and endangered species per taxonomic group, and $PotAll$ and $ActAll$, which aggregate $PotTax$ and $ActTax$ over the investigated taxonomic groups. In addition, we computed the biodiversity saturation index as $SatTax = ActTax/PotTax$ and habitat diversity as the fraction of suitable ecotopes present in the floodplain section per taxonomic group.

![Fig. 1. Biodiversity changes in the embanked floodplains of the Rhine delta between 1997 and 2012.](image)

(A) Location of the distributaries of the Rhine delta within the drainage basin in northwest Europe, center at 5.5°E, 52.0°N. (B) Spatial distribution of the flood hazard reduction at the once-every-1250-year flood. (C) Bivariate distribution of changes in $PotAll$ and $ActAll$ between 1997 and 2012. (D) Spatial distribution of the changes in aggregated biodiversity ($\Delta ActAll$) in all 179 floodplain sections. The colored lines alongside the sections indicate the measures implemented.
Between 1997 and 2012, the PotAll indices increased for 77% of the 179 floodplain sections and the ActAll indices increased for 82% based on the worst case (Fig. 1, C and D). Mean PotAll increased from 96 to 108, and mean ActAll increased from 9 to 13. The increase in ActAll is weakly related to changes in PotAll (Fig. 1C). For the worst case, we found a mean slope of 0.09 (n = 50), which indicates that actual biodiversity lags behind changes in ecotope composition. The standard deviation (SD) in slope, intercept, and explained variance of the regression equation was more than an order of magnitude smaller than the values themselves, which can be explained by reducing all sampled observations over the time periods to presence/absence vectors for BIOSAFE input. By comparison, the best-case regression showed both a higher slope (0.16) and a higher intercept (5.5) for the regression line (Fig. 1C, dashed line). Whether—and if so, how fast—potentials of a given area are fulfilled depends on species’ dispersal and migration capacities, as well as on the distance to the nearest source population and the presence of barriers and corridors for dispersal and migration (25–27). The positive y-axis intercept can point to a regional recovery of biodiversity or a radiating effect of biodiversity recovery in neighboring floodplain areas. No regional recovery is known because terrestrial systems remained stable or declined in the Netherlands (28). This leaves the positive effects of measures and land cover change taken within the river system as the main explanatory factor for the ActAll increase.

Habitat diversity (Fig. 2, A and B) increased for all functional groups, except for fast-spreading generalists of the dragonflies plus damselflies, and generalist fish (fast and slow). The mean SatTax for the worst-case scenario increased between 1997 and 2012. The increase was most notable for birds and mammals. Large differences were found in the SatTax values and changes of this index over time. Functional groups with high dispersal rate (black and red lines, Fig. 2) showed the highest mean values and the largest increase. Mean saturation increased from 32 to 44% for birds and from 8 to 11% for mammals. Dragonflies plus damselflies, and fish showed a small increase in mean saturation (~2%), mostly due to the fast-spreading

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**Fig. 2.** Temporal overview of habitat diversity (HabDiv) and saturation (SatTax) for the subsampled species observations (worst case). (A) Biodiversity changes over all floodplain sections with more than one observation in all periods (1997, 2005, 2008, and 2012). The x axis represents habitat diversity for each taxonomic group (HabDiv; scale, 0 to 100%); the y axis indicates the biodiversity saturation (SatTax = ActTax/PotTax; scale, 0 to 100%). (B) Temporal development of mean SatTax and habitat diversity per functional group. Note that the SatTax values of functional groups with high dispersal rates are higher and increase faster than species that disperse slowly.
specialists. Conversely, SatTax decreased for herpetofauna and higher plants, whereas the habitat diversity increased. Even the fast-spreading generalist plant species decreased slightly. For the best-case scenario, the same patterns in SatTax were present (fig. S4), although the changes were larger compared to the worst case.

Fish species show a trade-off with reducing limnophilic species in formerly isolated water bodies in the floodplains and increasing rheophilic species for water bodies connected to the main channel by recently constructed side channels. However, the increasing saturation also shows that these newly available habitats were rapidly colonized by other species without losing much of the species that were already present. Similar results were found for bird species. By exchanging production meadows, which are beneficial for meadow birds and geese, for more natural habitats, the 6% increase in habitat diversity resulted in a 12% increase in saturation. Also, fast-spreading mammals and dragonflies plus damselflies profited from the measures taken. However, for the latter group, recovery is certainly not occurring in all floodplain sections. More than 50% of the floodplain sections showed a SatTax of zero for dragonflies plus damselflies.

Effect of measures on biodiversity changes

Yearly overviews of the implementation dates of measures were unavailable. Therefore, we analyzed the changes in land cover to identify the floodplain sections where measures were carried out. These changes were detected by computing the transition matrix of 20 land cover classes, which consisted of aggregated ecotopes. The transition matrix contains the surface area for each transition in land cover between 1997 and 2012. The surface areas of transitions that represent specific measures were summed, and sections with large fractional changes were classified as “succession,” “side channel,” or “natural

Fig. 3. Effects of floodplain measures on ΔActTax (base year 1997) for species functional groups. Lines indicate mean values with transparent uncertainty bands representing ±1 SD. Blue dots represent significant differences in ΔActTax at that year (P < 0.1, by Mann-Whitney rank sum test carried out for 2005, 2008, and 2012). Floodplain sections with river restoration measures (in blue) mostly exceed the remaining floodplains (in red). Results for all functional groups are given in figs. S5 to S7.

Habitat diversity and SatTax (Fig. 2B) increased for the less mobile groups of higher plants, herpetofauna, and butterflies, but this did not translate in all cases to a higher saturation of their functional groups except for fast-spreading specialist butterflies (+11 percentage points). The decreasing saturation for herpetofauna and higher plants indicates that most species from these groups were not yet able to colonize the newly created habitats. Fifteen years of rehabilitation may not be sufficient yet to curb decades of habitat deterioration.
management.” A vegetation succession model (29) was used to identify succession. Because the first ecotope map dates from 1997, measures implemented before 1997 were not included, but it should be noted that they might still affect changes in biodiversity. We selected the 15% of the 179 floodplain sections with the largest fraction of modified surface area by measures to assess effects on biodiversity. The effect of these measures on the changes in PotTax and ActTax differed strongly between taxonomic and functional groups, although the results for floodplain sections with and without measures overlapped (Figs. 1, C and D, 3). Here, we highlight the effects of measures for fast-spreading species (Fig. 3). The full overview of PotTax and ActTax changes for the best and worst case is given in the Supplementary Materials (figs. S5 to S7). The ΔPotTax values differ significantly between floodplain sections with and without measures implemented (Fig. 4). ΔPotTax values for measures exceed those for floodplain sections without measures, except for slow-spreading generalist birds and butterflies (fig. S5). This shows that the implemented measures generally have a positive potential effect on the biodiversity of most functional groups. In contrast, the ΔActTax values differ much less between floodplains with and without measures in the best case (Fig. 3, middle two columns) and even more for the worst case (Fig. 3, two right-hand columns). Significant differences are shown for fast-spreading specialist mammals, butterflies, dragonflies plus damselflies and for slow-spreading generalist birds at the 95% confidence level. Other differences were significant only at 90 or 80%. In total, 14 of the 28 species groups showed significant differences due to the restoration measures at 90% for the best-case scenario (fig. S6), and 8 of 28 for the worst-case scenario (fig. S7). When combined into the seven taxonomic groups, all groups showed significant effects from measures at least at one time period for the best case (fig. S6). Fast-spreading groups showed significantly larger differences in ΔActTax than slow-spreading groups (figs. S6 and S7). The joint assessment of all functional groups (figs. S6 and S7; “All” column) smoothed out the effects of the separate groups. ΔPotTax scores of birds (fig. S5) were exceeded by their ΔActTax scores (Fig. 3).

**DISCUSSION**

Our analysis at the scale of the meta-community focused on species presence/absence data in a legal framework that necessitates action from managers, which is not required for other biodiversity indices such as the Shannon Index (30). Additional information on species abundance and composition would provide additional value in the assessment, but these data are unavailable or inconsistent at the spatiotemporal resolution of our study. Likewise, more detailed vegetation maps could also improve in discerning between measures, but these are also unavailable. Given the overall data richness of the Netherlands, it is unlikely that this is possible in other areas with the same level of detail. The key difference with long time series of standardized species inventories

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**Fig. 4. Transition matrix of aggregated ecotopes between 1997 and 2012 for the full study area.** The matrix should be read from left to right. For example, of the surface area of agriculture in 1997, 2 ha was converted to side channel, 20 ha was converted to lake/harbor, and 989 ha remained the same in 2012. Colors indicate the cells representing succession, side channel construction, and natural management floodplain meadows. The same kind of matrix was computed for each floodplain section to determine the extent and type of the land cover change.

Notwithstanding the limitations of our analyses, we reveal for the first time observational evidence that biodiversity decline can be reversed by combining large-scale physical reconstruction of floodplains for increasing flood safety with ecological rehabilitation in densely populated river deltas. Contrary to previous research on benthic invertebrates (27), we found evidence of significant effects of specific restoration measures, but the low significance levels point to the need of project-based field monitoring to assess the success of these measures. Disappointingly, habitat restoration ($\Delta PotTax$) alone is not enough for full biodiversity recovery ($SatTax < 100\%$) because flora and fauna species are subjected to multiple stressors both within and outside of the floodplain areas (26, 33). Our results also point to the need for river restoration designs that explicitly take all functional groups into account when a new habitat is created. Additionally, dispersal barriers need to be removed to facilitate recolonization of new habitat, and abiotic conditions must be optimized to support specialists. Given the degraded status of river deltas and floodplains globally, increasing the biodiversity in general, counteracting the decline in the richness of protected and endangered species over the whole delta region.

**MATERIALS AND METHODS**

We applied the BIOSAFE model (21, 22, 34, 35) to calculate biodiversity indices of protected and endangered species that are characteristic of fluvial environments. The main input consisted of the ecotope maps for the land use input and the species observations available from the NDFF database. The Supplementary Materials provide the details of these input data. Below, we describe our study area, the spatial analyses to drive BIOSAFE with spatiotemporal data, and the hydrodynamic model used to calculate the flood level lowering.

**Study area**

We considered all three distributaries of the Rhine River in the Netherlands, excluding the estuary. At the Dutch-German border, the Rhine River has a mean annual discharge of 2250 m$^3$ s$^{-1}$, draining a catchment area of 165,000 km$^2$ (36, 37). Just downstream of the border, the Rhine River splits into three main distributaries (Fig. 1D) with an average water gradient of 10 cm per kilometer. The total embanked area, that is, the main channel and floodplain area between the embankments, amounts to 440 km$^2$.

In the 1970s, the Rhine floodplains were predominantly used as agricultural production grasslands, and water quality was low. By 1995, water quality had improved (14, 38–40). This may have had a positive effect on fish, macroinvertebrates, and, to a lesser extent, amphibians and birds. A national-scale overview on biodiversity (28) showed that aquatic systems improved slightly, whereas terrestrial systems remained stable or declined. Whether habitat availability or chemical quality is the main limiting factor is undecided. After the 1993 and 1995 flood events, the “Room for the River” program started.

This €2.3 billion program consisted of 27 projects within our study area. Room for the River aimed at (i) increasing the conveyance capacity of the Rhine distributaries from 15,000 to 16,000 m$^3$ s$^{-1}$ to reduce the flood hazard (20) and (ii) improving the ecological status and increasing the biodiversity (21). The floodplains along the distributaries in the Rhine delta are almost entirely protected by the European Union Habitats directive (Council directive 92/43/EEC) and Birds directive (Council directive 79/409/EEC). Each distributary has specific protection goals in terms of carrying capacity for species and habitat types (41). The study area contains 179 individual floodplain sections with a mean surface area of 1.5 km$^2$, ranging from 0.15 to 11.5 km$^2$.

**Species field observations for actual biodiversity values**

We acquired field observations of species presence to compute actual biodiversity parameters from the Dutch NDFF, which serves as the national data warehouse for exchanging species observation data (24). The database currently contains more than 90 million observations, bringing together observations from volunteers and professionals (42) based on 40 different field protocols (table S2). Points, lines, or polygons geolocate the observations, enabling subsequent processing in spatial analyses. Before inclusion in the database, each observation is validated using a series of validation rules, and by experts per taxonomic group if necessary. Preprocessing of the NDFF data consisted of (i) spatial selection of records within the study area, (ii) temporal selection of records matching each of the ecotope maps, and (iii) linking records to floodplain sections. Details of the preprocessing are given in the Supplementary Materials.

**BIOSAFE extensions**

BIOSAFE was originally developed by Lenders et al. (22), extended by de Nooij et al. (21), and tested on sensitivity to input parameters (43, 44). The BIOSAFE conceptual model comprises a set of links between riverine species and legal and policy documents on the one hand and links between species and ecotopes [ecotope links (EL)] on the other hand. These two sets create a link between the legal domain and ecotopes via species (fig. S1). On the basis of these links, BIOSAFE computes biodiversity indices per ecotope and per taxonomic group. The Supplementary Materials provide an extensive description of the model, including a mathematical description. The spreadsheet version of BIOSAFE could compute floodplain-specific biodiversity indices and enabled scenario development. Now, we implemented BIOSAFE in the Python programming language (www.python.org) to automate the application and extended it with spatial functionality, aggregation of ecotopes, and species functional groups for each taxonomic group.

The spatial extension of BIOSAFE deals with two main input types: ecotope surface areas and species survey monitoring data. First, it tabularizes total ecotope surface areas for arbitrary floodplain sections based on a gridded representation of the ecotope map. The study area contained 179 individual floodplain sections plus adjacent water bodies represented by a unique identifier. With the tabulated surface areas per section, potential biodiversity indices were computed for each section. Raster analyses were carried out using the PCRaster Python software (45). Second, it constructs the species presence (SP) vector for each floodplain section based on the preprocessed NDFF species monitoring data, which is required for the actual biodiversity scores. Preprocessing of these data is necessary because monitoring data come in many file formats and database structures (24).

The aggregation extension was required to match the classes of the ecotope maps to the species-ecotope links contained in BIOSAFE. The
four ecotope maps contained 41 aggregated ecotope classes or additional classes that were not present in the original ecotope classification system (46–48). BIOSAFE did not contain these additions because it was based on the ecotope system and not on the ecotope maps. The aggregated classes account for a significant fraction of the floodplain area, which strongly affected BIOSAFE scores when not taken into account. We extended BIOSAFE with an aggregation function to include all ecotope classes present in the ecotope map. This function can further be used to upscale ecotope links to different land cover classifications, such as hydrodynamic roughness classes or CORINE land cover classes. The aggregation function adds a new ecotope class based on the species-ecotope links from the classes that are aggregated. For example, the species links to HG-1 and HG-2 are combined into the species links for the new ecotope class HG-1-2. Seven ecotopes were matched to a single RWES ecotope, effectively reducing the aggregation function to a lookup operation. All ecotope classes that featured in the four maps were included in the biodiversity estimates using this aggregation. Table S1 provides an overview of all ecotope classes and the underlying classes if aggregation was applied.

The species functional group extension provided insight into what species groups benefitted in terms of biodiversity indices. All species were attributed with two additional functional traits based on their habitat requirements and their dispersal speed. We distinguished two classes of habitat requirements: species that are purely linked to the fluvial environment (specialists) and species that also occur in different habitat but do not need the other environment per se (generalists). Species dispersal rate was classified as fast-spreading or slow-spreading. The combination of these two traits gives four functional groups: (i) slow-spreading generalist, (ii) fast-spreading generalist, (iii) slow-spreading specialist, and (iv) fast-spreading specialist (table S3). Traits were derived from species distribution maps and literature. Unfortunately, not all species could be attributed reliably with dispersal speed, in which case we labeled the trait as unknown (table S3). We created five subversions of the BIOSAFE model: one model included all species, and four represented the functional groups by specific subsets of species.

Regarding the classification of functional groups, we followed two routes. Deciding whether a species should be regarded as a fluvial specialist or as a generalist was determined on the basis of (historic) distribution patterns of species, derived from (digital) species distribution atlases and scientific literature. Important sources used are the series Nederlandse Fauna (Dutch Fauna) published by Naturalis, Leiden, especially volumes 4 (dragonflies and damselflies), 5 (butterflies), 7 (butterflies), 9 (amphibians and reptiles), and 12 (mammals); websites such as the NDFD Digital Distribution Atlases (www.verspreidingsatlas.nl) and Dutch Species Register (www.nederlandsesoorten.nl); and the sites of organizations specialized in monitoring of specific taxonomic groups, such as FLORON (www.floron.nl; plants), Butterfly Foundation (www.vlinderstichting.nl; butterflies, dragonflies, and damselflies), RAYON (www.rayon.nl; reptiles, amphibians, and fish), SOVON (www.sovon.nl; birds), and Dutch Mammal Society (www.zoogdiervereniging.nl; mammals). Species were qualified as either specialist or generalist, using available data on their (historic) distribution. Determining dispersal capacity proved to be much more arduous. For many species, there is little to no information on (actual or potential) dispersal rates; sometimes, information is even contradictory. For this reason, we consulted a large number of scientific publications and the abovementioned websites and classified species following a conservative best expert judgment approach either as slow-spreading or as fast-spreading.
in yellow cell borders, follows the natural vegetation succession (29). We added morphological succession describing the sequence of non-vegetated ecotopes from high hydromorphological dynamics to low dynamic areas, such as from sand bar to natural levee, because silting up of side channels was not included by Makaske et al. (29). Side channel recreation (Fig. 4, black cell outlines) comprised the change from any roughness class to the side channel class, or to the lake class if the channel is disconnected. Natural management (Fig. 4, red cell outlines) reflected the change from production meadow to natural meadow management. The other cells represented changes that were due to agricultural changes or classification errors. To detect where measures were implemented, we first computed the following ratios from the transition matrix between 1997 and 2012 for each floodplain section: floodplain management ratio (FMR), floodplain succession ratio (FSR), and floodplain side channel ratio (FCR)

\[
FMR = \frac{\sum \text{management area}}{\sum \text{floodplain section area}}
\]

\[
FSR = \frac{\sum \text{succession area}}{\sum \text{floodplain section area}}
\]

\[
FCR = \frac{\sum \text{new side channel area}}{\sum \text{floodplain section area}}
\]

We ranked the sections according to the three ratios and selected the sections with the top 15% for FMR, FSR, or FCR. This divided the study area in sections with and without measures implemented. The sections with measures were compared to those without measures. For both groups, we evaluated the changes in PotTax and ActTax indices compared to the 1997 base year, which is our first step. Next, we assessed the significance of the difference between sections with measures and sections without measures for 2005, 2008, and 2012 using the Mann-Whitney rank sum test. By definition, no change is present in 1997, which was used for standardization of the starting point. This means that the initial score of the section and whether this was a nature area or not did not affect the assessment of the change. We used a Mann-Whitney rank sum test with confidence intervals of 80, 90, and 95% to test the significance of the change for each year and species functional group. We compared the best- and worst-case results to delineate the full range of possible biodiversity developments.

**Flood hazard reduction from landscaping measures**

The increase in conveyance capacity was assessed using the WAQUA two-dimensional hydrodynamic model, which numerically solves the Saint Venant equations using a finite difference method (49). WAQUA is used by the Dutch Ministry of Infrastructure and Environment to calculate the flood hazard and discharge distribution in the complex channel and floodplain areas of Rhine distributaries in the Netherlands. Flood hazard is defined here as the water level at the river axis during a flood event with a return period of 1250 years. The WAQUA model that was used for this study is based on a staggered curvilinear grid. Each of the 886,861 cells represented a column-shaped volume of water with a variable surface area of 700 m² on average. The boundary conditions of the model included the river discharge at the upstream boundary and the water level at the downstream boundaries, which were determined using rating curves. The main spatial model inputs for the WAQUA model were a digital terrain model, a map with hydraulic structures (for example, groins and embankments), and a roughness class map. Roughness class maps were based on the ecotope map using the Baseline database and software (50), which are converted at runtime into hydraulic roughness. The landscaping measures that were carried out between 1997 and 2012 were geocoded, and the associated WAQUA geometric parameters were updated using the Baseline ArcGIS plug-in. The landscaping measures were decided on in the key decision on spatial planning (51, 52). The flood hazard reduction (Fig. 1B) was based on the 1996 reference situation and the measures as described by the key decision on spatial planning.

**SUPPLEMENTARY MATERIALS**

Supplementary material for this article is available at http://advances.sciencemag.org/cgi/content/full/3/11/e1602762/DC1

A detailed description of the BIOSAFE model

Details of the BIOSAFE input

A list of parameter abbreviations

fig. S1. Flow chart of the BIOSAFE methodology per floodplain section.

fig. S2. Graphical example of BIOSAFE parameter computation.

fig. S3. Number of observations per time slice and per surface area of the observation.

fig. S4. Temporal overview of habitat diversity (HabDiv) and saturation (SatTax) for all species observations (best case).

fig. S5. Effects of floodplain measures on ΔPotTax per functional group.

fig. S6. Effects of floodplain measures on ΔActTax per functional group, based on best-case scenario.

fig. S7. Effects of floodplain measures on ΔActTax per functional group, based on worst-case scenario.

fig. S8. Overview of ecotope classes included in BIOSAFE and connected land cover classes.

fig. S9. Overview of the data collection protocols in the NDFF database.

fig. S10. Number of species per functional group.

Excel file with BIOSAFE input and output

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Data and materials availability: All data needed to evaluate the conclusions in the paper are present in the paper and/or the Supplementary Materials. Additional data related to this paper may be requested from M.W.S. (m.w.straatsma@uu.nl).

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