

Genetic diversity loss in the Anthropocene

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More species than ever before are at risk of extinction due to anthropogenic habitat loss and climate change. But even species that are not threatened have seen reductions in their populations and geographic ranges, likely impacting their genetic diversity. Although preserving genetic diversity is key to maintaining adaptability of species, we lack predictive tools and global estimates of genetic diversity loss across ecosystems. By bridging theories of biodiversity and population genetics, we introduce a mathematical framework to understand the loss of naturally occurring DNA mutations within decreasing habitat within a species. Analysing genome-wide variation data of 10,095 geo-referenced individuals from 20 plant and animal species, we show that genome-wide diversity follows a power law with geographic area (the mutations-area relationship), which can predict genetic diversity loss in spatial computer simulations of local population extinctions. Given pre-21st century values of ecosystem transformations, we estimate that over 10% of genetic diversity may already be lost, surpassing the United Nations targets for genetic preservation. These estimated losses could rapidly accelerate with advancing climate change and habitat destruction, highlighting the need for forecasting tools that facilitate implementation of policies to protect genetic resources globally.

45 Anthropogenic habitat loss and climate change (1, 2) have led to the extinction of hundreds of species
46 over the last centuries (1, 2) and approximately one million more species (25% of all known species)
47 are at risk of extinction (3). It has been estimated that an even larger fraction—at least 47%—of plant
48 and animal species have lost part of their geographic range in response to the last centuries of
49 anthropogenic activities (4, 5). Though this loss might seem inconsequential compared to losing an
50 entire species, this range contraction reduces genetic diversity, which dictates species' ability to adapt
51 to new environmental conditions (6–8). The loss of geographic range can spiral into a feedback loop
52 where diversity loss further increases the risk of species extinction (9, 10).

53

54 Although genetic diversity is a key dimension of biodiversity (11), it has been overlooked in
55 international conservation initiatives. Only in 2021 did the United Nations' Convention of Biological
56 Diversity propose to preserve at least 90% of all species' genetic diversity (12, 13). Although analyses
57 of genetic markers in animal populations sampled over time with the aim of quantifying recent genetic
58 change are emerging (14, 15) and simulation studies with species distribution models or sensitivity
59 analyses suggest within-species range variation may be strongly impacted (5, 16, 17), theory and
60 scalable approaches to estimate genome-wide diversity loss across species do not yet exist, impairing
61 prioritization and evaluation of conservation targets. Here, we introduce a framework to estimate global
62 genetic diversity loss by bridging biodiversity theory with population genetics, and by combining data
63 on global ecosystem transformations with newly available genomic datasets.

64

65 The first studies that predicted biodiversity reductions in response to habitat loss and climate
66 change in the 1990s and the 2000s projected species extinctions using the relationship of biodiversity
67 with geographic area—termed the species-area relationship (SAR) (18) (see **Supplementary Materials**
68 **[SM] I** for a comparison of mathematical models for predicting biodiversity). In this framework,
69 ecosystems with a larger area (A) harbour a larger number of species (S) resulting from a balance of
70 limited dispersal, habitat heterogeneity, and colonisation-extinction-speciation dynamics. The more a
71 study area is extended, the more species are found. The SAR has been empirically shown to follow a
72 power law, $S = A^z$. It scales consistently across continents and ecosystems (19), with a higher z
73 characterising more speciose and spatially structured ecosystems. Given estimates of decreasing
74 ecosystem areas over time ($A_{t-1} > A_t$), Thomas et al. (20) proposed rough estimates of the percentage of
75 species extinctions in the 21st century ranging from 15 to 37% (**SM I.3**). Though this may be an
76 oversimplification, SAR has become a common tool for policy groups including the Intergovernmental
77 Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) (3).

78

79 As species richness is for to ecosystems' biodiversity, within-species variation can be
80 quantitatively described by the richness of genetic mutations within a species, defined here as DNA
81 nucleotide variants appearing in individuals of a species. Although population genetics theory has long
82 established that larger populations have higher genetic diversity (21), and it is known that geographic
83 isolation between populations within the same species results in geographically separated accumulation
84 of different mutations, there have been no attempts to describe the extent of genetic diversity loss driven
85 by species' geographic range reduction using an analogous “mutations-area relationship” (MAR).

86

87 We suspected that such a mutations-area relationship must exist given that another general
88 assumption is shared with species studies, namely that when mutations appear they are first in only one
89 individual, and they typically remain at low frequency in a population, though a few prevail to high
90 frequency through stochastic genetic drift and natural selection (22). This principle of “commonness of
91 rarity” is well-known for species (i.e. most species in an ecosystem are rare while only a few are

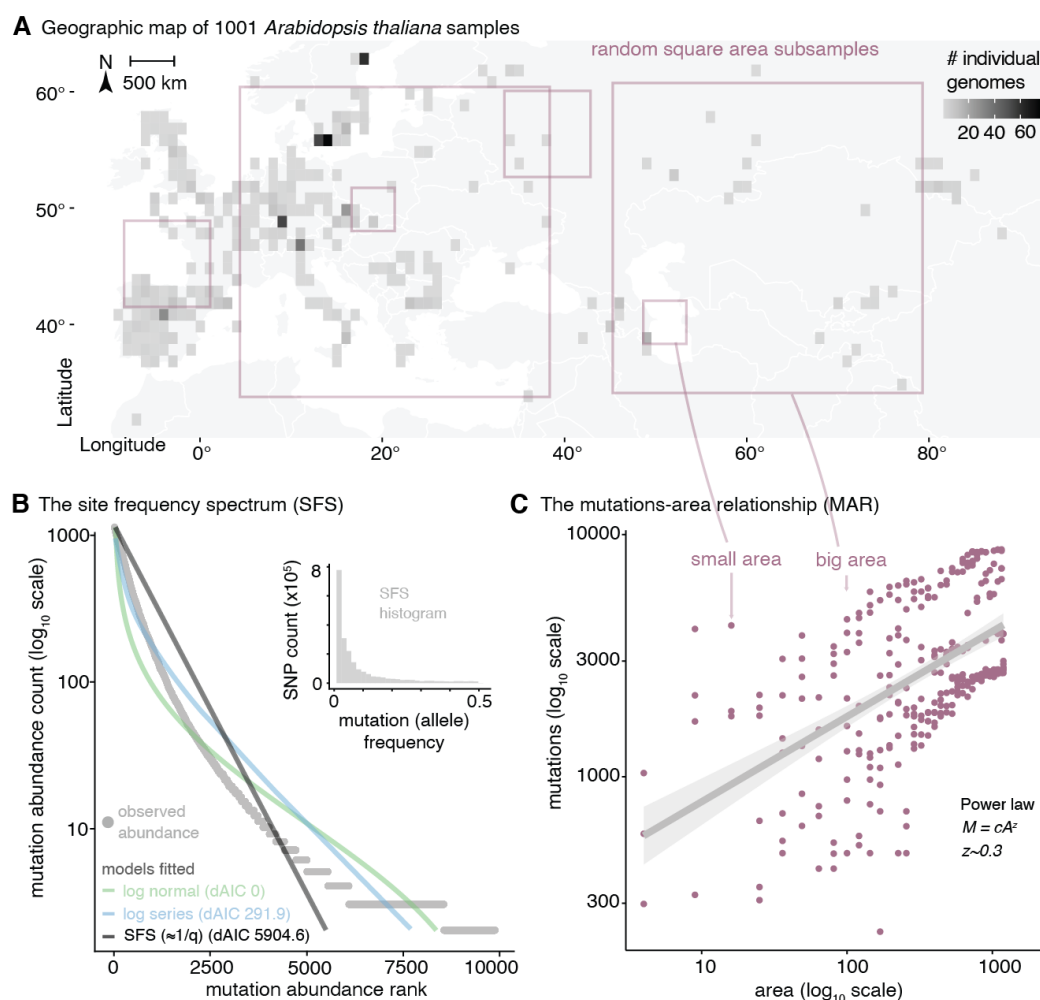
92 common) and, together with limited spatial dispersal of species and communities, is a key statistical
 93 condition that led to the power-law SAR.

94

95 To examine the expectation of a power-law MAR, we begin quantifying the rarity of mutations
 96 using millions of biallelic genetic variants of the *Arabidopsis thaliana* 1001 genomes dataset (Fig. 1A)
 97 (23) by fitting several common models of species abundances (24) to the distribution of mutation
 98 frequencies (q), termed the Site Frequency Spectrum in population genetics (Fig. 1B, SM II.1). The
 99 canonical L-shaped probability distribution ($1/q$) of this spectrum—which is expected under
 100 population-equilibrium and the absence of natural selection processes—fit this data well (Fig. 1B),
 101 although the more parameter rich Preston’s species abundance log-normal model achieved the best AIC
 102 value (Fig. 1B, SM III.1, Table S3, Table S10). Despite the small differences in fit, these models all
 103 showcase the similarities of abundance distributions of mutations within species and species within
 104 ecosystems, suggesting that they may behave similarly in their relationship to geographic area (22, 24).

105

106



107

108 **Fig. 1 | Mutations across populations follow a log-normal abundance distribution and a power**

109 **law with species range area.** (A) Density of individuals projected in a 1 x 1 degree latitude/longitude

110 map of Europe and exemplary subsample areas of different sizes. (B) Distribution of mutation (SNPs)

111 frequencies in 1,001 *Arabidopsis thaliana* plants using a site frequency spectrum histogram (grey inset)

112 and a Whittaker’s rank abundance curve plot, and the fitted models of common species abundance

113 functions in *A. thaliana* using a dataset random sample of 10,000 mutations also used in (C). The AIC

114 fit of the three models is indicated with respect to the top model, log-normal. (C) The mutations-area

115 relationship (MAR) in log-log space built from 10 random subsamples of different areas of increasing
116 size within *A. thaliana*'s geographic range along with the number of mutations discovered for each area
117 subset.

118

119 To quantify how genetic diversity within a species increases with geographic area, we
120 constructed the MAR by subsampling different regions of different sizes of *Arabidopsis thaliana*'s
121 native range using over one thousand geo-referenced genomes (**Fig. 1A, C**). As a metric of genetic
122 diversity, we modelled the number of mutations (M) in space (number of segregating sites) consistent
123 with the species-centric approach of SAR, which uses species richness as the metric of biodiversity
124 (**SM II.2**). The MAR also followed the power law relationship $M = cA^z$ with a scaling value $z_{MAR} =$
125 0.324 (CI95% = 0.238 – 0.41) (**Fig. 1C**). Naturally, subsamples of larger areas may also contain more
126 individuals, and therefore should also have more mutations. But the observed power law relationship
127 goes beyond what is expected from the increase of number of samples in an area (which only accounts
128 for increases of $M \approx \log(A)$, see theoretical derivation **SM II.3**). The remainder may be attributed to
129 population genetic drift and spatial natural selection causing structuring of genetic diversity across
130 populations. The discovered power law scaling appears robust to different methods of area
131 quantification, the effects of non-random spatial patterns, random area sampling, fully nested outward
132 or inward sampling (*I9*), raster area calculations, raster grid resolution (~ 10 – $1,000$ km side cell size),
133 and is adjusted for limited sample sizes (**SM II.3.2, III.3, Fig. S14-18, Tables S7-9**).

134

135 We then wondered whether MAR can predict the loss of genetic diversity due to species' range
136 contractions. We explored several scenarios of range contraction in *A. thaliana* by removing *in silico*
137 grid cells in a map representing populations that are lost (**Fig. 2B**). Our simulations included random
138 local population extinction as if deforestation was scattered across large continents, radial expansion of
139 an extinction front due to intense localised mortality, or local extinction in the warmest regions within
140 a species range (*4, 25*), among others (**SM III.4**). The MAR-based predictions of genetic loss, using $1 -$
141 $(I - A_t / A_{t-1})^z$ and assuming $z = 0.3$, conservatively followed the simulated local loss in *A. thaliana*
142 (pseudo- $R^2 = 0.87$, taking all simulations together) (**SM II.4, III.4**).

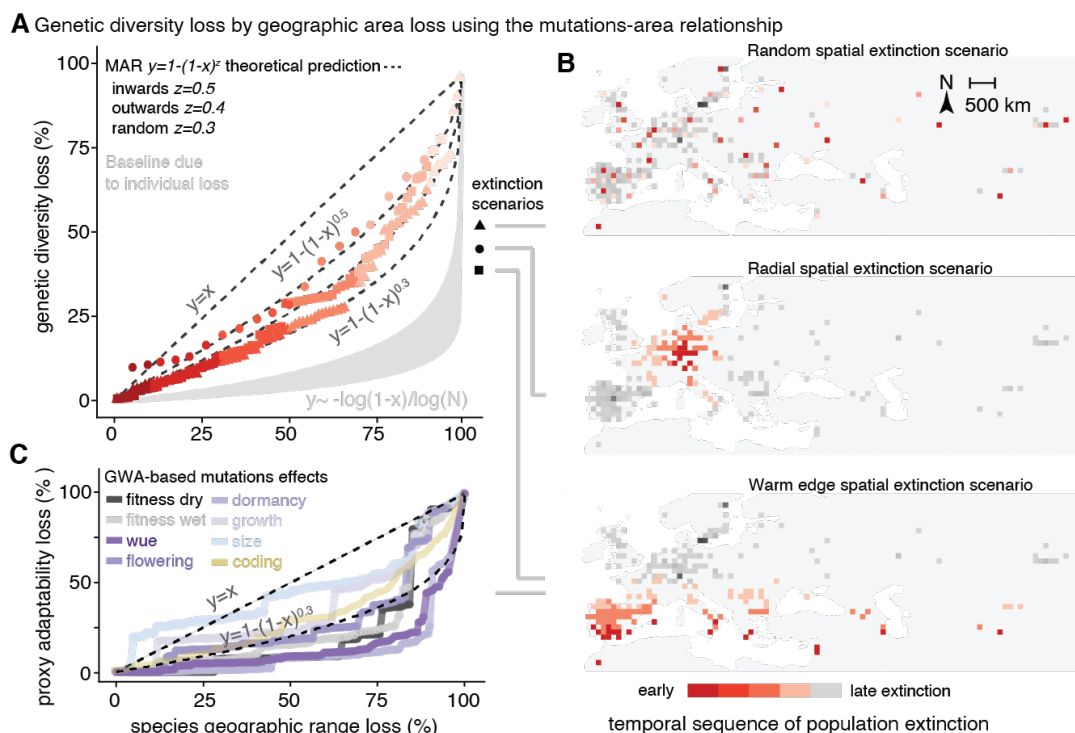
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144 Since genetic diversity is ultimately created by spontaneous DNA errors passed onto offspring
145 every generation, the loss of genetic diversity seems reversible, as these mutations could happen again.
146 However, the recovery of genetic diversity through natural mutagenesis is extremely slow (*57*),
147 especially for mutations affecting adaptation. Simulating a species undergoing only a 5–10% in area
148 reduction, it would take at least ≈ 140 – 520 generations to recover its original genetic diversity ($2,100$ –
149 $7,800$ years for a fast-growing tree or medium-lifespan mammal of 15 year generation length), although
150 for most simulations, recovery virtually never happened over millennia (see **SM II.4-5, Fig. S11, SM**
151 **III.6**).

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


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 156 **Fig. 2 | The power law of genetic diversity loss with range area loss.** (A) Percentage of loss of total
 157 genetic diversity in *Arabidopsis thaliana* from several stochastic simulations (red) of local extinction
 158 in (B), and theoretical model projections of genetic diversity loss using the MAR (dotted lines). The
 159 expectation for genetic diversity loss based only on individuals is in grey (using starting populations of
 160 $N=10^4-10^9$) (SM II.4). (B) Cartoon of several possible range contractions simulated by progressively
 161 removing grid cells across the map of Eurasia (red/grey boxes) following different hypothesised spatial
 162 extinction patterns. (C) A metric of adaptive capacity loss during warm edge extinction in (B). Using
 163 Genome Wide Associations (GWA) to estimate effects of mutation on fitness in different rainfall
 164 conditions, water use efficiency [wue], flowering time, seed dormancy, plant growth rate, and plant
 165 size. Plotted are the fraction loss of the summed squared effects ($\sum a^2$) of 10,000 mutations from the top
 166 1% tails of effects. We also plot (yellow) the fraction of protein-coding alleles lost (nonsynonymous,
 167 stop codon loss/gain, and frameshift mutations).

168
 169
 170 To test the generality of the MAR, we searched in public nucleotide repositories for datasets of
 171 hundreds to thousands of whole-genome sequenced individuals for the same species sampled across
 172 geographic areas within their native ranges (Table 1, SM IV). In total, we identified 20 wild plant and
 173 animal species with such published resources and assembled a dataset amassing a total of 10,095
 174 individuals of these species, with 1,522 to 88,332,015 naturally occurring mutations per species,
 175 covering a geographic area ranging from 0.03 to 115 million km². Fitting MAR for these diverse species,
 176 we recovered z_{MAR} values similar to *A. thaliana*, with many species overlapping in confidence intervals,
 177 with the exception of some outliers (mean (SE) $z_{MAR} = 0.31 (\pm 0.038)$, median = 0.26, IQR = ± 0.15 ,
 178 range=0.10–0.82, mean (SE) z^*_{MAR} scaled = 0.26 (± 0.048). See Table 1, SM IV, Fig. S22, Table S10).
 179 Theoretical derivations show that z_{MAR} is a consequence of fundamental evolutionary and ecological
 180 forces (mutation, dispersal, selection) and should range from 0 to 1, depending on the strength of
 181 population structure (SM II.3, see Fig. S10 for its relationship with isolation-by-distance). These
 182 predictions were further confirmed by spatial population genetics coalescent and individual-based

183 simulations in 2D and continuous space (**SM II.3**), as well as with mainland-island community
 184 assembly simulations according to the Unified Neutral Theory of Biodiversity (UNTB) (**SM V.3**).

185
 186

187 **Table 1 |The mutations-area relationship across diverse species.** Summary statistics of individuals
 188 sampled broadly across species distributions, sequencing method and mutations studied, and convex
 189 hull area extent of all samples within a species. The mutations-area relationship (MAR) parameter z ,
 190 which captures how spatially restricted mutations are, including a scaled correction z^* for low sampling
 191 genomic effort. Percent area that needs to be kept for a species to maintain 90% of its genetic diversity,
 192 using the per-species MAR value estimates. Area predictions are not provided for threatened species,
 193 as these have likely already lost substantial genetic diversity and require protection of their full
 194 geographic range (Fig. 3).

Species	N	M _{tot} Method	A _{tot} Km ² x10 ⁶	MAR z [CI95%]	MAR z* [CI95%]	scaledMin area 90% %
 <i>Arabidopsis thaliana</i>	1,135 (1,001) [#]	11,769,920 W	27.34	0.324 (0.238–0.41)	0.312 (0.305 - 0.32)	71–78
 <i>Arabidopsis lyrata</i>	108	17,813,817 W	2.79	0.236 (0.218–0.254)	0.151 (0.137–0.165)	50–66
 <i>Amaranthus tuberculatus</i>	162 (155)	1,033,443 W	0.80	0.109 (0.081–0.136)	0.142 (0.136–0.149)	48–65
 <i>Eucalyptus melliodora</i> ^{VU}	275 (36) [*]	9,378 GBS	0.95	0.466 (0.394–0.538)	0.403 (0.398–0.407)	77–82
 <i>Yucca brevifolia</i> ^{CA}	290	10,695 GBS	NA	[?] 0.128 (0.109–0.147)	0.049 (0.037–0.062)	-
 <i>Mimulus guttatus</i>	521 (286) ^{#*}	1,522 GBS	25.14	0.274 (0.259–0.29)	0.231 (0.221–0.241)	63–73
 <i>Panicum virgatum</i>	732 (576) [†]	33,905,044 W	6.29	0.232 (0.211–0.252)	0.126 (0.116–0.136)	43–63
 <i>Panicum hallii</i>	591	45,589 W	2.19	0.824 (0.719 - 0.928)	0.814 (0.745 - 0.883)	88–90
 <i>Pinus contorta</i>	929	32,449 GC	0.89	[?] 0.015 (0.014–0.016)	-0.061(-0.062-0.060)	-
 <i>Pinus torreyana</i> ^{CR}	242	478,238 GBS	NA	[?] 0.236 (0.19–0.282)	0.105 (0.099–0.11)	-
 <i>Populus trichocarpa</i>	882	28,342,826 W	1.12	0.275 (0.218–0.332)	0.165 (0.155–0.176)	53–67
 <i>Anopheles gambiae</i>	1142 (29) [*]	52,525,957 W	19.96	0.214 (0.164–0.264)	0.122 (0.111–0.132)	42–62
 <i>Acropora millepora</i> ^{NT}	253 (12) [*]	17,931,448 W	0.03	0.246 (0.209–0.283)	0.287 (0.28–0.294)	69–77
 <i>Drosophila melanogaster</i>	271 [%]	5,019 W	115.21	0.437 (0.397–0.477)	0.325 (0.314–0.336)	72–79
 <i>Empidonax traillii</i> ^{Decline}	219 (199) ^{&}	349,014 GBS/GC	7.03	0.214 (0.174–0.254)	0.074 (0.047–0.102)	24–54
 <i>Setophaga petechia</i> ^{Decline}	199	104,711 GBS	15.17	0.251 (0.236 - 0.267)	0.149 (0.135 - 0.163)	49--66
 <i>Peromyscus maniculatus</i>	80 (78) ^{&}	14,076 GBS	22.61	0.488 (0.264–0.713)	0.683 (0.615–0.751)	86–88
 <i>Dicerorhinus sumatrensis</i> ^{CR}	16	8,870,513 W	NA	[?] 0.412 (0.369–0.456)	0.127 (0.11–0.144)	-
 <i>Canis lupus</i>	349 (230) [†]	1,517,226 W	19.10	0.256 (0.232–0.28)	0.184 (0.175–0.193)	56–70
 <i>Homo sapiens</i>	2504 (24) [*]	88,332,015 W	80.76	[?] 0.431 (0.347–0.514)	0.281 (0.23–0.332)	NA

195 [#]Only individuals in the native range were used for the analyses.

196 [&]Only individuals with available coordinates or matching IDs were used for analyses.

197 [%]Numbers indicate pools of flies used for Pool-Sequencing.

198 ^{*}Number of geographically separated populations, as multiple individuals were collected per population.

199 [†]Only natural populations were used, excluding breeds, landraces, and cultivars.

200 Area was not reported for species with unknown locations or where less than 2 populations were sampled.

201 [?]Values excluded from global averages used for conservation applications due to uncertain estimates, suboptimal genomic data type, or
 202 because estimates should not be applied for conservation (i.e. humans or nearly extinct Sumatran rhinoceros).

203 Acronyms: W = whole-genome re-sequencing or discovery SNP calling. GBS = genotyping by sequencing of biallelic SNP markers. GC =
 204 genotyping chip; CR = Red List Critically Endangered. VU= Red List Vulnerable. CA = included in the California Endangered Species Act.
 205 Decline = population decline reported in the Red List.

206
 207

208 Although we expect species-specific traits related to dispersibility or gene flow to affect z_{MAR}
 209 (e.g. migration rate and environmental selection in population genetic simulations significantly
 210 influences z_{MAR} , **Table S2**), no significant association was found between z_{MAR} and different
 211 ecologically-relevant traits, mating systems, home continents, etc., for the 20 species analysed. Perhaps
 212 this is simply that there are still too few species that have large population genomic data to find such a
 213 signal (**Table 1, Table S12-13**). Nevertheless, the relative consistency of z_{MAR} across largely different
 214 species may be promising for conservation purposes, as an average $z_{MAR} \sim 0.3$ (IQR ± 0.15 , **Table 1,**
 215 **Table S11**) could be predictive of large-scale trends of genetic diversity loss in many range-reduced
 216 species that lack genomic information. Further, although species will naturally have different starting

217 levels of total genetic diversity prior to range reductions, for instance, due to genome size, structure, or
218 mating system differences (26), the application of z_{MAR} provides relative estimates of genetic diversity
219 loss. For instance, assuming $z_{MAR} \sim 0.3$, we would predict that an area reduction of $\sim 50\%$ creates an
220 approximate loss of $\sim 20\%$ of genetic diversity relative to the total genetic diversity of a given species.

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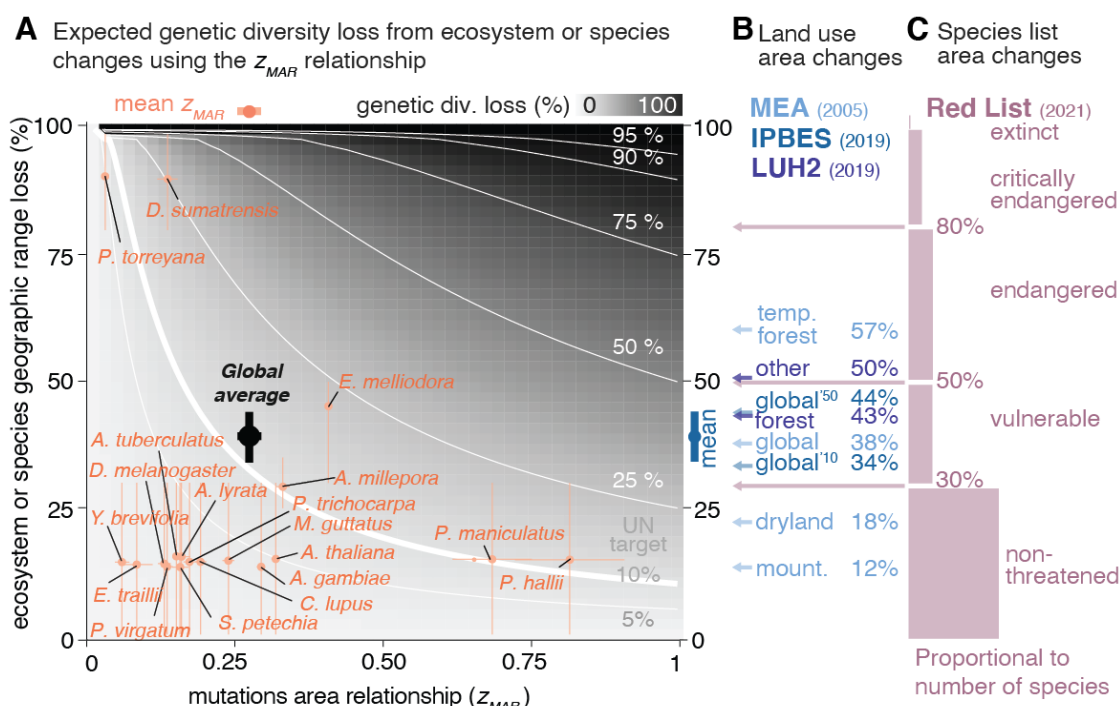
222 Finally, we used MAR to estimate the average global genetic diversity loss caused by pre-21st
223 century land transformations. Although accurate species-specific geographic area reduction data in the
224 last centuries are scarce, we leveraged global land cover transformations from primary ecosystems to
225 urban or cropland systems (3, 27) (Table S14-15). Using the average scaled z_{MAR}^* (Table S18) and
226 several global averages of Earth's land and coastal transformations for present day (38% global area
227 transformation from (27), 34% from (28), and 43-50% from (29)), we estimate a 10-16% global genetic
228 diversity loss on average across species (Fig. 3A). While these estimates may correctly approximate
229 central values across species in an ecosystem, we expect a substantial variation in the extent of loss
230 across species, ranging theoretically from 0 to 100% (Fig. 3, Fig. S26). One cause of this variation is
231 the heterogeneity in land cover transformations across ecosystems; for example, more pristine high-
232 altitude systems have only lost 0.3% of their area, while highly managed temperate forests and
233 woodlands have lost 67% (Fig. 3B, Table S14-15).

234

235 Another cause for the variability in genetic loss among species (even within the same
236 ecosystem) may be their differential geographic ranges and abundances, life histories, or species-
237 specific threats. We gathered data from species red-listed by the International Union for Conservation
238 of Nature (IUCN) (1), which evaluates recent population or geographic range area reduction over ± 10
239 years / ± 3 generations to place assessed species in different threat categories using several thresholds
240 (guidelines for assessments and thresholds available at www.iucn.org). Again, assuming that with the
241 average $z_{MAR} \sim 0.3$ we can capture general patterns, we translate these category thresholds into genetic
242 diversity loss (Fig. 3C, see SM V, Table S17). *Vulnerable* species, having lost at least 30% of their
243 geographic distribution, may have experienced $>9\%$ of genetic diversity loss, *endangered* species,
244 which have lost over 50% of their geographic distribution, should have incurred $>16\%$ of genetic
245 diversity loss, and *critically endangered* species, with over 80% area reduction, likely suffered $>33\%$
246 of genetic diversity loss (Fig. 3B). This clearly showcases that even species in no imminent risk of
247 extinction (e.g. least concern, near threatened, vulnerable), such as the majority of species for which
248 population genomic data exists, may already be losing substantial genetic diversity (Fig. 3A).

249

250



251
 252 **Fig. 3 | The parameter space of genetic diversity loss mapping pre-21st century ecosystem**
 253 **transformations and species threat categories against possible values of the mutations-area**
 254 **relationship.** (A) Possible values of two key parameters, the mutations-area relationship scaling
 255 parameter (MAR) and % of area reduction of a species geographic range (as a proxy of entire ecosystem
 256 transformation). The theoretical % of genetic diversity loss is represented as filled grey colour, with
 257 isolines in white. Estimates of scaled z_{MAR}^* from Table 1 per species are in orange with their 95%
 258 confidence intervals (for unscaled z_{MAR} see Fig. S23). Although exact area losses per species are
 259 unknown, species are plotted based on their IUCN Red list (C) status, using the broad ranges of
 260 minimum and maximum recent population or area decline per category. The global average is calculated
 261 with the average z_{MAR} across species and % of the Earth transformed from IPBES. (B) Percentage of
 262 transformed ecosystem area from the Millennium Ecosystem Assessment (MEA) (27) are represented
 263 by light blue arrows, from the Intergovernmental Science-Policy Panel for Biodiversity and Ecosystem
 264 Services (IPBES) (28) for 2010 and 2050 are dark blue arrows, and from the Land Use Harmonization
 265 2 (LUH2) dataset (29) are in dark purple. (C) The minimum criterion value of population or geographic
 266 area loss to be classified in each category of the IUCN Red List are indicated with pink arrows (the near
 267 threatened category does not have a range of values, instead we used 30% \pm 10%). The number of plant
 268 species (for which population abundance loss approximates area loss) included in each category is
 269 shown as box sizes (I). The IUCN ranges were used to place ranges of estimates in (A) per species.

270
 271 The ultimate challenge is to understand how genetic diversity loss relates to loss of adaptive
 272 capacity of a species. To this end, we leveraged the extensive knowledge of the effect of mutations in
 273 ecologically relevant traits in *A. thaliana* from Genome-Wide Associations (GWA) (Fig. 2C, SM III).
 274 We again conducted spatial warm edge extinction simulations, this time tracking metrics of adaptive
 275 capacity, including the total sum of effects estimated from GWA of remaining mutations ($\sum_i a_i$ for
 276 $i=1 \dots 10,000$ variants of putative a_i effect), the additive genetic variance ($Va = \sum_i p_i(1-p_i)a_i^2$, which
 277 accounts for each variant's population frequency p_i), and the loss of nonsynonymous mutations (SM
 278 III.5). Although determining the effect of mutations through GWA is technically challenging even in
 279 model species (30, 31), and variants may even be either deleterious or advantageous depending on
 280 genomic backgrounds (32) or environments (33), our simulations suggest putatively functional

281 mutations may be lost more slowly ($z < 0.3$, **Fig. 2C**) than neutral genetic diversity (**Fig. 2A**). In fact,
282 the additive variance V_a parameter, often equated to the rate of adaptation, appears rather stable (34)
283 until just before the extinction event when it sharply collapses (**Fig. S21**; see also **Fig. 2C**, and **SM**
284 **II.3.4** for simulations that replicate this pattern). This is analogous to the famous “rivet popper”
285 metaphor where ecosystem structure and function may suddenly collapse as species are inadvertently
286 lost (35). Projections of the MAR using genome-wide variation may crucially serve as early
287 conservation tool in non-threatened species (36, 37), before species reach accelerating collapsing
288 extinction dynamics—an acceleration that we expect to be even more dramatic due to elevated drift and
289 accumulation of deleterious mutations of small critically-endangered populations (38, 39).

290

291 To achieve the recently published United Nations target to protect “at least 90% of genetic
292 diversity within all species”(13), it will be necessary to aggressively protect as many populations as
293 possible for each species. Here, we have discovered the existence of a mutations-area relationship
294 (MAR) and provided a mathematical framework to forecast genetic diversity loss with shrinking
295 geographic species ranges. The MAR contrasts with existing studies on the risk of losing entire species
296 by focusing on quantifying the magnitude and dynamics of genetic diversity loss likely ongoing in most
297 species. This framework demonstrates that even with conservative estimates, substantial area protection
298 will be needed to meet the UN Sustainable Development Goals. For vulnerable or endangered species,
299 we may have likely already failed.

300

301 **ADDITIONAL INFORMATION**

302

303 **Author contribution** M.E.-A. conceived and led the project. M.E.-A., J.P.S., M.R., S.H., L.G., L.C.,
304 L.L., S.T.A., V.P., E.Z., P.L.M.L., C.C.K., T.B., C.W. conducted research, all authors interpreted the
305 results and wrote the manuscript.

306

307 **Data availability.** The analysed datasets are publicly available or were shared by authors upon request
308 (see Supplementary Materials for details). Code is available at Github
309 (<https://github.com/moiepositoalonso/lab/mar>) and Zenodo (<https://doi.org/10.5281/zenodo.6408624>).

310

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312 available and thus made this research possible: the 1001 Arabidopsis Genomes Consortium, the
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Supplementary Materials for

Genetic diversity loss in the Anthropocene

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120 SUPPLEMENTAL METHODS

121

122 I. Background on species biodiversity and biogeography

123 I.1 Theoretical models of biodiversity

124

125 Studies in biogeography have modelled the species-area relationship with several functions.

126 Below we summarise the different approaches using an example of richness of $S = 100$

127 species, with variable abundance or area, A .

128

129 We may visualise the different areas or abundances of species as a frequency

130 histogram (Fig. S1, Preston plot), with x-axis: logarithm of abundance bins (historically \log_2

131 as a rough approximation to the natural logarithm), and y-axis: number of species at given

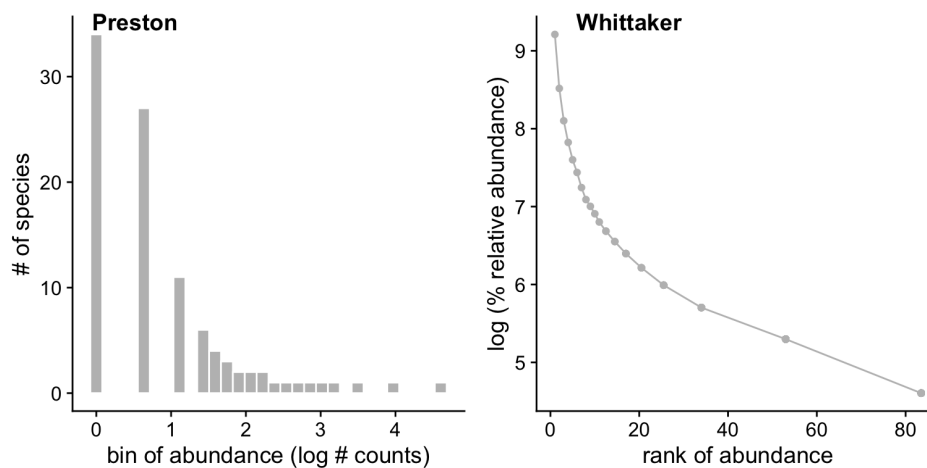
132 abundance. Alternatively, as a rank-abundance diagram (Fig. S1, Whittaker plot): x-axis:

133 species list, ranked in order of descending abundance (i.e. from common to rare), and y-axis:

134 logarithm of % relative abundance.

135

136



137

138 ***Fig. S1 | Example of typical plots used for species abundance curve studies***

139 *Due to their strong skew, Species Abundance Curves are often plotted using the Preston plot (left) where the x axis*
140 *represents bins of log2 abundances (also referred to as octaves), or using the Whittaker plot (right) where the x axis is the*
141 *rank of each species in a dataset and y axis the species' relative abundance.*

142

143

144

145 I.1.2. Niche apportionment approaches

146

147 A series of theoretical deterministic and stochastic "niche apportionment models" have been
148 put forward (summarised in (1) or (2, 3)).

149

150 The Motomura (4) geometric series suggests that each species that arrives takes half
151 the area. The first would take 50%, the second 50% of 50%, and so forth, which can be
152 expressed as:

153

$$154 P_i = 0.5^i$$

155

156 Similarly, one can imagine that as a species colonises a habitat, it takes up a fraction different
157 than 50%. This gives a geometric series with parameters k which can be written as

158

159 $P_i = k(1 - k)^{i-1}$.

160

161 Other geometric series-related models include stochasticity, where k instead of being a fixed
162 parameter is a random uniform variable and there is a k_i each time i a new species arrives to
163 the ecosystem. The "dominance preemption" model draws from 50-100% at any new arrival
164 of a species, the random fraction model draws from 0-100%. Then the abundance of a species
165 depends on the stochastic process of previous $f = 1 \dots i-1$ species arriving first:

166

$$E[P_i | P_1, \dots, P_{i-1}, k_i] = k_i \times \left(1 - \sum_{f=1}^{i-1} P_f\right)$$

167

168

169 Another approach is the broken stick by MacArthur (5), which theorised a habitat is broken
170 into $S-1$ places at random, which creates S fractions of an area. Then the relative area of a
171 species is:

172

$$E[P_i] = \left(\frac{1}{S}\right) \sum_{w=i}^S \frac{1}{w}$$

173

174

175

176 **I.1.2. Niche statistical approaches of species sampling**

177

178 Differently from niche partitioning functions, statistical approaches such as the log-series
179 from Fisher (6) and log-normal from Preston (7) are probability distributions, and approach
180 modelling in a conceptually different way: they model the sampling process of species
181 collections given an underlying relative abundance (see below).

182

183

184 Statistical-based derivations probably began with Fisher (6), with the log-series
185 distribution. It assumes that species abundances in the community are independent identically
186 distributed variables, sampling is a Poisson process, sampling is done with replacement, or
187 the fraction sampled is small enough to approximate a sample with replacement. Here,

188

$$189 S_n = \frac{\alpha x^n}{n},$$

190

191 where x is a constant $x \in [0, 1]$ related to the sample dataset (typically close to 1),

192 $x = \frac{N}{\alpha + N}$, and α is a new constant term (ecosystem-specific) that is used as a measure of
193 biodiversity. Fisher proposed the number of species could be estimated as:

194

$$195 S = \alpha \times \log\left(1 + \frac{N}{\alpha}\right).$$

196

197 Finally, Preston (8) posed that the skewness of previous proposals is due to lack of
198 sampling. With little data, common species are collected sooner, but with more abundant
199 sampling, the rarest species are also well-sampled and have abundances well above 0. Preston
200 then proposed that the octaves (bins of doubling abundance) follow a normal distribution,
201 making the raw abundance log-normal distributed. Given S_0 is the number of species in the
202 model octave of abundance and a variance composite of the log-Normal σ^2 , the number of
203 species per abundance (octave) bin $R (= \log(n))$ is:

204

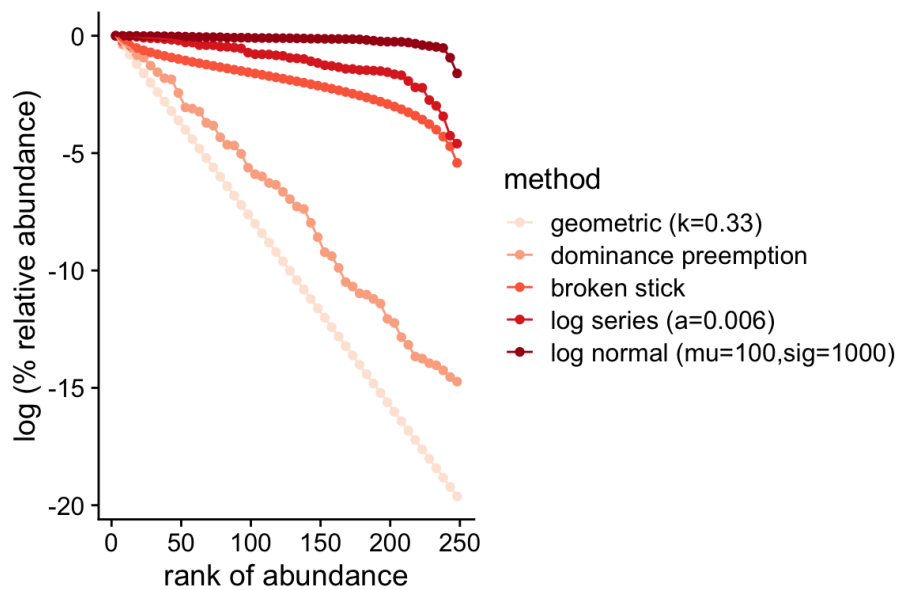
205 $S_R = S_0 e^{-R^2/2\sigma^2}$.

206

207 The Unified Neutral Theory of Biodiversity (UNTB) by Hubbell (1) takes a stochastic
208 approach of a community with immigrants, extinctions, and speciation in continuous
209 dynamics. Interestingly, the UNTB's key parameter, θ , coincides with Fisher's α , as the log-
210 series is a limiting case of UNTB. Hubbell's discovery was that $\alpha=2J_m v$, where J_m is the size
211 of the external metacommunity that provides migrants of species to the focal community, and
212 v is the speciation rate. Alonso and McKane (9) derived the so-called Metacommunity Zero-
213 Sum Multinomial (MZSM) distribution from the UNTB. In practice, both distributions have
214 almost-identical fits (lines completely overlapping in Fig. S2 below).

215

216



217

218 **Fig. S2 | Summary of theoretical models of Species Abundance Curves.**

219 *Five niche partitioning or statistical models shown in a Whittaker plot. The different models expect different levels of*
220 *evenness in abundance across the species in the community, from the lowest (geometric series) to the highest (log-normal).*

221

222

223 I.2 Metric of species diversity

224

225 Although a number of metrics exist to measure species diversity, such as the Shannon index,
226 $H' = -\sum_{i=1}^S P_i \log P_i$ (with P_i the relative proportions of species abundances) or Fisher's non-
227 dimensional α parameter, the study of species abundances and area relationships has focused
228 on species richness S , that is, the total number of species in a given location or area. Below
229 we therefore focus on species richness.

230

231

232 I.3 Biogeography of species and extinction.

233

234 SAD and SAR connection

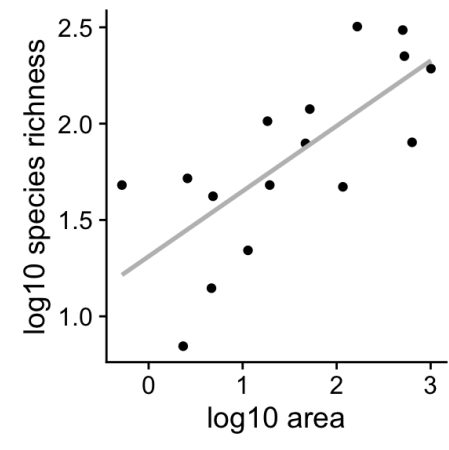
235

236 Due to many species being rare, it is expected that as researchers sample an area, the most
237 common species will be sampled first, and as the area studied increases, more and more
238 species will be discovered. This is thought to happen following a power law relationship,

239 where the number of species in that area S_A increases with the sampled area A , with scaling z
 240 (slope in a log-log plot), and with a constant c :

241
 242 $SAR(A) = cA^z$.

243
 244 Preston (7) derived theoretically that from a log-normal series, one would expect
 245 $z=0.27$, under a number of assumptions (Fig. S3). This has been empirically shown to be
 246 close to reality (7, 10), although there is some variation across ecosystems and spatial scales.
 247



248
 249 **Fig. S3 | Example of a Species-Area Relationship in Galapagos Islands**
 250 *Classic species richness dataset from the Galapagos Islands (Preston, 1962). It depicts species richness as a function of*
 251 *island area in a log-log plot.*

252
 253
 254 **I.4 Estimating extinction of species from the species area relationship**

255
 256 The first estimates of species extinction used the SAR relationship. Given a reduction of
 257 ecosystem area, A , by an area of a (11, 12). If these areas, as well as the SAR scaling, z , are
 258 known, then one can predict the number of species in the future as:

259
 260 $S_{\text{now}} - S_{\text{fut}} = cA_{\text{now}}^z - cA_{\text{fut}}^z$,

261
 262 However, we are normally interested in the fraction of species that will go extinct X_s , so we
 263 can take the ratio:

264
 265 $X_s = \frac{S_{\text{now}} - S_{\text{fut}}}{S_{\text{now}}} = 1 - \frac{cA_{\text{fut}}^z}{cA_{\text{now}}^z} = 1 - \left(\frac{A_{\text{fut}}}{A_{\text{now}}}\right)^z$.

266
 267
 268 **II. Population genetics models and the site frequency spectrum.**

269 **II.1 The Wright-Fisher model and the site frequency spectrum**

270
 271 Statisticians and population geneticists from the 20th century, Wright and Fisher, built a
 272 simple statistical model of evolution of a population. It assumes that each generation a
 273 population of N monoecious (hermaphrodite) individuals mate randomly to create a new
 274 generation of N individuals and then immediately die so that only N individuals remain in the
 275 population at any given time. This random sampling process causes the frequency of a variant

276 in one generation to possibly differ from its frequency in the previous generation—a process
277 known as genetic drift.

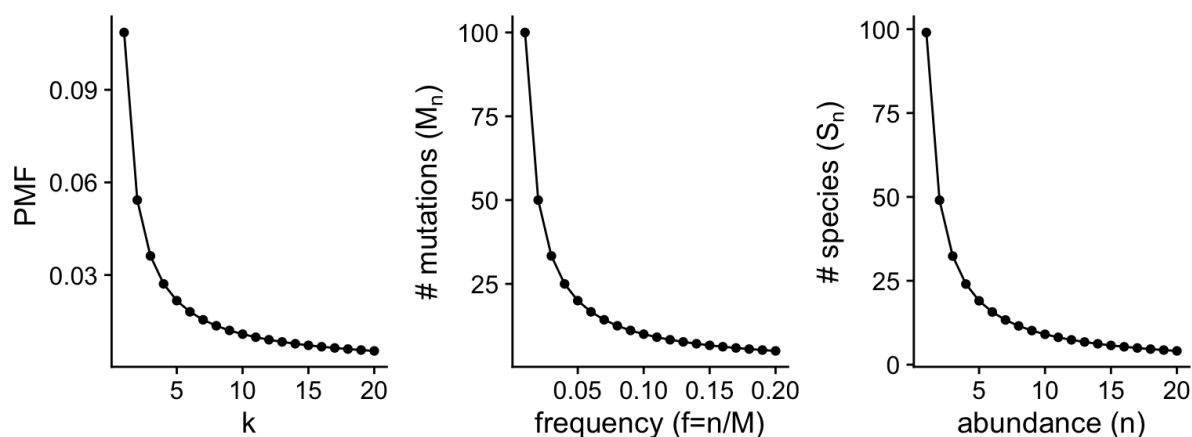
278
279 When a nucleotide mutation or variant (e.g. ACGAA → ACGTA) emerges by a
280 random process of, for instance, DNA replication error, it will first be in $1/N$ individuals (if
281 we consider these diploid, $1/2N$ chromosomes). Through random sampling that T mutation
282 may be lost, stay at the same frequency, or randomly move to higher frequency. Although
283 rarely, just by chance, the mutation may reach 100% frequency. This results in a
284 “commonness of rarity” when looking at mutations in a population, as we have seen in
285 previous sections for species. Since these genetic drift dynamics affect all mutations genome-
286 wide, we therefore expect the majority of mutations to be absent, or rare, and only a much
287 smaller proportion of variants to be at moderate or high frequencies.

288
289 The site frequency spectrum (SFS) refers to the distribution of frequencies of variants
290 in a population. This is the number of sites at which we observe a variant at frequency q in a
291 sample of n individuals. To derive the expected SFS distribution, we turn to Kingman’s
292 Coalescent (13). Both models describe the same ideal population of random mating, constant
293 population size, and mutations emerging at a low rate and drifting in frequency. But while the
294 Wright-Fisher model describes the dynamics of a whole population forward-in-time, the
295 Kingman’s Coalescent describes the genealogy of a sample of individuals from a population,
296 going backward in time. By building a model around the individuals that are sampled or that
297 survived, rather than of an entire population, the Coalescent provides a simpler way to derive
298 expectations in small populations or in cases, for example here, where a limited sample of
299 genomes are sequenced. Using the Coalescent (see (14) for details), one obtains that the
300 expected number of mutations of a given abundance, n , is inversely related to their frequency,
301 q :

302
303
$$M_n = c \frac{1}{q}$$

304
305 for some constant c that depends on the mutation rate and the population size. This SFS from
306 population genetics theory is remarkably similar to the Species Abundance Relationship. In
307 fact, Fisher himself (15) derived an expression similar to the above.

308
309 Rearranging terms, one can see this is a constrained version of the log-series
310 Probability Mass Function (PMF), which Fisher also proposed for the distribution of species
311 abundances (6). Below, one can graphically see the similarities (Fig. S4):
312



313

314 **Fig. S4 | Similarity between the Species Abundance Distribution and the Site Frequency Spectrum**
315 *Left is the Probability Mass Function of the log-series ($p=0.999$), center is the SFS ($N=100$, $c=1$), and right is*
316 *the log-series-based abundance of species ($\alpha=100$, $N=10000$).*

317
318 Keeping the abundance, n , constant (and low), when the number of individuals
319 $N \rightarrow \infty$, we know that the constant x from Fisher's SAD approaches 1, $x = \frac{N}{N+\alpha} \rightarrow 1$. Then,
320 we can rewrite the number of species at any given abundance (S_n) as:

$$321 S_n = \alpha \frac{\left(\frac{N}{\alpha+N}\right)^n}{n} = \alpha \frac{1^n}{n} = c \frac{1}{n} = M_n$$

322
323
324 So both have the same form as the log series PMF: $f(k) = \frac{-1}{\ln(1-p)} \frac{p^k}{k}$ when $p \rightarrow 1$. In
325 the next section we will see that the constants of the SAD and the SFS are proportional to
326 species and mutation diversity, although the Site Frequency Spectrum (SFS) is a specific case
327 of SAD. One can also see that because the constant in the SFS is the population scaled
328 mutation rate, $c = \theta = Ne\mu$, and Fisher's $\alpha \approx \theta$ for large N .

329 330 **II.2 Metrics of genetic diversity**

331
332 In population genetics, multiple measurements of genetic diversity have been put forward.
333 The most straightforward is the allelic richness, also number of mutations, or also called the
334 number of segregating sites. Segregating sites, M , is the direct equivalent of the species
335 richness, S , and it depends on the number of samples used and length of DNA sequence
336 explored (Note: we use the non-standard notation, M , as the standard in population genetics is
337 S [for segregating sites] but this is already in use for species richness. We then use M for
338 mutations and S for species). This metric can also be thought of as the area under the curve of
339 the SFS. Two other metrics that describe the SFS but that aim to be sequence-length- and
340 individual independent are Watterson's Theta, θ_W , and Nucleotide diversity, π , (also called θ_π
341). These two metrics of diversity are identical at population equilibrium and are estimates of
342 $4Ne\mu$ (when the SFS follows a $1/q$ relationship), with effective population size N_e and per-
343 generation mutation rate μ , whereas they differ in non-equilibrium demographics, under
344 natural selection, or under other behaviors not considered in the Wright-Fisher neutral model,
345 such as different mating systems (16).

346
347 First, π is described as:

$$348 \pi = \frac{\sum_{i=1}^{n-1} i(n-i)M_i}{n(n-1)/2},$$

349
350 and θ_W as:

$$351 \theta_W = \frac{\sum_{i=1}^{n-1} M_i}{\sum_{i=1}^{n-1} 1/i},$$

352
353 where $\sum_{i=1}^{n-1} 1/i$ is the $n-1^{th}$ Harmonic number, which serves to scale the segregating
354 sites based on the assumption that the abundance of mutations follows a $1/q$ SFS. The
355 diversity metrics π and θ_W are both functions of the SFS, as opposed to Fisher's α from the
356 Species Abundance Distribution, which is a parameter that changes the shape of the
357 distribution.
358
359

360

361 Although often nucleotide diversity π is reported as a typical measure of genetic
362 diversity of a species, since it can be calculated for a single genome and it captures the
363 process of inbreeding of a population (17), classic literature relating germplasm management
364 for conservation and breeding has advocated for allelic richness (18).

365
366

367 **II.3 Spatial genetics and the mutations-area relationship (MAR)**

368

369 Since its inception, a number of concepts in population genetics have dealt with genetic
370 variation in populations of different sizes, or populations separated in space. For instance, one
371 classic result in population genetics is the relationship of $\pi \approx 4N_e \mu$, which relates genetic
372 diversity π with the effective population size N_e and the mutation rate of the species μ . A
373 relationship which is still studied nowadays in an effort to reconcile data with theory (17).

374 In 1943, Sewall Wright turned to study the genetics of multiple populations within a
375 species. He proposed that populations sampled further apart geographically must differ more
376 in allele frequency due to more independent drift (19), leading to the commonly used
377 correlation between geographic distance and the metric of differentiation F_{ST} . Most
378 prominently, the use of correlation in the accumulation of mutations of populations that are
379 geographically close or share evolutionary history has been uncovered using dimensionality
380 reduction approaches such as PCA (20).

381 Despite these enormous advances in understanding spatial genetic structures,
382 surprisingly little quantitative work has been done to parametrize the loss of genetic diversity
383 by direct loss of habitat.

384 Because of the abundance of rare mutations in populations, it is straightforward to
385 think that the more area and individuals sampled, the more segregating sites will be found.
386 Analogous to the Species Area Relationship (SAR), $S=cA^z$, we should thus be able to
387 estimate the equivalent scaling for a mutations-area relationship (MAR):

388

$$389 \quad M=cA^z,$$

390

391 with a scaling $z = z_{MAR}$, which corresponds to the slope of best fit in a log-log-plot of
392 A and M for a given species. (Other functions are often fit empirically for SAR datasets,
393 which we explore later in section III.3. We work with the power law because of its historical
394 use, mathematical convenience, and because other more complicated functions only
395 improved fitting marginally, see Table S4).

396

397 This differs from other efforts to understand the number of segregating sites or
398 heterozygosity differences across species that differ in their total census size or geographic
399 distribution (21, 22). The MAR instead is built within a species, as its ultimate aim is to relate
400 the number of mutations left in a species as it loses spatial populations.

401

402 Below we derive what are the expectations of MAR taking two opposite scenarios of
403 neutral population evolution, and study how many segregating sites or mutations M are
404 discovered with increasing area in the simulations. We further test the scenario of meta-
405 populations in space with varying migration rates and neutral or natural selection processes.

406

407 **II.3.1 Panmictic population**

408

409 The expected number of mutations, M , is a constant that depends on the mutation rate, μ , and
410 the expected total branch length of the population genealogy, L , with $M=\mu L$. Under the

411 coalescent, the total branch length is equal to the number of lineages or individuals sampled
 412 from the population, n , times the time of the genealogy during which there are such lineages,
 413 T_n , plus $n-1$ times the time in the genealogy with such number of lineages, and so forth:

414
 415
$$L = nT_n + (n - 1)T_{n-1} + \dots + 2T_2.$$

416
 417 Under the coalescent,

418
 419
$$E[T_n] = \frac{2N_e}{n(n-1)},$$

420
 421 and thus:

422
 423
$$E[L] = n \frac{2N_e}{n(n-1)} + (n-1) \frac{2N_e}{(n-1)(n-2)} + \dots,$$

424
 425 which simplifies to

426
 427
$$E[L] = 2N_e \left(\frac{1}{n-1} + \frac{1}{n-2} + \dots + 1 \right) = 2N_e H_{n-1},$$

428
 429 where H_{n-1} is the $(n-1)$ th harmonic number. This is of course related to one of the
 430 diversity metrics (section II.2), where Watterson's Θ_W scales the number of segregating sites
 431 (M) by the harmonic number of sampled individuals. This is based on the expectation that as
 432 more individuals are sampled, we expect to discover more mutations proportional to the
 433 above harmonic number. Because such number is not so easy to work with to create an
 434 expectation for z_{MAR} , we further simplify this expectation following the Taylor expansion
 435 approximation of the harmonic number:

436
 437
$$H_n = \gamma + \log(n) + \frac{1}{2n} + O\left(\frac{1}{n^2}\right) \simeq \gamma + \log(n) + \frac{1}{2n},$$

438
 439 which we can further approximate as:

440
 441
$$E[L] \approx 2N_e \log(n-1) + c.$$

442
 443 Therefore, assuming a constant mutation rate and effective population size (N_e) under
 444 panmixia, M grows following $\log(n)$. In such a case, a log-log plot (typical power law plot)
 445 does not display a linear relationship, and the slope is asymptotic to $z \rightarrow 0$ for $N \rightarrow \infty$. On the
 446 other hand, with low values of x (area or individuals sampled close to 0), the slope z_{MAR} will
 447 be incorrectly high. We can show this effect trivially by studying the local derivative of the
 448 function $\log_{10}(M) = \log_{10}(\log(N))$. The local slope of that function is an approximation of our
 449 z_{MAR} parameter. This can be locally estimated at any given point N by taking the derivative:

450
 451
$$\frac{d \log_{10}(\log(N))}{d(\log_{10}(N))} = \frac{1}{\log_{10}(N) \log(10)}.$$

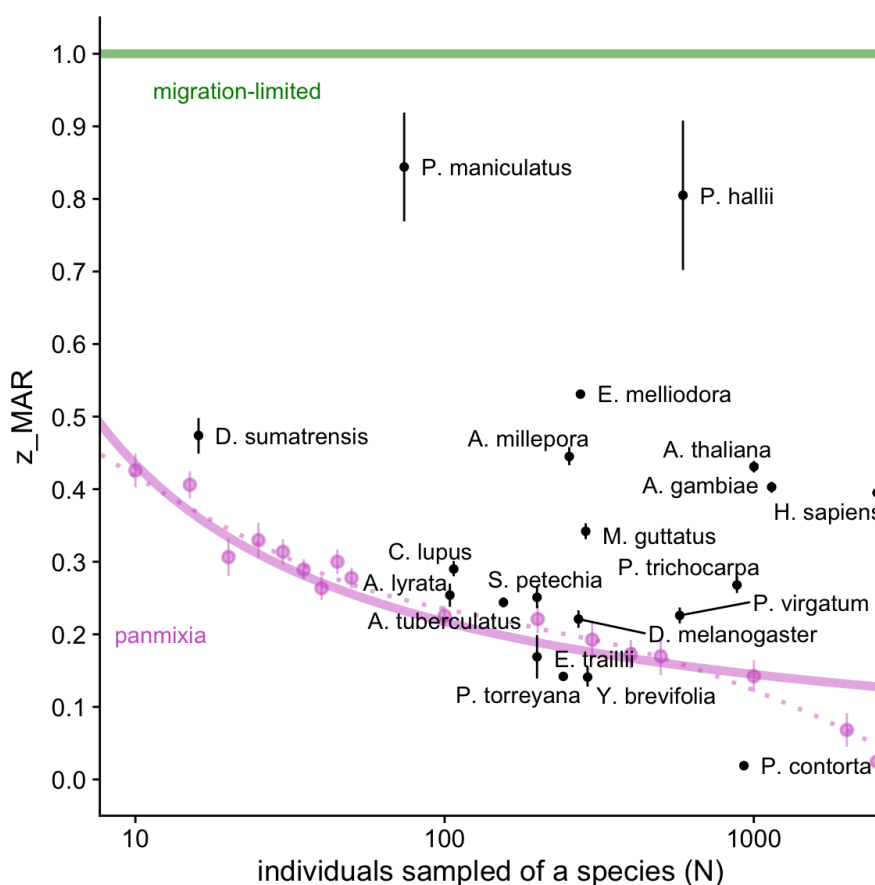
452
 453 The implication of this nonlinear function is that if we sampled only few individuals
 454 or areas of a species (e.g., $n=100$), even if this species was completely panmictic we would
 455 expect a non-zero z_{MAR} , a value that will change with sampling effort. We can roughly approximate
 456 z_{MAR} by the local slope of the number in the midpoint of the graph, e.g., for $n=100$ we look at
 457 the slope at $n=50$, and obtain $1/(\log_{10}(50) \times \log(10)) \cong 0.256$. Therefore, with small sample
 458 sizes, this parameter will not be helpful to understand whether a species behaves

459 panmictically or is limited by migration, which may be problematic for estimates of genetic
460 diversity loss later. We can visualise our expectation of the z_{MAR} under panmixia plotting the
461 first derivative above (Fig. S5). Because—as we will show below—we do expect a power
462 law relationship under a migration-limited scenario, z_{MAR} should theoretically not change with
463 sample size. The graphical study of the (non-)linearity of the log-log plots between the
464 number of mutations and area sampled should be diagnostic to this problem (We see for
465 instance that *Pinus contorta* has a highly nonlinear relationship, likely due to the use of
466 ascertained intermediate frequency markers instead of genome-wide data, Fig. S22).

467
468 Finally, we used msprime (23) to corroborate this finding (z_{MAR} being constant with
469 respect to sample size) with simulations, simulating 1600 demes in a 40x40 grid of demes or
470 populations of $N=N_e=1000$ that are completely panmictic (universal gene flow or dispersal,
471 so this is equivalent to a single panmictic deme). We observed the z_{MAR} for $t=100\dots 10,000$
472 generations in \log_{10} increments. After this time, we sample $n=1\dots 100$ individuals in
473 increasingly large groups of adjacent demes. The range of estimates of z_{MAR} in these
474 simulations was 0.07-0.15.

475
476 Fig. S5 indicates that the minimum average z_{MAR} even under panmixia would
477 continuously increase with lower numbers of individuals of a species sampled. This is due to
478 the fact that the site frequency spectrum is not fully sampled with small numbers of
479 individuals. Therefore, we devised an approach to rescale z_{MAR} .

480
481
482



483

484 **Fig. S5 | Expected ranges of z_{MAR} given sample sizes.**

485 *For increasing numbers of individuals sampled, we plot the expected mean z_{MAR} under two theoretical trends of a migration-*
486 *limited (green) and a panmictic (purple) species (Purple dots indicate averages from SLiM simulations under panmixia to*
487 *confirm the theoretical trend based on the derivative approach above). In black, z_{MAR} and 95% Confidence Interval of*
488 *species analyzed in section IV are plotted (see section for details).*

489

490

491 **II.3.2 Scaling z_{MAR} for low sampling and low census size**

492

493 Let $z_{pan-n} = E[z_{MAR} | n, panmixia]$, be the expected value of z_{MAR} of a panmictic
494 species given that we only have small sampling of n . Although theoretically z_{MAR} should
495 approach 0, with small samples it can be upwardly biased. In order to force the possible
496 values of z_{MAR} to range 0-1 despite small sample sizes, we can scale it as:

497

$$498 z_{naive\ scaled} = (z_{MAR} - z_{pan-n}) / (1 - z_{pan-n}).$$

499

500 In words, this moves the purple line in Fig. S5 to zero, stretching the space above it
501 accordingly.

502

503 Most species have census sizes so large that z_{MAR} should indeed approach 0 under
504 panmixia, so we should correct the sample estimate z_{MAR} to range 0-1. However, some
505 species have such low census size N that even if we sample all individuals of a species, the
506 sample size will still be small. In those cases, we should not scale z_{MAR} to range 0-1, but
507 rather scale it from $z_{pan-N} - 1$, where $z_{pan-N} = E[z_{MAR} | N, panmixia]$ is the expected value of
508 z_{MAR} given a census size N (plants or animals living in the wild). The updated scaling
509 approach for both census and sample size would then be:

510

$$511 z^*_{scaled} = (1 - z_{pan-N}) (z_{MAR} - z_{pan-n}) / (1 - z_{pan-n}) + z_{pan-N}.$$

512

513

514 Note that this scaled estimate must be conservative because while we adjust the
515 minimum z for the average value expected for low sample sizes, we do not adjust for the
516 maximum possible z , which only under very extraordinary theoretical conditions can be $z=1$,
517 namely under an unrealistic complete disconnection of populations by gene flow (see below).
518 Because deriving the maximum z would require more biological knowledge of the species'
519 demography, landscape connectivity, genome structure, etc., and because we rather create
520 conservative estimates, we do not create further scaling approaches.

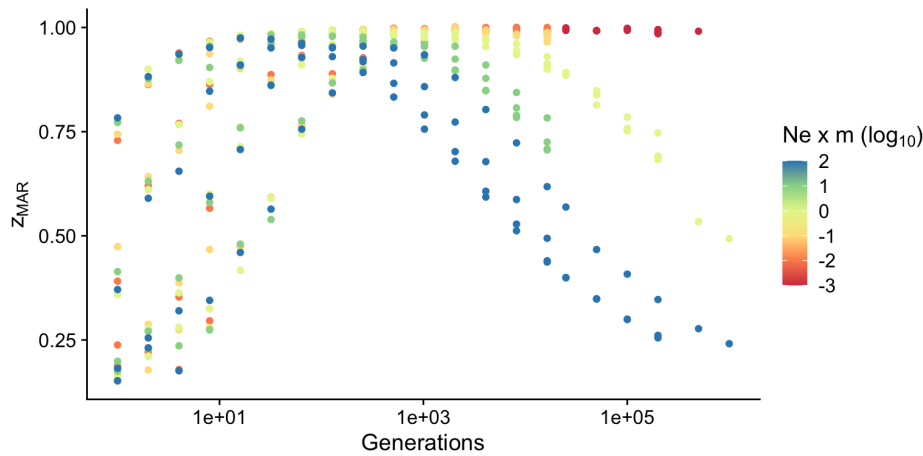
521

522 **II.3.3 Meta-populations in space**

523

524 A more realistic simulation than a panmictic population is that of the same 40x40 deme grid
525 where migration can happen between adjacent demes. This migration rate can be changed to
526 understand the effect of population structure and migration on z_{MAR} . Under no migration (or
527 very low migration), we expect the mutations in two distinct populations (and thus their SFS)
528 to be (almost) completely independent. Hence, when explored demes are doubled (N_e
529 doubles), we discover twice as many mutations. In this case, the number of mutations should
530 scale linearly with the area, so we expect the following to be true: $M=A$, $\log(M) = \log(A)$,
531 and $z_{MAR}=1$. Our analyses under different sampling schemes, and with different numbers of
532 "burn-in generations" (generations since a single deme colonised the full 40x40 space)
533 confirm that z_{MAR} approaches 1 in the limit of low migration (see Table S1 and Fig. S6).
534 Different from the panmictic situation, as we increase the sampled area, we not only increase
535 n , which would lead to a $\log(A)$ in mutations, but also increase N_e .

536
537
538



539

540 **Fig. S6 | msprime 2D deme simulations and the mutations-area relationship**

541 Simulations with different burn-in and migration rates under neutrality, and their corresponding z_{MAR} .
542

543 **Table S1 | msprime population genetic simulations in 2D**

544 Simulations summarised by grouping ranges of the resulting z_{MAR} parameters. The average parameters of the simulations
545 with similar z_{MAR} EW provided. (Acronyms: N_{emt} = product of effective population size, migration rate, and simulated
546 generations).
547

z_{MAR}	Samples/deme	Generations	Migration rate	N_{emt}
0.2 +/- 0.05	2.4	50001.7	0.0271675	5000044.23
0.3 +/- 0.05	20.25	70003	0.0561655	7000075.77
0.4 +/- 0.05	26.5714286	13057.4286	0.04450857	1305497.96
0.5 +/- 0.05	12.9230769	121759.462	0.04017769	752221.743
0.6 +/- 0.05	15.6111111	3218.77778	0.045735	321174.768
0.7 +/- 0.05	35.6842105	35034.8421	0.03395895	143791.614
0.8 +/- 0.05	35.030303	15655.1212	0.03055818	58023.5539
0.9 +/- 0.05	36.5806452	3057.12903	0.0253029	15290.4081
1 +/- 0.05	42.0140845	13625.4085	0.00861178	1798.36141

548

549

550 These simulations corroborated that we can recover z_{MAR} values ranging between 0-1
551 just varying migration and burn-in generation parameters. We found that it was both the time
552 of the system to reach an equilibrium as well as the migration rate that determined z_{MAR} . In
553 the future, it will be interesting to study different non-equilibrium scenarios to better
554 understand how genetic drift, gene flow, and different landscape structures may shape the
555 z_{MAR} .

556

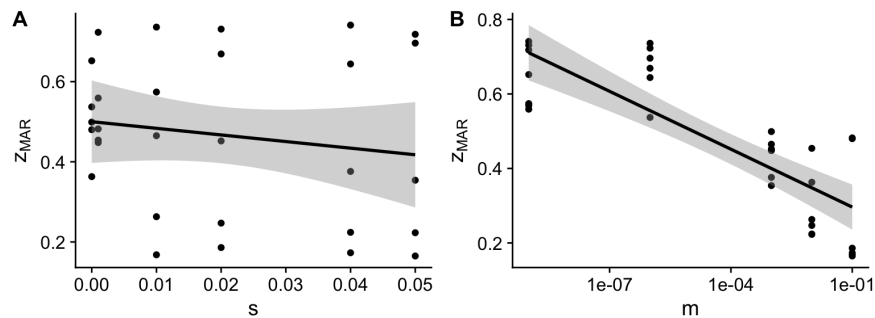
557 II.3.4 Metapopulations in space with local adaptation

558

559 In order to simulate local adaptation, we use the individual-based simulation software SLiM
560 (24) following the approach of (25). These simulations were set up for 196 demes arranged in
561 a 14 x 14 grid. Each grid cell contains a population of $N=1000$ and has an environment
562 attribute, e , which varied spatially from the lower-left to the upper-right corners (approx. $-7 <$
563 $e < 7$). 12 locations in the genome were allowed to be under directional natural selection. The
564 selection coefficient was fixed for a simulation, and grid runs were conducted with
565 $0 < s < 0.05$, but this selection would vary based on the environmental selection value of a grid
566 cell, according to $e \times s$. Therefore, these alleles are antagonistic pleiotropic. Selected
567 mutations across the 12 loci in the genome behaved additively (e.g. if an individual in grid

568 cell i had two of the selected mutations, fitness would be $w=1+2s \times e_i$. The migration rate
 569 varied from one individual in a billion (1×10^{-9}), to one individual every ten (1×10^{-1}). Finally,
 570 the mutation rate was set to 10^{-8} mutations/bp/generation and the recombination rate to 10^{-7}
 571 crossovers/bp/generation.

572
 573
 574



575

576 **Fig. S7 | SLiM population genetic simulations in 2D with selection and local adaptation**

577 Simulations were carried out with different combinations of migration rates and strength of antagonistic
 578 pleiotropic selection at 12 QTLs. (A) Marginal relationship between z_{MAR} with the strength of spatially-varying
 579 selection s . (B) Marginal relationship between z_{MAR} with the migration rate m .

580

581 These results, together with individual-based simulations, corroborate what we had
 582 observed with coalescent simulations, i.e. that z_{MAR} is lowest with a high migration rate. The
 583 simulations also appear to show a negative effect of selection on z_{MAR} . Generating a linear
 584 model fitting migration rate and selection and their interaction to understand what factors
 585 explain the scaling coefficient: $z_{MAR} \sim \log_{10}(m) + s + \log_{10}(m) s$; we confirm that both had a
 586 significant effect, and that selection significantly reduces z_{MAR} (Fig. S7, see below summary
 587 Table S2). This may seem counterintuitive, as one may expect that locally-adaptive mutations
 588 are rare and will be localised only to where they are adaptive. More work is necessary to
 589 understand the signatures that spatially-varying natural selection (and its different types)
 590 create on z_{MAR} , but we can think that under migration limited scenarios (where z approaches
 591 1) adaptive alleles and their linked mutations permeate faster to similar neighbour
 592 environments than neutral alleles.

593

594 **Table S2 | Linear model explaining z_{MAR} by migration rate and natural selection**

595 Summary table of the linear model $z_{MAR} \sim mig + s + mig:s$

	Estimate	SE	t-value	P-value
intercept	0.3385022	0.0469174	7.214859	0.0000001
mig	-0.0419733	0.0085804	-4.891792	0.0000407
s	-4.693492	1.6290184	-2.881178	0.0076725
mig : s	-0.4998393	0.2426463	-2.059950	0.0491621

596

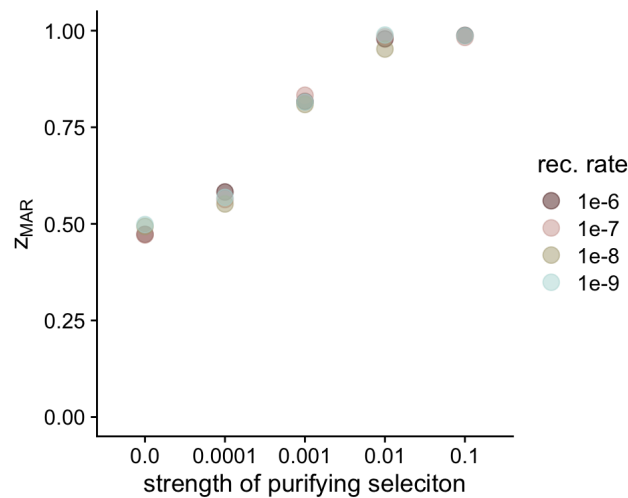
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598 II.3.5. Metapopulations in space with purifying selection

599

600 To understand the effect of purifying selection on z_{MAR} we also ran 2D simulations with a
 601 fraction of the genome allowed to be globally-deleterious (i.e. independent of the spatially-
 602 varying environment). We simulated an increasingly strong purifying selection ($|s|$ range
 603 from 0.0 to 0.1), simulating roughly that 29% of the genome of Arabidopsis is coding
 604 (arabidopsis.org) and mutations can be deleterious. We also varied the degree of
 605 recombination. Following our expectation, with stronger purifying selection deleterious

606 mutations are pushed to lower allele frequencies, stopping their geographic spread, which
607 increases z_{MAR} . Recombination rate appears to have a minor role on z_{MAR} (Fig. S8).
608
609



610

611 **Fig. S8 | SLiM population genetic simulations in 2D with purifying selection**

612 Simulations were carried out with varying strengths of purifying selection ($|s|$ range from 0.0 to 0.1) at coding positions,
613 representing about 29% of the genome. Different values of recombination rate were also used in all pairwise combinations
614 with $|s|$.

615

616 **II.3.6 Continuous-space non-Wright-Fisher models**

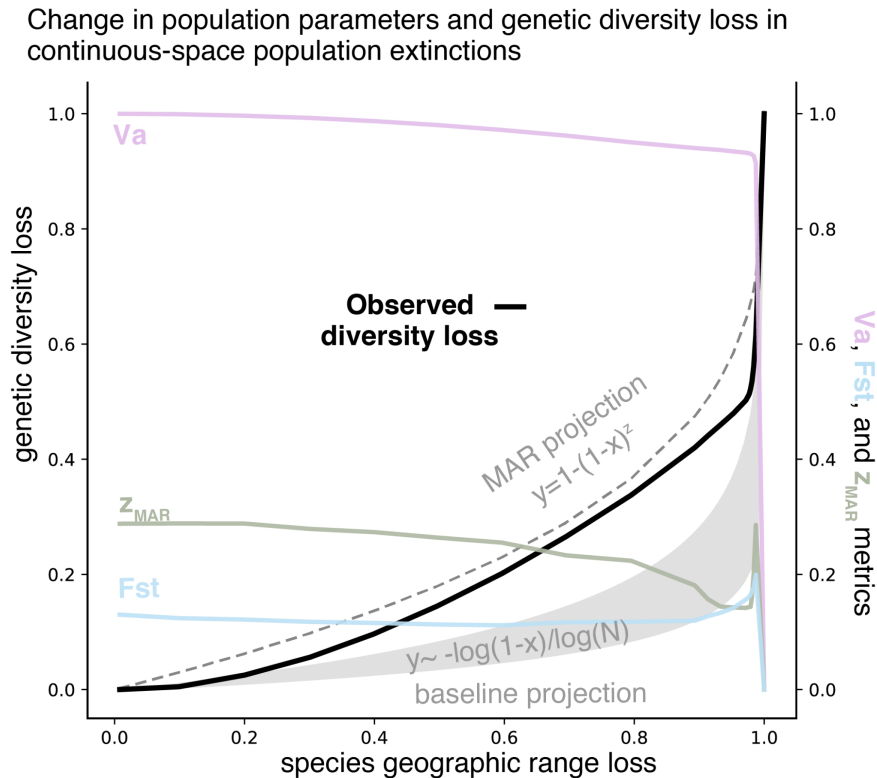
617

618 In order to confirm z_{MAR} generality in highly realistic conditions and its behavior through the
619 population extinction process (II.4), we set up SLiM simulations in continuous space using
620 non-Wright-Fisher dynamics (24). Spatial population structure in these simulations was
621 established through individual dispersal, local mate choice and spatial competition, which we
622 chose to lead to realistic values of F_{ST} across space. Spatial competition also acted as
623 population control, by keeping the total population size below a target carrying capacity
624 through direct effects on individual fitness. In addition to competition, fitness was also
625 affected by individual age as well as by a polygenic trait under stabilising selection. A subset
626 of variants (final proportion $\sim 10\%$) directly affected this trait with effect sizes drawn from a
627 Gaussian distribution with mean = 0.0 and standard deviation = 0.1, and a fitness penalty was
628 incurred by deviating from the optimal trait value using a Gaussian fitness function centered
629 at the optimum and with a standard deviation = 5.0. We initialised functional variation for
630 SLiM using neutral coalescent simulations with msprime (23) to reduce the computational
631 burden of burn-in, and loaded the resulting tree sequences into SLiM (26, 27). We drew
632 functional effect sizes for these variants, placed individuals into continuous space, and ran
633 simulations forward-in-time for 5,000 generations. After that, the geographic distribution of
634 the species experienced impacts as expected during global change: every generation, 0.001 of
635 one edge of the species distribution got its carrying capacity reduced to 0. This meant that
636 over 1,000 generations the whole species would disappear (note that this is a reasonable
637 fraction of area reduction given the estimates of yearly deforestation and habitat change in
638 section V). We subsequently overlaid neutral mutations on the tree sequence using
639 msprime, and analysed genomes sampled throughout the extinction process (by tracking them
640 in the tree sequence output) and extracted using tskit.

641

642

643



644

645 **Fig. S9 | Continuous space SLiM population genetic simulations**

646 *At 19 timepoints leading up to extinction, 1,000 individuals were sampled randomly in continuous space to quantify diversity*
 647 *loss (black line). The prediction of MAR (dashed line) using the starting z_{MAR} seemed to follow the real trend better than the*
 648 *baseline of just loss of individuals (dashed line). This suggests that even if z_{MAR} varies during the population extinction*
 649 *process, it is relevant to understand genetic loss by area reduction. We also tracked metrics of population structure (z_{MAR} ,*
 650 *F_{ST}) and a proxy of adaptive capacity (V_a), which showed qualitatively similar patterns as the GWA-based trends (Fig S21).*
 651

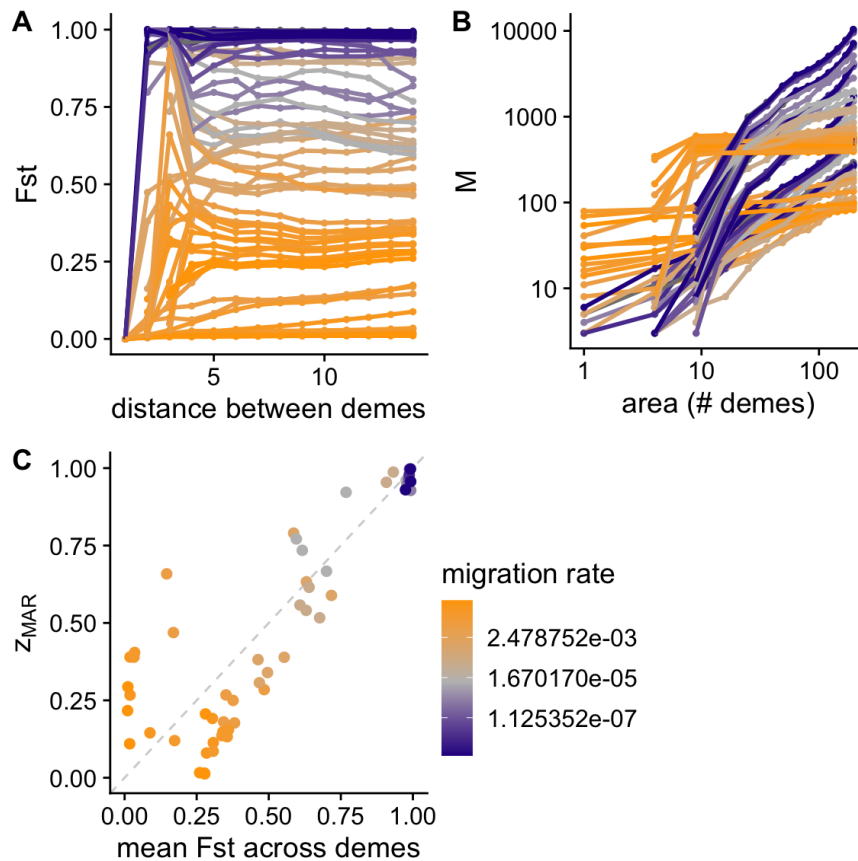
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653 **II.3.7 Connection of z_{MAR} with the isolation-by-distance pattern**

654

655 Ultimately, z_{MAR} is a complex integrator of evolutionary forces acting in space (mutation,
 656 migration, drift, selection) and captures how structured the distribution of a species'
 657 mutations is. Although the isolation-by-distance pattern conceptually resembles z_{MAR} , we have
 658 found no obvious analytical expression that relates both. Note that F_{ST} is defined based on
 659 heterozygosity or π , instead of the number of segregating sites (i.e., mutations M). For
 660 instance, using Hudson's estimator (28) to compute F_{ST} across a set of populations we
 661 calculate $F_{ST} = 1 - (\pi_w / \pi_b)$, where π_w is the diversity or heterozygosity within a population
 662 and π_b is the same parameter calculated for the meta-population. Plotting F_{ST} of a
 663 metapopulation by the distance of the farthest demes shows the typical non-linear trend of
 664 isolation-by-distance, which shows that very close populations have similar allele frequencies
 665 whereas populations further away drift apart. A challenge of F_{ST} is that it requires pre-
 666 defining discrete populations, which is straightforward in stepping-stone simulations but hard
 667 in real data. Comparing average F_{ST} of our 14x14 spatial demes and z_{MAR} , we see that the two
 668 parameters correlate (Fig. S10C). However, it appears that for low values of F_{ST} , z_{MAR} captures
 669 more variation across the simulations (Fig. S10). These patterns were also confirmed in
 670 continuous space simulations (not shown).
 671

671



672

673 **Fig. S10 | SLiM population genetic simulations in 2D comparing F_{ST} and z_{MAR}**

674 Neutral SLiM simulations with different degrees of migration. (A) Hudson's F_{ST} across populations with different area
675 subsamples. Following the expectation of the isolation-by-distance pattern, as the distance between the farthest demes in the
676 subsample increases, F_{ST} becomes larger and saturates at large distances. (B) The mutations-area relationship. (C)
677 Comparison between F_{ST} and z_{MAR} .

678

679

680 II.4 The loss of mutations (genetic diversity) in space

681

682 The aim is to predict the fraction of genetic diversity loss, x_M , from shrinking of an ecosystem
683 by an area a . To define all terms, we then have a past area A_{t-1} and a present reduced area
684 $A_t = A_{t-1} - a$, and a fraction of area extinct $x = a/A_{t-1}$

685

686 We first think of the loss of genetic diversity x_M through the basic process of losing
687 individuals. From the population genetics's coalescent theory derivation of the number of
688 mutations or segregating sites from individuals we got the approximation $M \sim \log(N)$.

689 Assuming the loss of area is simply the loss of individuals ($A=N$), we can derive the fraction
690 of genetic diversity loss as:

691

$$\begin{aligned}
 x_M &= 1 - \frac{M_t}{M_{t-1}} = 1 - \frac{\log(N_t)}{\log(N_{t-1})} = 1 - \frac{\log(N_{t-1}(1-x))}{\log(N_{t-1})} = 1 - \frac{\log(N_{t-1}) + \log(1-x)}{\log(N_{t-1})} \\
 &= -\frac{\log(1-x)}{\log(N_{t-1})}
 \end{aligned}$$

693

694

695 The loss of mutations is then in the scale of: $\log(1-x)$; which is very slow, as we

696 expected from having derived the trend that under panmixia $z_{MAR} \approx 0$. A substantial loss of

697 genetic diversity in this case only happens when population extinction is almost complete.

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Species do not typically behave perfectly panmictic given different z_{MAR} values. Under population structure, we can use our relationship to project the number of mutations (genetic diversity) lost as the geographic distribution due to habitat loss or climate change following equation:

$$x_M = 1 - \frac{M_t}{M_{t-1}} = 1 - \frac{MAR(A_t)}{MAR(A_{t-1})} = 1 - \frac{A_t^z}{A_{t-1}^z} = 1 - \left(\frac{A_t}{A_{t-1}}\right)^z = 1 - (1-x)^z$$

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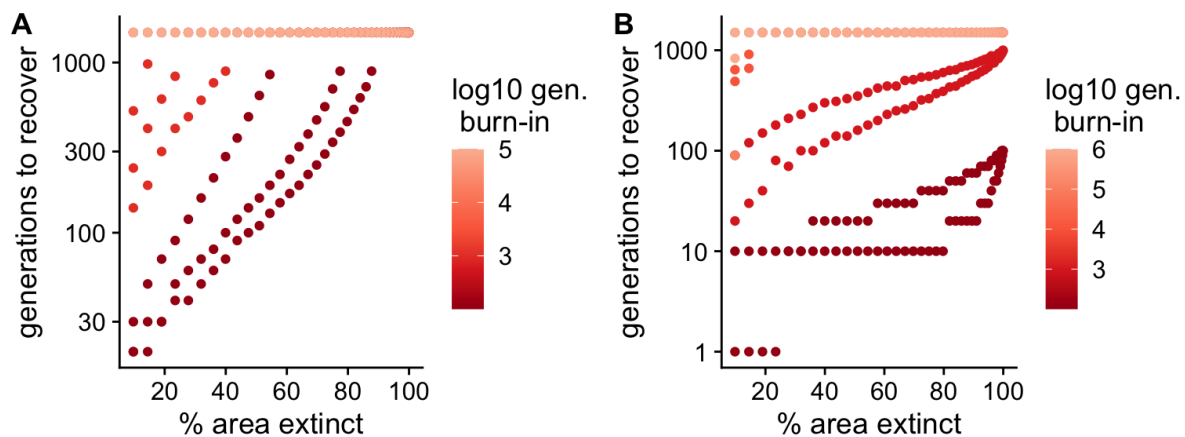
In the most extreme scenario of $z_{MAR} \approx 1$, the fraction loss of geographic area directly translates to the same fraction loss of genetic diversity.

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Reality should be in between the panmictic and fully-migration-limited cases. With combinations of environmental selection, non-equilibrium demography, and long-range dispersal, we may get intermediate z_{MAR} values, and it will be empirical estimates that can inform us how much may be lost (Section III).

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II.5 Recovery of genetic diversity after a bottleneck or local extinction



716

717 **Fig. S11 | 2D stepping-stone msprime simulations with extinction and recovery**

718 (A) Recovery of genetic diversity (number mutations) after loss of a fraction of the population. (B) Recovery of genetic
719 diversity after instantaneous loss of a fraction of the population and consecutive repopulation.

720 *Simulations with number of generations until recovery that are exceedingly large are assigned a value of 1,500, as none
721 are realistic for current conservation timelines.

722
723

724 The intuition that rapid recovery of genetic diversity may be possible is likely flawed.
725 While genetic recovery may be faster than speciation rates, which are on the order of millions
726 of years, the time for a set of populations that went through a simulation burn-in of 1,000
727 generations (not yet in diversity equilibrium), and that suffer an instantaneous 5% reduction
728 of area and an instantaneous recovery (e.g., through reforestation) would range from 20-90
729 generations. This number of generations for long-lived species would translate into centuries
730 or millennia of recovery without further impacts. About 49% of simulations – including every
731 simulation that reached equilibrium (burn-in generations >10,000) – have a recovery time of
732 more than a thousand generations (Fig. S11).

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735 SUPPLEMENTAL RESULTS

736

737 III. The mutations-area relationship with the 1001 Arabidopsis Genomes

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739 We begin testing the idea of a general mutations-area relationship using the extensive
740 sampling of the model plant species *Arabidopsis thaliana* and the 1001 Arabidopsis Genomes
741 Project (29). This section will serve as a case study to explore different approaches and biases
742 when building MAR to then apply the learned lessons across species (section IV).

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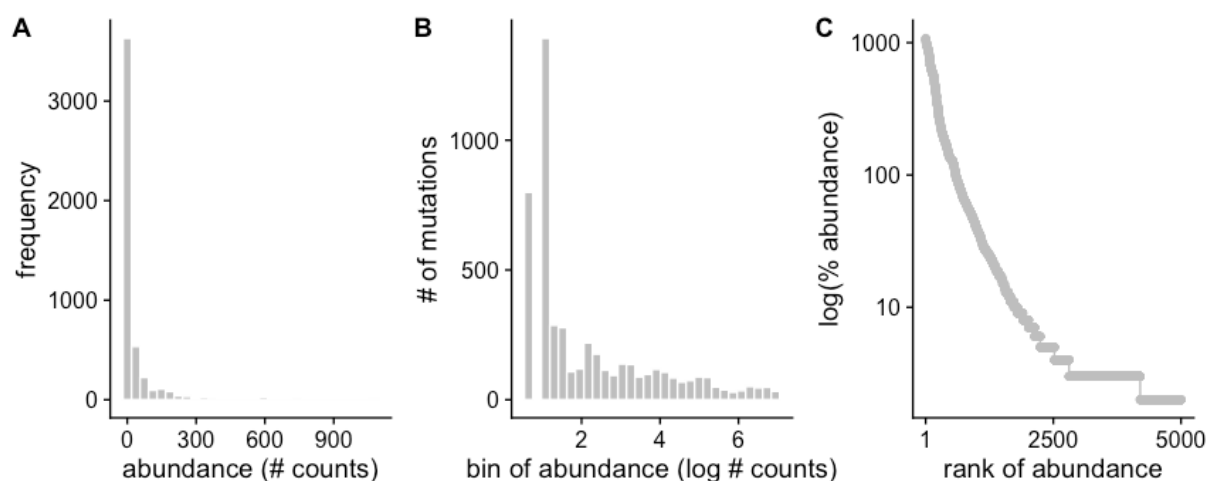
745 III.1 The Site Frequency Spectrum of the 1001 Arabidopsis Genomes

746

747 We began analyzing the frequency distribution of 11,769,920 biallelic genetic variants (i.e.,
748 mutations), which is typically called the Site Frequency Spectrum (SFS) in population
749 genetics.

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753 **Fig. S12 | Mutation abundance study in *A. thaliana***

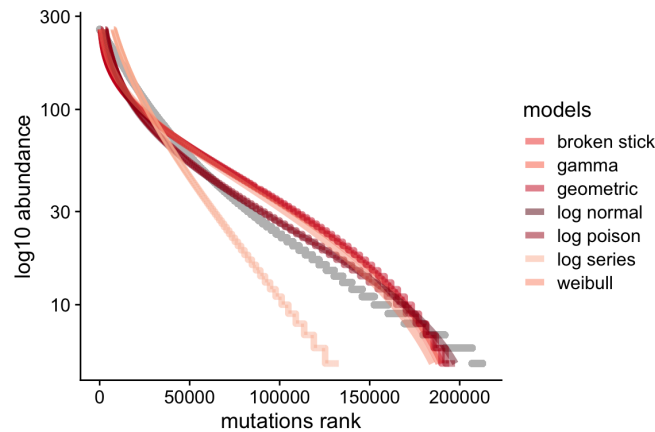
754 (A) Site Frequency Spectrum (SFS). (B) Preston plot of mutation abundances. (C) Whittaker plot of mutation rank
755 abundances.

756

757 To showcase the similarities to the Species Abundance Distributions (SAD), we use
758 the Whittaker plot of mutation rank abundance (Fig. S12) that suggests a log-normal of S-
759 shape may be the best fitting model (Table S3). For a review listing many popular models,
760 see (30), and for implementation details of 13 SAD models see the thorough manual of R
761 package SADS (31). As we shall see later, the log-normal distribution seems to be the best fit
762 across species.

763

764



765

766 **Fig. S13 | Fit of mutation abundance study in *A. thaliana* with different SAD models**

767 Representative models from Table S3 are plotted along with the observed frequency of 11,769,920 mutations.

768

769 Although model AIC captures best the fit of a curve accounting for the difference in
770 parameter complexity of each model and the statistical distributions behind, we often are
771 interested in the variance explained. We then calculated a proxy of predictive accuracy using
772 a pseudo- R^2 approach of the difference between the model fit and the observed data as:

773 $R^2 = 1 - \frac{SS_{res}}{SS_{tot}}$. For *A. thaliana*, we used 10,000 SNPs sampled at random to an accuracy of
774 over $R^2 > 0.999$ for both the top log-Normal model and the bottom log-Series model,
775 indicating that all “commonness of rarity” models must have a pretty good fit of mutation
776 frequency data.

777

778 **Table S3 | AIC values for model fit of common species distribution curves.**

779 For each SAD model, the degrees of freedom and the delta AIC compared to the top model are reported.

780

Model	dAIC	df
log-Normal	0	2
Poisson	7204.37509	2
Geometric	44267.5475	1
Weibull	45872.3678	2
Gamma	48805.6065	2
Broken Stick	49076.4368	0
UNTB (MTZSM)	168434.181	1
log-Series	168434.726	1

781

782

783 The typical SFS from population genetics is of course not implemented in current packages for Species
784 Abundance Distributions like R sads. For comparison, in the main text we also calculate the log
785 likelihood and AIC of this following the standard population genetics likelihood:

786

$$\log L = \sum_i \log\left(\frac{1}{Nq_i}\right) - \log(H_n(N-1))$$

787

788

789 where N represents the number of individuals in a sample, and q_i is the minor allele frequency of a
790 SNP in the sample, in the main text calculated for $i=1 \dots 10000$ random SNPs (see main text). As
791 before, H_n is the harmonic number function.

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III.2 Building the Mutations-Area Relationship

In the following, we explain how the area was estimated that was used to compute z_{MAR} on real world data. In short, we used a grid on the world map, with samples placed on the map based on their geo-coordinates of origin (Fig. 1). We first create square spatial subsamples of the *Arabidopsis thaliana* geographic distribution (Fig. 1, Fig. S15) and quantify diversity M as the total segregating sites. Excluding zeros, these two variables are fed to the `sars_power` function from the R SARS package (32).

Although the power law mutations-area relationship was already theoretically motivated (II.3), here we also fit different types of functions typically applied to the Species-Area Relationship. Doing this, we reach the conclusion that multiple models perform very similarly, and the classic power law is among the top models, see Table S4. Although small marginal fitting accuracy could be achieved with other models, for mathematical convenience and historical continuity, we use the power law for later sections and the study of MAR across species (Sections IV and V).

Table S4 | Different SAR curves fit to mutations.

We fit 20 different functions and calculated the variance explained (R2), Pearson's r, and Spearman's rho.

Model	R2	r	rho
Asymptotic regression	0.21825683	0.46717965	0.53510077
Beta-P cumulative	0.22012799	0.46917799	0.53374757
Chapman Richards	0	NA	NA
Cumulative Weibull 3 par.	0.21929646	0.468291	0.53374757
Cumulative Weibull 4 par.	0.21930145	0.46829633	0.53374757
Extended Power model 1	0.21833611	0.46726449	0.53026812
Extended Power model 2	0.21682584	0.46564561	0.53462775
Gompertz	0.16393078	0.40488366	0.45964364
Heleg(Logistic)	0.21929721	0.4682918	0.53531975
Kobayashi	0.22228406	0.47147011	0.53526975
Linear model	0.19579007	0.44248171	0.53510077
Logarithmic	0.20280401	0.45033767	0.53430311
Logistic(Standard)	0.22536996	0.47473146	0.53549765
Monod	0.22500999	0.47435217	0.53579276
Negative exponential	0.22801633	0.47751055	0.53447179
Persistence function 1	0.21929612	0.46829063	0.53501182
Persistence function 2	0.21760028	0.46647645	0.53409266
Power	0.21929556	0.46829004	0.53543785
PowerR	0.21753225	0.46640353	0.53493321
Rational function	0.22072491	0.46981369	0.53451874

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Because in the species literature it is recommended to only quantify richness of endemic species (33), we also count segregating sites that are private to the area subsample, creating the equivalent endemic-mutations-area relationship (EMAR) (33). The MAR slope and 95% Confidence Interval was $z = 0.324$ (0.238 - 0.41) (Table S5, Fig. S14 A), while the EMAR was $z = 1.241$ (1.208 - 1.274) (Table S6, Fig. S14 B). Interestingly, the endemics-area relationship of $z \approx 1$ resembles that of endemic species, whereas the total mutation relationship with area is above that of species relationships, which typically follows the canonical $z \approx 0.2 - 0.4$.

827 We must note that EMAR, the genetic analogy of the Endemic-(species)-Area
 828 Relationship (EAR) may not be that meaningful when analyzing genomic data (we did not
 829 find a way to theoretically motivate it in section II), and later we see it overestimates loss in
 830 our simulations (Fig. S18)

831

832 **Table S5 | The mutations-area relationship (MAR).**

833 Fitted values in a log-log power function between area sampled and mutations discovered.

	Estimate	Std. Error	t value	P	2.5%	97.5%	nls.Est.	nls.2.5%	nls.97.5%
c	494.565432	135.6314588	3.646392	0.0003138	223.3025141	765.8283493	494.5531270	278.1107276	822.829918
z	0.323727	0.0430277	7.523681	0.0000000	0.2376715	0.4097824	0.3237367	0.2430303	0.413162

834

835

836 **Table S6 | The endemic-mutations-area relationship (EMAR).**

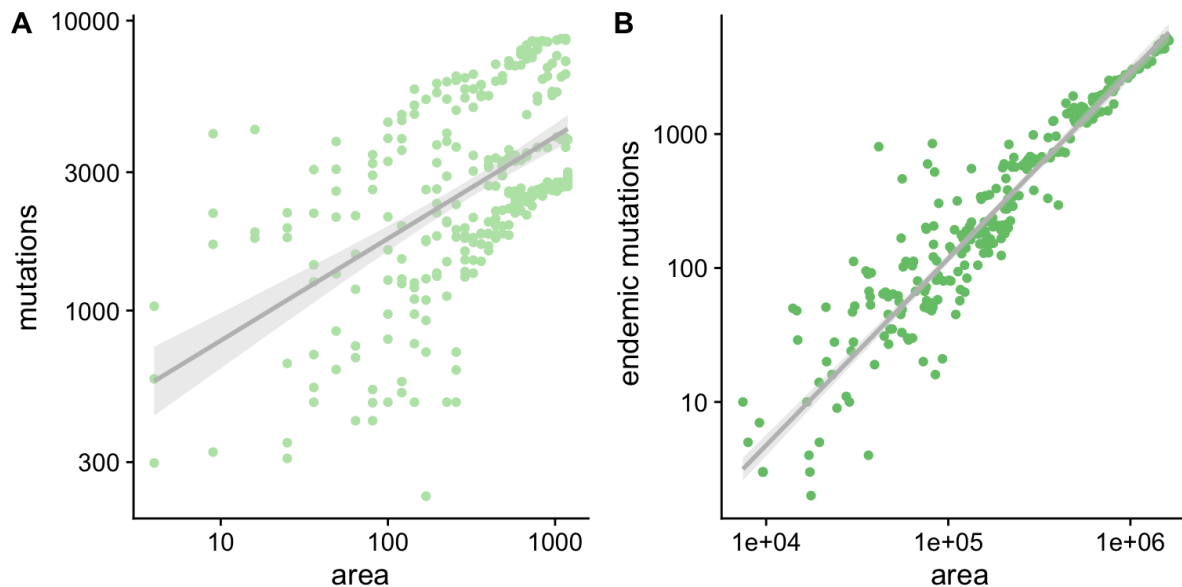
837 Fitted values in a log-log power function between area sampled and endemic mutations discovered.

	Estimate	Std. Error	t value	P	2.5%	97.5%	nls.Est.	nls.2.5%	nls.97.5%
c	0.0001001	0.0000231	4.337758	1.98e-05	0.0000539	0.0001463	0.0001001	0.0000635	0.0001555
z	1.2411831	0.0165268	75.101442	0.00e+00	1.2081296	1.2742366	1.2412125	1.2096087	1.2737927

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841

842 **Fig. S14 | The mutations-area and endemic-mutations-area relationships in *A. thaliana*.**

843 Dividing *A. thaliana* native geographic distribution into a 1 degree lat/long grid, square areas with 1 degree side-length to
 844 36 degrees side-length were randomly placed ($n=100$ for each size) across the distribution, and genetic diversity metrics
 845 were computed to produce the (A) Mutations-Area Relationship and (B) Endemic-Mutations Area relationship.

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847

848 III.3 Testing for potential numerical artefacts

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850 We wondered whether MAR estimates may be affected by some numerical artefacts in our
 851 software pipeline (available at <https://github.com/moiexpositoalonsolab/mar>). For instance,
 852 real world data may have uneven sampling in space, the spatial resolution of georeferenced
 853 samples may vary, projection of samples into gridded maps may have limited resolution,
 854 software pipelines may produce biased estimates, etc. To test this, we conducted several
 855 experiments:

856

857 **Lower bound of the method for z_{MAR} .** Our first experiment when building the MAR
858 aimed to make sure that spatial sampling, or some unknown bias in genome sequencing, or
859 the number of samples used, are not creating artificially large z_{MAR} . We then simulated a mock
860 dataset of *A. thaliana* with the same number of mutations, samples, and using the original
861 geographic locations. The number of SNPs were also sampled in a way that we created a
862 canonical $1/q$ SFS for the whole species. Under no biases, we then expect the MAR to follow
863 the theoretical derivation under panmixia with a $z \sim 0$. This exercise confirmed we get a value
864 approaching zero: $z = 0.033$, $(-0.095 - 0.162)$.
865

866 **Table S7 | MAR built with different area calculations and grid sizes**
867

Grid resolution (deg.)	z_{MAR} [CI95%] (cell area)	z_{MAR}[CI95%] (total area)
A=N	0.431 (0.423 - 0.439)	NA
0.1	0.435 (0.424 - 0.446)	0.367 (0.281 - 0.454)
0.25	0.454 (0.449 - 0.459)	0.422 (0.376 - 0.467)
0.5	0.488 (0.465 - 0.511)	0.352 (0.152 - 0.551)
1	0.543 (0.529 - 0.558)	0.389 (0.295 - 0.483)
2.5	0.644 (0.6 - 0.688)	0.388 (0.251 - 0.526)
5	0.617 (0.205 - 1.029)	0.403 (-0.204 - 1.011)

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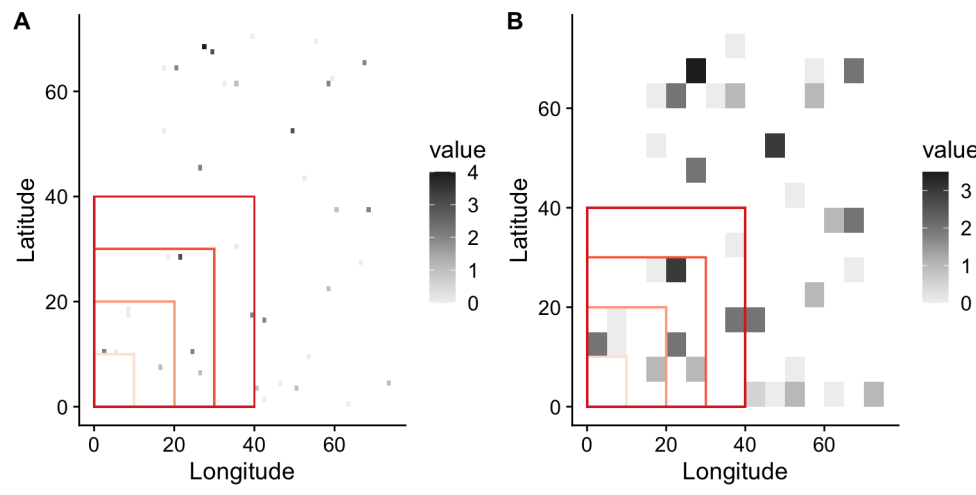
871 **Grid sizes, area calculations, and non-random spatial sampling.** In order to
872 streamline geospatial operations, we implemented the MAR relationship calculations in this
873 project using R raster objects (34). This required projecting the collected samples of a species
874 and the observations of any given mutation into a world map (i.e., each mutation's geographic
875 distribution). Necessarily, in order to be able to assign areas to sets of samples or mutations
876 on the map, the projection requires the choice of a grid size. The larger the grid size (e.g.,
877 lower spatial resolution), the faster the spatial operations can be performed. Further, for larger
878 grid sizes, we expect the slope of MAR to be more influenced by larger-scale patterns, while
879 for smaller grid sizes, the MAR will be influenced by smaller-scale patterns. To test this, we
880 repeated the subsampling of *A. thaliana* distribution with grid sizes ranging 0.1 degrees
881 latitude/longitude (roughly 10km side-length in temperate regions) to 10 degrees (roughly
882 1,000 km side-length). The estimates were roughly consistent between 0.4-0.6, but increases
883 in value at larger grid sizes (row in Table S7 for large grid size values), a scale-dependent
884 pattern that resembles results of SAR of species in ecosystems fitted at different scales (10).
885

886 Because we often have sparse samples of individuals in space, we devised two
887 strategies to calculate areas during the subsampling of MAR (see cartoon in Fig. S15): (A)
888 the total square area of the minimum and maximum latitude/longitude values of all the
889 samples analyzed. That is, simply the area of the red box in the figure. (B) the sum of areas of
890 grid cells that contain at least one sample. That is, the sum of the grey squares within the red
891 box in the figure. In addition, we also calculated the MAR relationship assuming the total
892 area is equal to the number of individuals ($A=N$) (which should be theoretically equivalent to
893 a grid of very high resolution where we end up with a maximum of one individual sampled at
894 any grid cell).
895

896 Table S7 values suggest there is a dependency of z_{MAR} with the grid size when areas
897 are calculated as the sum of grid cells with at least one sample. Our intuition for this pattern
898 is that lower resolution grids (e.g., 5 degrees side) lead to some grid cells having many
899 samples, which would increase the number of mutations discovered when discovering the

900 area. On the other hand, the calculation of z_{MAR} using the total area does not seem to affect the
 901 z_{MAR} estimate; however, because large areas often do not have samples (limiting the potential
 902 to find new mutations), it creates a higher variance in the estimate of z_{MAR} (see confidence
 903 intervals in Table S7 and Fig. S16). Here, we favored consistency of z at the expense of
 904 broader, more conservative confidence intervals. All the estimates reported below and in the
 905 main text therefore use the total area approach.

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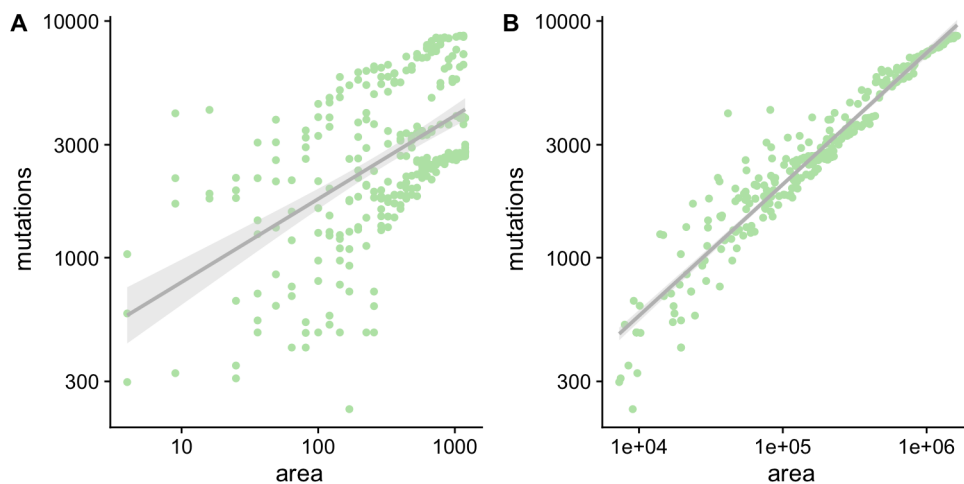


909

910 **Fig. S15 | Cartoon of raster sampling to build the MAR**

911 *Map of mock samples of a species projected into a raster. Grey scale indicates the number of samples per grid cell. Red*
 912 *boxes exemplify the process of spatial subsampling of increasing area to build the MAR relationship. Two example grid sizes*
 913 *were created for illustrative purposes: (A) Small grid size or high spatial resolution. (B) Large grid size or low spatial*
 914 *resolution.*

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918 **Fig. S16 | MAR comparison with different area calculations.**

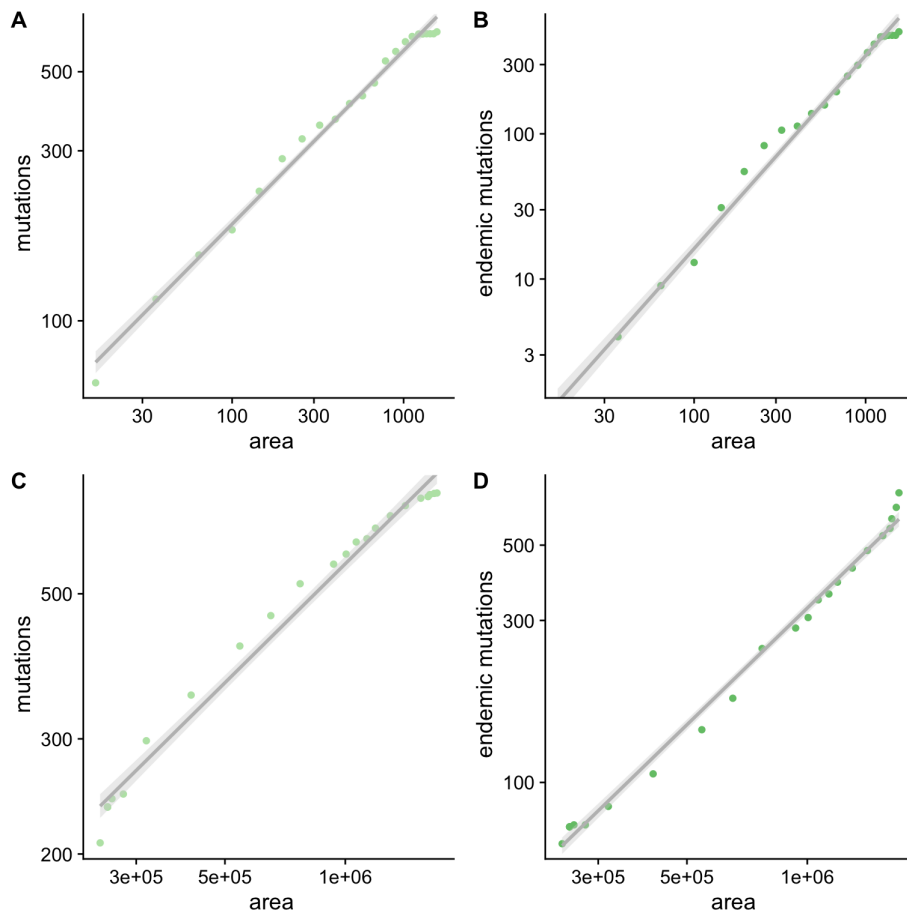
919 *(A) Using total area, (B) using grid cell sum with at least one sample. For 1 degree latitude/longitude grid cell.*

920

921 **Geographic subsampling strategy (inwards, outwards, random).** It has been
 922 indicated that the way the Species-Area Relationship (SAR) and Endemics-Area Relationship
 923 (EAR) are created may create differences in the scaling parameter z . The plots and estimates
 924 above were produced by randomly placing boxes of different size or area across the
 925 distribution of the species. Often, however, either discovery of species or extinction happen

926 in certain patterns. For instance, we often imagine sampling an ecosystem concentrically
 927 outwards from a focal point, whereas we may think of the extinction process of species
 928 reductions being concentrically inwards (33). Because these patterns seem of importance, we
 929 also calculated the MAR and EMAR outwards from the latitude and longitude median of all
 930 the samples in the map, moving outwardly until the map is filled (Fig. S17, Table S8).
 931 Likewise, the inward pattern is conducted in an inverse manner.

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936 **Fig. S17 | MAR and EMAR in *Arabidopsis thaliana* using outward and inward sampling.**

937 *Dividing *A. thaliana* native distribution in 1 degree lat/long grid, a square area of 1 degree was placed at the median of the*
 938 *sampling range and was expanded iteratively by 1 degree lat/long until all the area of the distribution was covered. (A-B)*
 939 *MAR and EMAR using a typical outward sampling. (C-D) MAR and EMAR using an inward sampling. The latter may not be*
 940 *a common process of sample collection, but it is common for extinction progress.*

941

942 **Table S8 | Outward and inward MAR and EMAR**

943 *The MAR and EMAR relationship computed with inward or outward nested subsampling, calculating area only as those*
 944 *cells with samples.*

945

Relationship	z
MAR outwards	0.444 (0.412 - 0.476)
EMAR outwards	1.086 (0.982 - 1.189)
MAR inwards	0.561 (0.524 - 0.597)
EMAR inwards	1.295 (1.192 - 1.399)

946

947

948 **Incomplete sampling of the species.** To check whether the relationship holds with
949 few individuals of a species or limited geographic distributions, we compared the species-
950 wide MAR with that of subset populations. Downsampling the native distribution of *A.*
951 *thaliana* to a region within North-East Spain (-2.00–4.25 degrees East, 36.52–42.97 degrees
952 North), or to a region within Germany (2.69–13.73 degrees East, 50.0–52.0 degrees North),
953 and using only 1,000 SNPs, we recovered $z_{MAR} = 0.423(0.233-0.614)$ for Spain and
954 $0.525(0.242-0.807)$ for Germany, which were close to the estimate based on the whole
955 distribution (Table 1). This result is reassuring in that if migratory patterns are relatively
956 homogeneous, one may be able to estimate this parameter from a subset of the species
957 distribution. For heterogeneous population structure cases, we expect incomplete sampling to
958 produce unreliable estimates.

959
960 **Number of genome-wide SNPs used.** To check whether different numbers of SNPs
961 used for the analyses would lead to different z_{MAR} , we conducted analyses with random
962 subsets consisting of 100, 1,000, and 10,000 SNPs, replicated 3 times. Estimates had a
963 coefficient of variation of 4.7%, which is way below the standard error of typical estimates
964 (Table 1).

965
966 **Locally-adaptive variants.** We then aimed to understand the effect of utilizing SNPs
967 that appear to be related to adaptation. To study this, we utilized an outdoor climate-
968 manipulated experiment that recorded fitness data (survivorship and reproduction output of
969 seeds) for 515 *Arabidopsis thaliana* ecotypes part of the 1001 Genomes set in 8 environments
970 (Exposito-Alonso, 2019). We devised two sets of alleles: 10,000 that were negatively
971 correlated with fitness in a Genome-Wide Association across 8 different environments, and
972 10,000 alleles that were associated positively with fitness in one environment but negatively
973 in another (antagonistic pleiotropic). The MAR relationship was computed as before and
974 compared to the original random (putatively neutral) set of alleles from the previous sections
975 (Table S9). Although we see a trend that locally-adaptive alleles have a slightly higher z ,
976 estimates overlap. The effects seen here of having smaller z for adaptive alleles than neutral
977 variation could, however, be due to top GWA SNPs often being ascertained to higher
978 frequency than background SNPs.

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980

981 Table S9 | MAR for putatively neutral, deleterious, and locally adaptive alleles in *Arabidopsis thaliana*
982

SNP set	z
neutral	0.324 (0.238 - 0.41)
globally deleterious	0.209 (0.13 - 0.288)
locally adaptive	0.291 (0.217 - 0.365)
globally positive	0.234 (0.137 - 0.332)

983

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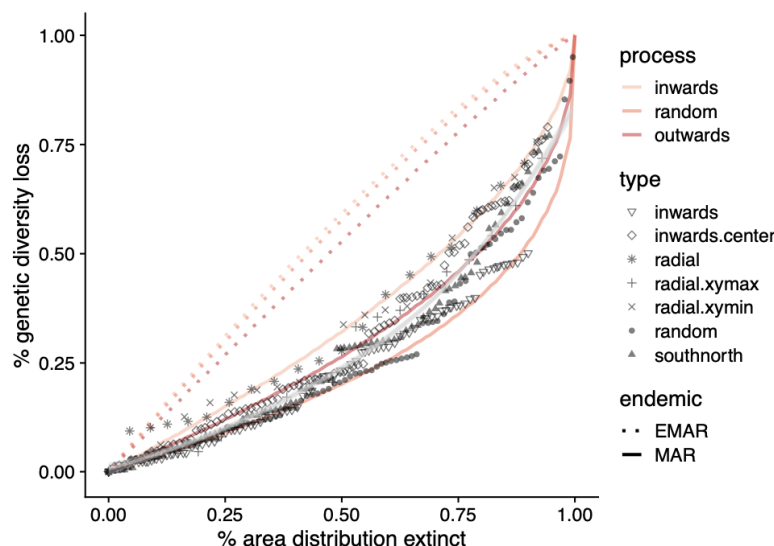
985 III.4 Local population extinction in *Arabidopsis*

986

987 Using the MAR framework, we can make projections of loss of mutations (or its inverse, the
988 remaining genetic diversity. By doing this, the known intuition is that with $z > 1$ (as from
989 EMAR) the decrease of diversity is much faster than the decrease of habitat, but with $z < 1$
990 (as from MAR), there is a (desirable) slower dynamics of genetic loss. In the latter, despite
991 habitats disappearing, reservoirs of mutations distributed across different locations enable
992 conservation of certain variation. To study which one is more likely and to observe the

993 stochastic nature of genetic diversity loss, we simulated in silico population extinctions of
 994 map cells from the Arabidopsis map (Fig. 1) and directly estimated from the genome matrix
 995 of remaining individuals the remaining genetic diversity. These simulations were
 996 implemented to capture different hypothesised patterns of extinction (see main text). All,
 997 however, agree with the more hopeful estimate of $z_{MAR} \approx 0.3$.

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1001

1002 **Fig. S18 | Loss of mutations with habitat loss in *A. thaliana*.**

1003 Predictions based on MAR and EMAR functions and in silico extinction stochastic simulations in *A. thaliana*.

1004

1005 To study the fit of the genetic loss predictions based on MAR relationships and the
 1006 results from computer simulations, we calculated a pseudo- R^2 based on the squared
 1007 differences between the predicted line and the “observed” genetic loss as: $R^2 = 1 - \frac{SS_{res}}{SS_{tot}}$.
 1008 This results in a high fit $R^2=0.872$ of the MAR, built from random samples of distribution
 1009 areas, while the EMAR had a poor fit due to overestimation of genetic loss: $R^2=-0.710$
 1010 (negative values indicate predictions are worse than the mean of the data).

1011

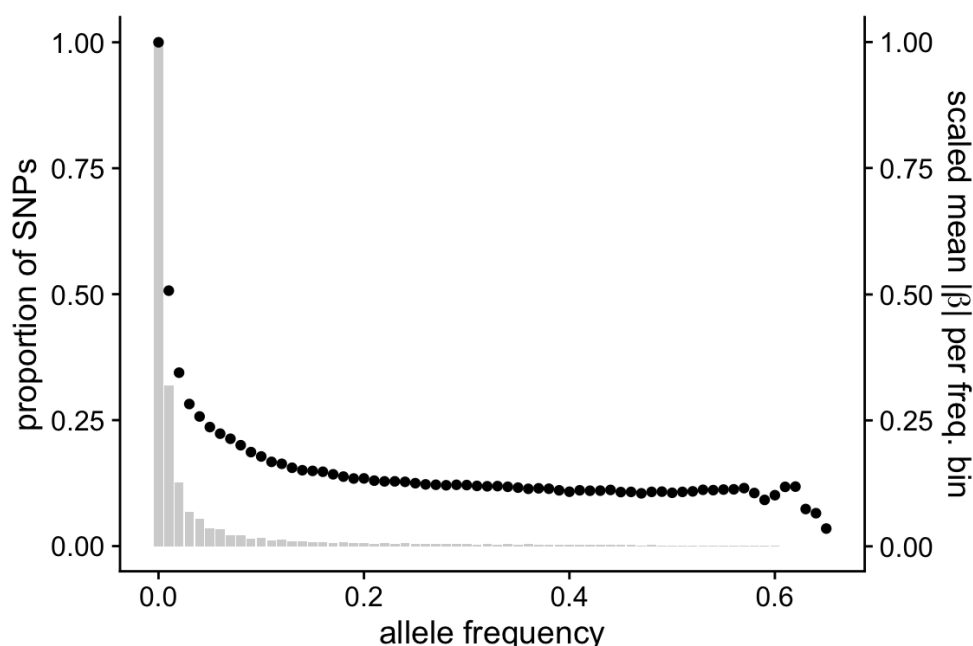
1012

1013 **III.5 Potential impacts of genetic loss in adaptability**

1014

1015 Although likely imperfect, Genome-Wide Associations could help to understand the
 1016 relevance of mutations in different frequency classes in model organisms such as *Arabidopsis*
 1017 *thaliana*. Fig. S19 shows the site frequency spectrum and a metric of the "total accumulated
 1018 effect in fitness" of the alleles in every bin. Effect sizes were retrieved from GWA on lifetime
 1019 fitness of 515 ecotypes in outdoor experiments (35). The average effect size across 8 fitness
 1020 GWA from 8 experimental combinations were used: high/low precipitation, high/low latitude
 1021 of outdoor stations, and high/low plant density. This exercise showcases the phenomenon that
 1022 low frequency variants often have strong effect sizes, which is expected under a stabilising
 1023 selection quantitative model (36). Because low frequency alleles will be the first to be lost
 1024 during a bottleneck (as would happen with the rapid extinction of populations of a species),
 1025 we may expect to lose variants that are related to fitness and thus potentially lose diversity
 1026 that could be advantageous in some environments. Alternatively, deleterious mutations are
 1027 also expected to be at low frequency, in which case would also make them more easily lost.

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1031 **Fig. S19 | Bias of low frequency mutations and effect size for fitness traits in *A. thaliana*.**

1032 *Grey bars represent the site frequency spectrum (scaled for visualisation purposes). The black dots represent the mean*
1033 *absolute effects of alleles as estimated from GWAs with 515 accessions scored for fitness traits in 8 outdoor experiments.*

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1045

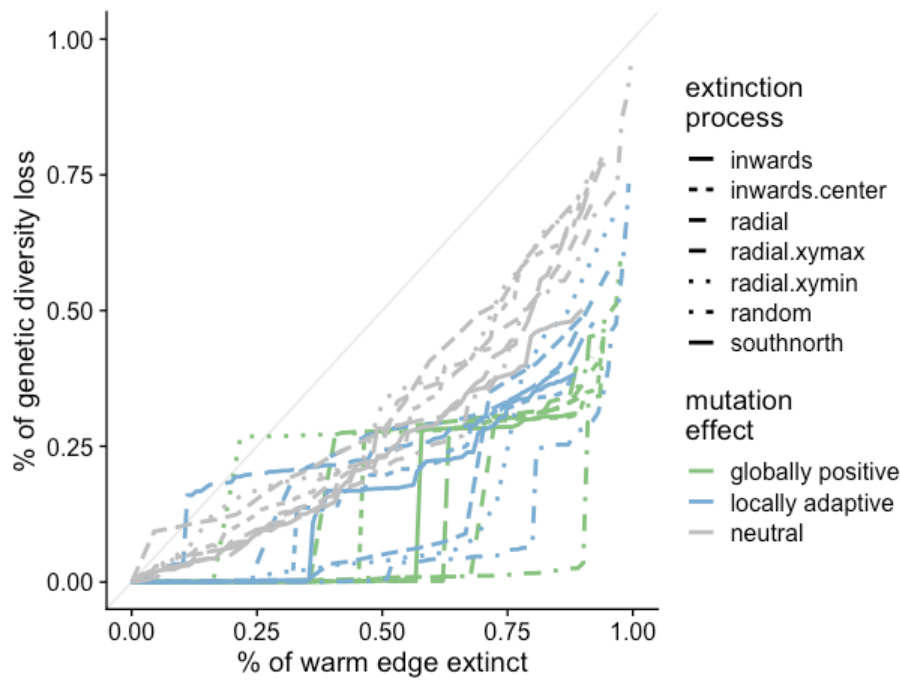
1046

1047

1048

1049

To further build intuition on the progress of extinction in relation to loss of genetic diversity that is not neutral, we repeated warm edge extinction simulations with several subsets of alleles: randomly selected SNPs, SNPs that were associated positively in 2 environments (low precipitation Spain and high precipitation Germany) (labelled globally positive), and SNPs that were associated positively in one environment and negatively in the other (labelled antagonistic pleiotropic or putatively locally-adaptive). This (Fig. S20) supports our intuition that although putatively functional alleles (or alleles tightly linked to such functional ones) may have slower loss dynamics than neutral variants due to a high frequency and z_{MAR} , certain population extinction patterns may actually lead to rapid loss of potentially-adaptive genetic diversity. The complexity of these patterns, together with the evolutionary feedback created by lowering genetic standing variation that affects fitness, make the inference of adaptive capacity loss even more difficult than just inferring the loss of genetic diversity itself.



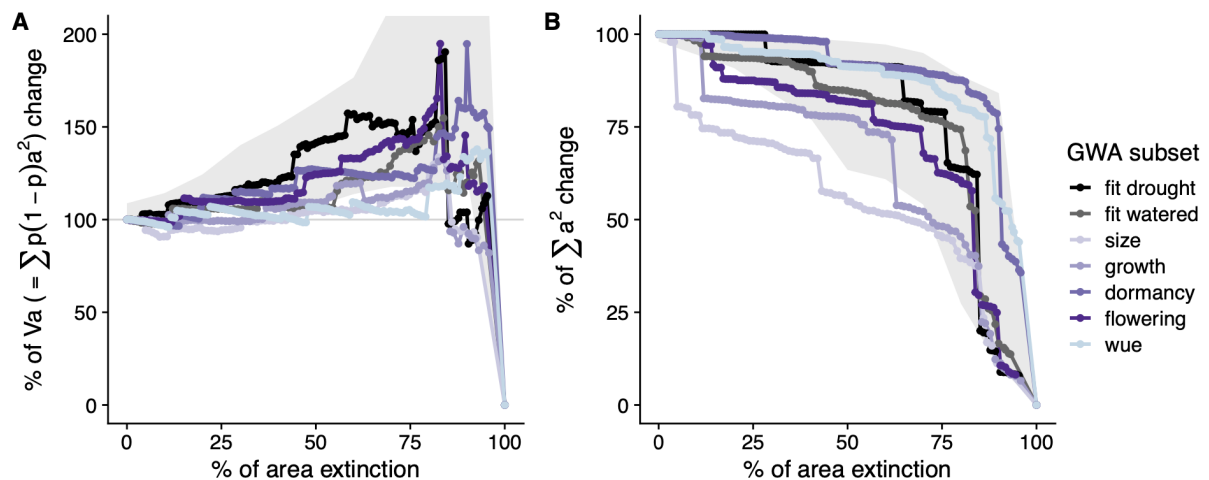
1050

1051 **Fig. S20 | Simulations illustrating the potential loss of locally-adaptive mutations in *A. thaliana*.**

1052 Simulations of extinction using multiple patterns of population losses with different subsets of alleles ascertained to show
 1053 positive associations in fitness GWA in two outdoor experiments (green), positive associations in one environment (e.g. low
 1054 precipitation) but negative in a second environment (e.g. high precipitation) or vice versa (green). These were compared to
 1055 a random set (grey).

1056

1057



1058

1059 **Fig. S21 | Extinction simulations showing proxies of adaptive capacity of *A. thaliana*.**

1060 Using estimated allele effect sizes from 10,000 SNPs in the 1% P-value tails of several Genome-Wide Associations, we show
 1061 (A) Percentage of change of V_a as a proxy of adaptive potential and (B) raw square sum of allele effects to showcase the
 1062 inflating effect of intermediate frequency alleles. Grey background shape indicates the minimum and maximum boundaries
 1063 of trajectories created by replicated frequency-matched non-effect sets of SNPs (one per GWA). The trajectories of some
 1064 effect alleles appear to show faster loss than the non-effect background trajectories.

1065

1066

1067 III.6 Case study of a massive natural bottleneck

1068

1069 A recent colonisation of North America by *Arabidopsis thaliana* can help us understand the
 1070 recovery of genetic variation. Whole-genome sequencing of 100 specimens of North
 1071 American *A. thaliana* indicates that it migrated from its native range of Europe to North

1072 America in the 17th century, and began spreading across the continent from a genetically-
1073 homogeneous population (37). Despite ideal conditions to re-gain genetic diversity—a
1074 continental population expansion aided by human travel (38, 39)—only ~8,000 new
1075 mutations were detected through spontaneous accumulation, equivalent to only ~0.067% of
1076 the species-wide native genetic diversity. Because most of these mutations are at very low
1077 frequency, as expected during population expansion, the scaling of genetic diversity with area
1078 is approximately 1 ($z_{MAR} = 1.025$ [CI95%: 0.878 - 1.173]).
1079
1080
1081

1082 **IV. The mutations-area relationship in diverse species**

1083

1084 Every dataset was retrieved online either from the published article in the form of VCF or
1085 fastq files, or provided by the study authors upon request. All datasets were first transformed
1086 into PLINK files using PLINK v1.9 (40). For computational efficiency, and since we showed
1087 random subsampling does not appear to affect calculations of z_{MAR} (Section III.3), we
1088 conducted all analyses with up to 10,000 randomly selected SNPs for each species sampled
1089 genome-wide, or in the largest chromosome for those species with large genomes. We aim to
1090 use mostly unfiltered SNP datasets to avoid ascertainment biased toward intermediate
1091 frequency SNPs, and therefore we did not apply a MAF filter for any analyses. By default,
1092 PLINK transforms SNP matrices into biallelic (if multiallelic, it takes the two most common
1093 alleles). Although the preservation of structural genetic variation may also be relevant and
1094 may have important consequences in adaptation (41), we do not expect dramatic differences
1095 in their scaling relationship compared to biallelic SNPs, as their SFS are relatively similar
1096 (Structural variants may show a skew to lower frequency, resulting in steeper z_{MAR} . By
1097 excluding those, our analyses may be conservative). In order to properly characterise the
1098 geographic distribution of a mutation using all available geo-tagged individuals, we filtered
1099 for genotyping rate (plink --geno), and the final value is reported per dataset.

1100

1101 Details for dataset processing or homogenization are described below.

1102

1103 - The 1001 Arabidopsis Genomes Consortium (29) generated a WGS Illumina
1104 sequencing dataset of *Arabidopsis thaliana* comprising 1,135 individuals and
1105 11,769,920 SNPs. The VCF with the data is available at: <https://1001genomes.org>.
1106 The raw sequencing data is available at
1107 <https://www.ncbi.nlm.nih.gov/bioproject/PRJNA273563>. These included recently
1108 colonised regions such as North America or Japan. Analyses of z_{MAR} were calculated
1109 only for the native range, which comprises most of the species diversity (>99%) and
1110 1001 individuals. For computational efficiency, we conducted analyses using
1111 randomly sampled SNPs from chromosome 1, as we did not observe any difference
1112 when sampling from other chromosomes. A number of MAR approaches were tested
1113 in this species (section III). For homogeneity, the final reported estimate (Table 1)
1114 was conducted following the same procedures as other species with a random sample
1115 of 10,000 SNPs.

1116

1117 - Lucek & Willi (42) recently published a dataset of WGS Illumina sequencing 108
1118 *Arabidopsis lyrata* individuals from North America, which the authors directly shared
1119 as a VCF. The raw data is available at
1120 <https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJEB30473>. We retrieved the
1121 latitude/longitude data from the supplemental material. We applied a genotyping rate
1122 filter ending with a dataset of 0.955431 genotyping rate. 10,000 SNPs were subsetted
1123 at random from the genome-wide data.

1124

1125 - Kreiner et al. (43) WGS Illumina sequenced 165 individuals of *Amaranthus*
1126 *tuberculatus*. The raw data is available in the link
1127 <https://www.ebi.ac.uk/ena/browser/view/PRJEB31711>. The authors provided a VCF.
1128 Overall, 155 individuals contained latitude and longitude information and were kept
1129 for the analyses. The genotyping rate was 0.98162 and we subsetted randomly 10,000
1130 SNPs.

1131

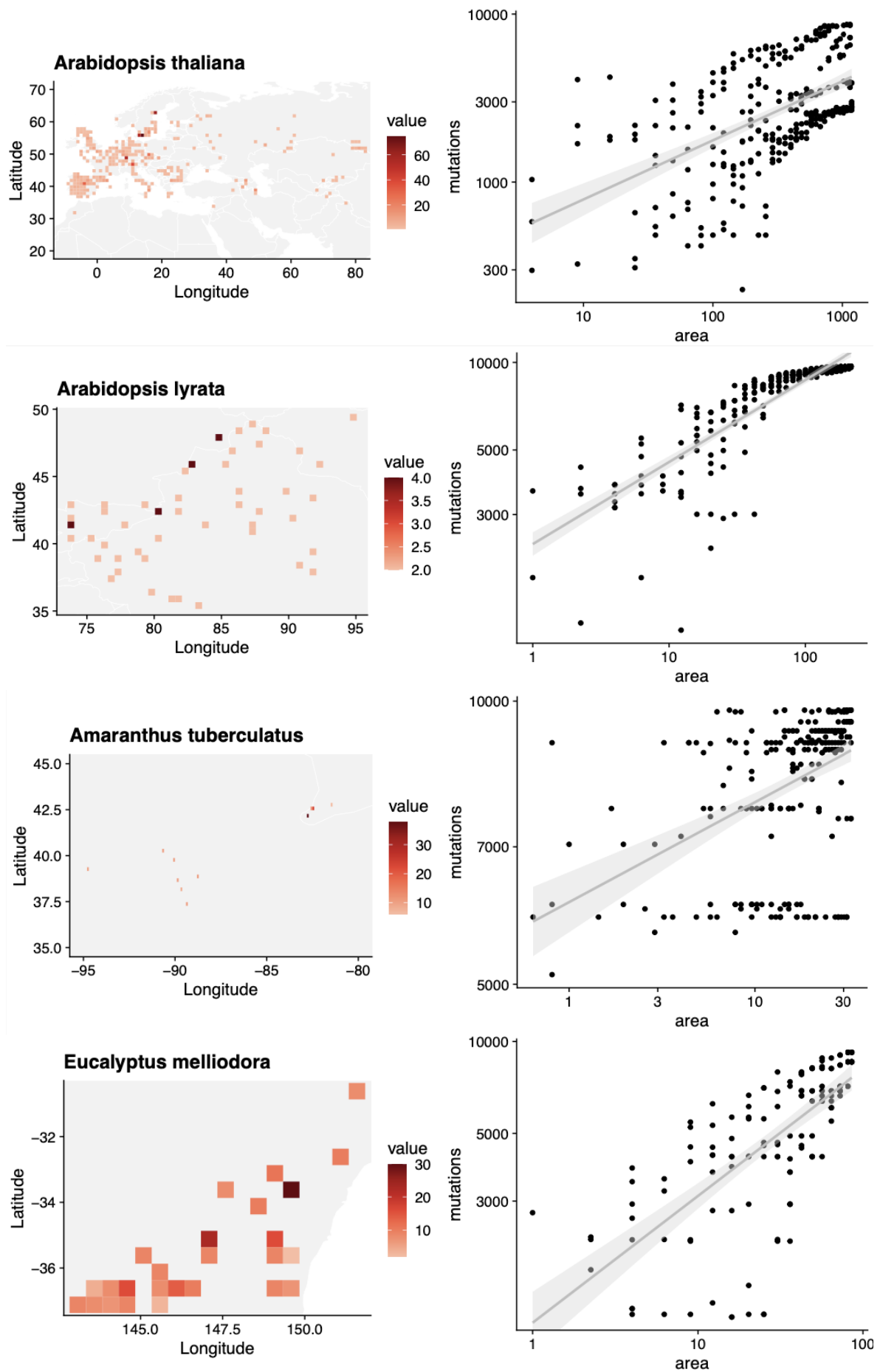
- 1132 - Supple et al. (44) generated a dataset of *Eucalyptus melliodora* of 275 individuals
1133 from 36 broadly distributed populations. The dataset was produced by Illumina
1134 sequence Genotyping-by-Sequencing (GBS) libraries digested with ApeKI as in
1135 Elshire et al. (2011). The raw data is available at
1136 <https://www.ncbi.nlm.nih.gov/bioproject/PRJNA413429/>. The authors provided the
1137 dataset in PLINK format. Genotyping rate was 0.769807 but we did not apply a
1138 further filter to avoid reducing the total number of variants. We conducted analyses
1139 with all 9378 SNPs. The genotyping rate in this dataset is likely not problematic as the
1140 total number of GPS locations is 36, with multiple individuals sampled closely. This
1141 sampling scheme probably allows to characterise an allele's distribution correctly
1142 despite the lower genotyping rate.
1143
- 1144 - Vallejo-Marin et al. (45) generated a GBS dataset of 521 *Mimulus* plants, with 286
1145 samples being *Mimulus guttatus* from its native distribution. Libraries for
1146 Genotyping-By-Sequencing were prepared with PstI enzyme as described in Twyford
1147 & Friedman (2015) and sequenced using Illumina. The VCF of this dataset is
1148 available at <http://hdl.handle.net/11667/168> and was also directly shared by the
1149 authors. After applying a filtering for missingness, we ended up with a genotyping
1150 rate of 0.904192 and 1,498 SNPs, which were used for the analyses.
1151
- 1152 - Lovell & MacQueen (46) generated a WGS Illumina sequencing dataset of
1153 Switchgrass, *Panicum virgatum*, of a collection of 732 individuals and 33,905,044
1154 variants. The raw data is available at:
1155 <https://www.ncbi.nlm.nih.gov/bioproject/PRJNA622568>. The authors provided a
1156 VCF file and latitude/longitude tables. 576 individuals were from natural collections.
1157 The dataset contains also other collections such as cultivars, which were not used to
1158 build the MAR. The genotyping rate was 0.976393 and analyses were conducted with
1159 10,000 SNPs drawn from the largest chromosome.
1160
- 1161 - MacLachlan et al. (47) generated a SNP chip dataset of *Pinus contorta* comprising
1162 929 trees with latitude and longitude information and 32,449 SNPs. Genotyping was
1163 conducted with the AdapTree lodgepole pine Affymetrix Axiom 50,298 SNP array
1164 and data was provided in the supplemental material of the paper along with custom
1165 scripts to parse the data. The database is available at
1166 <https://datadryad.org/stash/dataset/doi:10.5061/dryad.ncjsxkstp>. The genome matrix
1167 was transformed into PLINK. The genotyping rate was 0.959146, and analyses were
1168 conducted with 10,000 randomly drawn SNPs. The fact that this dataset was created
1169 with ascertained SNPs likely generates a frequency bias. In Fig. S22, one can see that
1170 this may be a problem to calculate z_{MAR} , as the mutations~area graph appears
1171 nonlinear and rapidly saturates. This confirms the expectation that SNPs are
1172 ascertained to be common, as they are discovered immediately with very few samples.
1173
- 1174 - Tuskan et al. (48) WGS Illumina sequenced 882 *Populus trichocarpa* trees. The
1175 dataset includes 28,342,826 SNPs. The data is available under this DOI
1176 <https://doi.ccs.ornl.gov/ui/doi/55> which redirects to a globus data sharing platform.
1177 The authors provided the dataset as a VCF along with latitude/longitude coordinates.
1178 This dataset was downsampled to the first chromosome. The genotyping rate was
1179 0.921191, and 10,000 SNPs were randomly sampled for analyses.
1180

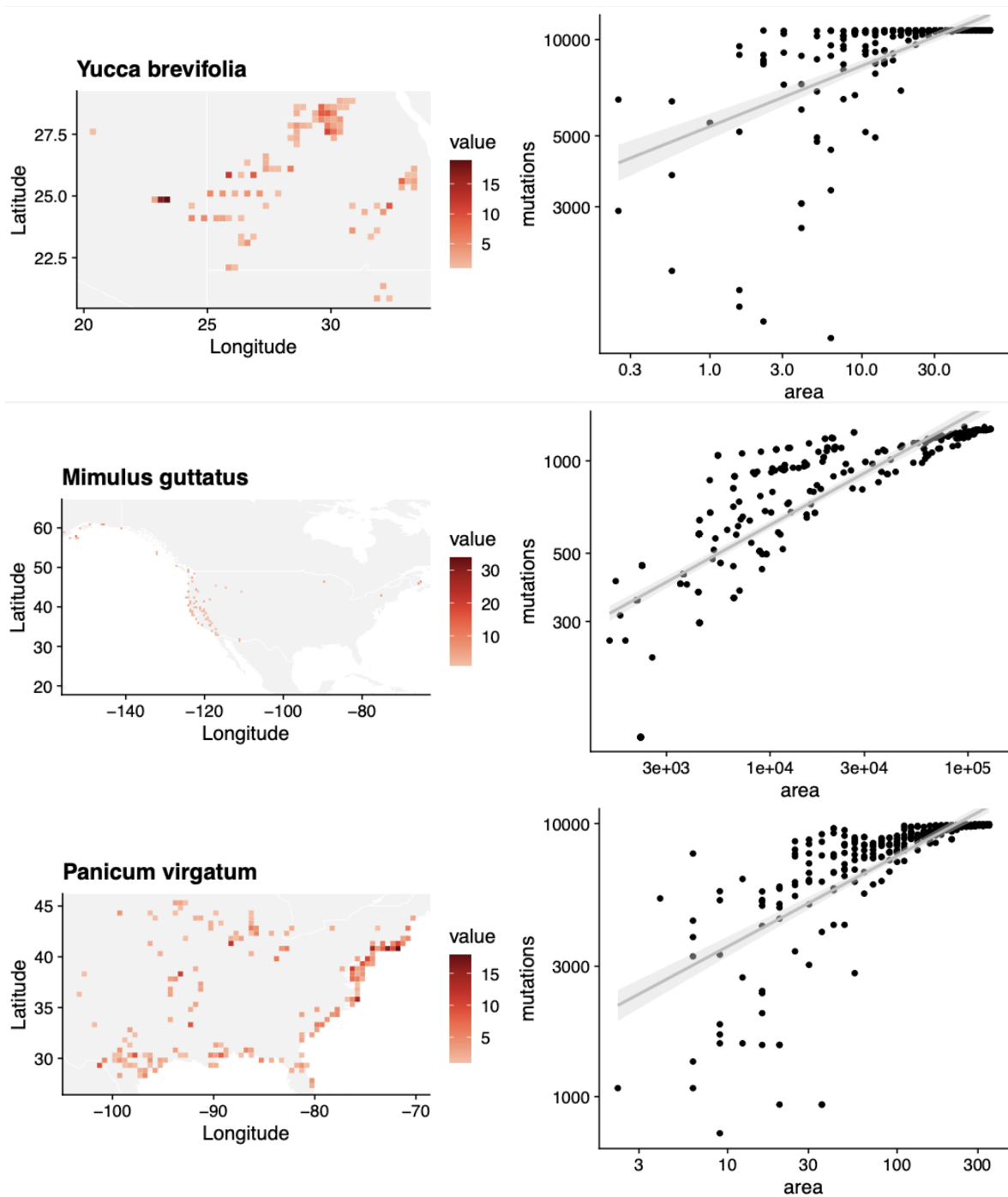
- 1181 - The Anopheles gambiae 1000 Genomes Consortium (49) (Phase 2) produced Whole-
1182 Genome Illumina sequencing data for 1142 wild-caught mosquitoes of *Anopheles*
1183 *gambiae*. All raw and processed data are available through
1184 <https://www.malariagen.net/data>. We downloaded a VCF and latitude/longitude
1185 coordinate files. The VCF was filtered for genotyping rate ending up at a 0.998895
1186 rate. For efficiency, 10,000 randomly-selected SNPs from the VCF of the largest
1187 chromosome 2L were used for analyses downstream.
1188
- 1189 - Fuller et al. (50) WGS Illumina sequenced 253 coral individuals of *Acropora*
1190 *millepora* in 12 reefs. The dataset was downloaded as fastq files from the published
1191 online material from <https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA593014>,
1192 and SNPs were called as described in the supplemental material ending with
1193 17,931,448, which were filtered to achieve a genotyping rate of 0.935709 for a total of
1194 2,512 SNPs, which were used in the analyses.
1195
- 1196 - Ruegg et al. (51) generated a dataset of 219 birds *Empidonax traillii*, for which 199
1197 could be matched with geographic coordinates. SNPs were ascertained from several
1198 publications using RAD seq and Fluidigm 96.96 IFC described and available in their
1199 repository <https://github.com/eriqande/ruegg-et-al-wifl-genoscape>. A total of 349,014
1200 SNPs were parsed using their custom scripts and we transformed them into PLINK
1201 files. A genotyping rate filter was applied ending with a 0.96061 rate and 195,700
1202 SNPs. 10,000 SNPs were selected at random for downstream analyses. Similarly, as
1203 with the *Pinus contorta*, the incorporation of some ascertained SNPs in the dataset
1204 based on Fluidigm technology could lead to quick saturation of the MAR curve (Fig.
1205 S22).
1206
- 1207 - Bay et al. (52) generated a dataset of 199 *Setophaga petechia* birds using a Restriction
1208 site-associated DNA sequencing (RAD-Seq). The raw data is available at
1209 <https://www.ncbi.nlm.nih.gov/bioproject/421926>. The authors shared a VCF file, with
1210 a genotyping rate of 0.962419 and a total of 104,711 SNPs. 10,000 SNPs were
1211 selected at random for downstream analyses.
1212
- 1213 - Kingsley et al. (53) produced a dataset of 80 *Peromyscus maniculatus* deermice, for
1214 which 78 could be matched with geographic locations. The SNP dataset was produced
1215 using MY-select capture followed by Illumina sequencing. The VCF and PLINK files
1216 are available via Figshare at <https://doi.org/10.6084/m9.figshare.1541235>. The dataset
1217 included a total of 14,076 variants which were filtered to achieve a genotyping rate of
1218 0.940411 for 2,946 SNPs, which were used in subsequent analyses.
1219
- 1220 - We identified two published datasets for wolves. Smeds et al. (54) produced a WGS
1221 Illumina sequencing dataset and combined it with pre-existing datasets for a total of
1222 349 local dog breeds and wolves, of which 230 were *Canis lupus* from natural
1223 populations. However, these samples did not have GPS locations assigned. The
1224 second dataset we identified was from Schweizer et al. (55), which contained 107
1225 geo-tagged grey wolves from North America using a capture and resequencing
1226 approach for 1040 genes. The raw data is available at
1227 <https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP065570>, and meta-data along
1228 with a VCF area available at <https://doi.org/10.1111/mec.13467>. This data contained
1229 13,092 SNPs at 0.993061 calling rate, and a better geographic resolution. We report
1230 data for the second dataset.

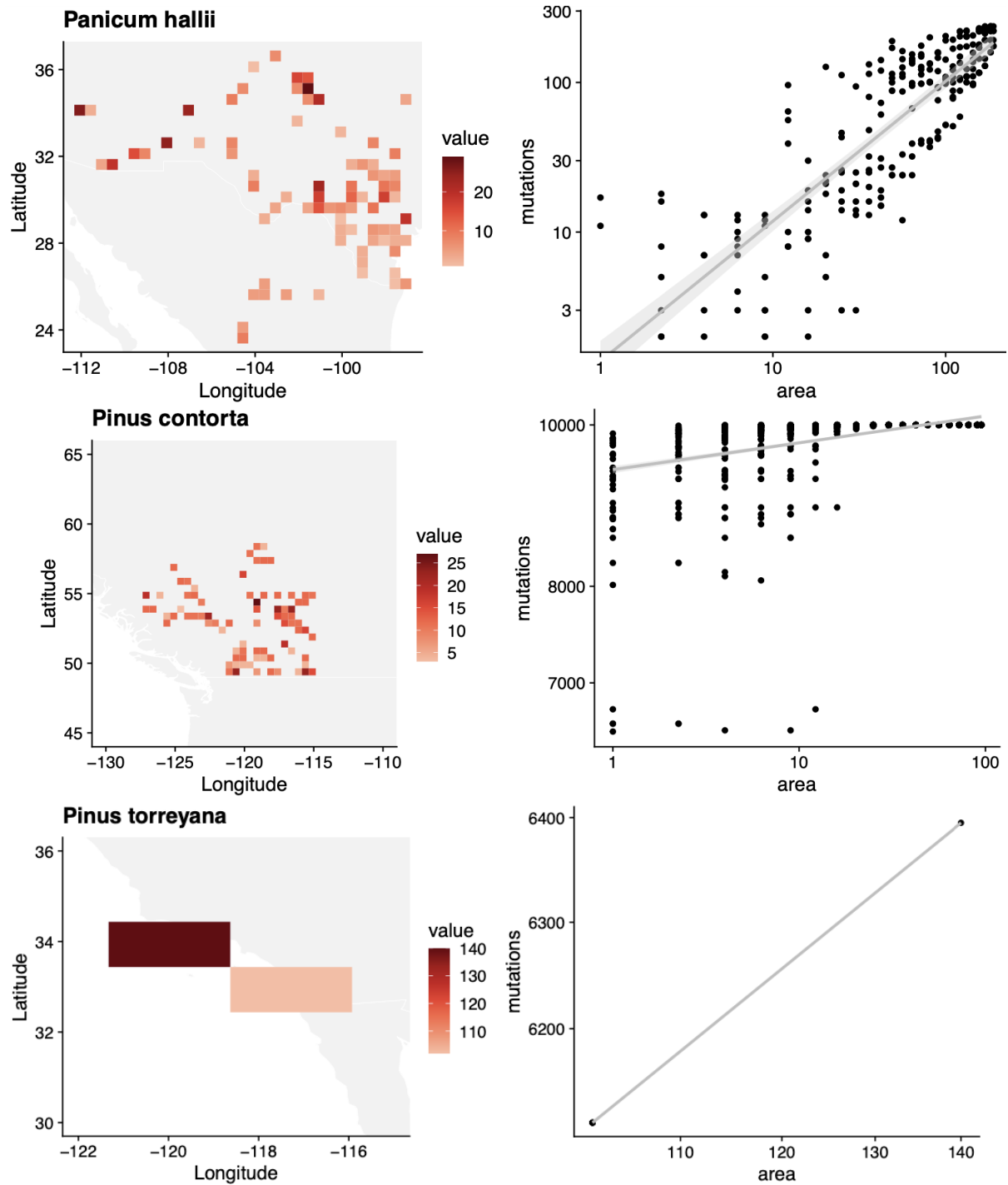
- 1231
1232 - The 1000 Genome Consortium (56) created WGS Illumina sequencing for over 2,504
1233 humans and 24 unique geographic locations. We downloaded chromosome 1 from
1234 [http://ftp.1000genomes.ebi.ac.uk/vol1/ftp/datacollections/
1235 1000G2504highcoverage/working/20190425NYGCGATK/](http://ftp.1000genomes.ebi.ac.uk/vol1/ftp/datacollections/1000G2504highcoverage/working/20190425NYGCGATK/) and gathered the
1236 population locations from [https://www.internationalgenome.org/data-
1237 portal/population](https://www.internationalgenome.org/data-portal/population). To conduct analyses, we subsampled 10,000 SNPs at genotyping
1238 rate 0.991069.
1239
1240 - Palacio-Mejia (57) used WGS for 591 *Panicum hallii* individuals to sequence at low
1241 coverage. The raw data is available at
1242 <https://www.ncbi.nlm.nih.gov/bioproject/PRJNA390994>. The authors shared an
1243 unfiltered VCF of 45,589 SNPs. Because of the low-coverage, stringent filters of
1244 calling rates as used for other species would lead to removing all SNPs, and we settled
1245 on a genotyping rate of 0.825824 for 242 variants, all of which were used for
1246 downstream analyses.
1247
1248 - Royer et al. (58) produced a SNP dataset using RAD-Seq based Genotyping-By-
1249 Sequencing of 290 *Yucca brevifolia* (Joshua Tree) individuals. A total of 10,695 SNPs
1250 with a genotyping rate of 0.897501 were used for the analyses. The data was available
1251 at Dryad <https://datadryad.org/stash/dataset/doi%253A10.5061%252Fdryad.7pj4t>.
1252
1253 - Kapun et al. (59) produced a WGS dataset of pooled *Drosophila melanogaster*,
1254 sequencing ~80 pooled individuals from each of 271 populations as part of the
1255 European "Drosophila Evolution over Space and Time" (DEST) project. A total of
1256 5,019 shared SNPs with a genotyping rate of 0.937697 were used for analyses. The
1257 dataset, both raw and processed, is available through <https://dest.bio>.
1258
1259 - Di Santo et al. (60) studied the highly-threatened species *Pinus torreyana*. They used
1260 Genotyping-by-Sequencing of 242 individuals of the last remaining populations. The
1261 dataset is not yet available through NCBI but the authors kindly shared a VCF directly
1262 with us. From a total set of 166,564 SNPs with a genotyping rate of 0.964632, 10,000
1263 were randomly selected for our analyses.
1264
1265 - von Seth et al. (61) studied the highly-threatened species *Dicerorhinus sumatrensis*.
1266 They used Illumina WGS of 16 individuals of the last remaining populations. The raw
1267 data is available at <https://www.ebi.ac.uk/ena/browser/view/PRJEB35511>. The
1268 authors shared a VCF. In total, this comprises a set of 8,870,513 SNPs, with a
1269 genotyping rate of 0.854862, which we did not further filter due to the small number
1270 of individuals. For computational efficiency we selected 10,000 SNPs from the largest
1271 chromosome.
1272

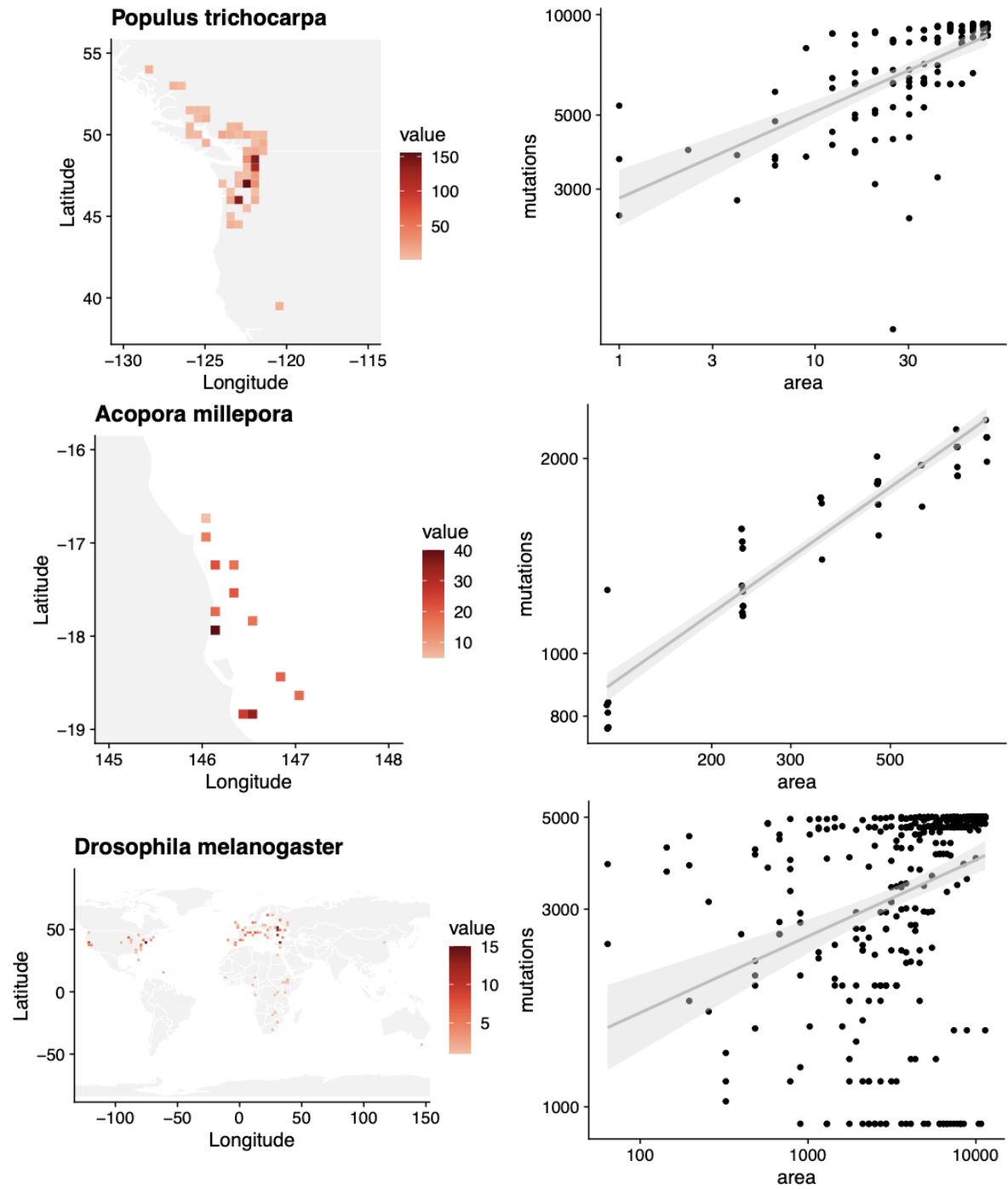
1273 Information and results per species are gathered in Table 1 and its extended version, Table
1274 S10, and the average z_{MAR} across species are provided in Table S11.

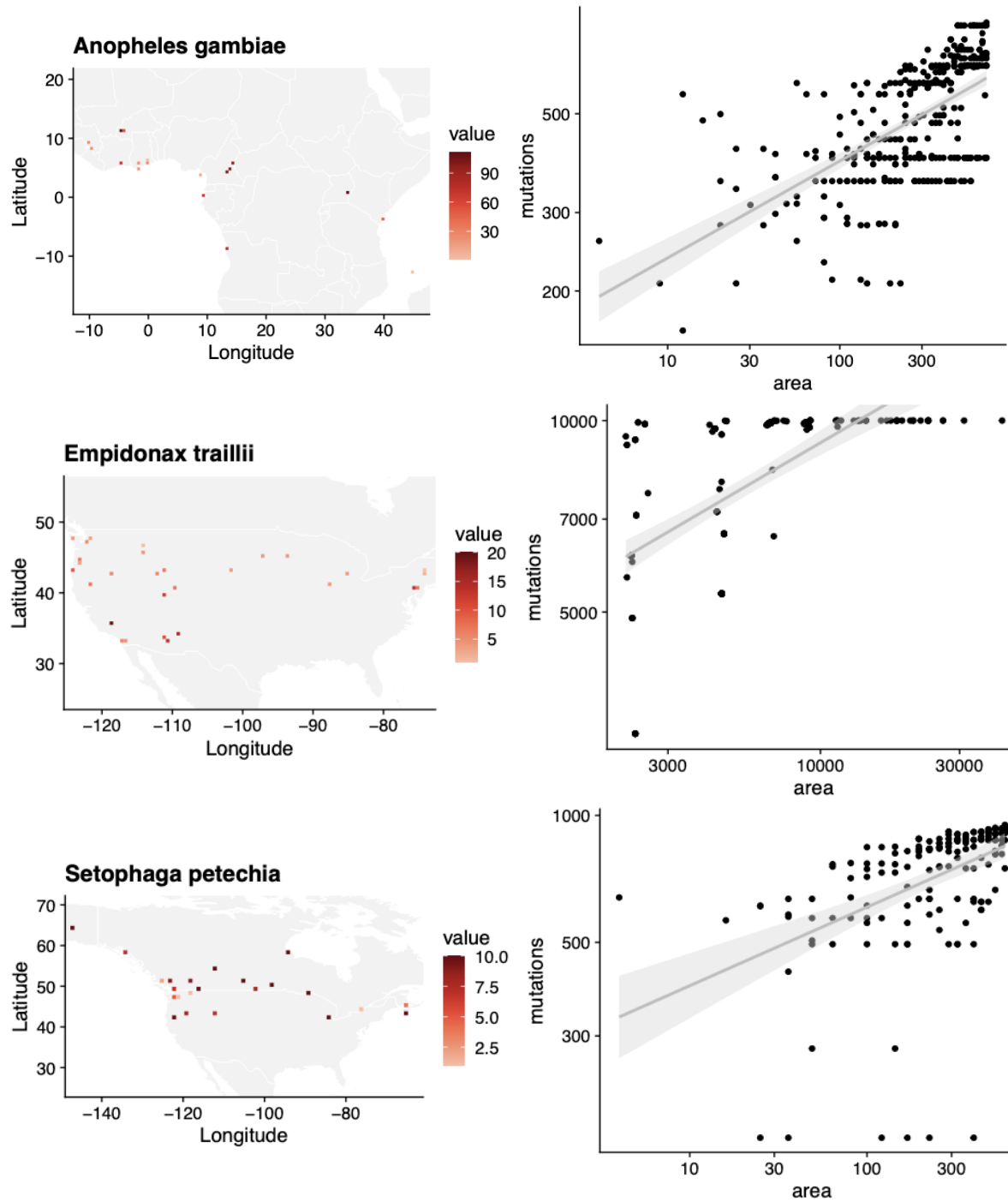
1275
1276

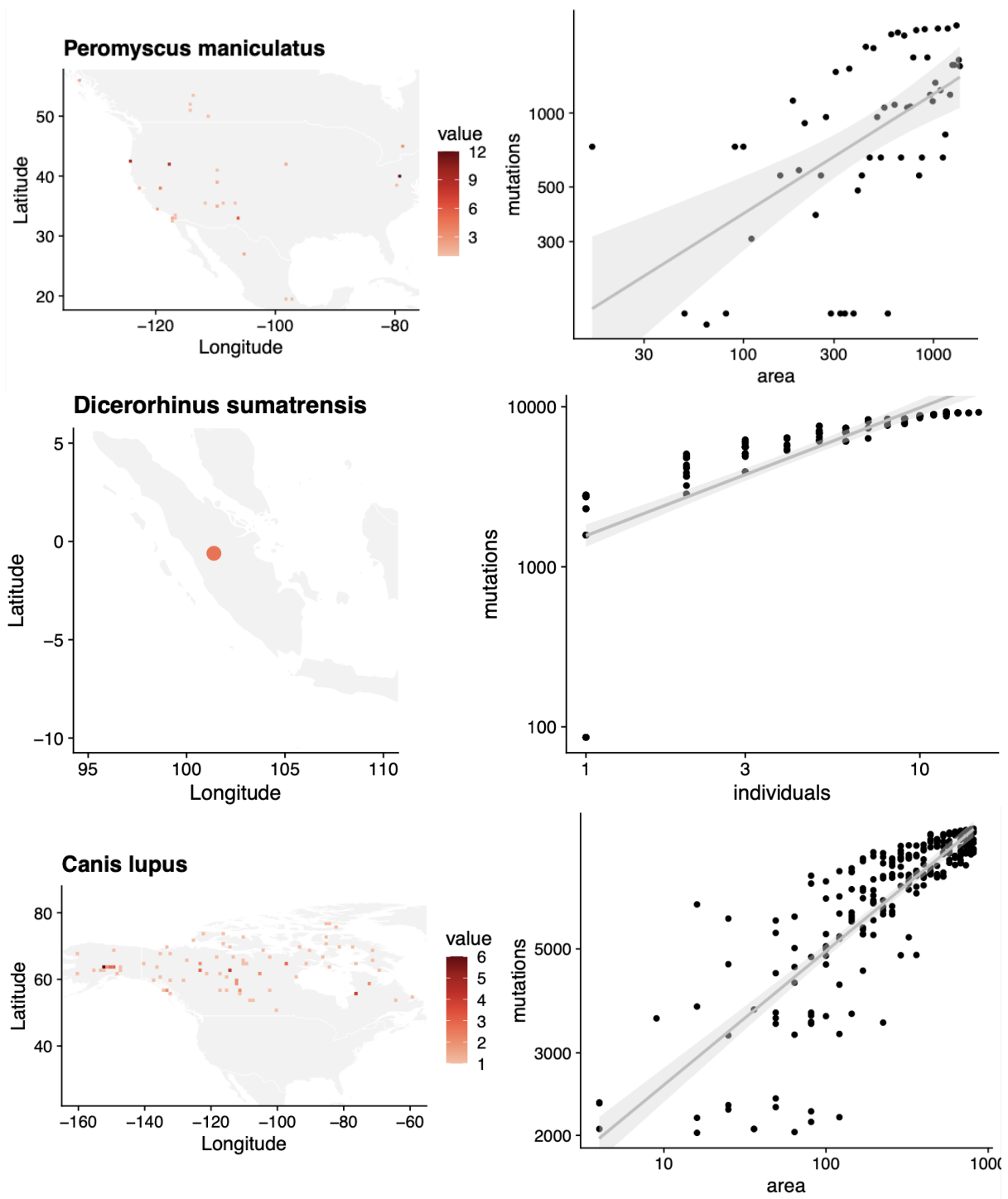


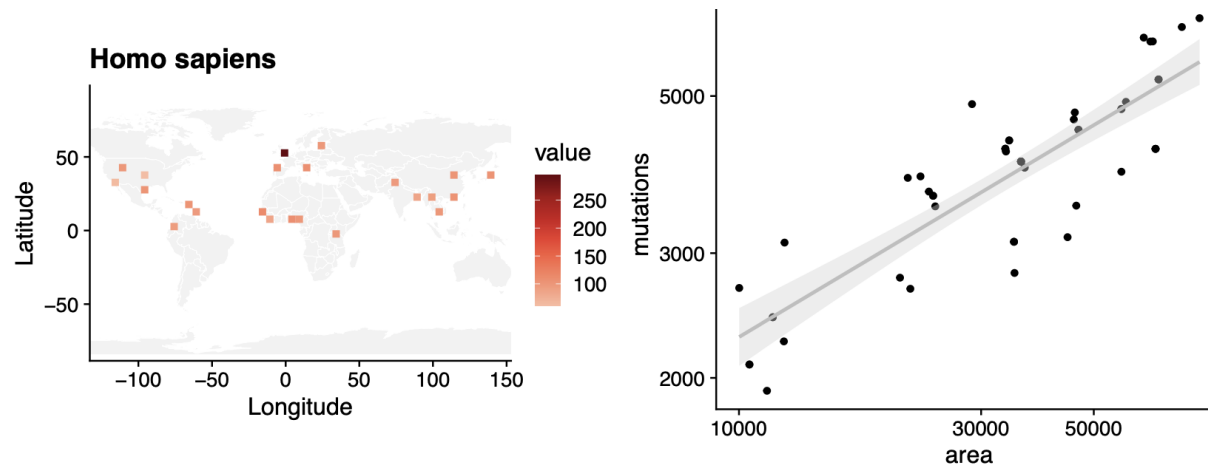












1277 **Fig. S22 | MAR summaries across species.**
 1278 For each species we plot (left) the map of sample density in space and (right) the mutations-area relationship. (The locations
 1279 of 16 *Dicerorhinus sumatrensis* are unknown so only Sumatra is shown. *Pinus torreyana* was only found in two extant
 1280 populations.)

1281

1282 **Table S10 | The mutations-area relationship across species. Extended Table 1**
 1283 The Mutations-Area Relationship (MAR) fitted with Area = Individuals and the scaled version. In the main text areas to
 1284 protect 90% of genetic diversity per species are provided given the scaled z^* . Here, we also provide the average estimated
 1285 area based on % of grid cells per species to be transformed from 2015 to 2050 using the LUH² dataset, the area where at
 1286 least 10% of grid cells will be transformed, and the genetic loss corresponding to those area transformations (see section
 1287 V.2).
 1288

Species (study)	SFS mod [<i>ΔAIC</i>]	MAR (A=N) z_N [CI95%]	MAR scaled z^* [CI95%]	LUH ² change '50	LUH ² >10% change '50	LUH ² extinct '50	LUH ² >10% extinct '50
<i>Arabidopsis thaliana</i> (29)	logN (85.8)	0.431 (0.423 - 0.439)	0.312 (0.305–0.32)	4.58	13.54	1.12	3.43
<i>Arabidopsis lyrata</i> (42)	logN (9592.4)	0.254 (0.238 - 0.27)	0.15 (0.136–0.165)	0.79	2.64	0.19	0.64
<i>Amaranthus tuberculatus</i> (43)	logN (7317.5)	0.244 (0.237 - 0.251)	0.142 (0.135–0.148)	4.86	11.13	1.19	2.79
<i>Eucalyptus melliodora</i> (44)	logN (157.5)	0.531 (0.526 - 0.536)	0.402 (0.397–0.406)	3.82	7.77	0.93	1.92
<i>Yucca brevifolia</i> (58)	logN(33300)	0.141 (0.128 - 0.155)	0.049 (0.037–0.062)	0.74	0	0.18	0
<i>Mimulus guttatus</i> (45)	logN (580.8)	0.342 (0.331 - 0.353)	0.231 (0.221–0.241)	3.78	NA	0.92	NA
<i>Panicum virgatum</i> (46)	logN (8345.2)	0.226 (0.215 - 0.237)	0.126 (0.116–0.136)	8.07	27.65	2	7.47
<i>Panicum hallii</i> (57)	logN (86)	0.983 (0.907 - 1.059)	0.814 (0.745 - 0.883)	3.78	11.36	0.92	2.85
<i>Pinus contorta</i> (47)	Wei (19413.7)	0.019 (0.018 - 0.02)	-	1.95	5.54	0.47	1.36
<i>Pinus torreyana</i> (60)	logN(766156)	0.239 (0.232 - 0.245)	0.105 (0.099–0.11)	25.4	NA	6.79	NA
<i>Populus trichocarpa</i> (48)	logS (0)	0.268 (0.257 - 0.28)	0.164 (0.154–0.175)	4.68	17.28	1.14	4.45
<i>Anopheles gambiae</i> (49)	logS (0)	0.221 (0.209 - 0.233)	0.121 (0.11–0.132)	9.95	21.96	2.48	5.78
<i>Acropora millepora</i> (50)	logN (452.3)	0.403 (0.395 - 0.41)	0.287 (0.28–0.293)	72.73	84.69	26.79	36.26
<i>Drosophila melanogaster</i> (59)	logN(33300)	0.445 (0.433 - 0.458)	0.324 (0.313–0.336)	0.95	NA	0.23	NA
<i>Empidonax traillii</i> (51)	Wei (640401.9)	0.169 (0.139 - 0.199)	0.074 (0.047–0.101)	5.55	15.14	1.36	3.86
<i>Setophaga petechia</i> (52)	ln (67138.5)	0.251 (0.236 - 0.267)	0.149 (0.135 - 0.163)	2.83	7.54	0.69	1.86
<i>Peromyscus maniculatus</i> (53)	logN (1449.7)	0.844 (0.769 - 0.919)	0.68 (0.613–0.748)	5.61	13.68	1.38	3.47
<i>Dicerorhinus sumatrensis</i> (61)	w (107864.2)	0.474 (0.449 - 0.498)	0.123 (0.106–0.14)	0.25	NA	0.06	NA
<i>Canis lupus</i> (55)	logN (85.8)	0.29 (0.28 - 0.301)	0.183 (0.174–0.193)	0.23	NA	0.06	NA
<i>Homo sapiens</i> (56)	logN (9592.4)	0.395 (0.339 - 0.451)	0.28 (0.229–0.331)	28.81	40.13	7.83	11.58

1289 Extended acronyms:
 1290 logN: log Normal distribution. logS: log Series distribution. Wei: Weibull distribution.
 1291

1292 **IV.1 Exclusion of species from global averages**

1293

1294 To avoid contaminating across-species averages of z_{MAR} with estimates of species whose data
 1295 we do not fully trust, we conducted global averages excluding species for which we are not
 1296 confident z_{MAR} reflects the correct species diversity-area relationships.

1297
 1298 *Pinus contorta* showed a lower z_{MAR} than what is expected in a theoretical baseline from
 1299 individual sampling (section II). This is most likely due to this being the only species for
 1300 which SNPs were previously ascertained to be intermediate frequency (i.e. the genome
 1301 technology was a SNP chip). This alters SFS, so we are not confident the z_{MAR} is the true
 1302 parameter of the species.

1303
 1304 *Yucca brevifolia* was a dense sampling of several local populations within a constrained area
 1305 that is a hybrid zone. Since this species was not sampled range-wide we do not feel confident
 1306 to include it in downstream analyses. The species also has a lower z than expected (Fig. S5)

1307
 1308 *Pinus torreyana* only has two wild populations left, and therefore the MAR is based on two
 1309 area sizes (Fig. S22). Because this is such a threatened species with already most of its range
 1310 loss, we do not have confidence in the z parameter.

1311
 1312 *Dicerorhinus sumatrensis* has only ~30 estimated adult individuals in the wild. Again we do
 1313 not have confidence in the z parameter in such extinction-edge cases.

1314
 1315 *Homo sapiens*. We exclude our own species.
 1316

1317 **Table S11 | Mean z_{MAR} and other summary statistics across species.**

1318 We selected those species that did not show artefacts in Fig. S22 or whose z_{MAR} overlapped with 0 to calculate a species-
 1319 wide mean. See section IV.1.
 1320

	z_{MAR}	$z_{MAR} (A=N)$	$z^*_{MAR} \text{ scaled}$
mean	0.31	0.39	0.27
mean se	0.038	0.053	0.048
median	0.25	0.29	0.18
IQR	0.15	0.19	0.17

1321
 1322
 1323 Although we could not see any obvious patterns relating z_{MAR} with certain groups of
 1324 species (Table 1), we wondered whether any life history trait of the species analysed could
 1325 explain the variation we observed (see Table S12 of traits). An ANOVA did not show any
 1326 significant relationship. Because we know theoretically this parameter must be related to the
 1327 degree of dispersal ability of genotypes of a species relative to the whole species geographic
 1328 range, we expect traits involved in determining these to be good predictors. Future work will
 1329 be necessary to validate this, as the sample size (n=19) may not permit enough power to
 1330 detect these expected patterns.
 1331

1332 **Table S12 | Traits, life history, and other characteristics of the analyzed species.**

Species	RedList	Known Decline	Kingdom	Reproduction	Pollination	Mobility	AreaRange
<i>Arabidopsis thaliana</i>	NO	NO	Plantae	Selfing	Selfing	Sessile	27337467.4
<i>Arabidopsis lyrata</i>	NO	NO	Plantae	Outcrossing	Vector	Sessile	2791301.4
<i>Amaranthus tuberculatus</i>	LC	NO	Plantae	Outcrossing	Vector	Sessile	804124.8
<i>Eucalyptus melliodora</i>	VU	NO	Plantae	Outcrossing	Wind	Sessile	948699.3
<i>Yucca brevifolia</i>	LC	YES	Plantae	Outcrossing	Vector	Sessile	1213454.4
<i>Mimulus guttatus</i>	LC	NO	Plantae	Outcrossing	Vector	Sessile	25138310.6
<i>Panicum virgatum</i>	LC	NO	Plantae	Outcrossing	Wind	Sessile	6291400.2

<i>Panicum hallii</i>	NO	NO	Plantae	Outcrossing	Wind	Sessile	2188807.4
<i>Pinus contorta</i>	LC	NO	Plantae	Outcrossing	Wind	Sessile	886182.2
<i>Pinus torreyana</i>	CR	YES	Plantae	Outcrossing	Wind	Sessile	30781.95
<i>Populus trichocarpa</i>	LC	NO	Plantae	Outcrossing	Wind	Sessile	1119664.1
<i>Drosophila melanogaster</i>	NO	NO	Animalia	Outcrossing	Activemating	Fly	115208408
<i>Anopheles gambiae</i>	NO	NO	Animalia	Outcrossing	Activemating	Fly	19959809.9
<i>Acropora millepora</i>	NT	YES	Animalia	Outcrossing	Activemating	Fly	26725.9
<i>Empidonax traillii</i>	LC	YES	Animalia	Outcrossing	Activemating	Fly	7027395.2
<i>Setophaga petechia</i>	LC	NO	Animalia	Outcrossing	Activemating	Fly	15172431.15
<i>Peromyscus maniculatus</i>	LC	NO	Animalia	Outcrossing	Activemating	Mobile	22609152.6
<i>Dicerorhinus sumatrensis</i>	CR	YES	Animalia	Outcrossing	Activemating	Mobile	3335605.58
<i>Canis lupus</i>	LC	NO	Animalia	Outcrossing	Activemating	Mobile	19102403.5
<i>Homo sapiens</i>	NA	NA	NA	NA	NA	NA	80763121.8

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Table S13 | Association of traits, life history, and other characteristics with z_{MAR} .

Acronyms: NO=not assessed but likely non-threatened, LC=low concern, VU=vulnerable, CR=critically endangered

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
RedList	4	0.0952396	0.0238099	0.5580988	0.7040464
KnownDecline	1	0.0275537	0.0275537	0.6458527	0.4580865
Kingdom	1	0.0011684	0.0011684	0.0273876	0.8750400
Reproduction	1	0.0003238	0.0003238	0.0075890	0.9339612
Pollination	1	0.0375975	0.0375975	0.8812784	0.3909509
Mobility	1	0.1600627	0.1600627	3.7518370	0.1104995
AreaRange	1	0.0174745	0.0174745	0.4095989	0.5503439
Residuals	5	0.2133125	0.0426625	NA	NA

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While no association between life history and z_{MAR} was found (Table S13), this may be due to limited power, as the sample size of species analysed here is still small, $n=20$. Further studies expanding the numbers of species will be necessary to confirm or reject this expected association.

1347 **V. An estimate of global genetic diversity loss**

1348

1349 Using the approach described in section II.4, we generated a number of estimates either per
1350 ecosystem or per species. All estimates below tried to be conservative, and thus we always
1351 used the scaled z_{MAR} values (section II.3.2.)

1352

1353 **V.1 Estimates of ecosystem area losses**

1354

1355 **Table S14 | Millennium Ecosystem Assessment land cover transformation.**

1356 *Changes of ecosystem area pre-21st century. Ecosystem names are repeated for ecosystem sub-classes.*

1357 Source: <https://www.millenniumassessment.org>

1358

1359

System	Area (km ² x10 ⁶)	Earth % surface	Protected areas (%)	Area transformed (%)
MARINE	349.3	68.6	0.3	NA
COASTAL	17.2	4.1	7	NA
- TERRESTRIAL	6	4.1	4	11
- MARINE	11.2	2.2	9	NA
INLAND WATER	10.3	7	12	11
FOREST/WOODLAND	41.9	28.4	10	42
- TROPICAL	23.3	15.8	11	34
- TEMPERATE	6.2	4.2	16	67
- BOREAL	12.4	8.4	4	25
DRYLAND	59.9	40.6	7	18
- HYPERARID	9.6	6.5	11	1
- ARID	15.3	10.4	6	5
- SEMIARID	22.3	15.3	6	25
- SUBHUMID	12.7	8.6	7	35
ISLAND	7.1	4.8	17	17
- STATES	4.7	3.2	18	21
MOUNTAINS	35.8	24.3	14	12
- 300-1000	13	8.8	11	13
- 1000-2500	11.3	7.7	14	13
- 2500-4500	9.6	6.5	18	6
- 4500+	1.8	1.2	22	0.3
POLAR	23	15.6	42	0.38
CULTIVATED	35.3	23.9	6	47
- PASTURE	0.1	0.1	4	11
- CROPLAND	8.3	5.7	4	62
- MIXED	26.9	18.2	6	43
URBAN	3.6	2.4	0	100
GLOBAL	510	NA	4	38

1360

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1362

1363 Ecosystem transformation has been tracked over decades. We extracted ecosystem
1364 transformations from the Millennium Ecosystem Assessment (62), which estimated
1365 ecosystem transformations from presumably native systems to cultivated or urban areas by
1366 GLC2000 land cover dataset (Table S14). The forest/woodland is calculated as percentage
1367 change between potential vegetation from WWF ecoregions to the current actual
1368 forest/woodland areas from GLC2000. These provide bulk ecosystem reductions, not for a
1369 given species, but may be a good proxy for an average across species.

1370

1371 **Table S15 | IPBES land cover transformation.**

1372 Source: <https://ipbes.net>

1373

Region	Area(Mkm2)	MSA 2010	MSA 2050 SSP2	MSA 2050 SSP1	MSA 2050 SSP3
North America	20	65	56	NA	NA
Central and South America	18	65	53	NA	NA
Middle East and Northern Africa	11	81	77	NA	NA
Sub-Saharan Africa	24	70	56	NA	NA
Western and Central Europe	6	37	29	NA	NA
Russian region and Central Asia	21	73	65	NA	NA

South Asia	5	44	35	NA	NA
China region	11	56	49	NA	NA
Southeast Asia	7	55	43	NA	NA
Japan, Korea and Oceania	8	71	57	NA	NA
Polar	2	96	91	NA	NA
World	132	66	56	62	54

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1378 The Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem
1379 Services (IPBES) recently used a PBL satellite product from the Netherlands Environmental
1380 Assessment Agency (<https://www.pbl.nl/en/nature-and-biodiversity>) to study the % of area
1381 ecosystem transformation in the world (Table S15). This provides an updated estimate to the
1382 Millennium Assessment as well as projections under several Shared Socioeconomic
1383 Pathways (1-3) for 2050. These were reported per region as of 2010, and for projections to
1384 2050 (scenario SSP2). Instead of direct area, the metric is a composite of land use
1385 information to predict Mean Species Abundance (MSA), a measure of the size of populations
1386 of wild organisms as a percentage of their inferred abundance in their natural state (% MSA).

1387
1388 A global transformation metric can also be captured by the most updated land use
1389 transformation data, the Land Use Harmonization 2 (release v2e for 2015-2011 and release
1390 v2h for baseline 1850-2015) (63). Baseline transformation of primary ecosystems was
1391 calculated subtracting the total area covered by primary forest (primf) and primary non-forest
1392 (primn) variables between year 1850 layer (roughly pre-industrial baseline) and the present,
1393 2015, as $I-A_{2015} / A_{1850}$ (Table S16). Analyses that use projections to mid-21st century were
1394 conducted similarly as in (64), summing over all transitions from primary forest (primf),
1395 primary non-forest (primn), secondary forest (secdf) and secondary non-forest (secdn) lands
1396 to any other category for all years within the 2015-2050 period (see Table S10).

1398 **Table S16 | Land Use Harmonization 2 from 1850 to 2015**
1399 Source: <https://luh.umd.edu/data.shtml>

	Area %
Primary forest transformed	43
Primary non-forest transformed	50

1401
1402 Finally, we searched for timely estimates of forest reduction (based on vegetation
1403 cover) reported in the Global Forest Watch website:
1404 <https://www.globalforestwatch.org/dashboards/global/> (accessed June 2021). From 2002 to
1405 2020, there has been a global tree cover loss of 10%, with an annual tree cover loss of 0.6-
1406 1.1%.

1407
1408 Although these are not direct area transformations, we also used the IUCN Red List
1409 resource (<https://www.iucnredlist.org>, Table S12 shows status of the species analysed here),
1410 which includes guides to categorise species as vulnerable, endangered, critically endangered,
1411 and extinct, and has conducted extensive assessments across thousands of species (Table
1412 S17).

1413
1414 **Table S17 | IUCN Red List categories of extinction risk and number of species.**
1415 Source: www.iucnredlist.org, January 2021

IUCN Red List	Description	Criterion of area or pop.	# plant species
---------------	-------------	---------------------------	-----------------

Category		reduction (>%)	
EX	Extinct	100	164
EW	Extinct in the Wild	100	
CR	Critically Endangered	80	4674
EN	Endangered	50	8593
VU	Vulnerable	30	8459
NC, LR, NT, DD,LC	No Concern, Low Risk, Near Threatened, Data Deficient, Least Concern, Other	0	32237

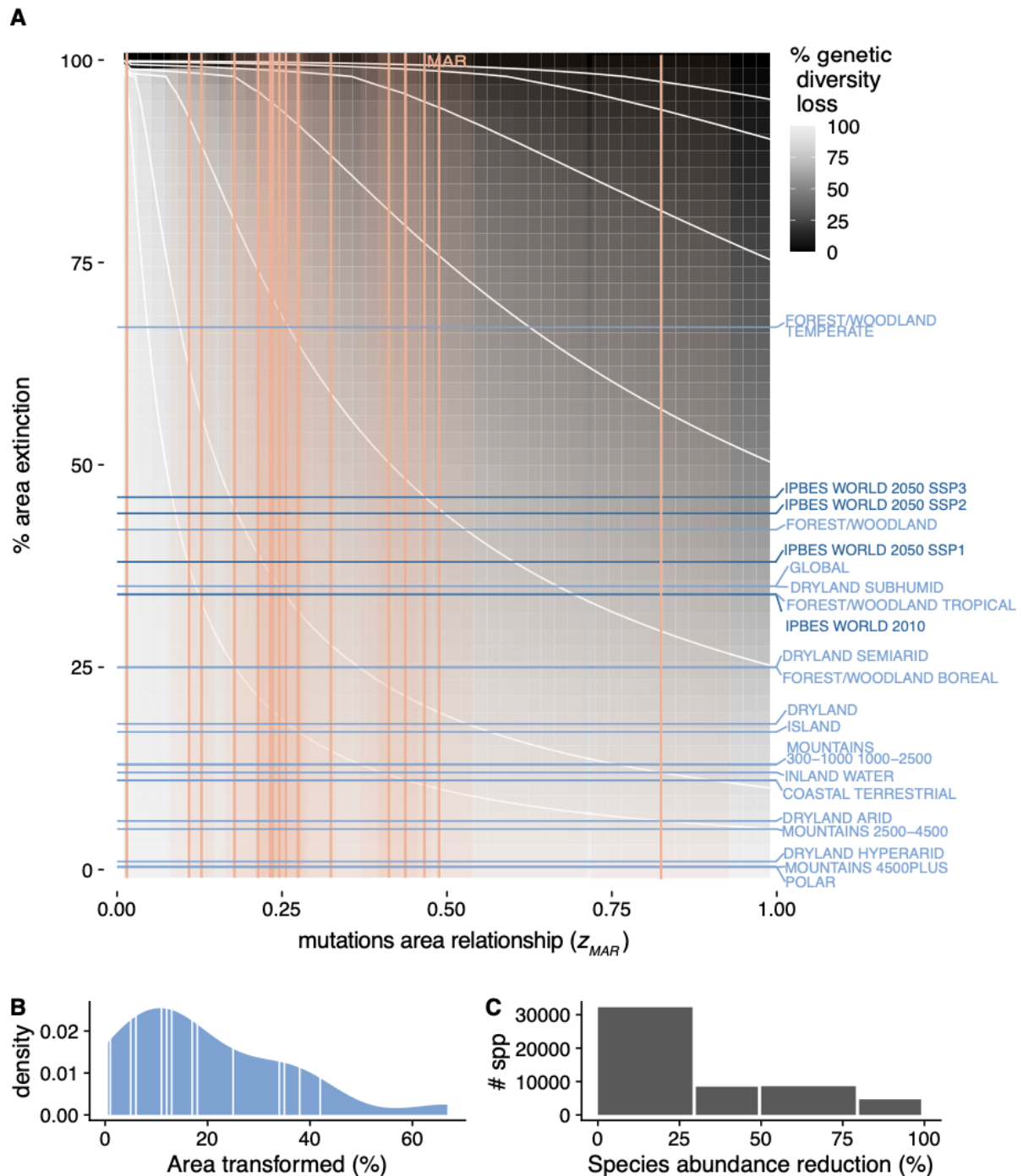
1417
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1419 **V.2 A global estimate of genetic loss**

1420

1421 Taking the estimates and standard error of z_{MAR} across species, and the world's reduction of
1422 ecosystems we can calculate the fraction of genetic diversity reduction following the MAR
1423 equation (section II.4), giving a range of estimates (Table S18).

1424



1425

1426 **Fig. S23 | The parameter space of genetic diversity loss, extended**

1427 (A) The theoretical space of genetic diversity loss. z_{MAR} values (using area, unscaled for samples, differently from Fig. 32)
 1428 computed for species analyzed here are marked as orange vertical lines, with confidence intervals as orange shading. Blue
 1429 horizontal lines correspond to ecosystem transformations from the Millennium Assessment (light blue) and IPBES
 1430 Assessment (dark blue) (B) Density histogram of percentages of area transformed across ecosystems from the MA, with
 1431 averages per ecosystem marked in the distribution as well as horizontal lines in (A). (C) The number of species of each of the
 1432 IUCN categories and the most optimistic range of area or abundance reduction for each of the category brackets.

1433

1434

1435 **Table S18 | Estimates of average expected genetic loss for different ecosystems.**

1436 Assuming ecosystem transformation approximately translates into average species distribution reduction, and using the
 1437 ranges of z_{MAR} from Table 1 of the main text, we project the average genetic loss using the Mutations Area Relationship.

1438

System	Area transformed (%)	Genetic loss % (mean z based)	Genetic loss % (min z based)	Genetic loss % (max z based)
--------	----------------------	-------------------------------	------------------------------	------------------------------

COASTAL TERRESTRIAL	11	3.2	0.9	9
INLAND WATER	11	3.2	0.9	79.7
FOREST/WOODLAND	42	14.0	4	35.8
FOREST/WOODLAND TROPICAL	34	10.5	3	28.7
FOREST/WOODLAND TEMPERATE	67	26.5	7.9	59.4
FOREST/WOODLAND BOREAL	25	7.7	2.1	20.9
DRYLAND	18	5.4	1.5	14.9
DRYLAND HYPERARID	1	0.3	0.1	0.8
DRYLAND ARID	5	1.4	0.4	4.1
DRYLAND SEMIARID	25	7.7	2.1	20.9
DRYLAND SUBHUMID	35	11.3	3.2	29.6
ISLAND	17	5.0	1.4	14.1
MOUNTAINS	12	3.5	0.9	9.9
MOUNTAINS 300-1000	13	3.8	1	10.7
MOUNTAINS 1000-2500	13	3.8	1	10.7
MOUNTAINS 2500-4500	6	1.7	0.5	4.9
MOUNTAINS 4500+	0.3	0.1	0	0.2
POLAR	0.4	0.1	0	0.3
GLOBAL	38	12.4	3.5	32.2

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Assuming the average z_{MAR} , and utilising tree cover from the Global Forest Watch (<https://www.globalforestwatch.org>), which estimates 0.6-1.1% of transformation per year across Canada, United States and Australia, we extrapolated genetic diversity loss in the next 50 years for tree species to be 8-15% genetic diversity loss.

Assuming that the calculated z_{MAR} estimates (Table 1) are representative of plant species, we conducted an experiment to create a distribution of % of genetic diversity loss in threatened species. We used the number of species in each IUCN category (Table S17) for a total of 54,127 plant species. For plant species, one of the evaluation criteria of percentage of population loss likely translates faithfully to area reduction in the species. Thus, the proportion of species per category gives a discrete probability distribution of the ranges of percentage of area loss: $P(0-29\%)=0.596$, $P(30-49\%)=0.156$, $P(50-79\%)=0.159$, $P(80-99\%)=0.086$, $P(99\%-100\%)=0.003$. Using a simulation-based sampling approach, we drew 350,000 random area reductions A_t/A_{t-1} from the previous distribution and a z_{MAR} from the mean and variance of our estimates from Table 1 for plants. These were plugged into the MAR equation (Section II.4) to calculate the percentage of genetic diversity loss of these 350,000 random draws. The resulting distribution had a median and interquartile range of 17.53 % [7.51- 31.82]..

Using the Land Use Harmonization 2 dataset, we also create per-species predictions based on the % transformation of each of the sampled regions per species (Table S14). As before, the land use transformations that merit be considered area losses are all transitions from primary forest (primf), primary non-forest (primn), secondary forest (secdf) and secondary non-forest (secdn) lands to any other category. Taking all the locations where each species has been sampled, we extracted the predicted % of land use change per cell and summed over all cells where individuals had been sampled (we call this LUH² change ‘50, see column in Table S10). We also produced the alternative area loss estimate taking that at least 10% predicted habitat transformation for a grid cell renders the entire area of that grid cell as impacted or lost (we call this LUH² >10% change ‘50). These per-species area losses, in combination with the matched z_{MAR} , provided a range of potential loss estimates to 2050 ranging 0-36% depending on the species (Table S10).

1473

1474 V.3 Community ecology simulations and MAR

1475

1476 To test whether intermediate levels of MAR would be expected across species in entire
1477 ecosystems, we conducted community assembly simulations of ~100-500 species following
1478 the Neutral Theory of Biodiversity (1, 41) and coalescent simulations (23) using the software
1479 MESS (65). These simulations are computationally demanding and could not run in a
1480 complete 2D spatial grid. Instead, they were simulated in a mainland-island system, with
1481 islands of increasing areas. The community forms by species colonising an empty island
1482 according to Hubbell's Unified Neutral Theory of Biodiversity and Biogeography (UNTB),
1483 where all species are equally likely to colonise and persist in the local community. Continued
1484 colonisation and migration to the local community continues to bring in new species that may
1485 or may not survive, while also continuously bringing in individuals of species already in the
1486 local community. The community assembly process ends when the community has reached
1487 an equilibrium denoted as the balance between local extinction and new species dispersing
1488 into the area (Hubbell 2001). Once the forward-time process has ended, we simulate the
1489 coalescent history of each species backward in time. For this, MESS considers the population
1490 size, divergence time, and migration rates of the meta and local communities. These
1491 coalescent simulations provide us with genetic data and ultimately diversity estimates for
1492 each species in the community.

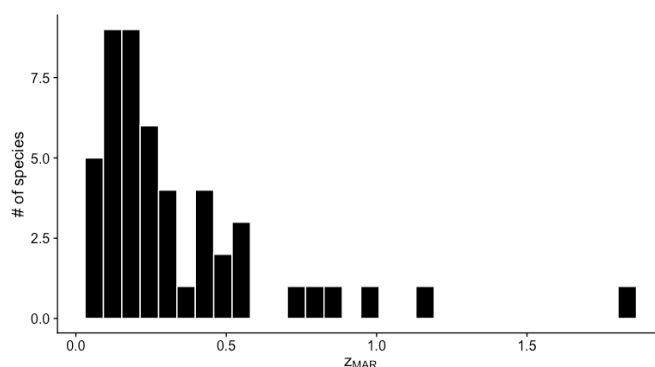
1493

1494 We simulated 100 MESS communities, and for each community the size of the local
1495 community was varied from 1K to 100K. We varied the size of communities to emulate
1496 variation in area occupied by a given community because we assume as the number of
1497 individuals in a community increases from 1,000 to 100,000, so does the area occupied. All
1498 other parameters were kept consistent across each of these community simulations, and most
1499 remained at their default value. The parameters changed were the length of the sequences
1500 simulated for the coalescent-based simulations, which was fixed at 10,000 bp, and the
1501 migration rate, which was fixed at 0.01.

1502

1503 The simulation output was used to then compute a single z_{SAR} for the system as
1504 $S=cA^{z_{SAR}}$, and one z_{MAR} for each species in the same way, $M=cA^{z_{MAR}}$. This resulted in the
1505 distribution of z_{MAR} from Fig. S24. This confirmed that we can recover typical z_{SAR} and z_{MAR}
1506 values from completely stochastic neutral yet spatially structured systems such as species in
1507 communities and mutations in populations of a species.

1508



1509

1510 **Fig. S24 | z_{MAR} calculated from MESS eco-evolutionary simulations**

1511 Using the MESS framework of a mainland-island model with different island sizes, z_{MAR} per species is recovered. The
1512 stochastic nature of the simulations results in each species having different abundances and migration histories that change

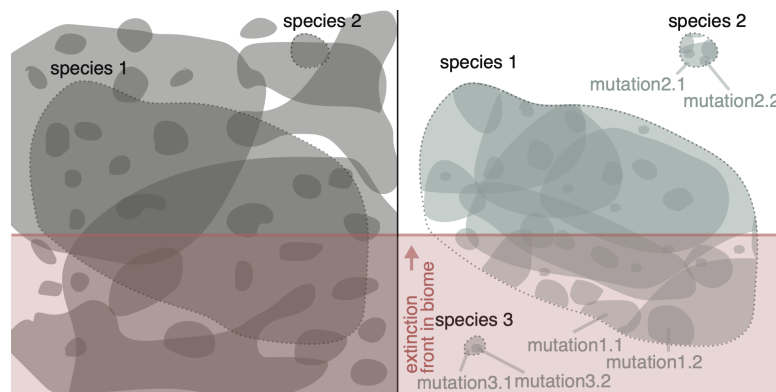
1513 *the scaling value. Values were typically around 0.3. Rarely some species had values above 1, which appear could be noisy*
1514 *estimates from recently colonising species in the simulations.*
1515
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1518 **V.4 The nested species extinction and genetic diversity loss processes**

1519
1520 Finally, we worried that our estimates of V.2 would be mistaken as overestimates. In fact, we
1521 believe these may be underestimated. Recent policy proposals for the United Nations'
1522 Sustainability Goals emphasize that the target of protecting 90% of species genetic diversity
1523 for all species cannot leave the already-extinct species behind (66) (That is, one cannot
1524 protect 90% of species and leave 10% to become extinct to meet this goal). This clearly
1525 exemplifies a problem in conservation biology that what researchers can study is (most of the
1526 time) what has escaped extinction, and therefore if we do not account for extinct species in
1527 our overall estimates of genetic diversity loss we may naively think ecosystems have not
1528 suffered genetic diversity loss (i.e. in the extreme scenario, an ecosystem that has lost all but
1529 one abundant species may not really appear genetically eroded if such species is in good
1530 shape).

1531
1532 We then created spatial simulations in R where 1,000 species are distributed in
1533 100x100 grid cells following a UNTB abundance distribution and then proceeded with an
1534 edge extinction of the ecosystem (see Fig. S25 for a cartoon).
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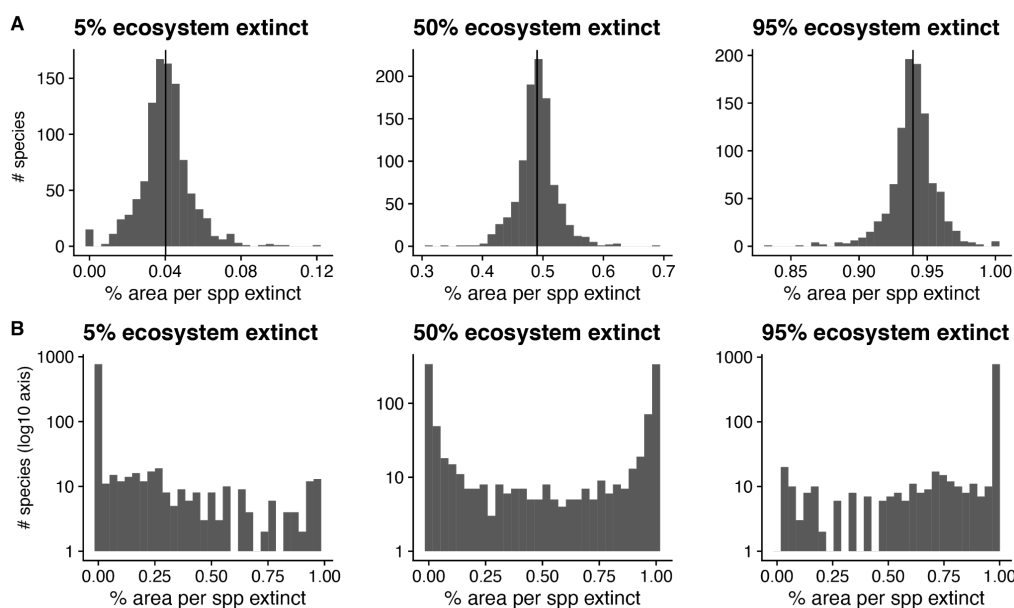
1539 ***Fig. S25 | Cartoon of nested extinction of species and genetic diversity loss.***

1540 *An ecosystem with multiple species within it (left), distributed in space, with few species broadly distributed and many*
1541 *narrowly distributed. Moving one level of biological organization lower, mutations within species (right) are also spatially*
1542 *distributed with many narrowly distributed. As extinction happens (red line moving bottom to top), all species below the red*
1543 *line go extinct, but only the mutations within species 1 below the line are lost, while mutations above the line remain.*
1544 *Species 3 has already become extinct, and therefore also all the mutations within it.*
1545

1546

1547 Two extreme types of distributions of species can be imagined: species are randomly
1548 placed in space, or species are found mostly in perfectly contiguous ranges (We ended up
1549 using as an example a simulation with 85% of the individuals of a species found in a core
1550 square continuous distribution and 15% found outside that core in fragmented observations,
1551 as this scenario produced the canonical SAR of $z \sim 0.3$). Spatial structure interestingly creates
1552 two extreme distributions of area reductions across species (Fig. S26): random placement of
1553 cell habitats essentially show that the average area reduction per ecosystem is followed by
1554 most species, while autocorrelated placement of cell habitats create a U distribution in area
1555 reductions, where at the beginning of the extinction process most species have not

1556 experienced any impact (Fig. S26B left) but at the end of ecosystem reduction virtually all
 1557 species are already extinct (Note we may be at the beginning of S26B process given the data
 1558 from IUCN, Fig 3C).
 1559
 1560

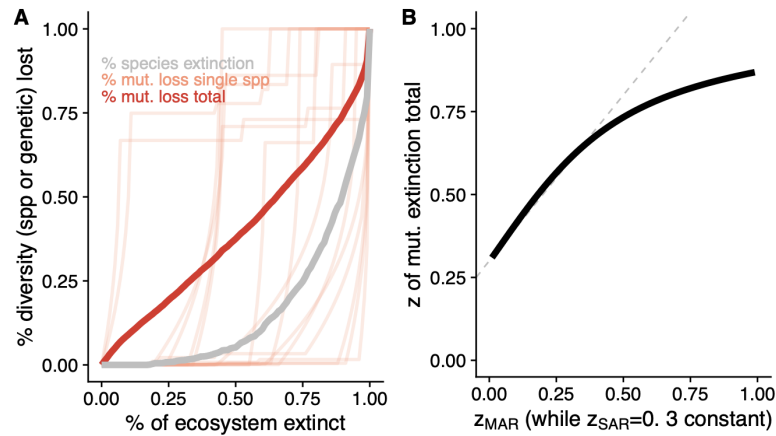


1561

1562 **Fig. S26 | The distribution of per-species area lost and total ecosystem extinction with 1000 species**

1563 *Two ecosystems of 100x100 cells with 1000 species. Species are either randomly distributed in cells (A) or spatially*
 1564 *autocorrelated with occupying mostly contiguous cells (B). As the extinction process wipes out part of the ecosystem*
 1565 *(snapshots are provided at 5%, 50%, and 95%), the area loss per species (and hence genetic diversity lost) is tracked. In (A)*
 1566 *the average area lost per species is roughly the total reduction of the ecosystem, whereas in (B) the distribution is U shaped*
 1567 *(note the log-scaled y-axis). While in (B) the mean area lost in the distribution correctly captures the area loss of the*
 1568 *ecosystem, per species losses are highly uneven.*
 1569

1570 To study the consequence of the above differential area loss and the effect of some
 1571 species going extinct on the total ecosystem genetic diversity, we conducted the next
 1572 analysis: For extant species, we assumed they would lose genetic diversity following the
 1573 MAR relationship (section II.4), with all species having $z_{MAR} = 0.3$ for simplicity (i.e. all
 1574 species lose genetic diversity at the same rate). For extinct species (100% of their area
 1575 reduced), we considered genetic diversity loss was 100%. The compound total genetic
 1576 diversity loss would then just be the sum of those $X_{Tot} = \sum_{i=1}^{1000} X_i$ (Of course, in reality species
 1577 may vary in their genome-wide diversity average, and we could for instance use Watterson's
 1578 Θ_W (see section II.2) to scale the total loss of genetic diversity in the ecosystem accounting
 1579 for different basal level of diversity per species: $\sum_{i=1}^{1000} \Theta_{Wi} X_i$). Interestingly, if we calculate the
 1580 z of the slope of compound genetic diversity across species in an ecosystem it is much larger
 1581 than MAR or SAR alone: $z_{compounded} = 0.6$ (Fig. S27).
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Fig. S27 | Numeric simulation of nested species and genetic diversity loss.

(A) Simulating the extinction of an ecosystem with 1,000 species that follow a log-normal species abundance curve. Extinction of the ecosystem creates a curve of species loss of $z \sim 0.3$ (grey). Likewise, each species trajectory (light red, 15 species drawn randomly) follows a simulated genetic diversity loss of $z_{MAR} \sim 0.3$ as they lose area. Because species' geographic distributions are by construction smaller than the whole ecosystem area, those distributed closer to the start of the extinction front lose area first, while those distributed farthest from the extinction front only lose area when the ecosystem is almost completely destroyed. Because genetic diversity loss is both due to complete extinction of species as well as area reduction of extant species, the compound genetic diversity loss curve (red) follows the faster loss dynamics. (B) Holding $z_{SAR} = 0.3$ constant, and varying z_{MAR} in independent simulations shows that the compound genetic diversity across species is close to the sum of both z slopes (the SAR and the MAR), but it saturates at ca. 0.85 (grey dotted line shows $z_{MAR} + z_{SAR}$).

1598 VI. Limitations and outlook

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1600 In this last section we list some potential limitations of an inherently simple scaling law, and
1601 what approaches could be used to address those and improve genetic diversity loss
1602 projections.

1603

1604 VI.1 Reasons for overestimations

1605

1606 Many researchers have posited that SAR likely overestimates species extinction (33, 67). For
1607 instance:

1608 - Ignoring that a diversity-area relationship can be defined outwards, inwards, or
1609 focusing on endemisms can have an impact (10, 33, 67). To address this, we
1610 confirmed relative consistency between inward, outward, and random placement
1611 MAR, and proposed that the EMAR may not be that appropriate to study genetic
1612 diversity loss (or at least EMAR does not show predictability in our simulation).

1613 - Species may persist in altered habitats, like some animals are known to do (68). We
1614 have focused some of the estimates in this study on plants, for which area loss should
1615 equate to population loss and vice versa, but further extensions could be applied in the
1616 future as described by Pereira and Daily (68).

1617 - SAR is not a mechanistic model (69). We have derived its ranges of possible values
1618 and averages analytically and are beginning to understand how evolutionary forces
1619 shape MAR. Realistic simulations can help understand in a process-based framework
1620 how populations (and their MAR) react to partial population extinction (continuous
1621 space simulations with progressive area reductions appear to fit well with the MAR
1622 predictions calculated before the extinction process starts, section III.2.6).

1623 - There is a scale dependence in the SAR slope, with slight increase in the slope at large
1624 scales (10). Since power laws are typically fit with large-scale datasets and used to
1625 predict local scale extinctions, predictions could be overestimated at local scales.

1626

1627 VI.2 Reasons for underestimations

1628

1629 While the simplicity of power laws to make predictions of species extinction may lead to
1630 overestimations, there are also important reasons to believe MAR would underestimate
1631 genetic loss.

1632 - Perhaps even more so than in species list datasets and census, the discovery of low
1633 frequency genetic variants is highly underpowered (70). These are highly prevalent,
1634 but genomic pipelines, with the aim to be conservative, often filter out rare variants.
1635 This would underestimate z_{MAR} and therefore the degree of genetic diversity loss with
1636 area shrinkage. This is clear in the pre-selected-only marker dataset of *Pinus contorta*.

1637 - Related to the previous: Although sequencing methods have an error rate that
1638 misreads true nucleotide sequences, this rate is typically extremely low (many
1639 sequencing projects described here used Illumina HiSeq series, which has a 0.112%
1640 error rate, or about 1 misread nucleotide in 1000). This could intuitively lead to
1641 overestimates in mutations in space but in fact, the mis-reading of DNA ends up
1642 causing an underestimation. This is because bioinformatic software that transforms
1643 raw data into SNP variant tables errs towards the conservative direction, often not
1644 calling mutations that have been observed very few times, and thus likely under-
1645 representing rare mutations (71).

1646 - The use of scaled z_{MAR} proposed in section II.3.2. accounts for that the minimum z_{MAR}
1647 is rarely exactly 0, especially when sample sizes are limited. We use this correction

1648 scaling down z_{MAR} to be conservative. However, z_{MAR} could only in very exceptional
1649 circumstances be 1, but we do not correct for this, again, to have a conservatively low
1650 z_{MAR} . Hence, our conservative approach would generally lead to underestimates of
1651 genetic diversity loss.

- 1652 - When species shrink in area, the effective population size of the remaining population
1653 decreases, increasing drift and moving towards a lower diversity equilibrium. This
1654 reactive process is not captured by the phenomenological MAR relationship.
- 1655 - The nested extinction of species and genetic diversity loss (section V.3) would lead
1656 us, by the right of “survival bias”, to underestimate how much genetic diversity has
1657 been lost cumulative in an ecosystem.

1658

1659 **VI.3 Final notes**

1660

1661 Ultimately, to make accurate predictions of genetic diversity loss and increased extinction
1662 risk of species, very detailed data and expert assessment per species will be required: census
1663 sizes, genome size, migration in metapopulations, mating system, detailed maps of genetic
1664 makeups, and finescale area transformations. This could enable mechanistic models projected
1665 forward-in-time such as discussed in section II.3.6. The production of new genomic datasets
1666 across entire ecosystems should further help create maps of genetic diversity at high
1667 resolution to track losses (72–74).

1668

1669 Our philosophy in this work has been to err on the conservative side when projecting
1670 genetic diversity loss (e.g. using area calculations that produce lower z_{MAR} values, scaling
1671 them for low sample bias, using lower estimates of ecosystem transformation, etc.). However,
1672 this conservative approach can also lead us into under-estimating loss. As described in V.4.,
1673 the phenomenon of survival bias likely leads us to underestimate what has been lost given we
1674 do not observe it. A phenomenon also highlighted as a possible explanation for the relatively
1675 shy difference in genetic diversity between threatened and non-threatened species (75, 76)

1676

1677 Because to our knowledge, no other approaches exist to project genetic diversity, we
1678 believe that MAR is a quantitative and scalable first-approximation of genetic diversity that
1679 would just require accurate understanding of abundance or area reductions and minimal
1680 information about population structure or mating/dispersal/range relationships. Given that
1681 scaling relationships are already applied by conservation policy (77), and given that
1682 assumptions and limitations are understood, we expect MAR to become a relevant tool to
1683 project losses of a dimension of biodiversity so far mostly invisible or unaddressable in large
1684 conservation projections.

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