

1 Manuscript in Preparation

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3 Range-wide differential adaptation and genomic vulnerability in  
4 critically endangered Asian rosewoods

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32

## 33 **Abstract**

34 In the billion-dollar global illegal wildlife trade, rosewoods have been the world's most  
35 trafficked wild product since 2005<sup>1</sup>. *Dalbergia cochinchinensis* and *D. oliveri* are the most  
36 sought-after rosewoods in the Greater Mekong Subregion<sup>2</sup>. They are exposed to significant  
37 genetic risks and the lack of knowledge on their adaptability limits the effectiveness of  
38 conservation efforts. Here we present genome assemblies and range-wide genomic scans of  
39 adaptive variation, together with predictions of genomic vulnerability to climate change.  
40 Adaptive genomic variation was differentially associated with temperature and precipitation-  
41 related variables between the species, although their natural ranges overlap. The findings are  
42 consistent with differences in pioneering ability and in drought tolerance<sup>3</sup>. We predict their  
43 genomic offsets will increase over time and with increasing carbon emission pathway but at a  
44 faster pace in *D. cochinchinensis* than in *D. oliveri*. These results and the distinct gene-  
45 environment association in the eastern coastal edge suggest species-specific conservation  
46 actions: germplasm representation across the range in *D. cochinchinensis* and focused on  
47 vulnerability hotspots in *D. oliveri*. We translated our genomic models into a seed source  
48 matching application, *seedeR*, to rapidly inform restoration efforts. Our ecological genomic  
49 research uncovering contrasting selection forces acting in sympatric rosewoods is of  
50 relevance to conserving tropical trees globally and combating risks from climate change.

51

## 52 **Significant statement**

53 In the billion-dollar global illegal wildlife trade, rosewoods have been the world's most  
54 trafficked wild product since 2005, with *Dalbergia cochinchinensis* and *D. oliveri* being the  
55 most sought-after and endangered species in Southeast Asia. Emerging efforts for their  
56 restoration have lacked a suitable evidence base on adaptability and adaptive potential. We  
57 integrated range-wide genomic data and climate models to detect the differential adaptation  
58 between *D. cochinchinensis* and *D. oliveri* in relevance to temperature- and precipitation-  
59 related variables and projected their vulnerability until 2100. We highlighted the stronger  
60 local adaptation in the coastal edge of the species ranges suggesting conservation priority. We  
61 developed genomic resources including chromosome-level genome assemblies and a web-  
62 based application seedeR for genomic model-enabled assisted migration and restoration.

## 63 **Main**

64 Rosewoods have been the world's most trafficked wild product since 2005, amounting  
65 to 30–40% of the global illegal wildlife trade<sup>1</sup>, which is estimated at 7–23 billion USD  
66 annually<sup>4</sup>. *Dalbergia cochinchinensis* Pierre and *D. oliveri* Gamble ex Prain are among the  
67 most sought-after and threatened rosewood species. Exploited for their extremely valuable  
68 timber<sup>2</sup>, alongside many other valued and threatened tree species in Asia's tropical and  
69 subtropical forests<sup>5</sup>, the growing demand and limited supply have driven prices as high as  
70 50,000 USD per cubic metre<sup>6</sup>. Both these *Dalbergia* species were classified as Vulnerable  
71 and Endangered in the 1998 IUCN Red List<sup>7,8</sup>. The Convention on International Trade in  
72 Endangered Species of Wild Fauna and Flora (CITES) has listed the entire *Dalbergia* genus  
73 in its Appendix II since 2017 to reduce sequential exploitation of other closely related  
74 species<sup>9</sup>. In the IUCN's latest re-assessment of their endangered status to Critically  
75 Endangered in 2022<sup>10,11</sup>, it is suspected that the populations of both species have already  
76 experienced a decline of at least 80% over the last three generations, and the decline is likely  
77 to continue<sup>12</sup>.

78 *D. cochinchinensis* and *D. oliveri* are sympatric species, endemic to the Greater Mekong  
79 Subregion (GMS) in Southeast Asia, an area of high ecological and conservation concern as  
80 84% of the GMS overlaps with the Indo-Burmese mega biodiversity hotspot<sup>13</sup>. The complex  
81 biogeographical and geological histories of the GMS have contributed to its high species  
82 richness, heterogeneous landscapes, and high endemism levels<sup>14</sup>. Ancient changes in the  
83 distribution of terrestrial and water bodies have been associated with changes in vegetation  
84 types and cover<sup>15</sup>. These forests contribute substantially to local livelihoods, economies, food  
85 security, and human health<sup>16,17</sup>, though overexploitation undermines their potentially central  
86 role to nature-based solutions and most of them are unprotected<sup>4</sup>.

87 Species- and environment- specific conservation approaches represent an immediate  
88 need in response to declining populations<sup>5</sup>. Conservation, collection, and use of genetically  
89 diverse germplasm are key to conserving diversity and restoring these rosewood populations.  
90 Genetic conservation actions were started in the early 2000s but were limited in scale, usually  
91 including fewer than 50 seed-producing trees per country<sup>18–20</sup>. Newer capacity-building  
92 initiatives targeting tree nurseries and seed value chain development<sup>21</sup> may still carry genetic  
93 risks associated with the supply and use of germplasm, and may compound the effects of  
94 over-exploitation. First, underrepresented genetic diversity during the sourcing of genetic  
95 materials can create a genetic bottleneck for the species and reduce the species' ability to  
96 adapt and evolve in a changing climate<sup>22</sup>. Second, mismatch of habitat suitability can result in  
97 maladaptation, if populations have strong local adaptation<sup>23</sup>. Third, climate change will likely  
98 impose new forces of selection on the current genetic diversity, thus reducing the species'  
99 adaptability, affecting population functioning<sup>24,25</sup>, and leading to increased risk of local  
100 extirpations and species' range collapse<sup>26</sup>. If unaddressed, these risks will reduce both short  
101 and long-term effectiveness of restoration projects. The genetic risks call for an  
102 understanding of adaptation and its genetic basis in *Dalbergia* species in the GMS to  
103 safeguard on-going conservation and restoration efforts. *Dalbergia* are high value species that  
104 could be used sustainably and generate income for farmers in developing countries if well-  
105 adapted planting material is available<sup>5</sup>. Planting for economic purposes and reducing risks to  
106 remaining natural populations of these species seem necessary, where ecological restoration  
107 alone is insufficient.

108 Of the 14,191 vascular plants that are listed as either Vulnerable, Endangered, and  
109 Critically Endangered in the IUCN Red List, only 0.1% have their genomes published, far  
110 fewer than the 1% reported for listed animals<sup>27</sup>. There is a critical lack of genomic resources  
111 in threatened species and a disproportionate representation across taxa, in contrast with the

112 rapid growth in genomic technologies. New reference genomes in threatened species will  
113 enable the analysis, of functional genes, higher-resolution studies of species delineation,  
114 association mapping and adaptation, genetic rescue, and genome editing<sup>28</sup>. These in turn will  
115 help to address important conservation (and restoration) questions such as genetic monitoring  
116 of introduced and relocated populations, predicting population viability, disease resistance,  
117 synthetic alternatives, and de-extinction<sup>29,30</sup>.

118 This paper develops an unprecedented understanding of adaptation in critically  
119 endangered rosewoods, which integrates genomic analyses, the creation of a novel evidence,  
120 and a resource base to inform and expand ongoing conservation efforts. (1) We present  
121 genome assemblies of *D. cochinchinensis* and *D. oliveri* at chromosomal and near-  
122 chromosomal scale respectively. (2) We analyse range-wide patterns of adaptation by  
123 genotyping ~800 trees, and identify differential drivers of adaptive genetic diversity between  
124 the two species by using gene-by-environment association analyses. (3) We project current  
125 genotypes onto future climate scenarios and predict the potential maladaptation of  
126 populations. (4) We deploy an interactive application to predict optimal seed sources, based  
127 on our landscape genomic results, in *D. cochinchinensis* and *D. oliveri* for use in restoration  
128 under future climate scenarios. Our ecological genomic study in the GMS fills crucial  
129 knowledge gaps for genomic adaptation in tropical tree species which are highly  
130 underrepresented in the current research literature.

131

## 132 **Chromosome-scale genome characterisation**

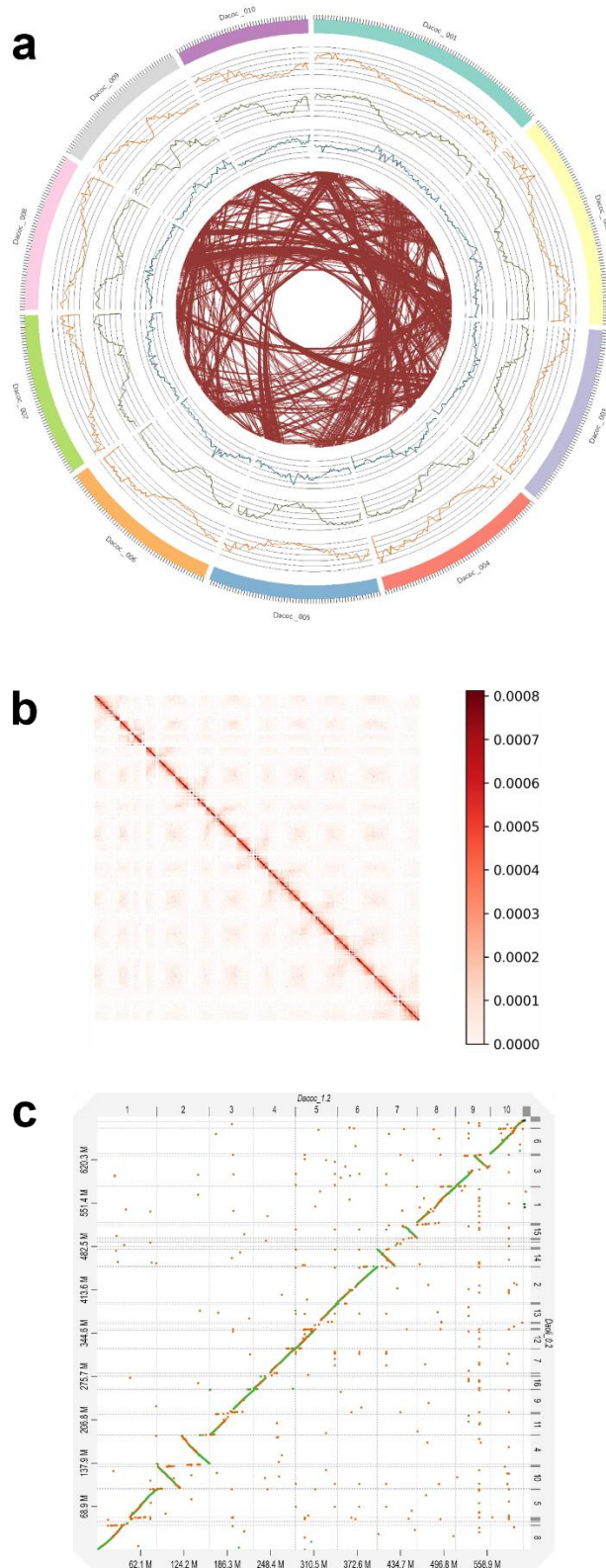
133 The *D. cochinchinensis* reference genome assembly (Dacoc\_1.4) was 621 Mbp in size  
134 comprised of 10 pseudochromosomes (Figure 1a, Supplementary Figure 1, Supplementary  
135 Table 1). Whole-genome sequencing of a single seedling of *D. cochinchinensis* produced 165  
136 Gbp (~260 X) long-read data. A diploid-aware draft assembly of 1.3 Gbp with 6,443 contigs

137 and a N50 of 1.35 Mbp was first obtained, with the longest contig between 33.2 Mb at  
138 chromosome-arm length. We purged the haplotig and scaffolded the draft genome with 54.97  
139 Gbp (~88.52X) Hi-C chromosome conformation capture reads into 511 scaffolds with a N50  
140 of 60.0 Mb (Supplementary Table 2). The 10 longest scaffolds were considered  
141 pseudochromosomes and 98.3% of the contigs were mapped onto them (Figure 1b).

142 The *D. oliveri* draft genome assembly (Daoli\_0.3) was 689.25 Mbp in size  
143 (Supplementary Figure 1, Supplementary Table 3). Whole-genome sequencing of a single  
144 seedling of *D. oliveri* produced 15.13 Gbp (~22X) long-read data. We first obtained a  
145 diploid-aware draft assembly of 814.69 Mbp with 3,249 contigs and a N50 of 474.02 Kbp.  
146 We purged the haplotig and scaffolded the draft genome with 13.46 Gbp (~20X) Pore-C  
147 multi-contact chromosome confirmation capture reads into 2,977 scaffolds with a N50 of  
148 38.43 Mbp. Syntenic analysis of the *D. oliveri* assembly (Daoli\_0.3) against the 10  
149 pseudochromosomes obtained in *D. cochinchinensis* (Dacoc\_1.4) showed that the 16 largest  
150 scaffolds in Daoli\_0.3 had 1-to-1 or 2-to-1 correspondences to Dacoc\_1.4, implying that  
151 Daoli\_0.3 was at chromosome-arm length (Figure 1c).

152 We constructed *de novo* repeat libraries of Dacoc\_1.4 and Daoli\_0.3, which contained  
153 402 Mbp and 453 Mbp of repeat elements respectively (64.80% and 65.71% of the genomes)  
154 (Supplementary Table 4, Supplementary Table 5), the majority of which were annotated as  
155 containing LTR elements (46.63% and 48.55%) such as Ty1/Copia (15.25% and 15.75%) and  
156 Gypsy/DIRS1 (30.51% and 31.96%). The repeat content of the two genomes was  
157 significantly higher than the average among Fabids (~49%), which may be due to the near  
158 double amount of LTRs (~22%)<sup>31</sup>.





159

160 **Figure 1.** (a) Genomic landscape of the 10 assembled pseudochromosomes of *D. cochinchinensis* (*Dacoc\_1.4*), showing tick  
161 marks every 1 Mb, gene density (orange), repeat density (green), 5-mC density (blue), and interchromosomal syntenic  
162 arrangement (brown). The densities are calculated in 1-Mb sliding window. (b) High-resolution contact probability map of  
163 the final *D. cochinchinensis* genome assembly after scaffolding, revealing the 10 pseudochromosomes at 100 Kbp resolution.  
164 (c) Syntenic dot plot of assemblies of *D. oliveri* (*Daoli\_0.3*) against *D. cochinchinensis* with a minimum identity of 0.25.

165 We predicted and annotated 27,852 and 33,558 gene models in Dacoc\_1.4 and  
166 Daoli\_0.3 respectively, using previous RNA sequencing data (Supplementary Table 6) and  
167 protein homology of *Arabidopsis thaliana* and *Arachis ipaensis*. The gene models had a mean  
168 length of 4,284.20 and 3942.71 bp respectively, of which 98.3% and 95.5% had an AED  
169 score less than 0.5, considered as strong confidence (Supplementary Figure 2). The gene  
170 models had a BUSCO v5.1.2 completeness of 96.2% and 88.3% using the eudicots\_odb10  
171 reference dataset, with 92.1% and 86.7% being both complete and single copy.

172

### 173 **Range-wide genomic scan for adaptive signals**

174 We obtained initial pools of 1,832,629 and 3,377,855 SNPs from genotyping 435 and  
175 331 individuals of *D. cochinchinensis* and *D. oliveri* respectively, across their natural ranges  
176 (Supplementary Table 7), and final pools of 180,944 and 193,724 SNPs after filtering for  
177 missing data, minimum allele frequency, and linkage disequilibrium. The samples  
178 represented previous sampling work<sup>32,33</sup> and new sampling that covered all known existing  
179 populations.

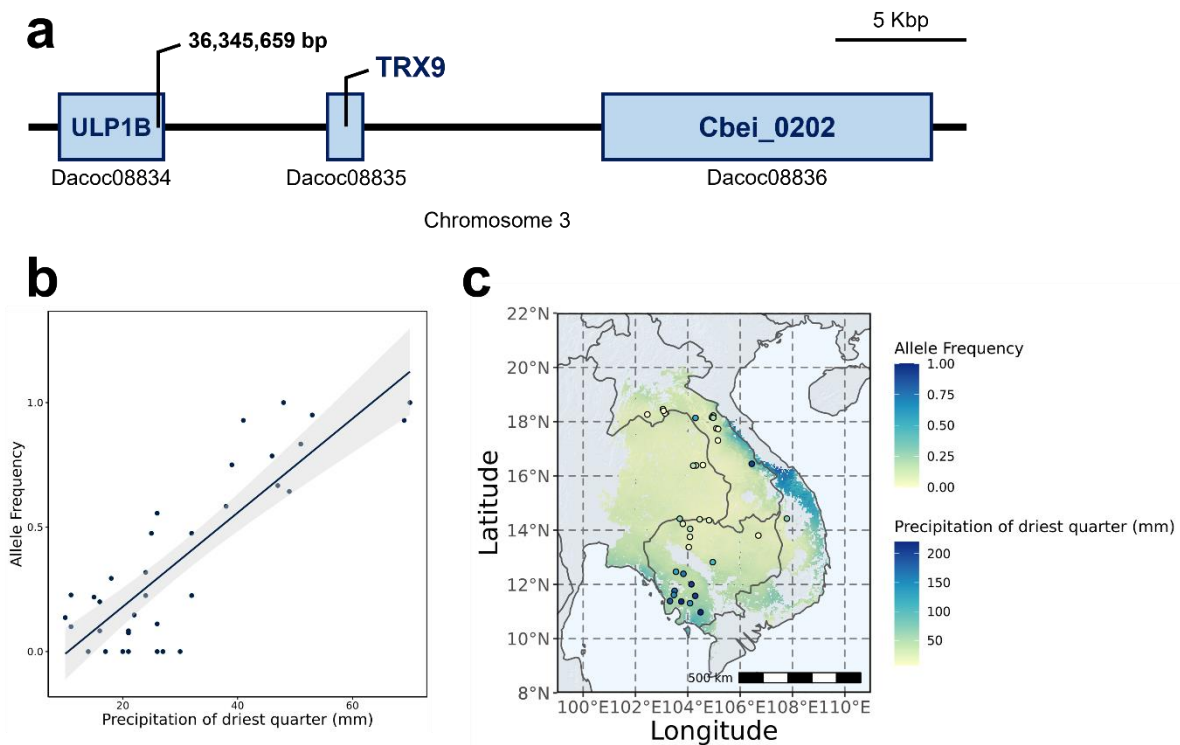
180 We employed the sparse non-negative matrix factorisation (sNMF) algorithm to  
181 determine the optimal number of ancestral populations (K) for *D. cochinchinensis* and *D.*  
182 *oliveri* as 13 and 14 respectively (Supplementary Figure 3, Supplementary Figure 4,  
183 Supplementary Figure 5). These results were much higher than the previous estimation of K  
184 = 5 – 9 for the same species using nine microsatellite markers and 19 SNPs<sup>32,33</sup>. The analysis  
185 revealed a highly resolved hierarchical genetic structure for both species and distinct  
186 population clusters around the Cardamon Mountains in southwest Cambodia and in northern  
187 Laos. Our calculation gave a larger genomic inflation factor ( $\lambda$ ) in *D. cochinchinensis* (range  
188 from 0.071 (evapotranspiration) to 0.25 (precipitation of driest quarter), mean of 0.13,  
189 standard deviation of 0.049) than that in *D. oliveri* (range from 0.038 (evapotranspiration) to

190 0.081 (mean diurnal range), mean of 0.056, standard deviation of 0.016 (Supplementary  
191 Table 8).

192 The numbers of SNPs found to be adaptive for at least one of the environmental  
193 variables were 20,373 (11.3%) and 6,953 (3.59%) in *D. cochinchinensis* and *D. oliveri*  
194 respectively ( $|Z\text{-value}| > 2$  &  $Q\text{-value} < 0.01$ ), after correcting for population structure  
195 (optimal K) and genomic inflation (Supplementary Figure 6, Supplementary Figure 7,  
196 Supplementary Table 9). Relatively few SNPs were associated with all or many  
197 environmental variables; 4 SNPs were associated with 11 out of 13 variables tested in *D.*  
198 *cochinchinensis*, and 46 SNPs were associated with all 12 variables in *D. oliveri*. These  
199 findings revealed the complex and polygenic nature of environmental adaptation, where  
200 multiple forces of natural selection can act together via different environmental cues and  
201 affect overlapping loci.

202 In *D. cochinchinensis*, ‘precipitation in the driest quarter’ was the environmental  
203 variable (wc2.1\_30s\_bio\_17) and the strongest gene-environmental association with a SNP  
204 on chromosome 3 at position 36,345,659 (LFMM  $Z = 6.07237$ ,  $Q = 4.77e-29$ ). The SNP was  
205 located within the gene Dacoc08834, a homologue of the Ubiquitin-like-specific protease 1B  
206 ULP1B. The highest allele frequencies of this SNP were found in the southwest of Cambodia  
207 with the highest precipitation of the driest quarter (Figure 2). ULP1B is one of the ubiquitin  
208 like-specific proteases that mediate the maturation and deconjugation of a small ubiquitin-  
209 like modifier (SUMO) from target proteins as part of post-translational modification<sup>34</sup>. The  
210 SUMO process in plants has been shown to regulate stress responses including to drought,  
211 heat, salinity, and pathogens<sup>35–37</sup> and timing of flower initiation<sup>38</sup>, which might explain the  
212 strong association with the drought stress associated with the said environmental factor. In an  
213 analysis of transcriptomes from 6 *Dalbergia* species, ubiquitin-related proteins were found to

214 be overrepresented compared to other legumes<sup>27</sup>. Taken together, these observations suggest  
215 that ubiquitin-related proteins have a role in *Dalbergia* adaptation to water assimilation.



216

217 **Figure 2.** (a) The most significant gene-environment association at 36,346,659 bp on chromosome 3, within the *Dacoc08834*  
218 gene and upstream of *Dacoc08835* and *Dacoc08836* genes, which are homologues of *ULP1B*, *TRX9*, and *Cbei\_0202*  
219 respectively. (b) and (c) Correlation between allele frequency and *wc2.1\_30s\_bio\_17* (Precipitation of driest quarter) for  
220 this locus.

221 By contrast, the strongest association in *D. oliveri* was between precipitation of the  
222 wettest quarter (*wc2.1\_30s\_bio\_16*), and a SNP on the scaffold *Daoli\_0035* at the position  
223 107,725 (LFMM  $Z = 6.1895$ ,  $Q = 6.36e-102$ ). The locus was 3,254 bp upstream of a  
224 predicted gene model *Daoli32516* and 5,010 bp downstream of the gene *Daoli32517*, a  
225 homologue of *tatC*-like protein *YMF16*.

226

## 227 Differential adaptation related to temperature and precipitation

228 Isothermality (*wc2.1\_30s\_bio\_3*) was identified as the most important overall driver  
229 of both neutral and adaptive genomic variation among non-spatial environmental variables in  
230 *D. cochinchinensis*, based on our gradient forest (GF) model (Figure 3, Supplementary

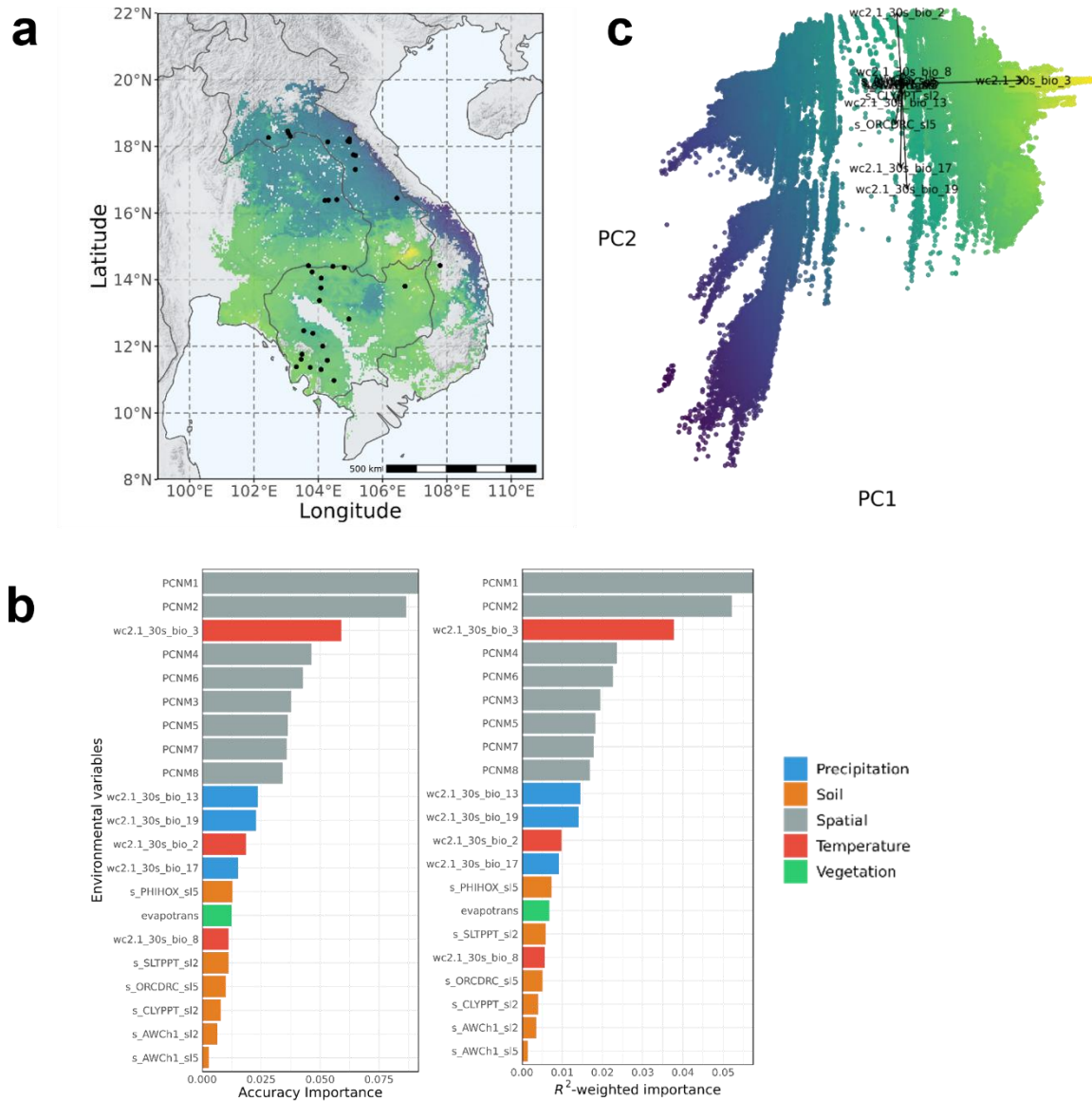
231 Figure 8a), in contrast to ‘precipitation of the wettest quarter’ (wc2.1\_30s\_bio\_16) in *D.*  
232 *oliveri* (Figure 4, Supplementary Figure 8b). Spatial variables, as principal coordinates of a  
233 neighbourhood matrix (PCNM), were the most important variables that explained both  
234 neutral and adaptive genomic variation, which was unsurprising given strong isolation by  
235 distance was known in these species<sup>32</sup> and environmental adaptation only affects a small  
236 portion of the genome<sup>39</sup>. Soil factors were among the lowest ranked variables for gene-  
237 environment associations for both species. We observed different patterns of geographic  
238 variation in *D. cochinchinensis* and *D. oliveri* when fitting the GF models across their native  
239 ranges. *D. cochinchinensis* had strong differentiation between North and South populations at  
240 around 16°N, that was mainly driven by isothermality (wc2.1\_30s\_bio\_3) as seen in the PCA  
241 loadings. On the other hand, *D. oliveri*’s major differentiation was between coastal and inland  
242 areas, driven by both precipitation of the wettest quarter (wc2.1\_30s\_bio\_16) and mean  
243 diurnal range (wc2.1\_30s\_bio\_2 ). The eastern coastal areas in Vietnam showed particularly  
244 strong differences in environmental associations with adaptive variation and neutral variation  
245 for both *D. cochinchinensis* and *D. oliveri* (Figure 5).

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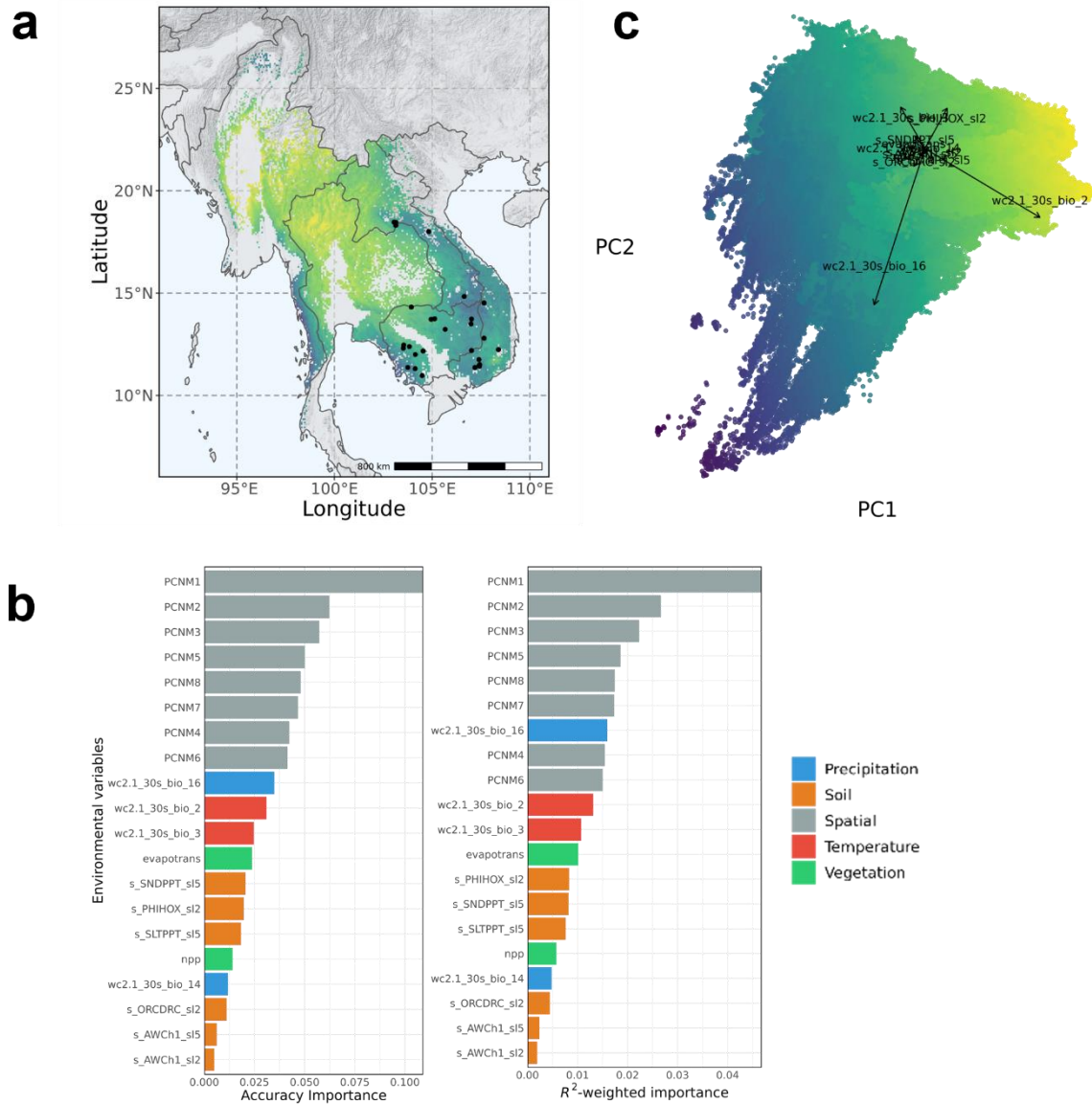
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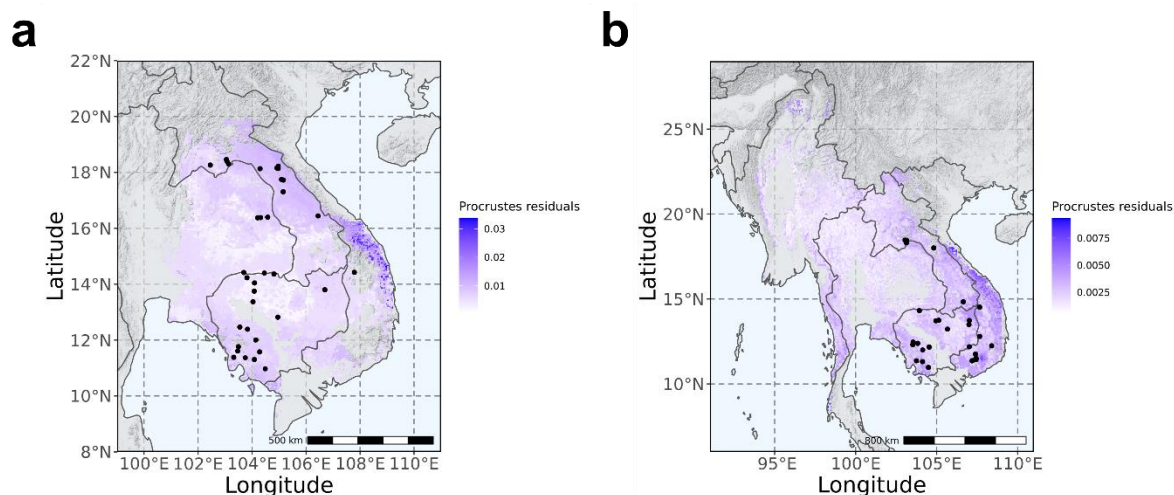
249

250 **Figure 3.** (a) Adaptive genomic variation across the species range predicted by GF model for *D. cochinchinensis*, visualised  
 251 using the first two principal axes from the PCA. (b) Accuracy and  $R^2$ -weighted importance for environmental predictor  
 252 variables which explained adaptive genomic variation (adaptive SNPs) by the GF model. (c) Principal component analysis  
 253 (PCA) of the adaptive genomic variation predicted by the GF model across the species range. Loadings are the  
 254 environmental factors.



255

256 **Figure 4.** (a) Adaptive genomic variation across the species range predicted by GF model for *D. oliveri*, visualised using the  
 257 first two principal axes from the PCA. (b) Accuracy and  $R^2$ -weighted importance for the environmental predictor variables  
 258 which explained the adaptive genomic variation (adaptive SNPs) by the GF model. (c) Principal component analysis (PCA)  
 259 of the adaptive genomic variation predicted by the GF model across the species range. The loadings are the environmental  
 260 factors.



261

262 *Figure 5. Procrustes residuals between neutral and adaptive gene-environmental associations for (a) D. cochinchinensis*  
263 *and (b) D. oliveri.*

264 We compared the allelic frequency turnover functions of the neutral and adaptive  
265 genomic variation for each environmental predictor variable. Adaptive genomic variation was  
266 significantly more strongly associated with environmental gradients than neutral variation  
267 (Supplementary Figure 9). There was only one exception, where available soil water capacity  
268 at a depth of 60 cm (s\_AWCh1\_sl5) was near-zero but of similar importance in explaining  
269 neutral and adaptive variation, regardless of the environmental gradient.

270 When exposed to drought stress under controlled conditions, *D. cochinchinensis* was  
271 more anisohydric than *D. oliveri*, which means that *D. cochinchinensis*, as a pioneering  
272 species with faster growth, optimises carbon assimilation and better tolerates reduced water  
273 availability<sup>3</sup>. *D. oliveri* is often found in moist areas and along streams and rivers<sup>40</sup>, and the  
274 morphological characteristics of its seeds suggest that secondary dispersal by water is likely<sup>32</sup>.  
275 This could explain how isothermality, which is a useful metric in tropical environments<sup>41</sup> and  
276 shown to influence plant height growth<sup>42</sup>, had a dominant effect in the adaptive variation only  
277 in *D. cochinchinensis*. Pioneering species maximise height growth in early successional  
278 habitats to meet their light requirements<sup>43</sup>, consistent with the observation of higher  
279 photosynthetic pigment levels in *D. cochinchinensis*<sup>3</sup>. On the other hand, the effect of



280 precipitation of the wettest quarter could act on selection in seed dispersal and survival in *D.*  
281 *oliveri* in the wet season. Temperature and precipitation, and their variability such as  
282 isothermality<sup>44</sup> have been widely reported as the most important drivers shaping patterns of  
283 productivity and adaptation in tree species across the world<sup>45–47</sup>.

284 To fill the current gaps in existing conservation actions, populations that are  
285 underrepresented but display distinct adaptive variation should be prioritised to avoid the  
286 potential loss of unique genetic diversity. Populations at the edge of the species ranges should  
287 be prioritised based on our findings on adaptive variation showing their distinct allelic  
288 frequencies and adaptation; however, they are currently underrepresented in conservation  
289 efforts and existing protected area networks. Importantly, hotspots of differential adaptive  
290 variation near the edges of species ranges are shared between *D. cochinchinensis* and *D.*  
291 *oliveri*. This observation reinforces the role of marginal populations in preserving  
292 evolutionary potential for range expansion and persistence due to their adaptation to distinct  
293 environmental conditions<sup>48</sup>.

294

## 295 **Genomic vulnerability under different climate change scenarios**

296 Genetic offset in the form of Euclidean distance represented the mismatch between  
297 current and future gene-environment association, which was modelled over five general  
298 circulation models (GCMs), namely MIROC6, BCC-CSM2-MR, IPSL-CM6A-LR, CNRM-  
299 ESM2-1, MRI-ESM2-0, under WCRP CMIP6 (Supplementary Figure 10). For both  
300 *Dalbergia* species, genetic offset generally increased over time ( $P = 2.71e-10$ ) and shared  
301 socioeconomic pathway ( $P = 4.54e-14$ ), which implies increased carbon emission (Figure 6a,  
302 Supplementary Table 10). However, *D. cochinchinensis* shows a significantly larger increase  
303 in genetic offset over time compared to *D. oliveri* ( $P = 0.025$ ), suggesting that *D.*  
304 *cochinchinensis* is more susceptible to any mismatch of current genotypes and future climate.

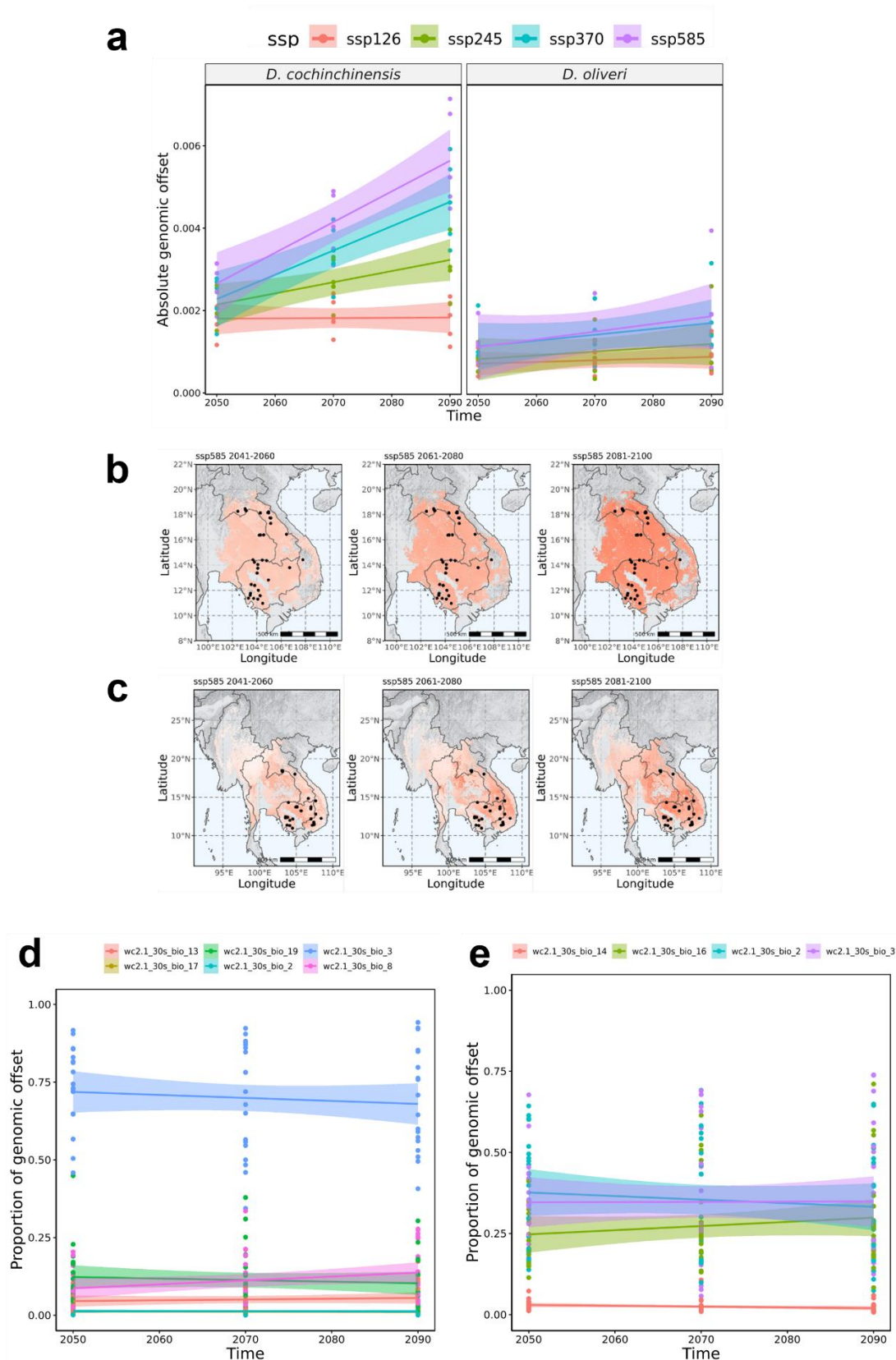
305 The geographic patterns of genetic offset also differed between the two species: *D.*  
306 *cochinchinensis* had an increasing offset across the entire range, while *D. oliveri* had a  
307 distinctly high offset in the southeast part of the range (Figure 6b–c). The variation in  
308 genomic offset between two species was mainly driven by the strong association with  
309 isothermality (*wc2.1\_30s\_bio\_3*) in *D. cochinchinensis*, as demonstrated in the GF model, as  
310 it contributed to ~75% of the genomic offset on average (Figure 6d). Isothermality had a  
311 smaller effect (~35%) in *D. oliveri* (Figure 6e).

312 Our prediction contrasts with a separate sensitivity-and-exposure modelling study  
313 which predicted that *D. oliveri* is likely to be slightly more vulnerable to climate change by  
314 2055 (2041–2070 period) than *D. cochinchinensis*<sup>12</sup>. It used growth rate and seed weight as  
315 proxy traits, predicting that both species have equally high sensitivity to climate change, but  
316 that *D. oliveri* is more exposed to the threat. Our findings predict that the dominant  
317 environment factor of isothermality could give more weight to the species' vulnerability. As  
318 discussed, isothermality is likely to affect the productivity and growth in pioneering species  
319 like *D. cochinchinensis* more than later successional species like *D. oliveri*. Our work  
320 supports that isothermality and other temperature variation factors will serve as more reliable  
321 indicators to predict the climate response of *D. cochinchinensis* and encourages further  
322 studies of this response, such as greenhouse or common garden experiments to validate the  
323 prediction with empirical data.

324 The different geographical patterns of genomic vulnerability support species-specific  
325 recommendations in conservation and restoration. While climate change is likely to affect *D.*  
326 *cochinchinensis* evenly across its range, greater attention is needed on the representation of  
327 adaptive variation in germplasm collection and conservation units; sampling should target  
328 edge populations in particular as they show potential signals of local adaptation, where the  
329 environmental associations between adaptive and neutral variation are the greatest. By

330 contrast, we recommend targeting hotspots of vulnerability in *D. oliveri*, especially around  
331 the borders between Cambodia, Laos, Vietnam, and Thailand, to improve conservation  
332 efforts.

333 In a rapidly changing environment, forest trees either persist through migration or  
334 phenotypic plasticity, or will extirpate<sup>45</sup> when environmental change outpaces adaptation  
335 potential. The spatially explicit model of genomic vulnerability helps to develop conservation  
336 decisions balancing between *in situ* adaptation and assisted migration, as populations with  
337 lower vulnerability are likely to persist through adaptation<sup>49</sup>.

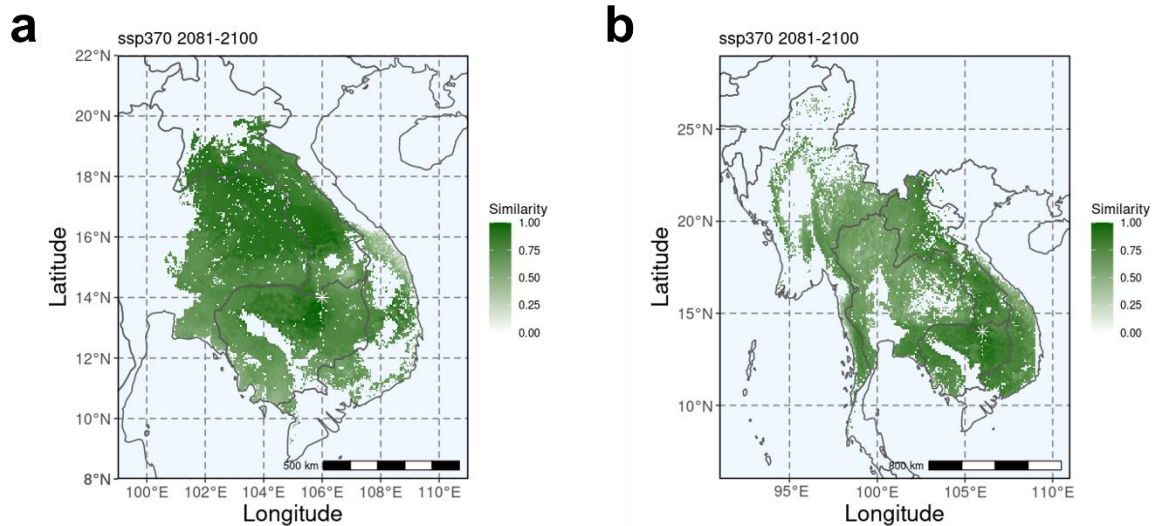


338

339 **Figure 6.** (a) Absolute genomic offset of gene-environment association, quantified as the Euclidean distance, of *D.*  
 340 *cochinchinensis* and *D. oliveri* in 4 SSPs (126, 245, 370, and 585) over three bidecades (2041–2060, 2061–2080, 2081–  
 341 2100) averaged across five GCMs (BCC-CSM2-MR, CNRM-ESM2-1, IPSL-CM6A-LR, MIROC6, MRI-ESM2-0). Scaled  
 342 genomic offset across the range of (b) *D. cochinchinensis* and (c) *D. oliveri*, using SSP585 between 2041 and 2060 as an  
 343 example. Proportion of genomic variation explained by environmental variables in (d) *D. cochinchinensis* and (e) *D. oliveri*.

## 344 **Genomic model-enabled assisted migration and restoration**

345 We developed *seedeR*, an open-source web application that is freely available from  
346 <https://trainingidn.shinyapps.io/seedeR/>, where users can input the species (*D.*  
347 *cochinchinensis* or *D. oliveri*), shared socioeconomic pathways (SSP), time period, and  
348 geographical coordinates of the target restoration or planting site. With these inputs, *seedeR*  
349 predicts the genomic similarity between a current germplasm source and target site from  
350 allelic frequency turnover functions and genetic offset and projects them onto the species  
351 range. We demonstrate the utility of *seedeR* for a hypothetical target restoration site (106° N,  
352 14° E) in northeast Cambodia for both *D. cochinchinensis* and *D. oliveri*, under the future  
353 climate scenario of SSP370 between 2081 and 2100 (Figure 7). In both predictions, the  
354 genomic similarity was the highest at proximity to several hundreds of kilometres and  
355 decreased when further away. Commonly, coastal regions in northeast Vietnam, which were  
356 predicted to have the strongest local adaptation in both species, showed a lower genomic  
357 similarity. The geographical scale of suitable seed sources has an important implication as too  
358 many forest landscape projects collect seeds from very close (a few kilometres) to restoration  
359 sites to feed the “local is best” paradigm<sup>50</sup>, while our predictions showed otherwise. It is also  
360 important to note that local tree populations in landscapes in need of restoration are often  
361 degraded and have low genetic diversity. Genetic quality of seed should be ensured by  
362 collecting seed from large populations and many unrelated trees, even if this means collecting  
363 from trees at distances much further from the target restoration site.



364

365 **Figure 7.** Genomic similarity (scaled between 0, most dissimilar, and 1, most similar) between a hypothetical future  
366 restoration site (106° N, 14° E) and the current potential germplasm sources under the future climate scenario of SSP370  
367 between 2081 and 2100 for (a) *D. cochinchinensis* and (b) *D. oliveri* predicted on *seedeR*  
368 (<https://trainingidn.shinyapps.io/seedeR/>).

369

Matching seed sources and restoration sites remains one of the keys for effective

370

conservation and restoration<sup>51</sup>, in line with the importance of adaptive variation and potential

371

in genetic materials. Our genome-enabled prediction tool considers the future climate of

372

restoration sites, which in turn will greatly influence the future resilience and productivity of

373

these species. In the case of maladaptation and extirpation due to environmental change<sup>52</sup>,

374

when the classical preference for local provenance may no longer hold, deliberate transfer of

375

germplasm along climate gradients may be necessary<sup>53</sup>. Especially in the case of *Dalbergia*,

376

when many local populations have extirpated or are very small in size, and large

377

environmental association was predicted, assisted migration based on admixture and

378

predictive provenancing are deemed more appropriate for the species to facilitate adaptation

379

of the populations under climate change<sup>54</sup>. Genetic materials from regions with strong

380

adaptive genomic variation, such as coastal Vietnam, can be moved to suitable regions using

381

the *seedeR* prediction to facilitate gene flow and maintain unique genetic components of the

382

population by admixture<sup>53</sup>. Hotspots of vulnerable populations such as those in northern

383

Cambodia are suitable to be moved to new suitable areas to prevent loss of genetic diversity.



384           The *seedeR* application helps to visualize these spatially explicit predictive models of  
385 genomic vulnerability and match, which are most useful to frontline practitioners and  
386 managers<sup>55</sup>. Not only can it inform conservation and management strategies, but by  
387 simplifying the analytical pipelines through a user-friendly platform, it will also directly  
388 reduce the gap between conservation and genomics; a challenge faced for dissemination of  
389 genomic knowledge<sup>56</sup>.

390

## 391 **Narrowing the gap between conservation and genomics**

392           Our study characterises range-wide gene-environment association in two sympatric  
393 endangered species, *D. cochinchinensis* and *D. oliveri*, for which there was virtually no prior  
394 knowledge on adaptability. Building on previous understanding of their different  
395 physiologies, we demonstrate their differential adaptive characteristics, which point to  
396 species-specific implications for their conservation. These findings on differential genomic  
397 adaptation between sympatric species sheds novel understanding on tropical forests, which in  
398 particular harbour many threatened species, at risk from threats associated with climate  
399 change.

400           We show how genomic technologies can directly support rapid decision-making and  
401 conservation activities. The separation between scientific and conservation communities  
402 represents a long-standing challenge, such that advances in scientific research and  
403 specifically genomic technologies are often inaccessible to the conservation side, which  
404 hinders translational science<sup>57,58</sup>. Through engagement with diverse stakeholders and  
405 conservation activities, we were strongly motivated to deliver the results of this study in a  
406 user-friendly (e.g. *seedeR*) and spatially explicit manner that can be integrated with ongoing  
407 conservation work.

## 408 **Methods**

### 409 *Plant materials and sample preparation for genome assemblies*

410 Dried seeds of *Dalbergia cochinchinensis* and *D. oliveri* were collected from the  
411 Bolikhamxay, Khamkend, Laos, and Phnom Penh, Cambodia in 2018 by their forestry  
412 authorities respectively. We germinated the seeds in a greenhouse at 30°C with 16L/8D  
413 photoperiod. Leaf tissues were harvested from a selected 1-year-old individual for each  
414 species and ground in liquid nitrogen with a mortar and pestle.

415 High-molecular-weight genomic DNA was extracted from the reference individual  
416 with Carlson lysis buffer (100 mM Tris-HCl, pH 9.5, 2% CTAB, 1.4 M NaCl, 1% PEG 8000,  
417 20 mM EDTA) followed by purification using the QIAGEN Genomic-tip 500/G. The  
418 quantity and quality of genomic DNA were determined with NanoDrop 2000 (Thermo,  
419 Wilmington, United States) and Qubit 4 (Thermo Fisher Scientific, United Kingdom). DNA  
420 integrity was preliminary assessed with a 0.4% agarose gel against a NEB Quick-Load® 1 kb  
421 Extend DNA Ladder. A DNA sample passed the quality check only when a single band could  
422 be mapped near a lambda DNA band (~ 48.5 kb).

423

### 424 *Genomic sequencing and assembly of D. cochinchinensis*

425 For Oxford Nanopore sequencing, 9 µg of extracted DNA was size-selected using the  
426 Circulomics Short Read Eliminator XL Kit (Maryland, United States) to deplete fragments <  
427 40 Kbp. Three libraries were prepared each starting from 3 µg of size-selected DNA was  
428 used in each library preparation with the Oxford Nanopore Technologies Ligation  
429 Sequencing Kit (SQK-LSK110). The libraries were sequenced on two R10.3 (FLO-109D)  
430 flow cells on a GridION sequencer for ~ 72 hours. Real-time basecalling was performed in  
431 MinKNOW release 19.10.1. Raw reads with Phred score lower than 8 were filtered.



432 For PacBio sequencing, DNA samples were sent to the Genomics & Cell  
433 Characterization Core Facility at the University of Oregon for DNA library preparation and  
434 sequencing. Throughout the sample preparation, the quality of DNA was assessed using  
435 Fragment Analyzer 1.2.0.11 (Agilent, United States). 20 µg of unsheared genomic DNA was  
436 used for library preparation using the SMRTbell Express Template Prep Kit 2.0 (Pacific  
437 Biosciences, United States). The library was size selected using the BluePippin system (Sage  
438 Science, United States) at 45 kb and then sequenced on a single SMRT 8M cell on a Sequel II  
439 System (2.0 chemistry) using the Continuous Long-Read Sequencing (CLR) mode with a  
440 movie time of 30 hours.

441 For Hi-C sequencing, we harvested 0.5 g of fresh leaf from the same reference  
442 individual and immediately cross-linked the finely chopped tissue in 1% formaldehyde for 20  
443 minutes. The cross-linking was then quenched with glycine (125 mM). The cross-linked  
444 samples were ground in liquid nitrogen with a mortar and pestle and shipped to Phase  
445 Genomics (Seattle, USA) for library preparation and sequencing. The Hi-C library was  
446 prepared with the restriction enzyme DpnII, proximity-ligated, and reverse-crosslinked using  
447 Proximo Hi-C Kit (Plant) v2.0 (Phase Genomics, Seattle, USA). The library was sequenced  
448 on a HiSeq4000 for ~300 M 150-bp paired-end sequencing.

449

#### 450 ***Genomic sequencing of D. oliveri***

451 For Nanopore sequencing, the same protocol and procedure were used as for *D.*  
452 *cochinchinensis* (see above).

453 For Pore-C sequencing, the library was prepared with the protocol and reagents  
454 described by Belaghzal et al.<sup>59</sup> with minor modifications. We harvested 2 g of fresh leaf from  
455 the same reference individual as for the Nanopore library and immediately cross-linked the  
456 finely chopped tissues in 1% formaldehyde for 20 minutes. The cross-linking was quenched

457 with 125 mM glycine for 20 minutes and then the samples were ground in liquid nitrogen  
458 with a mortar and a pestle. Cell nuclei were isolated with a buffer containing 10 mM Trizma,  
459 80 mM KCl, 10 mM EDTA, 1 mM spermidine trihydrochloride, 1 mM spermine  
460 tetrahydrochloride, 500 mM sucrose, 1% (w/v) PVP-40, 0.5% (v/v) Triton X-100, and 0.25%  
461 (v/v)  $\beta$ -mercaptoethanol, and then passed through a 40  $\mu$ m cell strainer. The suspension was  
462 centrifuged at 3,000 g, according to the estimated genome size of  $\sim$  700 Mbp. Chromatin was  
463 denatured with the restriction enzyme NlaIII at a final concentration of 1 U/ $\mu$ L (New England  
464 Biolabs, United Kingdom) at 37°C for 18 hours. The enzyme was heat-denatured at 65°C for  
465 20 minutes at 300 rpm rotation in a thermomixer. Proximity ligation, protein degradation,  
466 decrosslinking, and DNA extraction were performed according to the original Belaghzal  
467 protocol. The Pore-C library was prepared with the Oxford Nanopore Technologies Ligation  
468 Sequencing Kit (SQK-LSK110), then sequenced on two R10.3 (FLO-109D) Nanopore flow  
469 cells on a GridION sequencer for  $\sim$  72 hours. The flow cell was washed once every 24 hour  
470 with the Flow Cell Wash Kit (EXP-WSH003).

471

### 472 ***Assembly pipelines***

473 Raw reads shorter than 500 bp were filtered. Due to the heterozygous nature of the  
474 wild individual, we assembled the sequences with Canu 2.1.1 using the options  
475 “corOutCoverage=200 correctedErrorRate=0.16 batOptions=-dg 3 -db 3 -dr 1 -ca 500 -cp  
476 50”. We then used purge\_haplotigs v1.1.1 to collapse the assembly by separating the primary  
477 assembly and haplotigs.

478 Hi-C reads (for *D. cochinchinensis*) were mapped to the draft genome assembly using  
479 hicstuff 2.3.2<sup>60</sup> to generate the contact matrix, which was then used to scaffold and polish the  
480 assembly using instaGRAAL 0.1.2<sup>61</sup> with default options to produce the final assembly  
481 Dacoc 1.4 after removing contamination.

482 Pore-C reads (for *D. oliveri*) were mapped to the draft genome assembly and used to  
483 generate contact map with the Pore-C-Snakemake ([https://github.com/nanoporetech/Pore-C-](https://github.com/nanoporetech/Pore-C-Snakemake)  
484 [Snakemake](#)) and produce a merged\_nodups (.mnd) file, which contains a duplicate-free list of  
485 paired alignments from the Pore-C reads to the draft assembly. The draft assembly and the  
486 merged\_nodups file were used for scaffolding in 3D-DNA (version 180419) and produce the  
487 final genome Daoli 0.3.

488 To validate the scaffold arrangement, Daoli 0.3 was aligned to that of *D.*  
489 *cochinchinensis* (Dacoc 1.4) using minimap2 and D-GENIES<sup>62</sup> to produce a dot plot for  
490 visualising similarity, repetitions, breaks, and inversions, with a minimum identity of 0.25.

491

#### 492 ***De novo repeat library***

493 A *de novo* repeat library was constructed using RepeatModeler 2.0.1<sup>63</sup>, which  
494 incorporated RECON 1.08<sup>64</sup>, RepeatScout 1.0.6<sup>65</sup>, and TRF 4.0.9<sup>66</sup> for identification and  
495 classification of repeat families. We then used RepeatMasker 4.1.1<sup>67</sup> to mask low complex or  
496 simple repeats only (“-noint”). A *de novo* library of long terminal repeat (LTR)  
497 retrotransposons was constructed on the simple-repeat-masked genome using LTRharvest<sup>68</sup>  
498 and annotated with the GyDB database and profile HMMs using LTRdigest<sup>69</sup> module in the  
499 genomertools 1.6.1 pipeline. Predicted LTR elements with no protein domain hits were  
500 removed from the library. We applied the RepeatClassifier module in RepeatModeler to  
501 format both repeat libraries. We merged the libraries together and clustered the sequences  
502 that were  $\geq 80\%$  identical by CD-HIT-EST 4.8.1<sup>70</sup> (“-aS 80 -c 0.8 -g 1 -G 0 -A 80”) to  
503 produce the final repeat library.

504

#### 505 ***Gene models and annotation***

506 Filtered mRNA-sequencing data for *D. cochinchinensis* (50.5 Gbp) and *D. oliveri*  
507 (54.4 Gbp) from a previous project<sup>27</sup> (NCBI Bioproject: PRJNA593817) were aligned against  
508 the genome assembly using STAR v2.7.6 and assembled using the genome-guided mode of  
509 Trinity v2.13.2. Protein sequences were obtained from *Arabidopsis thaliana* (Araport11)<sup>71</sup>  
510 and *Arachis ipaensis* (Araip1.1)<sup>72</sup>. After soft-masking the genome with the *de novo* repeat  
511 library using RepeatMasker (Dfam libraries 3.2), the transcript and protein evidences were  
512 used to produce gene models using MAKER 3.01.03<sup>73</sup>. The MAKER pipeline was iteratively  
513 run for two more rounds to produce the final gene models. In between each run of MAKER,  
514 the gene models were used to train the *ab initio* gene predictors SNAP (version 2006-07-28)<sup>74</sup>  
515 and AUGUSTUS 3.3.3<sup>75</sup> which were used in the MAKER pipeline. tRNA genes were  
516 predicted with tRNAscan-SE 1.3.1<sup>76</sup>. The quality of the gene models was assessed with two  
517 metrics: the annotation edit distance (AED) in MAKER 3.01.03<sup>73</sup> and the BUSCO score  
518 (v5.1.2)<sup>77</sup>.

519

### 520 ***Population sampling***

521 We obtained a collection of 435 and 331 foliage samples of *Dalbergia*  
522 *cochinchinensis* and *D. oliveri* from 35 and 28 localities across their native range  
523 (Supplementary Table 11). These samples were a combination of those collected in a  
524 previous study<sup>32</sup> and newly between 2019 and 2020. Genomic DNA was purified using a two-  
525 round modified CTAB protocol (2% CTAB, 1.4 M NaCl, 1% PVP-40, 100 mM Tris-Cl pH  
526 8.0, 20 mM EDTA pH 8.0, 1% 2-mercaptoethanol) with sorbitol pre-wash (0.35 M Sorbitol,  
527 1% PVP-40, 100 mM Tris-Cl pH 8.0, and 5 mM EDTA pH 8.0) as the samples were rich in  
528 polyphenols and polysaccharides<sup>78</sup>. Genomic DNA was treated with 5 µL RNase (10  
529 mg/mL). Quality and quantity of the genomic DNA were assessed using NanoDrop One

530 (Thermo, Wilmington, United States) and Qubit dsDNA BR Assay kit on Qubit 4 (Thermo,  
531 Wilmington, United States) respectively.

532

### 533 ***Genotyping-by-sequencing (GbS)***

534 DNA samples were normalised to 200 ng suspended in 10  $\mu$ L water and sent to the  
535 Genomic Analysis Platform, Institute of Integrative and Systems Biology, Université Laval  
536 (Quebec, Canada) for GbS library preparation. DNA was digested with a combination of  
537 restriction enzymes PstI/NsiI/MspI, ligated with barcoded adapter, and pooled to  
538 equimolarity. The pooled library was amplified by PCR and sequenced on a Illumina  
539 NovaSeq6000 S4 with paired-end reads of 150 bp at the G enome Qu ebec Innovation Centre,  
540 (Montreal, Canada).

541

### 542 ***Variant calling***

543 DNA sequence variant calling was done with the Fast-GBS v2.0 pipeline<sup>79</sup>: Illumina  
544 raw reads were demultiplexed with Sabre 1.0<sup>80</sup> and trimmed with Cutadapt 1.18<sup>81</sup> to remove  
545 the adaptors. Trimmed reads shorter than 50 bp were discarded. Reads were aligned against  
546 the Dacoc 1.0 genome (Hung et al., unpublished) and the Daoli 0.1 genome using BWA-  
547 MEM 0.7.17<sup>82</sup>. The SAM alignment files were converted to BAM format and indexed using  
548 SAMtools 1.9<sup>83</sup>. Variant calling was performed in Platypus<sup>84</sup> and variants were filtered with  
549 proportion of missing data of 0.2 and minimum allele frequency (MAF) of 0.01 using  
550 VCFtools 0.1.16<sup>85</sup>. Missing genotype was imputed using Beagle 5.2. Finally, linkage  
551 equilibrium among SNPs was detected using BCFtools 1.9<sup>83</sup>, and one SNP was removed from  
552 all SNP pairs with  $r^2 > 0.5$  in a genomic window of 5 Kbp.

553

### 554 ***Environmental heterogeneity characterisation***

555 Environmental data were obtained from different sources (34 variables in total,  
556 Supplementary Table 12) and represented different measurers of temperature, precipitation,  
557 their seasonality, soil, elevation, and vegetation. We calculated a correlation matrix across the  
558 sampling localities and highly inter-correlated variables (pairwise correlation coefficient  $| >$   
559 0.7) were detected. For each inter-correlated variable pair, the one variable with the largest  
560 mean absolute correlation across all variables was removed.

561

### 562 ***Population genetic structure and identification of putatively adaptive loci***

563 Population genetic structure was assessed with sparse non-negative matrix  
564 factorisation (sNMF) to estimate the number of discrete genetic clusters ( $K$ )<sup>86</sup>. The sNMF  
565 was run for 10 repetitions for each value of  $K$  from 1 to 15 with a maximum iteration of 200.  
566 The optimal  $K$  was selected based on the lowest cross-entropy value from the sNMF run, or  
567 where the value began to plateau. Admixture plots were drawn for  $K = \{2, 4, 8, \text{optimal } K\}$ .  
568 Population structure-based outlier analysis was also conducted with sNMF, in which outlier  
569 SNPs that are significantly differentiated among populations, based on estimated  $F_{ST}$  values  
570 from the ancestry coefficients obtained from sNMF<sup>87</sup>, were obtained and mapped on the 10  
571 putative chromosomes for *D. cochinchinensis* or the 16 longest scaffolds for *D. oliveri* in a  
572 Manhattan plot.

573 We used latent factor mixed modelling (LFMM) to test for significant associations  
574 between environmental variables and SNP allele frequencies. The optimal  $K$  obtained from  
575 the sNMF was used in LFMM to correct for the neutral genetic structure. LFMM was run for  
576 3 repetitions with a maximum iteration of 1,000 and 500 burn-ins.  $Z$ -scores were obtained for  
577 all repetitions for each environmental variable, and then the median was taken for each SNP.  
578 Next, the genomic inflation factor  $\lambda$ , defined as the observed median of  $Z$ -scores divided by

579 the expected median of the chi-squared distribution for each environmental association<sup>88</sup>, was  
580 calculated to calibrate for *P*-values:

$$\lambda = \frac{\text{median}(Z^2)}{\chi_1^2(0.5)}, \text{ such that } P_{\text{adjusted}} = \chi_1^2\left(\frac{Z^2}{\lambda}\right).$$

581

582 The calibration was then inspected on a histogram of *P*-values for each environmental  
583 association. Finally, multiple testing was corrected with the Benjamini and Hochberg method  
584 to obtain *Q*-values.

585 The sNMF and LFMM calculations were performed in R 4.1.0 using the packages  
586 LEA 3.4.0<sup>89</sup>.

587

### 588 ***Gradient forest modelling***

589 For all predictions in gradient forest models, resampling was necessary because not  
590 all environmental raster layers had the same resolution and extent. They were all cropped to  
591 the latest-updated modelled and expert-validated species distribution<sup>12</sup> and reprojected to the  
592 WorldClim bioclimatic rasters, as they have the highest resolution, using bilinear  
593 interpolation or nearest neighbour method for continuous and categorical variables  
594 respectively.

595 To correct for the genetic structure, spatial variables were generated using the  
596 principal coordinates of neighbour matrices (PCNM) approach<sup>90</sup>. Only half of the positive  
597 PCNM values were kept. Gradient forest model was used to predict and rank the importance  
598 of environmental variables in genomic variation, as its machine learning algorithm worked  
599 best with minimal prior and confounding variables. Putatively neutral SNPs and putatively  
600 adaptive SNPs were used as the response variables and all the filtered environment variables  
601 and PCNM variables were used as the predictor variables in the gradient forest model for 500  
602 regression trees. The maximum number of splits to evaluate was determined as follows:

$$\text{Maximum number of splits} = \log_2 \frac{(0.368 \times \text{number of predictor variables})}{2}$$

603

604 The turnovers of allelic frequencies were then projected spatially across the latest-  
605 updated predicted species distribution ranges<sup>12</sup> using the fitted gradient forest model and the  
606 environmental values across the range. Principal component analysis (PCA) was used to  
607 summarise the genomic variation across the distribution and the first three principal  
608 components (PC1, PC2, and PC3) were used for visualisation of genomic variation across the  
609 range.

610 The PCAs of turnovers of allelic frequencies between adaptive SNPs and neutral  
611 SNPs were compared using the Procrustes rotation, and its residuals were used to map where  
612 adaptive genomic variation deviates from neutral variation.

613

#### 614 ***Prediction of genomic vulnerability***

615 Future climate projections were obtained from five general circulation models (GCM)  
616 (MIROC6, BCC-CSM2-MR, IPSL-CM6A-LR, CNRM-ESM2-1, MRI-ESM2-0)  
617 participating in the World Climate Research Programme Coupled Model Intercomparison  
618 Project 6 (WCRP CMIP6) for four shared socio-economic pathways (SSPs) (126, 245, 370,  
619 and 585) over four 20-year periods (2021–2040, 2041–2060, 2061–2080, 2081–2100). The  
620 gradient forest model was used to predict patterns of genetic variation and local adaptation  
621 under future environmental scenarios. The allelic frequency turnover function was fitted on  
622 the future landscape and the genomic offset, defined as the required genomic change in a set  
623 of putatively adaptive loci to adapt to a future environment<sup>91</sup>, was calculated in a grid-by-grid  
624 basis using the following equation for Euclidean distance, where  $p$  is the number of  
625 environmental (predictor) variables:



$$\text{Genetic offset} = \sqrt{\sum_{n=1}^p (\text{Future allelic turnover} - \text{Current allelic turnover})^2}$$

626

627 The genetic offset was then scaled across all SSPs and time periods.

628

### 629 ***Prediction of genomic similarity between current germplasm source and future restoration***

#### 630 ***site***

631 It is of practical interest to a range of forestry stake-holders to predict if a current  
632 germplasm source is a good match for future restoration sites, or where to source suitable  
633 germplasm for a proposed restoration site. We developed an interactive web application  
634 based on R Shiny and hosted the application on the shinyapps.io server. *seeder* v 1.0 is open  
635 source and freely available from <https://trainingidn.shinyapps.io/seeder/>. The analysis  
636 workflow consists of the selection of species of interest, time period and future climate  
637 scenario, and the restoration site's geographical coordinates (Supplementary Figure 11).

638 The application maps the predicted turnover of allelic frequencies at a hypothetical  
639 future restoration site onto the current landscape on a grid-by-grid basis, with the genetic  
640 offset calculated as described above. After scaling, the values are reversed on a 0-1 scale to  
641 represent the genomic similarity between the current germplasm source and future restoration  
642 site.

643

#### 644 ***Data availability***

645 The research materials supporting this publication, including genomic assemblies, raw  
646 reads, and annotations, can be publicly accessed either in the Supplementary Information or  
647 in NCBI GenBank under the BioProjects PRJNA841235 and PRJNA841689.

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854 **Competing interests statement**

855 The authors declare no competing interests.

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857 **Author contributions**

858 T.H.H.: designed the study, processed the samples, conducted the Oxford Nanopore  
859 sequencing, conceived and conducted the bioinformatic analyses, drafted the manuscript, and  
860 secured funding for the project;

861 T.S.: collected the samples, revised the manuscript, and secured funding for the project;

862 B.T.: collected the samples, revised the manuscript, and secured funding for the project;

863 V.C.: collected the samples, and revised the manuscript;

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865 C.P.: collected the samples, and revised the manuscript;

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868 H.G.: provided expertise and materials for species distribution models, and revised the  
869 manuscript;

870 R.J.: revised the manuscript, and secured funding for the project;

871 D.H.B.: supervised the study, revised the manuscript, and secured funding for the project;

872 J.J.M.: designed and supervised the study, revised the manuscript, and secured funding for  
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874

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