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Good things take time – diversity effects on tree growth shift from negative to positive during stand development in boreal forests

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1 **Good things take time – diversity effects on tree growth shift from negative**
2 **to positive during stand development in boreal forests**

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[1]

19 **ABSTRACT**

20 1. Long-term grassland biodiversity experiments have shown that diversity effects on
21 productivity tend to strengthen through time, as complementarity among coexisting
22 species increases. But it remains less clear whether this pattern also holds for other
23 ecosystems such as forests, and if so why.

24 2. Here we explore whether diversity effects on tree growth change predictably during stand
25 development in Finland's boreal forests. Using tree ring records from mature forests, we
26 tested whether diameter growth trajectories of dominant tree species growing in mixture
27 differed from those in monoculture. We then compared these results with data from the
28 world's longest running tree diversity experiment, where the same combinations of species
29 sampled in mature forests were planted in 1999.

30 3. We found that diversity effects on tree growth strengthened progressively through time,
31 only becoming significantly positive around 20 years after seedling establishment. This
32 shift coincided with the period in which canopy closure occurs in these forests, at which
33 time trees begin to interact and compete aboveground. These temporal trends were
34 remarkably consistent across different tree species sampled in mature forests, and broadly
35 matched growth responses observed in the much younger experimental plots.

36 4. *Synthesis.* Our results mirror those from grassland ecosystems and suggest that canopy
37 closure is a key phase for promoting niche complementarity in diverse tree communities.
38 They also provide a series of testable hypotheses for the growing number of tree diversity
39 experiments that have been established in recent years.

40 **Key words:** biodiversity–ecosystem functioning; canopy packing; competition for light; non-
41 linear growth models;overyielding; plant–plant interactions; tree diversity experiments; tree rings

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42 INTRODUCTION

43 All things being equal, diverse tree communities generally sequester and store more carbon
44 from the atmosphere than their species-poor counterparts (Morin *et al.* 2011; Vilà *et al.* 2013;
45 Jucker *et al.* 2014a; Fichtner *et al.* 2018). Yet underlying this overall positive relationship
46 between tree diversity and productivity is a considerable degree of spatial and temporal
47 variation in the strength of diversity effects on tree growth (Forrester 2014; Jucker *et al.*
48 2014b, 2016; Searle & Chen 2020). Recent work has highlighted how differences in climate,
49 soils, canopy structure and species composition account for much of the spatial variation in
50 the strength and direction of these diversity effects (Forrester 2014; Toigo *et al.* 2015; Jucker
51 *et al.* 2016; Ratcliffe *et al.* 2016; Baeten *et al.* 2019). However, considerably less is known
52 about how and why diversity effects on tree growth change through time during stand
53 development (Zhang, Chen & Reich 2012; Taylor, Gao & Chen 2020).

54 Long-term grassland biodiversity experiments have shown that diversity effects on
55 productivity tend to strengthen through time (Cardinale *et al.* 2007; Reich *et al.* 2012;
56 Zuppinger-Dingley *et al.* 2014; Guerrero-Ramírez *et al.* 2017). This pattern has been
57 attributed to diverse communities progressively optimizing the use of limiting resources,
58 resulting in stronger complementarity and lower redundancy among coexisting species (Reich
59 *et al.* 2012; Zuppinger-Dingley *et al.* 2014). In forests, numerous mechanisms have been put
60 forward to explain the positive effects of diversity on tree growth, including reduced pest and
61 pathogen loads, trophic interactions, and increased water- and nutrient-use efficiency
62 belowground (Jactel & Brockerhoff 2007; Sapijanskas, Potvin & Loreau 2013; Brassard *et al.*
63 2013; Ammer 2019). But perhaps the most important of these is that by combining species
64 with contrasting crown architectures and abilities to tolerate shade, trees in mixed-species

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65 forests are able to use canopy space more efficiently (Sapijanskas *et al.* 2014; Pretzsch 2014;
66 Jucker, Bouriaud & Coomes 2015; Kunz *et al.* 2019). These crown complementarity effects
67 can alleviate competition for light among neighbouring trees, allowing them to grow faster in
68 mixture (Sapijanskas *et al.* 2014; Williams *et al.* 2017; Kunz *et al.* 2019; Searle & Chen
69 2020).

70 However, unlike in grassland ecosystems where community dynamics are relatively fast, in
71 forests the process of canopy filling is a slow one which unfolds over the course of multiple
72 successive growing seasons during which neighbouring trees expand their crowns and begin
73 competing for light. Consequently, overyielding – whereby species in mixture outperform
74 those in monoculture – may take years to manifest in regenerating stands. This may help
75 explain why, in contrast to observational studies conducted in mature forests, most tree
76 diversity experiments established in temperate and boreal forests in the last 5–10 years have
77 so far found little evidence of overyielding (Haase *et al.* 2015; Verheyen *et al.* 2016;
78 Grossman *et al.* 2018; Kambach *et al.* 2019; although see Williams *et al.* 2017). The problem
79 is that testing this hypothesis would require long-term, annually resolved growth records for
80 trees exposed to different levels of diversity, data which are not typically recorded in forests.

81 Here we overcome this challenge by using tree ring records to reconstruct the growth
82 trajectories of individual trees from stands that span a tree diversity gradient ranging from
83 monocultures to 3-species mixtures. Using this dataset, we explore how diversity effects on
84 tree growth change during the early stages of stand development in regenerating boreal
85 forests in Finland. We hypothesise that diversity effects should become increasingly positive
86 with time and that this shift should coincide with the period of canopy closure – which occurs
87 approximately 20–25 years after a stand-replacing disturbance in these forests (Angelstam &

88 Kuuluvainen 2004; Shorohova *et al.* 2009). To complement this analysis, we then compare
89 these growth responses with those observed in the Satakunta experiment in Finland – one of
90 the world’s longest running tree diversity experiments where the same combinations of
91 species we sampled in closed-canopy forests were planted two decades ago. We expect that
92 temporal trends in the strength of diversity effects on tree growth in these experimental plots
93 should mirror those observed in closed-canopy forests. However, because of the relatively
94 young age of trees in the Satakunta experiment, overyielding will be less evident.

95 **MATERIALS AND METHODS**

96 **Overview**

97 To explore how diversity effects on tree growth vary through time, here we take advantage of
98 two complementary research platforms: the FunDivEUROPE plot network, which captures
99 closed-canopy forests characterised by different levels of tree diversity, and the Satakunta
100 tree diversity experiment. Below we provide an overview of these two platforms before
101 detailing the approach we used to model the effects of diversity on tree growth. For a
102 comprehensive description of the FunDivEUROPE project and of the Satakunta experiment
103 see Baeten *et al.* (2013) and Verheyen *et al.* (2016), respectively.

104 Note that while the FunDivEUROPE network spans multiple sites across Europe, here we
105 focus exclusively on the site in Finland. This is for two main reasons. Firstly, this site lies less
106 than 400 km east of Satakunta (see Appendix S1 in Supporting Information), which is one
107 longest running tree diversity experiments anywhere in the world. The two platforms share
108 the same target tree species – which include *Pinus sylvestris*, *Picea abies* and *Betula pendula*
109 – and replicated plots with all possible combinations of these species are found at both sites

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110 (Table 1). This provides a unique opportunity to compare tree growth responses to diversity
111 in natural and experimental forests in a way that would be hard to do anywhere else.
112 Secondly, the FunDivEUROPE plots in Finland all consist of even-aged stands that have
113 regenerated naturally following clear cutting in the past 40–60 years (Table 1 and Appendix
114 S1). This makes comparing growth trajectories through time and across plots much simpler
115 than would be the case in older, uneven-aged stands.

116 **FunDivEUROPE plot network**

117 As part of the FunDivEUROPE project six study sites were established across Europe,
118 including one in the region of Northern Karelia in eastern Finland. At this site, 28 permanent
119 plots (30 × 30 m in size) with all possible combinations of the three locally dominant tree
120 species – *P. sylvestris*, *P. abies* and *B. pendula* – were established in 2012 in closed-canopy
121 forest stands. This includes seven possible species combinations – three monoculture
122 treatments, three 2-species mixtures and one 3-species mixture – each of which was
123 replicated at least 3 times (Table 1). This full factorial design mimics that of most tree
124 diversity experiment, thus allowing diversity effects to be teased apart from identity and
125 compositional effects. To enable statistically rigorous comparisons across diversity levels, the
126 final list of 28 plots was selected from a wider pool of candidates following a screening
127 procedure that aimed to maximise community evenness while minimising differences in
128 topography, soil properties, climate, stand development stage and management history among
129 plots (for details see Baeten *et al.* 2013 and Jucker *et al.* 2014a). In particular, all plots were
130 established in even-aged stands that regenerated naturally following clear cutting and have
131 not been actively managed. Stand age varied between 40–60 years, resulting in predictable
132 differences in stem density and mean tree size among plots (Table 1). Importantly, however,

133 we found no evidence that these differences in stem density and mean tree size were related
134 to variation in tree diversity among stands when the plots were established (see Appendix S2
135 for details).

136 *Reconstructing temporal growth trends from tree ring data*

137 Within each FunDivEUROPE plot, all stems ≥ 7.5 cm in diameter were mapped, identified to
138 species and permanently marked ($n = 2,146$ stems). For each stem, we measured diameter at
139 1.3 m aboveground (D , in cm) using diameter tape and tree height (H , in m) using a vertex
140 hypsometer (Haglöf AB, Sweden). To reconstruct the growth trajectories of individual trees,
141 in September 2012 we extracted bark-to-pith increment cores from a subset of trees in each
142 plot following a size-stratified random sampling approach (for details see Jucker *et al.*
143 2014a). Specifically, we cored 12 trees per species in monoculture plots and 8 trees per
144 species in all mixture plots ($n = 438$ cores). This approach ensures that the tree size
145 distribution of each plot is adequately captured by the subsample without needing to core all
146 trees in a plot (Nehrbass-Ahles *et al.* 2014). This is important, as growth trajectories and
147 responses to competition of canopy dominant and suppressed trees can vary considerably
148 (Luo *et al.* 2020).

149 Wood cores were extracted using a 5.15 mm diameter increment borer (Haglöf AB, Sweden)
150 and stored in polycarbonate sheeting to air dry. Cores were then mounted on wooden boards
151 and sanded with progressively finer grit sizes before being digitally scanned using a high-
152 resolution flatbed scanner (2400 dpi optical resolution). From the scanned images we
153 measured annual radial increments for all cored trees using the software CDendro (Cybis
154 Elektronik & Data, Sweden). Individual chronologies were crossdated against species-level
155 reference curves generated by pooling all samples belonging to a given species to detect any

156 misplaced or missing ring boundaries. From these chronologies we calculated the annual
157 diameter increment of each cored tree (D_{incr} , in cm yr^{-1}), as well as its age. For trees in which
158 cores did not include the pith, we estimated the number of missing rings by first calculating
159 the distance to pith from the innermost visible ring using the pith locator tool in CDendro and
160 then dividing this distance by the mean increment of the five innermost rings (Rozas 2003).
161 Finally, the true age of each tree was adjusted to account for the number of years needed for
162 trees to reach a height of 1.3 m at which cores were extracted. We did this by fitting species-
163 specific height–age functions using data from the Satakunta experiment (see section below
164 and Appendix S3 for details). We chose to use D_{incr} to represent tree growth instead of basal
165 area increments because the former showed a simpler relationship with tree age which we
166 were able to capture using well established non-linear plant growth models (see below and
167 Appendix S4 for details). The disadvantage of D_{incr} is that, compared to basal area increments,
168 it is a poorer surrogate of whole-tree biomass growth. We note, however, that replacing D_{incr}
169 with basal area increments in our analysis did not affect our results (Appendix S4).

170 **Satakunta tree diversity experiment**

171 The Satakunta tree diversity experiment was established in the Satakunta region of
172 southwestern Finland in 1999. It forms part of TreeDivNet – a global network of tree
173 diversity experiments – of which it is the longest running study and the only one in the boreal
174 forest biome (Verheyen *et al.* 2016). The experiment includes 114 plots (20×20 m in size) in
175 which different combinations of five target tree species were planted in clear-cut areas (Table
176 1). Diversity treatment include monocultures, 2-, 3- and 5-species mixtures. Plots are
177 grouped into three blocks, with all species compositions replicated twice within each block.
178 The target species include *P. sylvestris*, *P. abies* and *B. pendula*, as well as *Larix sibirica* and

179 *Alnus glutinosa*. For the purposes of this study only plots which feature combinations of *P.*
180 *sylvestris*, *P. abies* and *B. pendula* were analysed (42 plots; 14 × 3 blocks). 169 seedlings
181 were planted in each plot (13 × 13 rows with seedlings 1.5 m apart). Seedlings of *P. abies*
182 were two years old at the time of planting, while those of *P. sylvestris* and *B. pendula* were
183 one. An equal number of seedlings was planted for each species in the mixture treatments,
184 but planting locations inside the plots were assigned randomly.

185 *Tree growth measurements*

186 Tree growth was monitored at four points in time during the experiment. In 2004, 2009 and
187 2011, *D* and *H* were measured for a random subset of 10 trees per species in each plot.
188 Additionally, because only 53% of selected trees had reached a height of 1.3 m by age seven,
189 in 2004 we also recorded the basal stem diameter at 10 cm aboveground (D_{base} , in cm) of
190 each tree. While D_{base} was, on average, 2.3 cm greater than *D*, the two measures of tree size
191 were closely correlated to one another (Pearson's correlation coefficient = 0.77, $P < 0.0001$).
192 In 2016, an additional census was conducted, during which *D* was measured for a random
193 subset of 5 trees per species in each plot. However, because half of the Satakunta plots were
194 experimentally thinned in 2013, for the 2016 census we only included growth data from 18
195 unthinned plots. This included three replicate plots per treatment (one per block) for all
196 species combinations, except for *P. sylvestris* monocultures, *P. sylvestris* + *P. abies* 2-species
197 mixtures and *P. sylvestris* + *B. pendula* 2-species mixtures, for which only two replicate plots
198 were sampled.

199 **Using tree ring data to test how diversity effects on growth vary through time in the**
 200 **FunDivEUROPE plots**

201 *Comparing alternative tree growth models*

202 Having reconstructed diameter growth trends from the tree ring records, we then used these
 203 data to model the growth trajectory of trees across the FunDivEUROPE plots to determine
 204 how diversity effects on tree growth vary through time (Fig. 1). We started by comparing
 205 different diameter growth models using the approach outlined in Paine *et al.* (2012). Because
 206 diameter growth tends to vary non-linearly with tree age – with initial increases in growth
 207 rates followed by a decline and levelling-off phase – we used non-linear regression to model
 208 changes in growth rate through time. All models were fit using the *nls* function in R (R Core
 209 Development Team 2019). Following a comprehensive comparison of alternative models
 210 based on AIC (Appendix S4), we settled on the Ricker function (Bolker 2008) to capture how
 211 D_{incr} varies as a function of tree age (A ; in years):

$$D_{incr} = \alpha + \beta A e^{-\gamma A} \quad (1)$$

212 where α , β and γ are parameters to be estimated from the data using a non-linear least squares
 213 approach. This flexible function outperformed all other non-linear plant growth models we
 214 tested (Appendix S4). Integrating eqn 1 provides a function for modelling cumulative
 215 diameter increments through time:

$$D = \alpha A + \frac{\beta(\gamma A + 1)e^{-\gamma A}}{\gamma^2} + \frac{\beta}{\gamma^2} \quad (2)$$

216 where α , β and γ are the same parameters estimated for eqn (1). Eqn 2 allows the diameter of
 217 a tree to be estimated based on its age. This is particularly convenient as it provides a way to

218 directly compare growth trends in the FunDivEUROPE plots to those observed at Satakunta,
219 where tree growth increments were not measured on an annual basis.

220 *Testing the effects of diversity on tree growth through time*

221 Having identified a growth function that captures age-related variation in tree growth for all
222 three study species, we then used this model to quantify how diversity effects on tree growth
223 change through time. To do this, for each species we first fit separate growth models for trees
224 growing in all possible species combinations (i.e., monoculture, the three possible 2-species
225 mixtures and the 3-species mixture). We then used the fitted models to predict D_{incr} and D as
226 a function of tree age for each of these treatments and calculated the differential between tree
227 growth trajectories in monoculture and the mixtures through time (see Fig. 1 for a schematic
228 representation). This allowed us to not only test whether trees in mixture grow faster than
229 those in monoculture, but also determine at what age diversity effects emerge. For the
230 purposes of model fitting we restricted the analysis to include only the first 30 years of
231 growth, as beyond this threshold the number of trees with complete chronologies dropped off
232 sharply (Appendix S1). In order to test whether growth differences between treatments were
233 statistically significant, we used Monte Carlo simulations as implemented by the *predictNLS*
234 function in the *propagate* R package to estimate 95% confidence intervals for each fitted
235 model (Spiess 2018).

236 Our analysis makes two important assumptions about the FunDivEUROPE data which are
237 worth stating explicitly. The first is that species composition and diversity have remained
238 relatively stable since stand establishment. If true, current-day species composition can be
239 combined with tree ring records to infer how diversity effects on growth have changed
240 through time. While we have no information on the community composition of the plots prior

241 to their establishment in 2012, a second census was conducted in 2017. This shows that in the
242 five years following our initial sampling, the species composition of the plots has remained
243 unchanged (Appendix S2). While these observations do not capture the initial phases of stand
244 development in the FunDivEUROPE plots, a second census of the Satakunta plots in 2011
245 revealed almost no changes in community composition during the first 12 years of the
246 experiment (Appendix S2). Together, these data suggest that species composition and
247 diversity are likely to have remained relatively constant during the initial stages of stand
248 development in these forests.

249 The second assumption is that stand structural attributes known to influence tree growth –
250 such as the number and size of trees in a plot (Coomes *et al.* 2014) – vary independently of
251 tree diversity. Note that this does not mean we assume that the number and size of trees in a
252 plot has remained constant through time. Instead, the assumption is that changes in the
253 number and size of trees have been similar among plots, allowing us to directly compare the
254 growth trajectories of trees across the diversity gradient. Supporting this premise, the repeat
255 census data from the FunDivEUROPE plots shows that the number and mean size of trees
256 varies closely with stand age (Appendix S2), following a classic self-thinning pattern (Yoda
257 *et al.* 1963). Crucially, however, at the time of establishing the plots we found no significant
258 differences in mean tree size and density across diversity levels (Appendix S2). A very
259 similar pattern emerged from the Satakunta plots, where rates of stem exclusion during the
260 initial 12 years of the experiment were statistically indistinguishable across the diversity
261 treatments (Appendix S2).

262 **Comparing diversity effects on growth in the FunDivEUROPE and Satakunta plots**

263 To compare diversity effects on tree growth between the FunDivEUROPE plots and the
264 Satakunta experiment, we used mixed-effects models to estimate differences in diameter
265 between trees in monoculture and mixture at each census period of the experiment (2004,
266 2009, 2011 and 2016). For each species, we modelled stem diameter as a function of census
267 year, species composition and their interaction, with plot and experimental block as nested
268 random effects. Year was treated as a categorical variable in the models, as surveys were too
269 few and infrequent to fit continuous tree size–age functions. The interaction between year and
270 species composition tests whether the effects of species mixing on growth changed during the
271 experiment. Fitted models were used to estimate differences in stem diameters between trees
272 in monoculture and mixture at each census period, which we then compared to those
273 observed in FunDivEUROPE plots.

274 Models were fit using the *lme4* package in R (Bates *et al.* 2015). Parametric bootstrapping as
275 implemented by the *bootMer* function was used to generate 95% confidence intervals for the
276 predictions. Note that for the 2004 census we used D_{base} instead of D as a measure of tree
277 size, as by age seven only around 50% of surveyed trees had reached a height of 1.3 m. For
278 all other years we modelled differences in D between treatments. The few trees that had not
279 yet reached a height of 1.3 m by 2009 and 2011 were assigned a value of $D = 0$ (15 and 9
280 trees, respectively).

281 RESULTS

282 Diversity effects on growth in the FunDivEUROPE plots

283 While the shape of the relationship between D_{incr} and age was similar across the three
284 species, clear quantitative differences in their growth trajectories also emerged (Fig. 2). Of
285 the three, *P. sylvestris* was the fastest growing early on (mean D_{incr} before age 15 = 0.81 cm
286 yr^{-1} , compared to 0.69 and 0.72 cm yr^{-1} in *P. abies* and *B. pendula*, respectively). However,
287 *P. sylvestris* also showed the steepest decline in diameter growth rate with age of all three
288 species, and by age 30 growth differences between species had reversed (mean D_{incr} after age
289 30 = 0.31 cm yr^{-1} in *P. sylvestris* compared to 0.41 and 0.40 cm yr^{-1} in *P. abies* and *B.*
290 *pendula*, respectively). As a result, by age 30–35 all three species had reached similar
291 diameters on average (Fig. 2). Clear between-species differences were also observed for
292 height growth, although in this case *B. pendula* grew fastest early on, while the two conifers
293 progressively narrowed the height gap with time (Appendix S3).

294 When we compared the growth trajectories of trees in monoculture and mixture, we found
295 that on average diversity effects on growth tended to shift from mostly negative to
296 overwhelmingly positive during stand development (Fig. 3). This pattern matched our
297 predictions and was remarkably consistent across species and diversity treatments (Fig. 3 and
298 Table 2). By age 35 the average diameter growth rate of a tree in mixture was 25% faster than
299 that of a tree in monoculture (Table 2). This overyielding effect was significantly strongest
300 for trees in the 3-species mixtures (+32%, compared to +22% in the 2-species mixture) and
301 for *B. pendula* (+39% across treatments, compared to +21% and +15% for *P. sylvestris* and
302 *P. abies*, respectively). Moreover, when comparing across species and treatments we found

303 that the average age at which diversity effects on growth shifted to significantly positive was
304 21 (Table 2). This coincides with the period in which regenerating boreal forests in Finland
305 typically achieve canopy closure.

306 **Comparing diversity effects on growth in the FunDivEUROPE and Satakunta plots**

307 The cumulative diameter growth trajectories of trees in the Satakunta experiment were very
308 similar to those observed in the FunDivEUROPE plots (Fig. 2 a–c), although on average *P.*
309 *sylvestris* grew quicker at Satakunta (*D* at age 18 = 11.2 cm, compared to 9.9 cm in the
310 FunDivEUROPE plots). When we compared the effects of diversity on diameter growth
311 between the two platforms, we found good or partial agreement for 7 of the 9 possible species
312 combinations (Fig. 4). In particular, *P. abies* showed similar responses to diversity in the
313 FunDivEUROPE and Satakunta plots, particularly when mixed with *P. sylvestris* (Fig. 4 d)
314 and in the 3-species mixture (Fig. 4 f). Equally, for all three species, temporal trends in
315 diversity effects in the 3-species mixtures were broadly consistent with those observed in the
316 FunDivEUROPE plots (Fig. 4 c,f,i).

317 The clear exception where growth responses to diversity did not match between the two
318 research platforms was the *P. sylvestris* + *B. pendula* mixture. In contrast to what we
319 observed in the FunDivEUROPE plots, *P. sylvestris* trees in this mixture grew significantly
320 slower than their counterparts in monoculture at Satakunta, with no sign of this trend abating
321 by the time of the last census in 2016 (Fig. 4b). As for *B. pendula*, at Satakunta trees in this
322 mixture showed strong signs of overyielding much earlier than in the FunDivEUROPE plots
323 (Fig. 4g). By age 18, the average *B. pendula* tree growing in mixture with *P. sylvestris* at

324 Satakunta was 3.0 cm larger in diameter than its equivalent in monoculture (+34% increase in
325 size).

326 **DISCUSSION**

327 Across the FunDivEUROPE plots we found a clear pattern whereby diversity effects on tree
328 growth shifted from mostly negative to positive during the first 35 years of stand regeneration
329 following clear cutting. This trends was remarkably consistent across species and mixture
330 types (Fig. 3), and closely matches what has previously been observed in long-term grassland
331 biodiversity experiments (Cardinale *et al.* 2007; Reich *et al.* 2012; Zuppinger-Dingley *et al.*
332 2014; Guerrero-Ramírez *et al.* 2017). Observational studies conducted across a range of
333 forest ecosystems have revealed a considerable degree of variation in the strength and even
334 the direction of diversity effects on productivity (Paquette & Messier 2011; Vilà *et al.* 2013;
335 Ratcliffe *et al.* 2016). Previous work has shown that this context-dependency can be partially
336 explained by environmental differences among forest types, such as those associated with
337 climate or soils (Forrester 2014; Jucker *et al.* 2014b, 2016; Toïgo *et al.* 2015; Ratcliffe *et al.*
338 2017). Our study highlights how changes in species interactions during stand development
339 can also play an important role in determining the strength of diversity–productivity
340 relationships in forests (Lasky *et al.* 2014; Taylor *et al.* 2020). It also illustrates the value of
341 focusing on how individual trees respond to species mixing in order to better understand
342 community level responses (Chamagne *et al.* 2017; Fichtner *et al.* 2018).

343 **Canopy packing as a driver of diversity–productivity relationships in forests**

344 On average, overyielding in the FunDivEUROPE plots first became apparent around 20 years
345 after seedling establishment (Fig. 3 and Table 2). This coincides with the period in which

346 boreal forests in norther Europe typically undergo canopy closure and enter the phase of stem
347 exclusion (based on observations in the Satakunta experimental plots; see also: Angelstam &
348 Kuuluvainen 2004; Shorohova *et al.* 2009), lending support to our hypothesis that the process
349 of canopy filling is key to promoting positive diversity–productivity relationships in forests.
350 Growing evidence suggests that by combining tree species with complementary crown
351 architectures, phenologies and abilities to tolerate shade, diverse forests are able to use
352 canopy space more efficiently (Pretzsch 2014; Jucker *et al.* 2015; Williams *et al.* 2017). This
353 in turn alleviates the effects of competition for light among neighbours, allowing trees to
354 grow faster in mixture and pack more densely in space (Sapijanskas *et al.* 2014; Williams *et*
355 *al.* 2017; Kunz *et al.* 2019; Searle & Chen 2020).

356 Despite the low number of tree species present in our study system, differences in their
357 ecological strategies still present numerous opportunities to maximise the use of aboveground
358 space. Firstly, phenological differences between the evergreen conifers and the deciduous *B.*
359 *pendula* can reduce competition for light among neighbouring trees at the onset and end of
360 the growing season. Secondly, while both *P. sylvestris* and *B. pendula* (in particular) are
361 light-demanding species, *P. abies* is able to persist and grow even in low-light conditions
362 (Niinemets & Valladares 2006). These contrasting abilities to tolerate shade are also reflected
363 in differences in the way the three species invest in vertical growth and crown expansion
364 (Appendix S3), which enables them to vertically and horizontally partition canopy space.
365 Finally, these crown complementarity effects can be further enhanced by the ability of
366 individual trees to plastically adapt the vertical distribution of their branches and leaves to
367 suit that of their neighbours (Sapijanskas *et al.* 2014; Pretzsch 2014; Jucker *et al.* 2015). For
368 example, previous work conducted across the FunDiveEUROPE network revealed that trees in

369 mixed-species stands had significantly wider and deeper crowns than their counterparts
370 growing in monoculture (Jucker *et al.* 2015). When scaled up from individual trees to whole
371 stands, these crown complementarity effects allow mixed-species forests to use canopy space
372 more efficiently, thus contributing to overyielding at the community level (Pretzsch 2014;
373 Jucker *et al.* 2015; Williams *et al.* 2017).

374 While our results are consistent with our hypothesis and match patterns observed in faster-
375 developing ecosystems such as grasslands, the FunDivEUROPE plots in Finland only capture
376 the early-to-mid stages of stand development: canopy closure and the beginning of stem
377 exclusion. Understanding how diversity effects on tree growth are likely to change in the
378 latter stages of stand development – when understorey re-initiation begins and stands become
379 multi-layered and uneven aged – remains a priority. However, because of the timescales
380 involved, very few studies have actually tracked stand development long enough to robustly
381 address this type of question (for rare examples see Pretzsch *et al.* 2014 and Madrigal-
382 González *et al.* 2015).

383 Tree rings provide one way to address this challenge by allowing the long-term growth trends
384 of individual trees to be accurately reconstructed. However, they tell us nothing about the
385 past composition of a stand. Consequently, attributing growth responses to diversity becomes
386 progressively harder the further back in time one goes. One way around this is to use a space-
387 for-time substitution, where plots at different stages of stand development are compared.
388 Using this approach, Taylor *et al.* (2020) recently showed that in Canada's boreal forests
389 diversity–productivity relationships tended to peak in mid-successional stands. However, the
390 challenge with this type of study is that accounting for differences in management practices is
391 often made challenging by a lack of historical data, particularly for older stands. Moreover,

392 because of recent climate change, conditions under which forests are regenerating today will
393 often be substantially different to those in which currently mature stands developed in the
394 past. To complement these analyses, it can therefore be useful to pair them with simulation
395 models of forest dynamics (Morin *et al.* 2011). In this respect, Holzwarth *et al.* (2015) used
396 the ecosystem model LPJ-GUESS parameterised for temperate forests to show that diversity
397 effects on productivity are likely to be strongest in early-to-mid successional stands. This is
398 consistent with what we know about forest dynamics in European temperate forests, where
399 shade-casting species such as beech tend to outcompete light-demanding ones, leading to
400 lower tree diversity in late successional stands (Pretzsch *et al.* 2015).

401 While our results are predominantly observational and representative of a single, low-
402 diversity ecosystem, they provide a series of testable hypotheses for the growing number of
403 tree diversity experiments established in recent years. Large-scale syntheses will clarify
404 whether the tendency of diversity effects to strengthen through time is a general one, and if
405 so, help elucidate the mechanisms driving it. Here we focused on one possible explanation for
406 these temporal trends – the slow onset of canopy interactions among neighbouring trees. But
407 other processes are also likely to be at play. For instance, studies in both grasslands and
408 forests have shown that trophic interactions are key to promoting positive biodiversity–
409 ecosystem functioning relationships (Eisenhauer 2012; Ammer 2019), but these interactions
410 take time to establish (Eisenhauer, Reich & Scheu 2012). Similarly, soil nutrients have been
411 shown to influence how quickly diversity effects emerge in grasslands by constraining rates
412 of ecosystem development (Guerrero-Ramírez *et al.* 2017).

413 Future work leveraging networks of tree diversity experiments will also help clarify whether
414 some of the other trends we observe in our data – such as the tendency of diversity to

415 negatively influence growth in the early stages of stand development – also emerge across
416 different species and forest types (Kambach *et al.* 2019). Contrary to our expectations, which
417 were for diversity effects in the earliest stages of stand development to be mostly neutral, 7 of
418 the 9 species combinations in the FunDivEUROPE plots showed negative effects of diversity
419 on tree growth between ages 5–15 (Fig. 3). This initial negative relationship between
420 diversity and growth likely explains why we found no significant differences in mean tree
421 size across the diversity gradient (Appendix S2), as it would have offset any subsequent
422 increases in growth in mixed-species plots. Early synthesis work from tree diversity
423 experiments outside tropical and subtropical regions has mostly revealed neutral effects of
424 diversity on aboveground productivity at a community level (Grossman *et al.* 2018; Kambach
425 *et al.* 2019). This pattern could emerge even if diversity were to negatively influence the
426 early-stage growth of individual trees, provided that survival rates were higher in mixtures.
427 However, even if this were the case, it still begs the question of what might cause individual
428 trees to grow more slowly at first when in mixture. Aboveground interactions seem an
429 unlikely candidate, as competition for light among neighbouring trees would initially be
430 weak. Trophic interactions, both above and belowground (e.g., slower colonization by
431 mutualistic fungi or increased pest and pathogen loads in mixed-species plots), are possible
432 explanations worth exploring further (Eisenhauer 2012; Ammer 2019).

433 **Bridging the gap between observational studies and tree diversity experiments**

434 The fact that positive diversity effects on tree growth in the FunDivEUROPE plots tended to
435 strengthen with time and only became apparent once stands matured enough to achieve
436 canopy closure may explain why most tree diversity experiments established outside the
437 tropics have so far found little evidence that diverse tree communities are more productive

438 than species-poor ones (Haase *et al.* 2015; Verheyen *et al.* 2016; Grossman *et al.* 2018;
439 Kambach *et al.* 2019). Currently, the average duration of the 26 globally-distributed tree
440 diversity experiments that form TreeDivNet is nine years (range 1–20 years, with Satakunta
441 being the oldest; for details see: <http://www.treedivnet.ugent.be> and Verheyen *et al.* 2016).
442 Our results from the FunDivEUROPE plots suggest this may simply not be long enough for
443 the aboveground interactions that underpin the positive effects of diversity on tree growth to
444 manifest themselves, particularly in slower-growing boreal and temperate forests.

445 Exceptions to this pattern are tree diversity experiments established in the tropics and
446 subtropics, where stand regeneration occurs much more rapidly. The two best examples of
447 this are the BEF-China project (Huang *et al.* 2018; Fichtner *et al.* 2018; Kunz *et al.* 2019) and
448 the Sardinilla experiment in Panama (Sapijanskas *et al.* 2014; Schnabel *et al.* 2019), both of
449 which have shown strong effects of diversity on productivity in the first 10 years since
450 planting. What is particularly interesting about these experiments is that both have shown that
451 crown complementarity and canopy filling are key to explaining the positive effects of
452 diversity on productivity (Sapijanskas *et al.* 2014; Kunz *et al.* 2019). Moreover – just as we
453 find in the FunDivEUROPE plots – recent work suggests that in the BEF-China experiment
454 the strength of these diversity effects has been progressively increasing through time (Huang
455 *et al.* 2018).

456 Outside the tropics, experimental evidence for positive diversity–productivity relationships in
457 the early stages of stand development is much more mixed (for a review see Grossman *et al.*
458 2018). The one notable exception are studies from the IDENT network (Tobner *et al.* 2014).
459 For instance, Williams *et al.* (2017) found positive effects of diversity on productivity
460 emerging relatively soon after planting in an experiment established in 2009 at the temperate-

461 boreal forest ecotone in Quebec. Crucially, this study also concluded that increased canopy
462 packing in mixed-species plots was driving positive diversity effects on productivity. The fact
463 that these effects emerged so early in the experiment is likely attributable to the study's
464 design, which involved planting seedlings at extremely high densities to speed up their
465 interaction (planting density = 40,000 seedlings ha⁻¹, almost 10 times as high as Satakunta;
466 Tobner *et al.* 2014).

467 When comparing early-stage tree growth responses to diversity in the Satakunta and
468 FunDivEUROPE plots, we generally found reasonable agreement between the two research
469 platforms (Fig. 4). However, there were a few exceptions, the most notable of which was the
470 behaviour of both *P. sylvestris* and *B. pendula* when grown in combination with one another
471 (Fig. 4b,g). In contrast to what we observed in the FunDivEUROPE plots where both species
472 benefitted from growing in mixture with each other (Fig 3 b,g), at Satakunta only *B. pendula*
473 showed evidence of overyielding when mixed with *P. sylvestris*. By contrast, *P. sylvestris*
474 grew noticeably slower when mixed with *B. pendula*. The fact that we found such marked
475 differences in the behaviour of the same combination of species growing within a few
476 hundred kilometres of each other is less than promising for future efforts to bridge
477 observational and experimental studies of forest dynamics (Kambach *et al.* 2019).

478 There are several plausible explanations for the mismatch we observed. For instance, spatio-
479 temporal differences in climate and soils can strongly influence species interactions
480 (Forrester 2014; Jucker *et al.* 2014b; Pretzsch *et al.* 2015), and generally speaking diversity
481 effects on tree growth have been shown to be strongest in more stressful and less productive
482 environments (Toigo *et al.* 2015; Jucker *et al.* 2016). Mean annual temperature at Satakunta
483 is around 3 °C warmer than in Northern Karelia where the FunDivEUROPE plots were

484 established (Table 1) – a difference that would have been further amplified by the fact that
485 Finland has warmed considerably in the decades that separate when the FunDivEUROPE
486 stands established and the Satakunta experiment was planted. These differences in climate
487 may explain why *P. sylvestris* grew faster at Satakunta (Fig. 2) and could have contributed to
488 shifting the competitive balance between the two species.

489 Another possible explanation for the contrasting responses to diversity in the two platforms is
490 differences in tree density and spatial arrangement (Table 1). As is fairly common practise in
491 tree diversity experiments (e.g., Tobner *et al.* 2014), planting density in the Satakunta plots
492 was higher than what is typically found across managed forests in northern Europe (4,225 ha⁻¹
493 ¹, compared to 1,600–2,000 ha⁻¹ in commercially planted stands in Finland). Planting
494 seedlings at high density encourages species interactions to begin sooner, but it may also
495 fundamentally alter their outcome (Ammer 2019). Finally, an additional contributing factor
496 which is worth considering is herbivory. In particular, browsing pressure by moose has been
497 shown to increase in mixed stands of *P. sylvestris* and *B. pendula* relative to monocultures
498 (Milligan & Koricheva 2013; Nevalainen *et al.* 2016). Moreover, work by Muiruri *et al.*
499 (2015) at Satakunta showed that these differences in browsing can actually alter the growth
500 response of *B. pendula* to mixing, shifting it from positive-saturating at low browsing
501 intensities to neutral under high browsing pressure. Given that between the 1980s – when
502 trees in the FunDivEUROPE plots would have been short enough to be susceptible to moose
503 browsing – and the early 2000s damage by moose more than doubled across Finland’s forests
504 (Nevalainen *et al.* 2016), it is possible that differences in browsing pressure between the two
505 platforms contributed to the discrepancy in the results.

[23]

506 **Conclusions**

507 Using a combination of tree ring records and data from a long-term tree diversity experiment,
508 we find that diversity effects on tree growth change predictably during the early stages of
509 stand development in Finland's boreal forests. In doing so, we take a further step towards
510 reconciling the results of previous studies which suggest that while diversity effects in forests
511 are generally positive, they can also vary substantially through space and time. Our results
512 point to canopy closure as a key phase of stand development during which positive diversity
513 effects on tree growth first emerge. This reinforces the importance of canopy space filling as
514 an ecological mechanism for explaining why diverse forests are, on average, more productive
515 than species-poor ones. It also provides a testable prediction for when positive diversity
516 effects on tree growth should emerge across different forest types. This is critical when it
517 comes to bridging the gap between observational studies – from which most of our
518 understanding of how diversity relates to productivity in forests has traditionally come from –
519 and tree diversity experiments – which have grown rapidly in number and ecological realism
520 in recent years. Overall, our study lends further support to the growing evidence that
521 management and conservation strategies aimed at increasing tree diversity in forests have the
522 potential to enhance carbon sequestration. However, as with most good things, a little
523 patience is needed before we can reap the benefits of what we sow.

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531 **AUTHOR CONTRIBUTIONS**

532 D.A.C., L.F. and O.B. helped design the FunDivEUROPE research platform, while J.K. runs
533 the Satakunta tree diversity experiment; T.J. designed the study, collected the tree ring data,
534 performed the analyses and wrote the first draft of the manuscript. G.I. and O.B. collected
535 and curated the data from the second census of the FunDivEUROPE plots. All authors
536 contributed substantially to revisions.

537 **DATA AVAILABILITY**

538 The authors confirm that data supporting the results of this manuscript will be archived and
539 made freely available on Figshare and that the corresponding DOI will be included at the end
540 of the article.

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- 766

767 TABLES

768 **Table 1:** Summary of the FunDivEUROPE plot network and the Satakunta tree diversity
 769 experiment.

| | FunDivEUROPE network | Satakunta experiment |
|---|--|---|
| Location | 29°04' – 30°22'E, 62°08' – 63°01'N | 21°42' – 22°09'E, 61°39' – 61°42'N |
| Climate ^a | MAT = 2.1 °C ; MAP = 632 mm | MAT = 5.3 °C ; MAP = 586 mm |
| Species pool (target species in bold) | <i>Pinus sylvestris</i> , <i>Picea abies</i> , <i>Betula pendula</i> , <i>Betula pubescens</i> | <i>Pinus sylvestris</i> , <i>Picea abies</i> , <i>Betula pendula</i> , <i>Larix sibirica</i> , <i>Alnus glutinosa</i> |
| No. of plots | 28 plots | 42 plots arranged in 3 blocks ^b |
| Plot size | 30 × 30 m | 20 × 20 m |
| Stem density ^c | 852 stems ha ⁻¹ (range = 444–1911) | 4225 stems ha ⁻¹ |
| Quadratic mean stem diameter ^d | 19.0 cm (range = 12.5–23.1) | |
| Stand age | 42 years (range = 32–49) | 19 years |
| Study design ^e | 3–4 × monocultures 4–5 × 2-species mixtures 3 × 3-species mixtures | 6 × monocultures 6 × 2-species mixtures 6 × 3-species mixtures |
| Sampling design | 12 trees cored in monoculture plots 8 trees cored per species in all mixtures | 10 trees per species per plot in 2004–11 5 trees per species per plot in 2016 |
| No. of growth measurements | 438 individual trees cored 14970 annual growth measurements | 852 individual trees measured 2103 diameter measurements ^f |

^aMean annual temperature (MAT) and mean annual precipitation (MAP) between 1981–2010.

^bThe Satakunta experiment includes a total of 114 plots (38 plots × 3 blocks). Only plots which feature combinations of *P. sylvestris*, *P. abies* and *B. pendula* were used for this study (42 plots; 14 × 3 blocks).

^cFor the FunDivEUROPE plots stem densities include all trees with $D \geq 7.5$ cm in the plot. For the Satakunta experiment 169 trees were initially planted in each plot (13 × 13 rows with seedlings 1.5 m apart).

^dCalculated as $\sqrt{\sum D^2/n}$, where n is the number of stems with $D \geq 7.5$ cm in the plot. See Appendix S2 for the relationship between stem density, quadratic mean stem diameter and stand age in the FunDivEUROPE plots.

^eIn the FunDivEUROPE network *B. pendula* monocultures were replicated 3 times and the 2–species mixture of *B. pendula* and *P. sylvestris* was replicated 4 times.

^fTree diameters in the Satakunta plots were measured in 2004, 2009, 2011 and 2016.

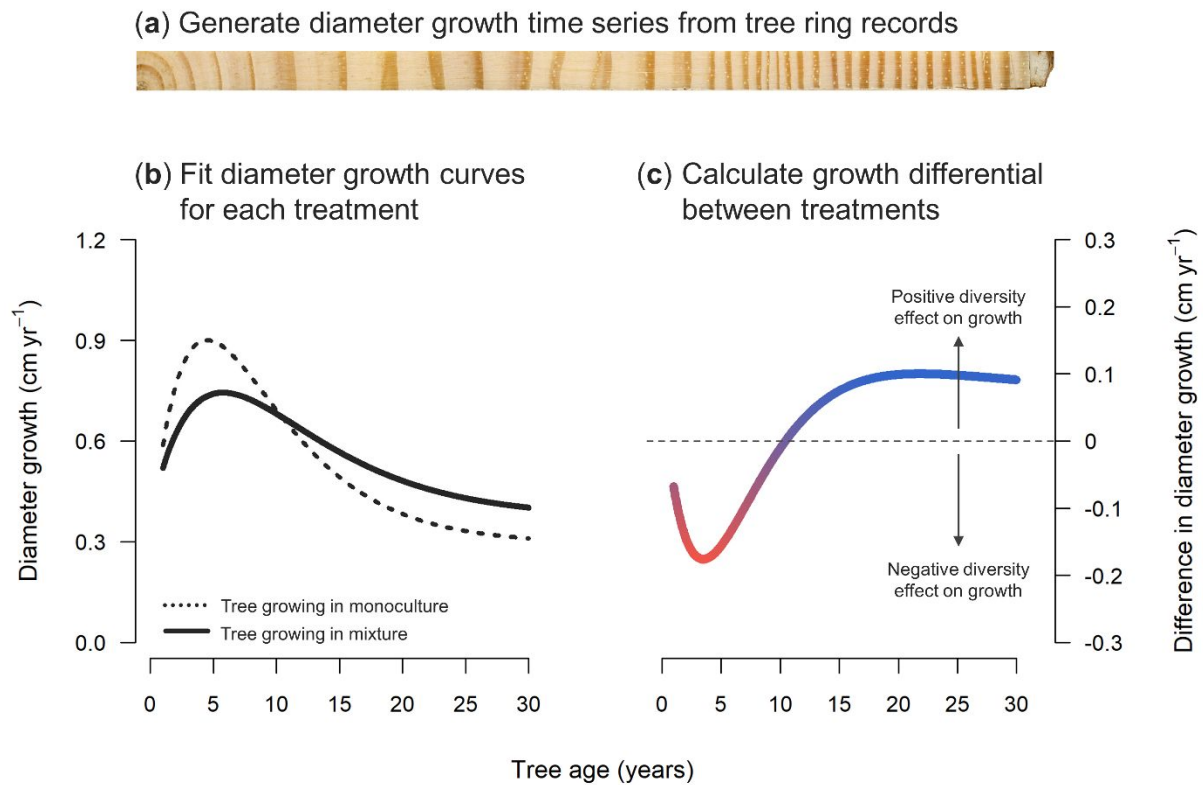
770

771 **Table 2:** Summary statistics of diversity effects on tree growth for the three study species in
 772 the FunDivEUROPE plots (PINSYL: *Pinus sylvestris*; PICABI: *Picea abies*; BETPEN:
 773 *Betula pendula*). The age at which diameter growth in mixture first becomes significantly
 774 greater than that in monoculture was determined by comparing the 95% confidence intervals
 775 of the diameter growth model predictions.

| Species combination | Difference in diameter growth relative to monoculture at age 35 | | | Age at which diameter growth in mixture exceeds that in monoculture | | |
|--------------------------|---|--------|--------|---|--------|--------|
| | PINSYL | PICABI | BETPEN | PINSYL | PICABI | BETPEN |
| PINSYL + PICABI | +16% | +17% | | 22 | 23 | |
| PINSYL + BETPEN | +18% | | +35% | 26 | | 20 |
| PICABI + BETPEN | | +10% | +35% | | 12 | 22 |
| PINSYL + PICABI + BETPEN | +29% | +19% | +47% | 25 | 27 | 16 |

776

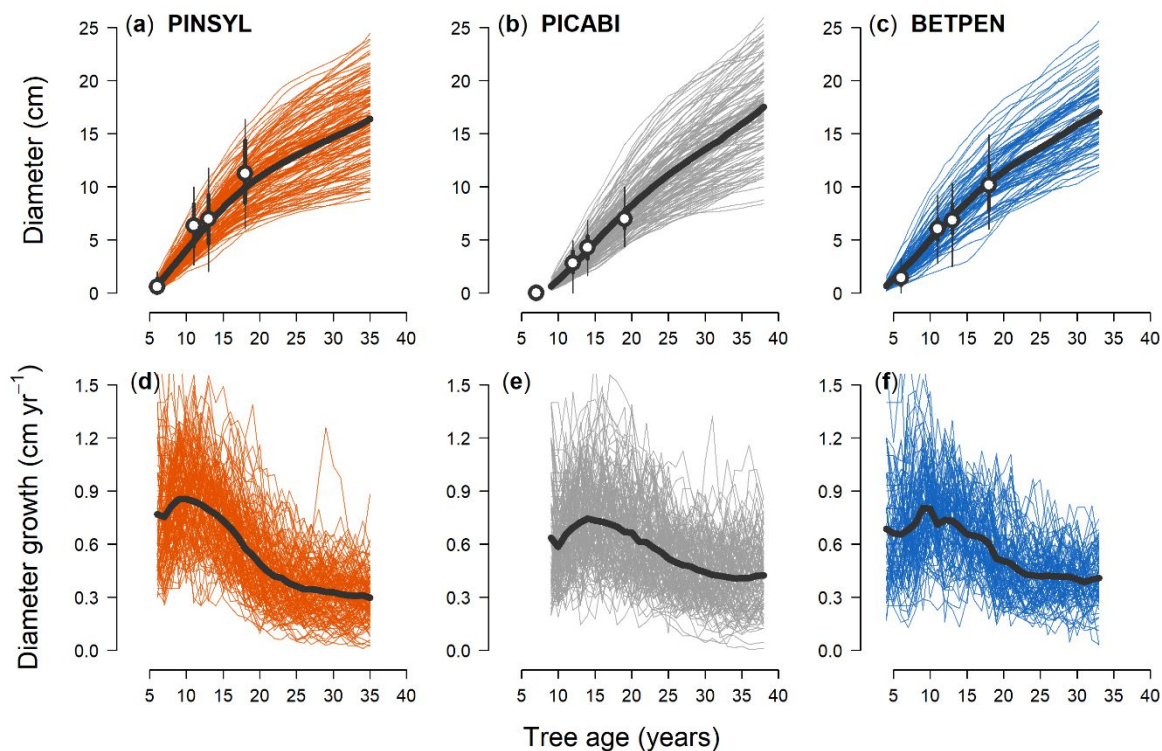
777 FIGURES



778

779 **Fig. 1:** Schematic diagram illustrating how tree ring data from the FunDivEUROPE plots
 780 were used to test how diversity effects on tree growth vary through time. (a) Radial
 781 increments measured from tree cores were used to generate diameter growth time series for
 782 each sampled tree. (b) Non-linear growth models were used to fit diameter growth curves for
 783 trees growing in monoculture (dashed line) and in mixture with other species (solid line). (c)
 784 By calculating the difference between the two growth trajectories we can identify periods
 785 when growth was faster in monoculture (in red below the dashed line) or in mixture (in blue
 786 above the dashed line).

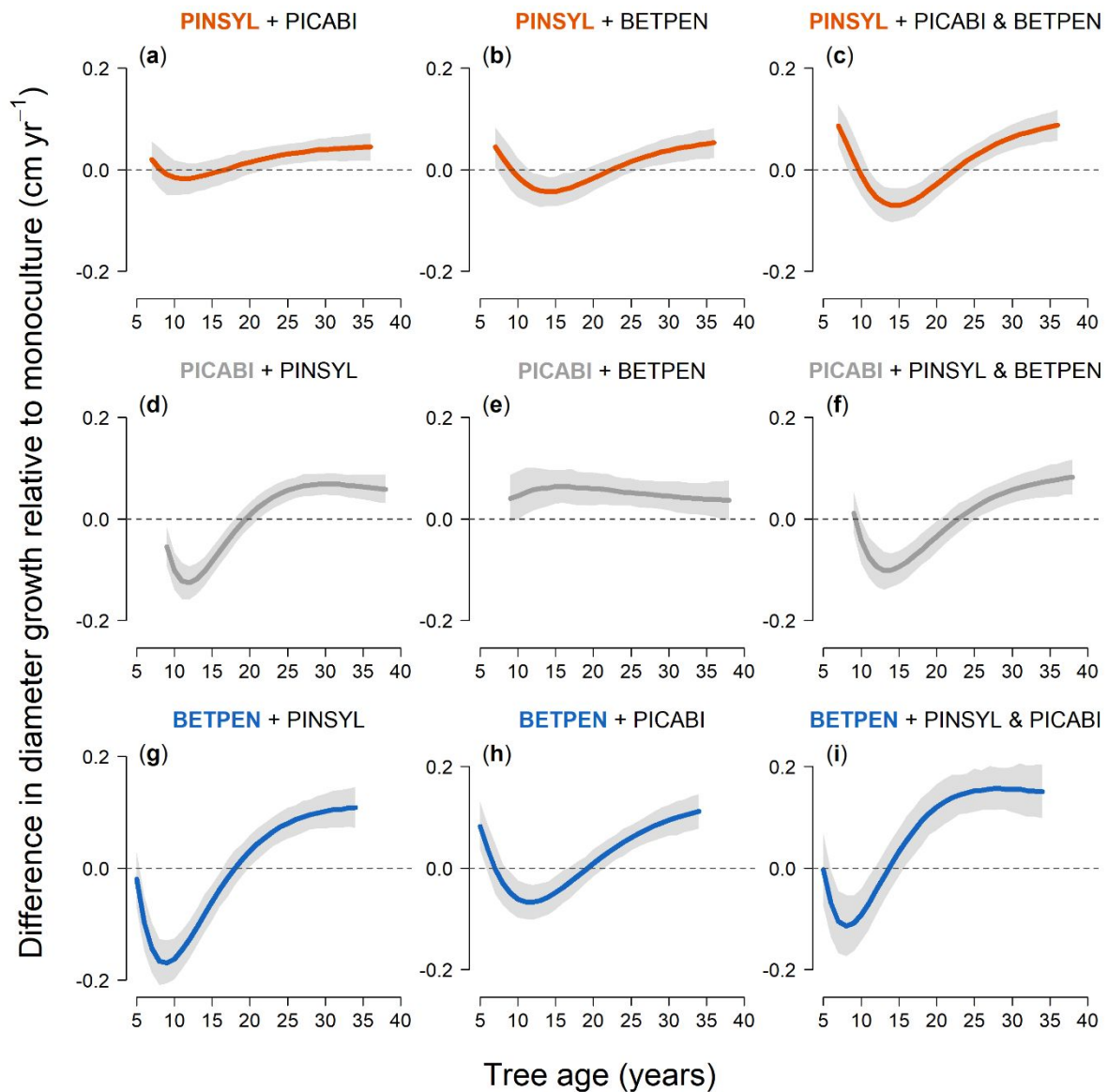
[34]



787

788 **Fig. 2:** Cumulative diameter increment (a–c) and annual diameter growth rate (d–f) through
 789 time for each study species in the FunDivEUROPE plots (PINSYL: *Pinus sylvestris*;
 790 PICABI: *Picea abies*; BETPEN: *Betula pendula*). Thin coloured lines show the growth
 791 trajectory of individual trees, whereas thick black lines correspond to mean values across all
 792 sampled trees. For comparison, empty circles in panels (a–c) show the mean diameter value
 793 of trees in the Satakunta experiment at the four time periods in which they were measured.
 794 Error bars show the interquartile range (thick lines) and 95% range (thin lines) of the
 795 diameter values of the Satakunta trees. Note that a correction was applied to the age of trees
 796 in the FunDivEUROPE plots to account for the fact that tree cores were sampled at a height
 797 of 1.3 m above-ground (see main text and Appendix S3 for details).

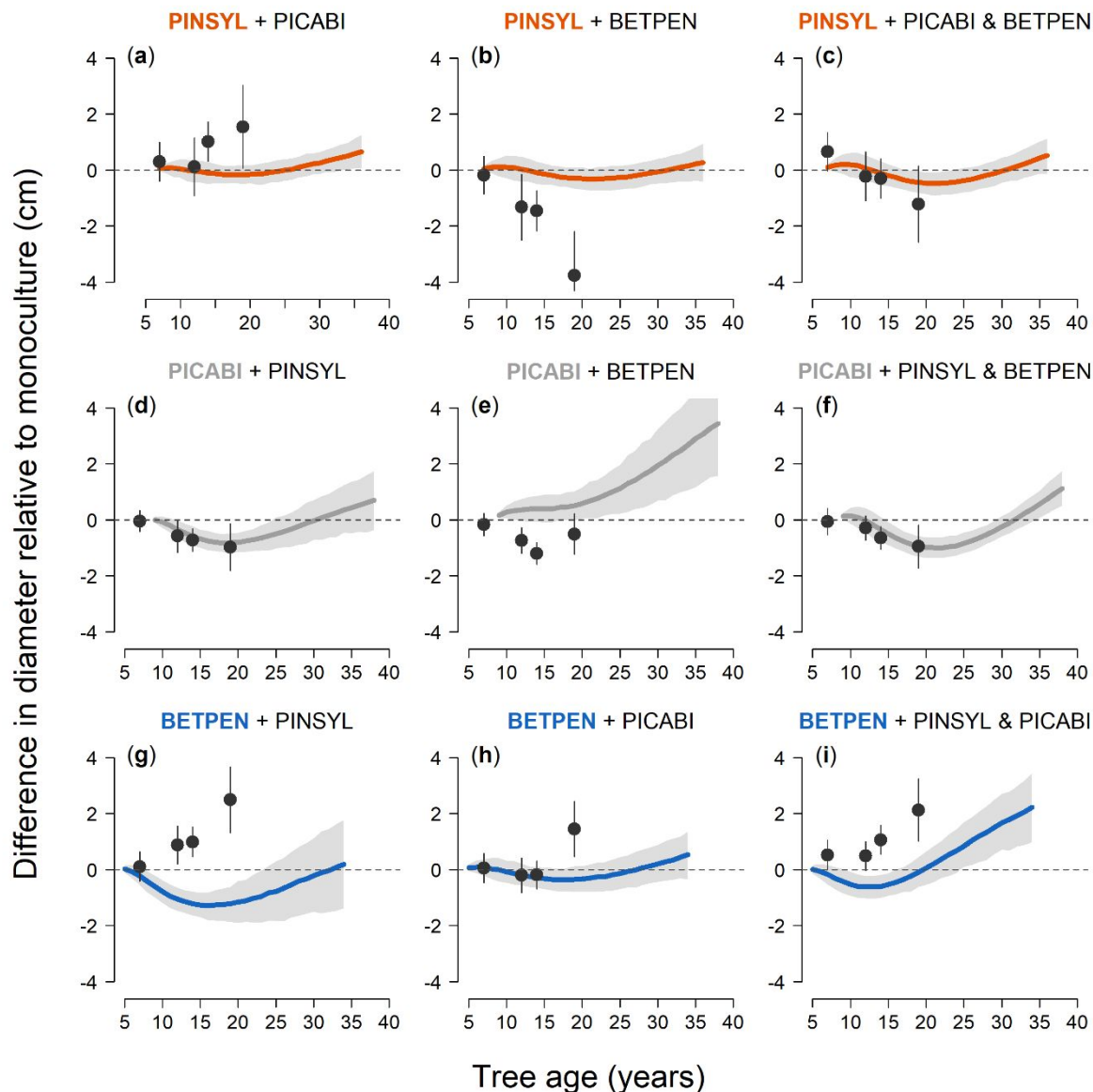
[35]



798

799 **Fig. 3:** Difference in diameter growth between trees in monoculture and those in mixture as a
 800 function of tree age for (a–c) *Pinus sylvestris* (PINSYL), (d–f) *Picea abies* (PICABI) and (g–
 801 i) *Betula pendula* (BETPEN) in the FunDivEUROPE plots. Shaded regions in grey
 802 correspond to the 95% confidence intervals of the curves. See Fig. 1 for a schematic
 803 interpretation of the results.

[36]



804

805 **Fig. 4:** Difference in diameter between trees in monoculture and those in mixture as a
 806 function of tree age for (a–c) *Pinus sylvestris* (PINSYL), (d–f) *Picea abies* (PICABI) and (g–
 807 i) *Betula pendula* (BETPEN) in the FunDivEUROPE plots. Shaded regions in grey
 808 correspond to the 95% confidence intervals of the curves. For comparison, the results of the
 809 same analysis conducted on trees from the Satakunta experiment are shown as filled circles
 810 (mean difference in diameter between monoculture and mixture \pm 95% confidence intervals).

[37]

811 **SUPPORTING INFORMATION**

812 Additional supporting information may be found in the online version of this article:

813 **Appendix S1:** FunDivEUROPE plot network and tree ring data

814 **Appendix S2:** Changes in species composition and stand density through time in the
815 FunDivEUROPE and Satakunta plots

816 **Appendix S3:** Tree height–age curves

817 **Appendix S4:** Comparing alternative tree growth models

Good things take time – diversity effects on tree growth shift from negative to positive during stand development in boreal forests

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Supporting information

| | |
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Appendix S1 | FunDivEUROPE plot network and tree ring data

Plot locations

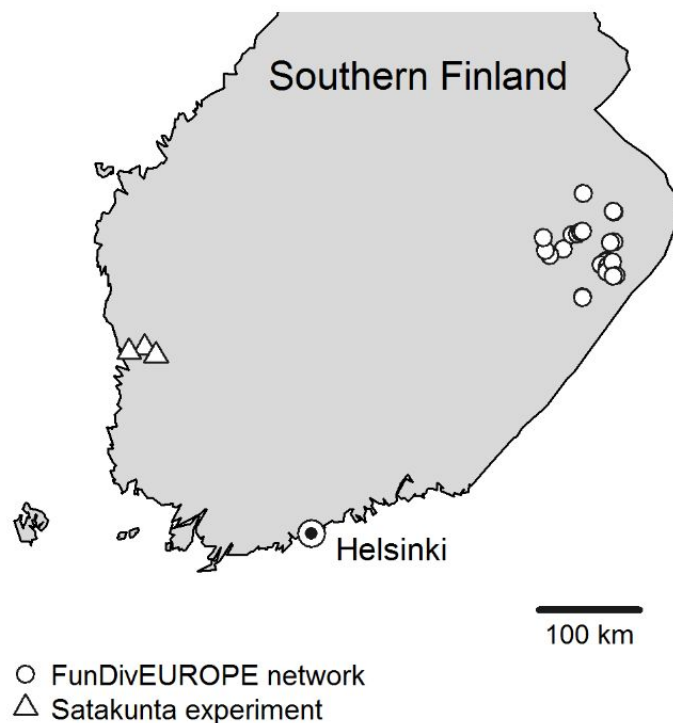


Fig. S1 | Map of southern Finland showing the location of the FunDivEUROPE plots (circles) relative to the three sites of the Satakunta tree diversity experiment (triangles).

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Tree age variation within and among FunDivEUROPE plots

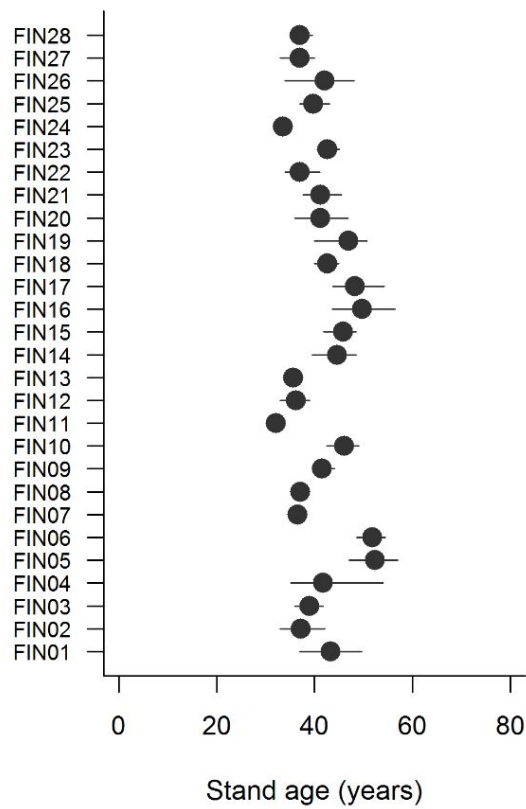


Fig. S2 | Tree age (mean and range) across the 28 FunDivEUROPE plots based on tree ring records.

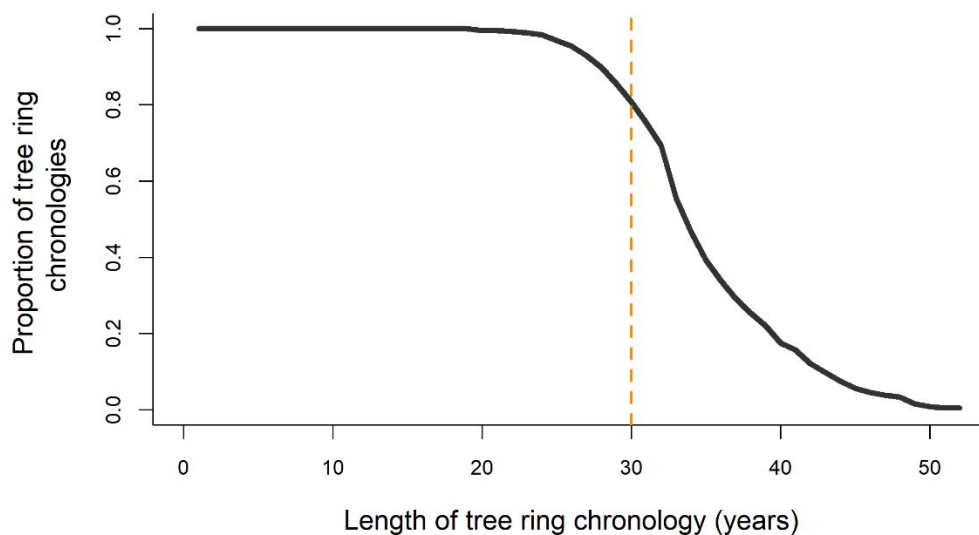


Fig. S3 | Proportion of the 438 tree ring samples that exceed a specific length.

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Appendix S2 | Changes in species composition and stand density through time in the FunDivEUROPE and Satakunta plots

FunDivEUROPE plots

In addition to the initial 2012 census, the FunDivEUROPE plots were re-surveyed a second time in 2017. During this second census, the diameter (D , in cm) of all previously tagged stems was measured again and any trees that died or recruited between census periods were recorded. Using these data, we can test the extent to which the species composition of the FunDivEUROPE plots changed over a 5-year period. To do this, for each plot we calculated the exponential of the Shannon diversity index in both 2012 and 2017, which Jost (2006) defines as a measure of the ‘effective number of species’ of a community:

$$\text{Effective no. species} = \exp \left(- \sum_{i=1}^S \frac{BA_i}{BA} \ln \left(\frac{BA_i}{BA} \right) \right) \quad (\text{S1})$$

where S is the number of unique species within a plot, BA_i is the basal area of species i and BA is the total basal area of the plot. This provides a measure of diversity that directly account for species’ relative abundances (i.e., evenness), while also being easily interpretable and directly relatable to species richness (as when species’ relative abundances in a plot are equal, species richness = effective number of species; Jost 2006). By comparing the effective number of species recorded in 2012 and 2017 across the FunDivEUROPE plots, we found that species composition remained almost identical over this 5-year period (Fig. S4).

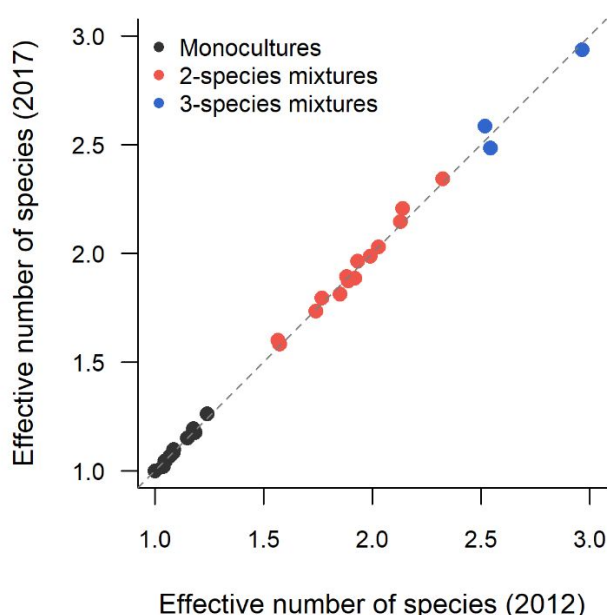


Fig. S4 | Relationship between the effective number of species recorded in the FunDivEUROPE plots in 2017 and 2012. A 1:1 line is shown in grey. Plots categorised as monocultures, 2-species mixtures and 3-species mixtures are shown in black, red and blue, respectively. Note that because some of the monoculture plots contain a small number of non-target trees ($\leq 5\%$ of the plot basal area in all cases), their

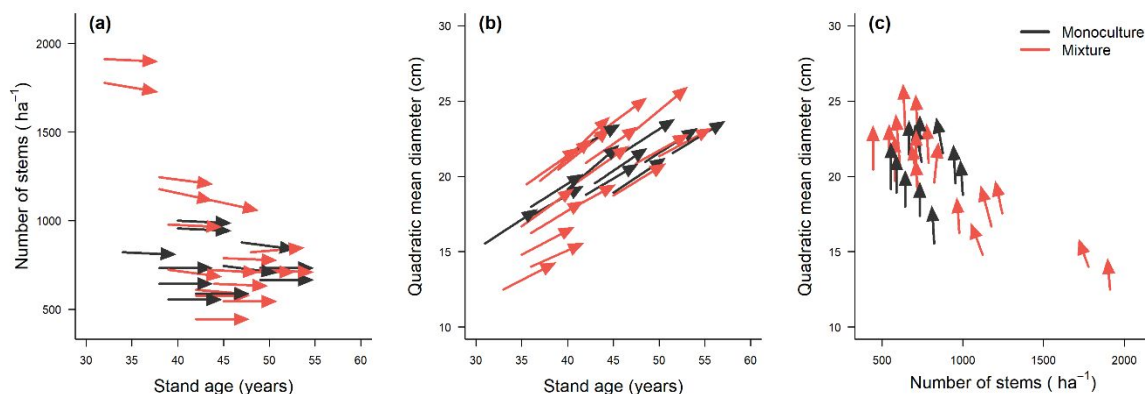
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effective number of species is >1 . See Baeten *et al.* (2013) for details on the criteria used to select the FunDivEUROPE plots, including thresholds for non-target species.

The repeat-census data from the FunDivEUROPE plots also provide an opportunity to explore how stand density has changed through time and how this varies among plots at different stages of stand development and in relation to tree diversity. In particular, it allowed us to test one of the key assumptions of our analysis: that differences in stand density among the FunDivEUROPE plots simply reflect differences in development stage (i.e., stand age) and not ones in species composition or diversity. To do this, we first used the census data from both 2012 and 2017 to calculate two measures of stand density which together capture information on both the number and size of trees in a plot: stem density (N , in stems ha^{-1}) and the quadratic mean stem diameter (QMD , in cm), which is calculated as $\sqrt{\sum D^2/N}$. Combined together, QMD and N determine the basal area of a forest stand (Curtis & Marshall 2000; Jucker *et al.* 2016) and the relationship between QMD and N captures key information on stand development and self-thinning (Yoda *et al.* 1963; Westoby 1984). We then used linear models to explore whether the relationship between (i) N and stand age (as estimated from the tree ring data), (ii) QMD and stand age and (iii) QMD and N are modulated by the species richness of the plot (tested by including an interaction term between species richness and the explanatory variable). N , QMD and stand age were all log-transformed prior to model fitting to normalise the residuals.

This analysis revealed clear changes in N and QMD during stand development, with N declining sharply and QMD increasing steadily with stand age (Fig. S5a–b). This resulted in older stands being characterised by fewer, larger stems – a pattern consistent with self-thinning (Fig. S5c). However, we found no significant difference in the shape of these relationships for plots characterised by different levels of tree diversity (i.e., interaction terms between tree species richness and the explanatory variable were not statistically significant in all three models). These results support our assumption that differences in stand density among the FunDivEUROPE plots reflect differences in stand development stage, and not ones in tree diversity or species composition.



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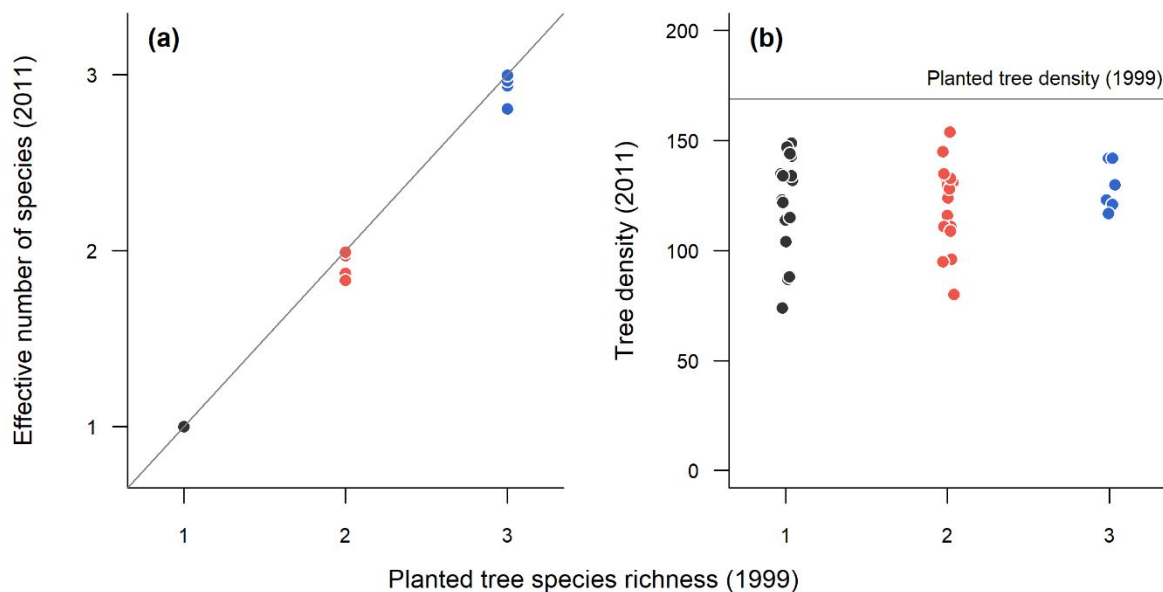
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Fig. S5 | Relationship between (a) stem density (N) and stand age, (b) quadratic mean diameter (QMD) and stand age and (c) QMD and N across the FunDivEUROPE plots. Arrows depict temporal changes in QMD and N that occurred between the 2012 (starting point of the arrow) and 2017 census (tip of the arrow). Monoculture plots are shown in black, while mixed-species plots are in red.

Satakunta plots

In 2011 a complete second census of the Satakunta plots was conducted, at which time any trees that had died since planting in 1999 were recorded. These data provide an opportunity to determine how species composition and tree density changed during the early stages of stand development at Satakunta. To explore how species composition may have changed since the experiment was first established, we used the 2011 census data to calculate the effective number of species in each plot based on the relative abundance of live stems (as described above for the FunDivEUROPE plots). When we compared these values to those of the initial tree species richness at the time of planting in 1999, we found that species composition in the Satakunta plots had remained very consistent during the first 12 years of stand development (Fig. S6a).

In terms of tree density, by 2011 the number of live stems per plot had declined to 123 ± 20 (mean \pm 1 standard deviation) from the initial 169 that were planted in 1999. However, an ANOVA conducted on the 2011 data revealed no significant differences in tree density across the diversity gradient (Fig. S6b) or among the various species composition treatments. So despite changes in stem density consistent with the initial phases of self-thinning, mortality rates were found to be similar across the tree diversity gradient during the early stages of stand development.



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Fig. S6 | Relationship between planted tree species richness in 1999 and (a) effective number of species in 2011 and (b) tree density in 2011 across the Satakunta plots. In (b) we applied a jitter to the x-axis so that overlapping points could be more easily distinguished.

Appendix S3 | Tree height–age curves

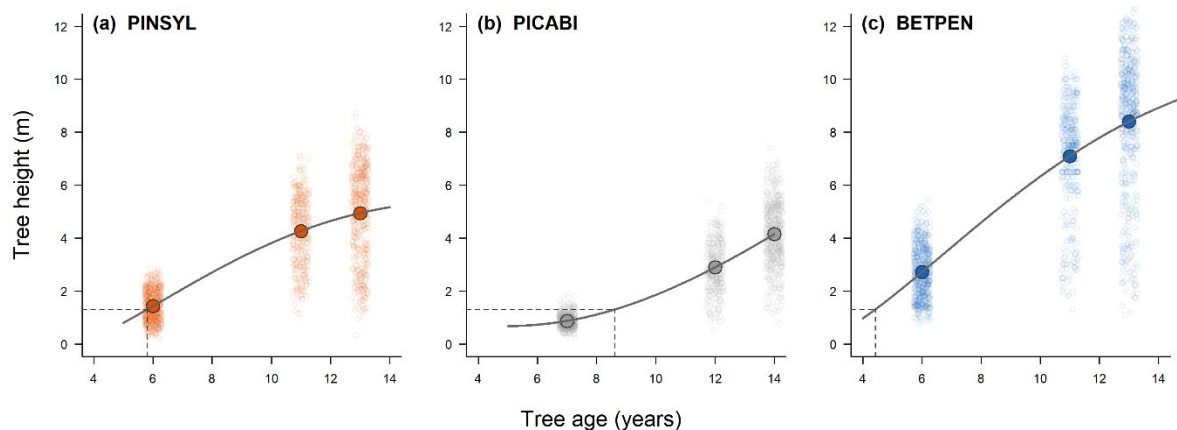
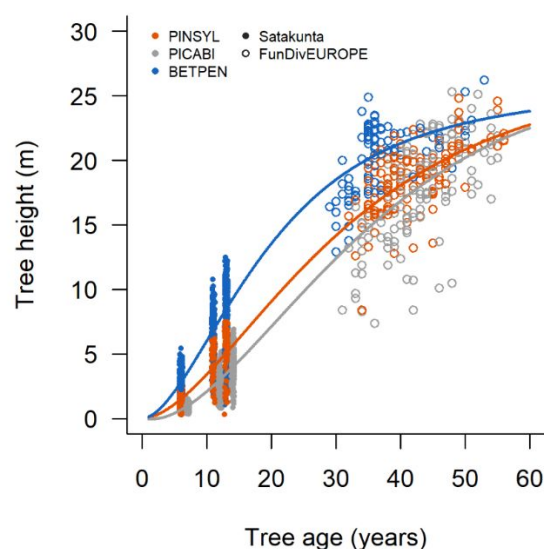


Fig. S7 | Height–age curves for trees in the Satakunta biodiversity experiment (PINSYL: *Pinus sylvestris*; PICABI: *Picea abies*; BETPEN: *Betula pendula*). Tree height was measured during three census periods (age 7, 12 and 14). Small empty circles are individual trees, while large filled circles are mean height values for each census year. The following height (H , in m) – age (T , in years) function was used to estimate the age at which the average tree reaches a height of 1.3 m for each study species: $H = \alpha + \beta T e^{-\gamma T}$ (see where dashed lines intercept the height – age curves).



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Fig. S8 | Tree height as a function of tree age for each study species (PINSYL: *Pinus sylvestris*; PICABI: *Picea abies*; BETPEN: *Betula pendula*) in the FunDivEUROPE plots (open circles) and the Satakunta biodiversity experiment (filled circles). Height – age curves for each species were fit using the function described in Fig. S7 using data from both the FunDivEurope and Satakunta plots.

Appendix S4 | Comparing alternative tree growth models

Modelling diameter growth

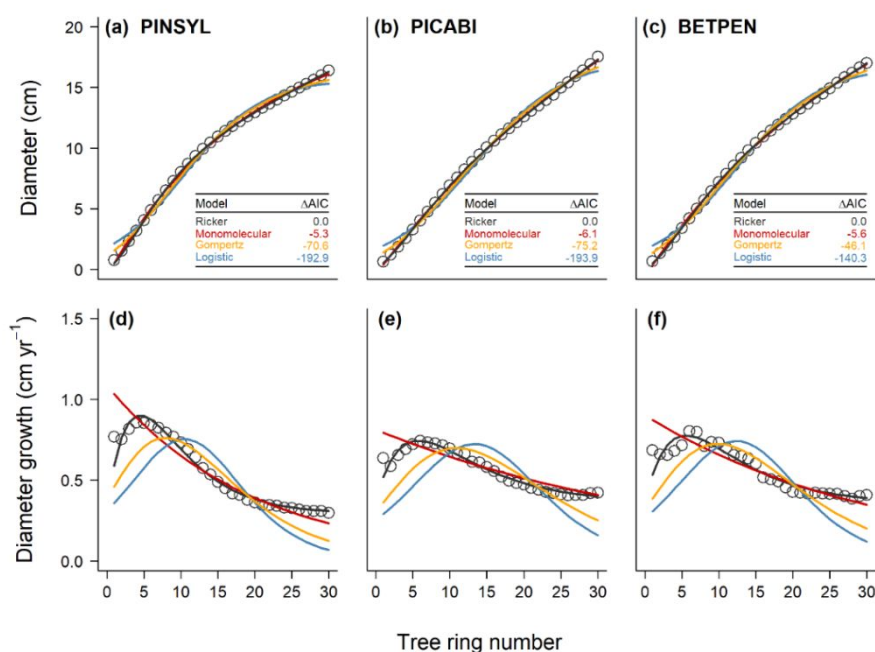


Fig. S9 | Comparison of alternative non-linear models of tree growth for each target species (PINSYL: *Pinus sylvestris*; PICABI: *Picea abies*; BETPEN: *Betula pendula*). Lines show to the fit of four different growth models (Ricker, monomolecular, Gompertz, and a four-parameter logistic), while open circles correspond to observed mean growth values for each year. For both cumulative diameter increments (top row) and annual diameter growth rate (bottom row), the Ricker function outperformed other growth models. A monomolecular function showed a reasonable fit to the cumulative diameter increments (top row), with Δ AIC values within 10 points of those obtained with the Ricker function. However, when the monomolecular function is expressed in terms of annual diameter growth rates (bottom row), the limitations of this function for modelling ontogenetic trends in tree diameter growth become apparent: the monomolecular function fails to capture both the initial inflection point in diameter growth (years 0 – 10) as well as the levelling-off of diameter increment with age. Diagnostic plots of the residuals of the Ricker models are shown in Fig. S10.

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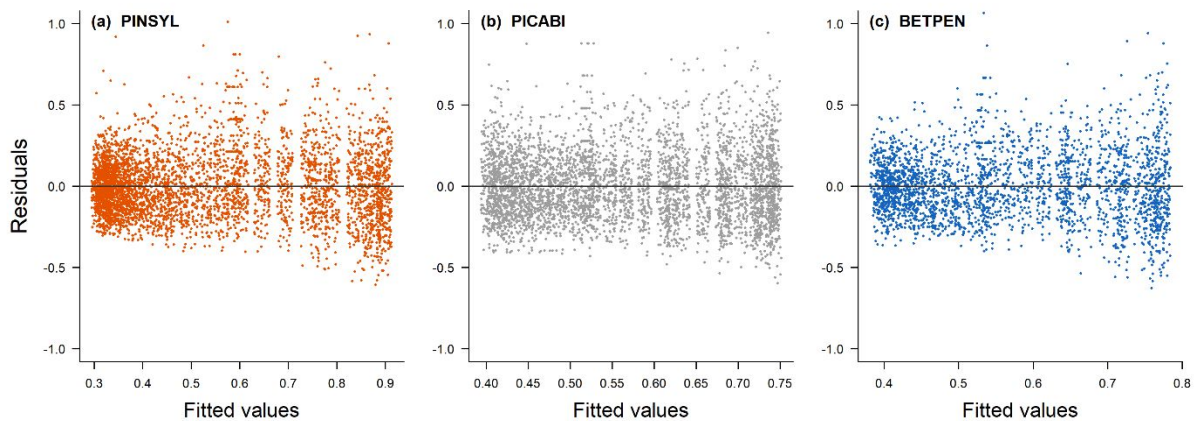


Fig. S10 | Diagnostic plots showing the relationship between residuals and fitted values of the Ricker diameter growth models for each study species.

Modelling basal area growth

Compared to diameter growth (Fig. S9d–f), basal area growth (BA_{incr} , in $\text{cm}^2 \text{yr}^{-1}$) trajectories exhibited much more complex oscillating non-linear temporal trends (Fig. S11). We compared the ability of several non-linear growth models to capture the BA_{incr} trends through time and found the best fitting model to be a four-parameter Weibull implemented using the *SSweibull* function in R:

$$BA_{incr} = \alpha - \beta \times \exp(-\exp(\gamma) \times A^\delta) \quad (\text{S2})$$

where A is the age of a tree in years and α , β , γ and δ are the four parameters to be estimated from the data. While this function recreates the early phase of BA_{incr} trends well for all three study species, it does not capture the second phase in which BA_{incr} slows before gradually increasing again (dashed black curves in Fig. S11). In fact, we found that we were able to better capture this complex pattern by simply converting predicted diameter growth increments obtained using the Ricker growth model [eqn (1) in the main text; black curves in Fig. S9d–f] into basal area increments (red curves in Fig. S11).

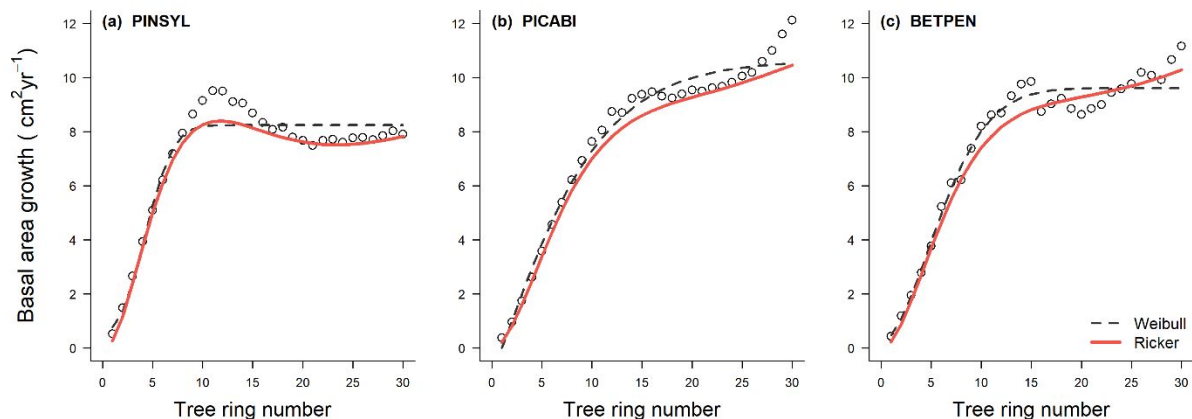


Fig. S11 | Comparison of two different non-linear models of basal area growth for each target species (PINSYL: *Pinus sylvestris*; PICABI: *Picea abies*; BETPEN: *Betula pendula*). Dashed black curves

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show the fit of the four-parameter Weibull function presented in eqn (S2). Red curves were generated by converting diameter growth increments predicted from the Ricker growth model presented in eqn (1) in the main text into units of basal area growth.

Based on this we chose to use the Ricker function to model differences in basal area growth trajectories of trees in monoculture and mixture. This revealed very similar temporal trends to those highlighted for diameter growth in the main text. In particular, the effects of species mixing on basal area growth tended to strengthen with time in all three study species and across all different possible species combinations (Fig. S12).

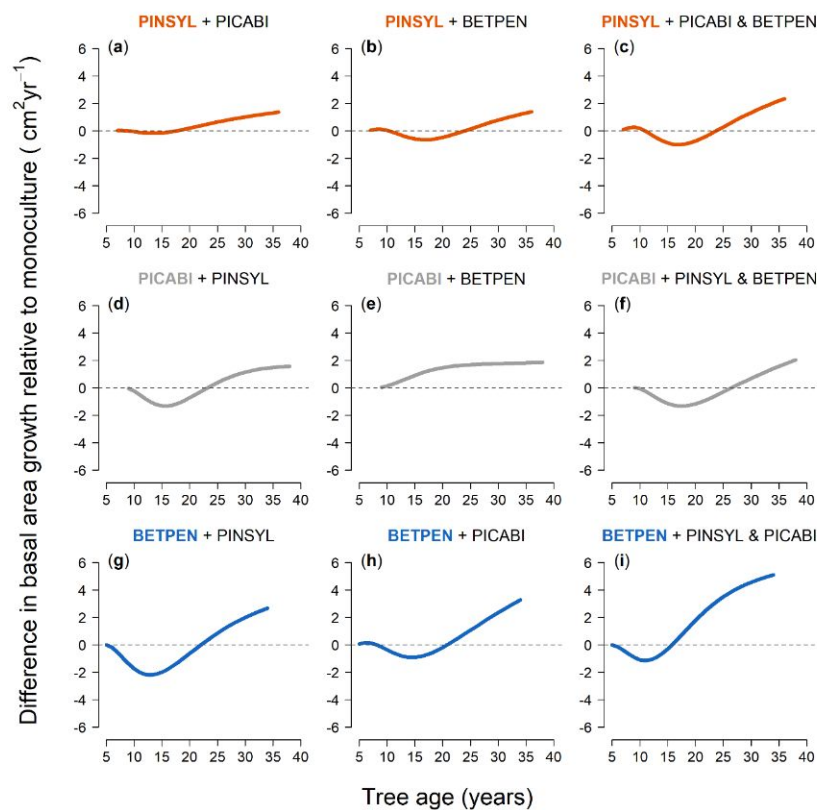


Fig. S12 | Difference in basal area growth between trees in monoculture and those in mixture as a function of tree age for (a–c) *Pinus sylvestris* (PINSYL), (d–f) *Picea abies* (PICABI) and (g–i) *Betula pendula* (BETPEN) as a function of tree age in the FunDivEUROPE plots. The interpretation of the figure is analogous to that of Fig. 3 in the main text.

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