In the present study, the evolutionary dynamics of three quantitative traits (drought tolerance, shade tolerance, and maximal growth rate) are integrated into ForCEEPS, a pre-existing process-based individual-based model designed to predict forest growth dynamics. The ability of two species (beech and fir) to adapt to warming temperatures is evaluated for different values of heritability and phenotypic variability and under different scenarios: monospecific stands, two-species mixtures, two-species mixtures with pre-adapted individuals introduced during the warming period, and two-species mixtures with new species introduced during the warming period.

The hypotheses explored in the present study are of great interest for guiding management and conservation strategies. The modeling approach appears robust and considerable effort has been made to summarize the findings For these reasons, I believe this paper meets the requirements for publication in PCI Ecology.

However, I think the clarity of the paper could still be largely improved.

In my opinion, the introduction should provide more explanation on how evolutionary dynamics have already been implemented in previous process-based models, and should more clearly present the specific type of process-based model used in the study (and how it differs from other models). I also think that the introduction should be more specific about how adding evolutionary dynamics may "impact models' projections of climate change impacts on forest ecosystems and their interactions with forest management practices" (L38-39). Last, the study objectives should be more clearly presented at the end of the introduction.

I also found the method and result sections very hard to understand, which undermines the study's replicability. Some terms are used without being previously defined and without explanation on how they are quantified, e.g. recovery, slow vs fast evolutionary scenarios. I also recommend checking throughout the manuscript that the same terms are used to describe the same parameters / scenarios.

I am not an English speaker, but I also think the manuscript would benefit from proofreading to improve the English and thereby facilitate reading and comprehension. As an example, I am not sure that the syntax of the first sentence is correct (L3-4). As another example, the sentence L31-33 is hard to understand and I think the grammar is not correct. Is this a question or an affirmation? I will not comment further on the syntax of the manuscript, but I recommend that it be reworked to improve clarity.

Specific comments

Abstract. I think the part of the abstract describing the background (from "In recent years" to "global warming on forests") could be shortened to give more space to the explanation of the study's modeling approach (which type of model was used, which parameters were studied, how the model performance was evaluated, etc), the hypotheses tested and more details about the case study (for example, which species or scenarios were tested). Indeed, I found that the abstract is not clear about the study's goal: is the objective to build a model that predicts the evolutionary dynamics of the species tested? Or is the aim to better integrate the evolutionary dynamics of the species into larger models (aimed at predicting the dynamics of species on a broad scale)?

The paragraph L26-L40 in the introduction conveys the idea that evolutionary processes have almost not yet been included in process-based models. I may be mistaken, but I do not think this is

true; there are already a number of studies that have developed process-based models incorporating evolutionary processes. Therefore, I think that the introduction should provide an overview of the different ways evolutionary processes have already been integrated into existing process-based models and should also clarify in which aspects the model presented here differs from previous work. For instance, evolutionary processes have been included in demo-genetic agent-based models by explicitly modeling changes in allele frequencies, mutations, and recombination, whereas the model presented here does not explicitly model changes in allele frequencies. I think briefly presenting the different methodologies that have already been explored in the literature would be highly useful.

Because of the lack of an overview of the literature on process-based models in the introduction, I did not clearly understand what the novelty of the model presented here is. Is the novelty in the fact that the current model incorporates both evolutionary processes and multi-species interactions?

L9-11. Please add a citation to support this statement.

L14. What are these "inherent requirements"?

L32. I would suggest defining "evolutionary rescue".

L34. I think it would be useful to be more specific, maybe giving some examples of new processes and parameters that need to be incorporated in the models to account for evolutionary processes.

In the first paragraph, the term "process-based models" (e.g., L9) is used, then the term "forest models" is used in the second paragraph (e.g., L34), and then "vegetation models" is used in the third paragraph (L41). If these terms refer to the same models, I suggest maintaining consistent terminology throughout the manuscript to avoid confusion. If these terms refer to different models, it is necessary to explain the differences between them.

L41. How did the previous studies incorporate evolution in the process-based models? I think it would be interesting to explain in the introduction how evolution has been incorporated in previous models.

L44. The previous sentence is related to the interaction between evolution and species diversity, so shouldn't be "evolutionary" processes instead of "community" processes?

L47. What do the authors mean by "general models"?

L49. I think adding one sentence explaining the goal of the ForCeeps model (i.e. what does it predict?) and how it works would be useful.

L53. I would suggest specifying what these three traits are.

L48-56. I think the aims of the paper should be explained more clearly in this paragraph. Indeed, I would say that adding "a new evolutionary module allowing species-specific parameters to evolve within the course of the simulation" (L51-52) is not the purpose of the paper, but the method. What is the objective behind adding an evolutionary module? An improvement in predictions (if so, which ones)? A better understanding of certain processes (if so, which ones)?

L61. Is there a paper showing that? (ie the extinction of beech populations in ForCEEPS simulations without evolution)

L70. Maybe specify here which new species are added in this third scenario.

I think it would be useful to indicate in the introduction whether this model applies to natural populations, managed populations or both.

Figure 1. "to activate a**n** uniform seed rain", "genetic componants" => "genetic components" I do not understand the meaning of "Starting from an inventory"

L80. Remove "of the".

L81. How environmental/climate conditions mediate competition for light? Please provide a citation for this statement.

Paragraph 77-83. I suggest adding a little more detail on how the ForCEEPS model works here, eg: - Is ForCEEPS spatially explicit? (L82)

- What is the link among patches? Are they simulated independently? (L83)

- How is population density limited in ForCEEPS? (L83) How is population density limited in ForCEEPS? Is there a carrying capacity? Or the population density is limited through the tolerance to shade?

L85. This is the first time that "gap models" is used. Is ForCEEPS a gap model? If yes, I think it has to be specified in the introduction and a definition should be given. Also, I think it may also be useful to specify whether this way of simulating regeneration is similar or not to the other process-based models that incorporate evolutionary processes, and mention the differences if there is any.

L91. Does the site composition correspond to the patch composition? I mean, is the local regeneration simulated for each patch independently?

L96. Is this migration parameter binary or quantitative (with an infinite number of values between 0 and 1)? And when M=1, what is the proportion of local regeneration vs migration regeneration?

I also wonder: is the term 'migration regeneration' commonly used in gap models? If so, I agree that it is best to use the same terminology as other models. However, if it is not a common term, I find it confusing because it can imply regeneration based on migration from other patches (which is not the case if I have well understood). I think a term like 'general,' 'large,' or 'broad' might be more appropriate.

L101. "inheritable" => "heritable"

L101. Evolutionary forces are mutation, genetic drift, gene flow and natural selection. If I am not misleading, only natural selection (and genetic drift?) is modeled here (which is already very cool!). So maybe it would be more appropriate to write "natural selection and genetic drift" here instead of evolutionary forces.

L107. When does seedlings become adults?

L105-111. As the species parameters change throughout the simulation and are specific to each individual, wouldn't it be more accurate to add the index *i* to the parameters? e.g. $DrTol_{s,i} \Rightarrow DrTol_{s,i}$

L112-113. "Base species values, i.e. the initial trait values before modification by the simulated evolutionary dynamics" may be simplified to "The initial trait values before evolution".

L118. I am not a native English speaker but I find this part a bit clumsy: "The three formerly described traits". I would write something like "The three traits described above".

L119. I would remove "additive" in "by a large number of additive genes" because these are not the genes which are additive, but their effects. And the following part of the sentence is enough to explain that quantitative trait variation is explained by a large number of genes with small effects on the phenotype.

L125. In my opinion, it would be more accurate and comprehensive to talk about "initial species specific parameters" than "former ForCEEPS species specific parameters" or "the old ForCEEPS parameterization" (L127). And I suggest keeping the same terms throughout the manuscript to avoid confusion.

L130. "assumed here to be equal for all traits ranging from 0.1 to 0.4" Does it mean that heritability is the same for the three traits in a given simulation but that its value can vary among simulations (between 0.1 to 0.4)? This is not clear to me.

L131. Could we say that Σ_{P} is the *phenotypic* variance-covariance matrix?

L131-133. I think this sentence is not grammatically correct.

I am not sure I fully understand how Σ_P is obtained. I would advise making it clearer which parameters have values set at the initiation of the simulations and then that change during the simulations, which parameters have fixed values throughout the simulations, and which parameters have values based on empirical estimates from the literature.

Regarding VR, where does the initial value of VR come from? Is it fixed throughout the simulation? And is it a common value for all species?

I am not sure I understand what sd_inter is, the interspecific standard variation of the traits?

L137. Are these correlations among traits values between species, within species, or both? I would suggest to mention here the trait correlations that are important to interpret the results, e.g. the correlation between drought-tolerance and shade-tolerance which is mentioned in L282.

L139. "data on drought and shade tolerance from" => remove "from"?

L142. How were the values aggregated across data sources? By taking the mean?

L144-146. I am not sure that we can say that *ShTolseedling*_{*i*,*s*} was "linearly inferred" by *ShTol*_{*i*,*s*} and *ShTol*_{*s*}, as this parameter is not inferred but calculated from three other parameters. And would it be possible to provide further explanation of this way of calculating *ShTolseedling*_{*i*,*s*}? And why dividing by 8?

L187-188. I would suggest providing more explanation on why the first site is considered a "typical ecological site" and the second one a "complementary site."

L202-204. Does it mean that regeneration is only by migration during the first 1000 years?

L207. I would talk about "values" instead of "scenarios".

L213-214. I am not sure to understand the part "with the number differing in order to keep a similar number of individuals of each species." Does it mean that there is the same number of firs in the 50 mixed plots than in the 11 monospecific plots (and the same number of beeches in the 50 mixed plots than in the 11 monospecific plots)? What is proportion of beach vs fir in the mixed plots? Is the size of the patches the same across all the simulations? In L79, it is specified that the size of the patches is "usually ca. 1000 m²". I think it would be helpful to make clear which patch size was used in the case study.

L221. Was the number of seedlings from local vs migration regeneration the same between question 1 and question 2? And were the phenotypes of the immigrants randomly drawn from the distribution of phenotypes from the simulations in the Montagne noire forest? And to what extent were the phenotypes in the Montagne Noire forest different from those in the Drôme? Does the distribution of phenotypes in the two regions overlap? I think more explanation would be useful.

L222. I think this is confusing to talk about new genotypes as this model does not explicitly model the genotypes - it simulates genetic variation at the level of the phenotypes. So I would suggest to use either "phenotypes" (but only if the phenotypes of the immigrants are really different from the phenotypes of the local seedlings) or new "individuals".

L227. Add "s" to "mixture".

L233. Were the initial values obtained from simulations in the Montagne noire? Which are the eight additional species? Are they more or less drought-tolerant than beech and fir in the simulations? What is the proportion of migrants from each species? More explanations are needed here.

L241. How were evolutionary rates calculated? Give the equation if possible.

L249. How was the median minimal Relative Basal Area calculated? Is it the minimal basal area over the reference period basal area? I would suggest to add the equation either in figure 2 or in the main text. And a suggestion for figure 2D – the reference period basal area might be called the reference basal area – to keep it simpler and shorter.

Figure 2. A) To what correspond the "exact recovery percentages"? I do not understand what it means. B) the colors of the time periods on the graph do not match those in the legend, I would suggest to also fade the colors in the legend. A) et C) How do we know whether the monospecific patches contain beeches or firs? Can we really say that VR corresponds to trait variability? From what I understood, VR is the ratio of intra vs interspecific variance of the phenotypic traits, so I do not understand how it can correspond to "trait variability". D) I think this subplot should be the first one (A) as we need it to understand the other plots of the figure.

L255. In which aspects some scenarios are "slower"? How has it been evaluated? Same comment for "faster evolutionary scenarios" in L262.

L261-262. How is defined and quantified the "recovery"?

L263. Please keep the same wording across the manuscript when referring to the beech-fix mixtures. They are then called "mixed species forests" L263, or two-species mixed populations in L273, or "two-species mix treatment" in L285.

L268. Do the initial values of drought tolerance systematically higher for beech than for fir? It would be highly interesting to run some simulations in which beech and fir have the same abundance but different initial values of drought tolerance, and some simulations in which beech

and fir have different abundances but the same initial values of drought tolerance, to assess which hypothesis (monopolization vs preadaptation hypotheses) is the most likely.

L274-275. Which are the two scenarios with identical evolution rates? I did not understand. What do the values 0.23 [0.22; 0.25] and 0.23 [0.20; 0.25] correspond to?

Figure 3. "Years" instead of "Date" on the x-axis? How was the mean individual relative light availability calculated?

Figure 4. I do not understand what the three plots on the third row represent: the community weighted Δ DrTol calculated for the reference period, the last decade of the simulations, and which period for the third plot?

L282. I do not understand the sentence "the general evolutionary path of target traits was a selection toward higher DrTol at the cost of unconstrained ShTol evolution" Is there a trade-off between these traits? What do the authors mean by "unconstrained"?

L285. "with the two-species mix treatment (as in Question 1)" => "with the beech-fir mixture used for question 1."?

L289. "genetic enrichment led to a higher safety margin (minimal RBA)" for both species? Or is it calculated by making no differences among the species-specific basal areas?

L293. What do the authors mean by "evolutionary regimes"? I think it would be simpler and clearer to talk about different combinations of h2 and VR values.

L296. What do "at the community scale" mean?

L304. Which result or figure shows the role of trade-offs among traits in the outcome of the simulations?

Figure 5A and B. I think it would be helpful to specify that the change in tolerance is calculated over the stabilization period and that $\Delta DrTol = DrTol_year3100 - DrTol_year2100$, so that it is clearer that a positive difference corresponds to higher values at the end of the stabilization period than at its beginning.

Figure 5B. It's very hard to see and understand the patterns on these graphs, and the graphs are too small. What represent the gray lines? If the populations did not go extinct, how do we see the trait values at the end of the simulation? What are these areas without any points or crosses on the bottom right of the plots on the right ? Are they areas of the parameter space that were reached by the parameters over the course of the simulations but then the parameter values moved away from these areas toward the end of the simulations? And why are there no crosses on the plots on the right?

L311. Were the additional species preadaptated to the dry conditions? If yes, it has to be specified in the method section. And how was the tolerance to shade and g of these additional species compared to beech and fir? Can it also explain their success ?

L331-332. I do not understand this sentence. From what I understood, there are almost no beech or fir anymore at the end of the species enrichment scenarios, so how can beech and fir have larger leaf cover at the end of these scenarios ?

L332. What do the author mean by "management treatments" ? Again, please keep the same working across the manuscript, this is highly confusing.

Supporting Information.

Fig S1. What do the points on the lower-left graphs represent? What do the lines on the diagonal represent? Why are the parameters called NiiShTol / NiiDrTol instead of ShTol and DrTol? Please explain further.

Fig S2. Please arrange the frames in the same order as used in the manuscript in the *Simulation plan* section.