Dear Pr Giraud and Rodríguez de la Vega,

We are happy to read that our manuscript could in principle be considered for recommendation by PCI genomics, and we thank you for these additional suggestions. We have taken them all into account, as we explain in details below.

Best regards,

Amélie Carré, Vincent Castric and Pierre Saumitou-Laprade

-L39 : Modes of sexual reproduction are strikingly diverse

Done

-L97 : add a reference

Done

-L99 : italics for « P. angustifolia »

Done

-L108 : explain briefly here what is this stigma test and in details in M&M

We have clarified what the stima test is by providing key methodological features. All experimental details have been reported in Saumitou-Laprade *et al.* (2010, 2017).

-L110 : coma after the bracket

Done

-L115 : unclear what « its » refers to

We have replaced "its" by "homomorphic diallelic SI determinant".

-L112, L356, 358, 370, 372, 373, 397, 422 and elsewhere : tense should be homogeneous within sentences ; I would keep the past tense all along

Done

-L145 : M allele

Done

-L152 : it has not been clarified that this represents experimental data, and it is unclear as the previous sentence mentions a model

We have clarified the sentence to replace "the observation" by "the segregation patterns".

-L177 : delete specific

Done

-L212, L297 : no capital within a sentence even for explaining acronyms

Done

-L234, L244, L723 : no plural when a name is before another name, so either just SNPs or SNP markers

Done

-L277 : it is still not clear what is the principle of this method (ant not only its goal), i.e., how it differs from just classical association genetics

In a classic genetic association analysis, it would have been necessary to generate a separate map for each phenotype (one with all the individuals for sex and one restricted to the hermaphrodite offspring; SI group is not expressed in males). SEX-DETector allows us to test the genetic hypotheses on individuals sub-samples and to place the markers a posteriori on the map. This tool also makes it possible to have a probability of following the model (XY or ZW) for each of the SNPs and thus to follow their association to the SI group or sex along the linkage group. An additional advantage of SEX-DETector is that it can analyse the segregation of any marker, regardless of whether it could be positionned on the linkage map. This is important since these loci can still be placed on the *Olea europeae* genome and represent a substantial fraction of all markers (for example for SI, the text mentions that 38998 SNPs could be analysed by SEX-DETector *vs.* only 15814 SNPs positioned on the map).

-L321, L323 : give the P values and N

We now reporte the Khi2 and P values. The number of samples is given in the previous sentences.

-L325 : no number at the beginning of a sentence or written in full letters

Done

-L331 : revise sentence, the two numbers and two comas are unclear

We modified the sentence.

-L377 : fewer instead of less

Done

-L304 : I would recommend using sequence similarity instead of homology, which has a different meaning in evolution, ie with a notion of shared ancestry

Done

-P11 : is it possible to plot the differentiation between alleles in the scaffold of interest to assess whether the differentiation is much higher at the SI and sex deterining loci than alsewhere, or even if there is a pattern of evolutionary strata ? Even if the contigs cannot be fully ordered, the differentiation levels may add further strong support to the findings and interpretation.

We fully agree that this would be a very interesting analysis, but we feel that at this stage the GBS markers are too short and sparse to achieve the density that would be necessary to reveal these patterns with sufficient confidence.

-P12 : it could be interesting to discuss the mating-type system in oomycetes that also resembles XY sex-determining systems (DOI:https://doi.org/10.1016/j.cub.2020.07.057)

We now introduce the oomycetes system at the end of the paragraph.

-L471, L484, L493, 497, 530 : I would use the term homologous instead of orthologous ; Orthologous is used for genes, to distinguish paralogous and orthologous genes among homologous genes, but you have not studied or found paralogs here, and it cannot be used with « functionnally » to my understanding

We have carefully checked the text and corrected the use of homologous/orthologous/ paralogous accordingly.

-L478-479 : I do not understand this sentence, it seems to have a syntax issue

We have modified the sentence.

-L493 : sexes or sexual morphs instead of sex

Done

-L496 : « such as » is redundant with « eg »

Done

-L14 : I find frustrating not to have some speculations about what can cause this distortion… meiotic drive ? more complex genetic system than a single locus ? selection for balanced male and female functions in the population, which can be different from the sexual morph census numbers ?

We agree that the causes of the distortion are intriguing, but at this stage we have no element to discuss the underlying mechanism. Our ongoing effort to develop genomic resources in this species should enable us to study this phenomenon in much more details in the near future, and we therefore feel that speculating on this point in the present manuscript would be premature.