REVIEW NO. 1

Comments to the authors:
They examine the role of particulate inheritance (which they call meiotic) and patterns of gene dominance in the population dynamics of a model system. Although they discuss this in terms of speciation, it would be more appropriate to discuss it in term of genetic diversity, as the groups that they call species generally interbreed.

"Numerical results are shown in Table I, which gives the count of the number of populations present at the end of each run for the various conditions."
I don't understand the table. What does the "populations" column correspond to? Are there as many as 44 populations at the end of a run? Eventually I conclude that this description should be reworded to something like this:
"For 48 independent runs of the simulation, Table 1 counts the number of runs for which the number of populations present at the end of the run is 0, 1, 2, or 2+, for the various conditions."

"This trait allowed the meiotic populations to exploit the full range of available resources"
In the context of evolution, "trait" has a common meaning, which causes some cognitive dissonance with its use in this sentence. Perhaps best to replace "trait" with something like "property"

"reducing the range of the running mutation rate from 0.310 to 0.00. We also quadrupled the initial mutation rate to 0.980 to give the starting population"
I'm not clear on how this works. Do you run it for a while with mutation and then stop? If so, how long do you run it with mutation? Elsewhere you said:
"the initial population was sampled from a Gaussian distribution with a mean 5.5 and a standard deviation of 0.5"
These two statements appear inconsistent. Please clarify the initial conditions with respect to starting genetic diversity and mutation rates, and clarify if mutation rates vary over the course of the run.

"For the first test, we widened the initial population to cover both niches by quadrupling the initial mutation rate to 0.980. In the second test, we reduced the initial population by halving the initial mutation rate to 0.1225"
So again I wonder if you are talking about initial genetic diversity as sampled from a Gaussian distribution, or actual mutation rates. If actual mutation rates, then is "initial mutation rate" different from the ongoing mutation rate?
This wording is also confusing: "widened the initial population", "reduced the initial population". At first read, it appears you are talking about population size, not genetic diversity. Try something like this wording: "widened the genetic diversity of the initial population", "reduced the genetic diversity of the initial population"

"the only phenotypic expression possibilities considered in this work were complete dominance and no dominance."
What?! You used complete dominance (CD) and incomplete dominance (ID)!

"it could be argued that the distinct bands that arise in meiotic populations in the bimodal seeds and random mating scenario do not actually comprise distinct species"
It is good that you mention this. You might want to be more up-front about it. If breeding occurrs between these distinct groups, they are not biological species. This is certainly the case for "random mating". This dramatically limits any claims that you can make about biological speciation. It would be more biologically accurate to make claims about the maintenance of genetic diversity, rather than claims about speciation. I would go so far as suggesting a change of title.
Either:
Meiotic Inheritance and Gene Dominance in Synthetic Sympatric "Speciation"
or
Meiotic Inheritance and Gene Dominance in Maintenance of Genetic Diversity

typos:

it is not expected to be make -> it is not expected to make

REVIEW NO. 2

Comments to the authors:
    Great paper! I certainly enjoyed reading this and believe it will be of great interest to the target audience.

    The paper describes a set of simulation experiments that demonstrate that demonstrate that gene inheritance and expression mechanisms on speciation. The experiments are clearly motivated, correctly designed and convincingly interpreted. They represent an extension of previous work by the second author (with a number of other co-authors).

    The results are interesting not just for their main message, but also because they convincingly demonstrate that a great amount of attention needs to be paid to the fine details of a biological simulation. Details, from which many works aim to abstract without worrying the impact this may have on the outcomes.

    The paper walks a fine line between biology and evolutionary computation and manages to be relevant and interesting for both sides. (I do appreciate that the authors are careful not to make any strong claims about immediate applicability to evolutionary computation).

    The presentation is exemplary and of exceptional clarity.

    While my area of specialisation is not close enough to the subject matter of the paper to be certain of this, I believe the results to be novel.

My only quibble with the paper is that the sensitivity of the results to the parameter choices (population size, mutation rates, population density, etc.) does not seem to have been investigated. I would strongly suggest to do so.

Also, could you please make the caption of Table 1 self contained? "Results" is not terribly enlightening". One can consult the text in Page 3, Column 2 to find out, but it would be better better to have this information directly available in the caption. The only flaw in an otherwise great presentation.

REVIEW NO. 3

Comments to the authors:
This paper discusses the effect of meiotic inheritance and gene dominance on the sympatric speciation. The paper is very well written.