**Associate Editor  
Comments to the Author:**  
First I would like to apologise to the authors for the very long period we have had their ms in review. In fairness, as AE, I knew as soon as I read the title that I would struggle to get reviewers. I did struggle and then when finally I had some, it followed their return was repeatedly delayed (separate issue).  
  
The title is quite off-putting and unnecessarily indirect and with jargon (while also being obvious that selection affects introgression). Especially the term 'intrusion'. I suggest you revise the title but I won't insist.

Suggestions:  
  
The other comments from reviewers are helpful and I request you consider them all. Reviewer 2 is brief and not constructive, but I agree that it's hard to see how the paper moves beyond this running of the model. Reviewer 1 and 3 are more specific and deep in their comments. All of us struggle with interpreting the details of the model and its application.  
  
Further, for my own reading I find the handling of hard and soft selection (eg in the introduction) a bit too focused on that one paper. Intra-population aspects such as frequency dependence have long been recognised, as has the role of competition among individuals, and complex interplay of biotic and abiotic environment. Moving beyond terminology, the concepts are more broadly shared than is explained here. I think it would help the reader see both the foundation and the novelty, if this is addressed. There is a bit more even handed exploration of this in the discussion and I suggest it be revised and clarified in the Introduction.

There is only one correct interpretation of soft selection and that’s the one of Wallace (1970). All the material regards intra-population aspects is a misappropriation of the original term coined by Wallace. Furthermore, selection acts on populations not on meta-populations.  
  
For the methods and results, I echo the comments from reviewer 1 and 3 that these can be considerably refined.  
  
I can see the value of the model for exploring some anticipated scenarios and counter-intuitive outcomes, though the utility of the paper and the model will critically depend on the accessibility of the code to others.

Code will be made available via my Github. We mention this in the paper. We could also register it on Zenodo to get a DOI minted for it.

REVIEWER(S)' COMMENTS:  
  
Reviewer: 1  
  
Comments to the Author  
The article takes a (potentially first?) stab at quantifying the potential real-world implications of co-occurring soft and hard selection on ecological and evolutionary dynamics in a loosely based model of Atlantic salmon.  The topic of soft and hard selection is surprisingly neglected in ecology, evolution, and population genetics.  Nevertheless, and as the manuscript shows, these two different forms of natural selection have very important implications for a variety of population level phenomena.  Overall, I think this manuscript is analytically very well done.  And from an applied perspective, it will be quite useful in that it helps illuminate some of the paradoxical results that can occur when both soft and hard selection influence adaptation/maladaptation.  
  
I have one general comment to consider.  I’m definitely biased because I’ve thought a lot about hard and soft selection and agree they are vitally important concepts when thinking about the ecological consequences of evolutionary dynamics.  That being said, I’m confident we are in the minority in this situation.  I strongly suggest the authors carefully try to make this manuscript accessible to:  
  
1.      Non-quantitative geneticists (e.g., ecologists, evolutionary biologists, conservation biologists, even population geneticists) who are unfamiliar with these concepts but would benefit from better understanding why they are critically important in eco-evolutionary dynamics.  
2.      Biologists/managers that have to deal with genetic introgression.  
  
At present, I think the manuscript is a bit too technical.  I think the manuscript would benefit from very careful (and likely moderate/major) revision that tries to make this more accessible to a more generalized audience.  In its current format, the realized audience might be limited to the relatively small subset of scientists who have thought about the nuances of hard and soft natural selection, and in turn, already anticipate these results (after all, this is a deterministic model).  I strongly urge the authors to try to make this work more accessible.  
  
More specifically, I suggest (1) trying to reduce as much jargon and technical terminology as possible, and (2) focus on several key findings that are most important to report and discuss.  Some of the issues (e.g., mean trait values, genetic variance?) and even simulation scenarios could be moved to Supplemental.  This also applies to the Figures.  This is a lot of information (response variables and scenarios) to sift through, especially given that the principal issues of hard and soft selection are not particularly intuitive, at least for the un-initiated.  On the bright side, there is a lot of great information here, but it will help to separate some of the what from the chaff, at least for purposes of messaging.  
  
Minor comments:  
  
Line 40:  I think it would be more appropriate to call “adaptive linkage disequilibrium” either “co-adaptive gene-complexes” or “adaptive epistatic interactions”.  Maybe I’m being too semantic in thinking about this through the lens of population genetics, but I don’t think “adaptive linkage disequilibrium” is the best term.  
  
Lines 133-134:  I don’t follow here.  Linkage disequilibrium could occur either because of physical linkage (not an issue in this model), or because of finite population size.  The latter, due to drift, would be random/ephemeral, and fairly weak unless populations sizes are very small.  Even then, any non-random association should still be random/ephemeral and not “build up”.  
  
Line 134-137:  I might be missing something, but a single diagnostic locus would provide an imprecise estimate of ancestry at the individual and population level with many generations of backcrossing.  If you want to track and report on the proportion of non-native ancestry, more diagnostic loci should be used.  But, it does make me wonder, is this response variable necessary?  If a primary goal is to describe admixture dynamics in the face of soft/hard selection, then yes. If instead the authors focus on the ecological consequences of hard/soft selection (e.g., population demography/dynamics), then perhaps not.  Again, a more focused approach would help clarify what is important to track and report and what can be ignored, or simply fodder for future efforts.  
  
Lines 189-195:  I think this way of parameterizing soft selection is completely appropriate for this effort, but there is no stochasticity.  Might be worth mentioning that in nature, competitively inferior individuals would occasionally luck out, that is, soft selection will rarely be “perfect”?  
  
  
Reviewer: 2  
  
Comments to the Author  
The manuscript, entitled “Soft selection affects introgression dynamics and the viability of populations experiencing intrusion of maladapted individuals”, investigated the rates of introgression variation by developing an eco-genetic model to understand the influence of soft selection. They then employed a generalised salmonine lifecycle to test the model and found that the effects of both acute and chronic intrusion depended strongly on the relative competitiveness of intruders versus locals. Overall, this manuscript is not in deep. I think the manuscript is not suitable to the journal Evolutionary Applications.  
  
  
Reviewer: 3  
  
Comments to the Author  
This paper presents an original approach to examining the consequences of human-mediated introgressive hybridisation for conservation and management. It explores the effects of eco-evolutionary interactions arising from the interplay between density-dependent soft selection and maladaptation. The key aspect considered is the extent to which soft selection, resulting from density regulation during reproduction, influences the rate of introgression and subsequent demographic consequences outcomes shaped by density-independent survival later in the life cycle. A model of sequential soft and hard selection events is developed to explore the eco-evolutionary consequences of intrusion, and to evaluate how the relative competitiveness of locals versus intruders impacts the extent of introgression and population productivity. In this model, soft selection determines the magnitude of genome-wide introgression, which then determines how the introgressed population is pushed away from a phenotypic optimum under strong stabilising (hard) selection. The model mimics a salmonid life cycle, with acute or chronic intrusion of aquaculture fish that differ phenotypically from locals on both soft and hard selected traits. The authors examine the effects of intrusion intensity, the degree to which invaders exhibit competitive inferiority/superiority and maladaptation relative to locals, the level of reproductive excess, and traits heritability. Clear predictive hypotheses were made in the Materials and Methods section for each type of simulation. The results were generally well explained and the discussion reads well. However, I have to admit that I had to read the whole paper twice to understand it properly.  
  
The results show that the relative competitiveness of invaders versus locals determines the eco-evolutionary consequences of maladaptive hybridisation. While the finding that competitive inferiority of intruders leads to lower introgression may seem trivial, the consequences of interactions between density-dependent and independent selection are less intuitive. When intruders are competitively superior, the rate of introgression is enhanced, reducing the mean fitness and therefore the survivorship and productivity of the population, potentially leading to population decline or genetic replacement.  
  
I enjoyed reading this thought-provoking study that invites us to look at the effect of supplemental stocking from a different angle than is usually considered in genetic studies. The results will provide guidance for assessing the risks associated with aquaculture and restocking practices. However, the manuscript would benefit from a clearer explanation of the methods to maximise the impact of the results.  
  
  
MAIN CONCERNS  
  
The use of an advanced simulator such as SLiM would have made the model easier to understand and reproduce. It would also have facilitated the simulation of a more realistic architecture of traits, including mutations with a non-uniform distribution of effects on the traits.  
  
I'm not asking to rewrite the model in SLiM, but I have a number of comments about the complexity of the model, which in some cases seems unnecessary and confusing. There are also repetitions in the Materials and Methods, for example, the part common to both traits under soft and hard selection (i.e. genetic basis, phenotype construction using environmental variation) could be explained in the same selection instead of being repeated twice.  
  
The way in which the genotype matrices of local individuals for each trait are constructed in generation 1 to make the initial allele frequency at each locus equal to pSOFT and pHARD is difficult to understand on first reading and unnecessarily complex. As I understand it, this is equivalent to randomly drawing alleles from a binomial distribution using the probability of success pSOFT or pHARD.  
  
The 20 generation "burn-in" period needs to be justified. At first I thought it was just to generate more variance in allele frequencies across loci around pSOFT and pHARD, but then I realised it was helpful in the results to compare trends before and after intrusion.  
  
L153-157, the construction of the genotype matrix for non-local intruders follows the same method as for local individuals, so this could be explained all at once in the same paragraph.  
  
The genetic basis of the selected traits (i.e. positive additive effects with uniform allele frequencies across loci) is not realistic. This is acknowledged in L131, which states that this should not qualitatively affect the outcome of the model. However, the fact that locals and intruders differ in their value of 𝑝, combined with the fact that 𝑝 is uniformly distributed across loci, means that the additive genetic variance between locals and intruders differs. As a consequence, L174-175, it is unclear whether heritability or only VE also differ between locals and intruders.  
  
I was a bit surprised by the ranking strategy to determine reproducers following density regulation. The fact that only the top fraction of individuals reproduce does not include any stochastic effect beyond the random contribution of VE to the phenotypic value. Is this a realistic choice?  
  
L238-240 Here also (as for genotypes drawing) survival looks like a random binomial drawing process of parameter Wi.  
  
  
MINOR POINTS:  
  
ABSTRACT: The abstract is a little too vague, which makes it difficult to get the main message learned from the simulations. For example L21-22, specify that the effect of intrusion depends of the relative competitiveness for reproduction. It is also difficult to understand from the abstract whether the paper is about soft selection in the context of density-dependent regulation or weak selection.  
  
INTRODUCTION  
L40-41: “breakdown of adaptive linkage disequilibrium” could be replaced by “breakdown of coadapted gene complexes”  
  
MATERIALS AND METHODS  
L267-269: As I understand it, an average RPS of 1 should be obtained with Wmax=0.5, given that the number of offspring per parent was set to 2. Does this mean that the Wmax=0.53 value will produce an RPS slightly higher than 1 (i.e. a low reproductive excess, as stated in the results section)? This should be more clearly stated here.  
  
L296-299: In the Acute intrusion simulations set 1, the difference in ZHARD between locals and intruders implies a (very) strong directional selection. I was wondering if such a strong selection effect could be considered realistic?  
  
RESULTS:  
L369: As I understand it, additive genetic variance is progressively eroded by drift even before allele fixation occurs at any loci, simply because the initial genetic architecture was made up of common variants (allele frequency = 0.75) that are likely to drift away from 0.5 (the frequency at which genetic variance is maximised).  
  
L410: dipped to a much lower number?