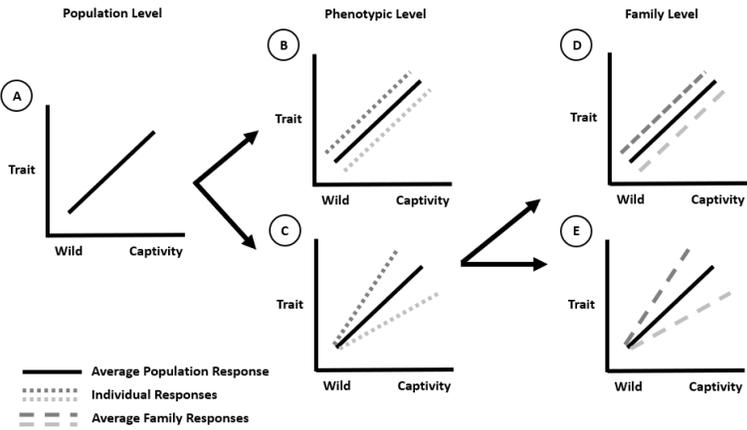


Editor Comments	Responses
<p>Abstract: Currently lack a sentence describing the problem. So, please, mention how phenotypic changes (e.g. due to genetic adaptation to captivity) can be a problem for e.g. reintroductions.</p>	<p>Thank you, below is the new abstract with additional or edited sentences in bold.</p> <p>Human activities are resulting in altered environmental conditions that are impacting the demography and evolution of species globally. If we wish to prevent anthropogenic extinction and extirpation, we need to improve our ability to restore wild populations. <i>Ex situ</i> populations can be an important tool for species conservation. However, difficult to prevent deviations from an optimal breeding design and altered environments in captivity seem likely to lead to evolutionary or plasticity-induced phenotypic change that could make reintroduction more difficult. Quantitative genetic analysis can help disentangle the causes of phenotypic change in <i>ex situ</i> populations. Consequently, quantitative genetics can improve the management of these populations and the success of <i>in situ</i> population management actions that they support. In this review we outline methods that could be used to improve the management of <i>in situ</i> and <i>ex situ</i> populations in a One Plan Approach. We discuss how quantitative genetic models can help measure genetic variation, phenotypic plasticity, and social effects on phenotypes. Finally, we discuss how phenotypic change can be predicted using measurements of additive genetic variance and selection. While previous work has highlighted the value of <i>ex situ</i> populations for the field of quantitative genetics, we argue that quantitative genetics can, in turn, offer opportunities to improve management and consequently conservation of populations of species at risk. We show that quantitative genetic analyses are a tool that could be incorporated into and improve <i>ex situ</i> management practices.</p>
<p>Main text – minor edits.</p>	<p>We've fixed these mistakes.</p>
<p>L. 792 (Fig 3): change “phenotypic level” into “individual level”; it is also not clear why there are two parallel lines at the family level and why these purple ‘family’ lines are parallel if there are differences between families (situation E). I guess the purple lines are NOT specific for families but that is not clear from the legend. I suggest to keep the solid black line specific for the population level, dotted lines for the individual level and striped lines for the family level. Different individuals (and families) can then be symbolized by different colors (but not black).</p>	<p>Thank you, this is a good point and helps the clarity of the figure. See the new version of the figure below and in the updated manuscript.</p> 

Reviewer Comments	Responses
<p>Mainly satisfied with the modifications to the manuscript which have fulfilled my previous comments. Argumentation is now clearer and more precise. The only point where I have still some concerns is related to the ambiguity regarding the citation of the classical management methodology currently being applied in ex-situ conservation programs. In several places of the manuscript (e.g., line 65 or line 399) the expression ‘mate-pairing based on kinships’ seems to mean that minimisation of the kinship (coancestry) is only used to decide the mating scheme to limit the rise of inbreeding when, actually, this parameter is also to be accounted in the selection process itself, determining the ‘redundant’ individuals or the ones belonging to underrepresented lineages which should be promoted to produce offspring (maintenance of the genetic diversity).</p>	<p>Thank you, on line 65 we mentioned selection pressure to acknowledge that an optimal design should also minimize selection. We removed the mention on line 399 because it does not relate to the main topic of this sentence.</p> <p>Line 70-74: Many breeding programs follow a mate pairing method based on mean kinship and inbreeding avoidance derived from pedigrees to minimize genetic drift, inbreeding, and selection pressure while maintaining genetic diversity (Montgomery et al. 1997; Ralls et al. 2000; Willoughby et al. 2014; Ballou et al. 2020).</p>
<p>Minor edits</p>	<p>Thank you, we have fixed both these mistakes.</p>