

Some complexities in interpreting apparent effects of hitchhiking: A commentary on Gompert et al. (2022)

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Abstract

We write to address recent claims by regarding the potentially important and underappreciated phenomena of “indirect selection,” the observation that neutral regions may be affected by natural selection. We argue both that this phenomenon—generally known as genetic hitchhiking—is neither new nor poorly studied, and that the patterns described by the authors have multiple alternative explanations.

KEYWORDS

demography, epistatic selection, genetic hitchhiking, linkage disequilibrium, selective sweeps

We wish to express a number of concerns about the recent paper by Gompert et al. (2022), who propose a “widespread indirect selection hypothesis,” and assert that “functionally neutral genetic regions can be affected indirectly by natural selection, via their statistical association with genes under direct selection.” They add that “the genomic extent of such indirect selection, particularly across loci not physically linked to those under direct selection, remains poorly understood.” The authors present analyses of several data sets; they suggest that this process could be an important phenomenon over both short and long timescales, and may serve to make “aspects of evolution more predictable” given that “conditional on patterns of LD, indirect selection is a deterministic process.” We have concerns about both their conceptual framework and their interpretation of the experimental results.

First, the concept of “indirect selection” as they use it appears to be equivalent to genetic hitchhiking, which is only mentioned towards the end of their paper—see Barton and Servedio (2015) for a general discussion of direct and indirect selection in this context. However, the term indirect selection is also used by quantitative geneticists to refer to the covariance between a trait and fitness due to selection on a trait with which it is correlated (e.g., Morrissey, 2014). The term hitchhiking is most often used in relation to the effects of the spread of a beneficial mutation on variability at linked sites (Maynard Smith & Haigh, 1974), often referred to as a selective sweep, or to the similar effects of the elimination of deleterious mutations (background selection: Charlesworth et al., 1993; incorrectly

attributed by Gompert et al. (2022) to Begun and Aquadro (1992)). As noted in the recent review by Charlesworth and Jensen (2021), the various forms of hitchhiking can all be described in general terms by the Price–Robertson identity, which states that the change in mean of a trait is governed by the additive covariance between the trait and fitness (Price, 1970; Robertson, 1968). In this case, the trait is the allele frequency at the neutral locus, and the covariance is the product of the coefficient of linkage disequilibrium, D , and the additive fitness effect of the locus under selection (Charlesworth & Jensen, 2021; Santiago & Caballero, 1995). Furthermore, variation maintained by long-term balancing selection or divergent selection between populations can also affect variability at linked sites, but this does not involve changes in allele frequencies that are noticeable over the short timescales considered by Gompert et al. (2022), except in the initial phase of their establishment (see Zeng et al., 2021 for a recent theoretical analysis).

Thus, in one sense their remark about the deterministic nature of indirect selection is correct. However, the initial value of D is generated by various forms of chance associations between alleles at the neutral and selected loci, as is indicated by the title of their paper, so that there is inherently a stochastic element to hitchhiking. Furthermore, D is reduced by a factor of $1 - c$ each generation, where c is the frequency of recombination between the two loci concerned (Charlesworth & Charlesworth, 2010, p. 381). Multiple theoretical analyses of hitchhiking have shown that significant effects of selection on linked neutral sites only occur if the ratio of c to the selection

coefficient at the selected loci is small, or the neutral loci are embedded within a large number of loci that are simultaneously experiencing selection (Charlesworth & Jensen, 2021). A neutral locus can only be affected by a selective sweep at an unlinked locus ($c = \frac{1}{2}$) if there is extremely strong selection, involving a much greater than two-fold selective advantage to the beneficial allele. Similarly, background selection caused by unlinked loci is likely to have only a minor effect on neutral variability unless there is an implausibly large deleterious mutation rate per genome (Charlesworth, 2012). Detectable hitchhiking effects involving unlinked loci are therefore likely to be very infrequent.

Second, their assertion that widespread hitchhiking effects are “relatively untested” seems misplaced. One of the most consistent patterns to emerge from the study of DNA sequence variation over the past few decades is the generally positive correlation between neutral variability and the local rate of recombination (Begun & Aquadro, 1992; Charlesworth & Jensen, 2021). Genetic hitchhiking has long been discussed as a major factor in generating this genome-wide correlation, although in some species the mutagenic effect of recombination may contribute as well (Arbeithuber et al., 2015; Pratto et al., 2014). Indeed, the abundant evidence for pervasive background selection effects has prompted numerous authors to argue that it should be an essential component in any evolutionary null model when conducting population genomic studies (e.g., Comeron, 2017; Jensen et al., 2019; Pouyet et al., 2018).

Third, the authors suggest that, while hitchhiking effects have been studied over long periods of time, “it remains unclear whether indirect selection is pervasive on shorter time scales, such as generations or decades.” Although it is not obvious how hitchhiking effects could operate over long timescales without also acting at short timescales, this remark reflects a more fundamental misunderstanding. As described above, recombination events between directly selected mutations and linked variants act to diminish hitchhiking effects, so that the footprints associated with recent hitchhiking events are naturally stronger than older ones. In fact, recombination, subsequent mutations and genetic drift cause these patterns to decay so rapidly that most effects of individual selective sweeps are *only* detectable over relatively brief periods of time since their occurrence (Kim & Stephan, 2002; Przeworski, 2002). If there has been strong directional selection at certain loci in the experimental set-ups that are described by Gompert et al. (2022), the short timescale involved is certainly favourable for the detection of their hitchhiking effects (although the statistical power associated with the relatively small experimental sample sizes and limited number of generations can be problematic: Barrett et al., 2019).

When considering the evidence for hitchhiking effects in the cases described by Gompert et al. (2022), we focus specifically on their primary example—the stick insect *Tisema cristinae*. Previous work has documented the existence of an interesting colour polymorphism, controlled by a 10-Mb region, the *Mel-Stripe* locus, which appears to be potentially associated with a chromosomal inversion

(Lindtke et al., 2017). Among approximately 7 million single nucleotide polymorphisms (SNPs) in their sample, Gompert et al. (2022) found 64 SNPs that had $r^2 \geq 0.1$ with *Mel-Stripe* and were also on different chromosomes, where r is the correlation coefficient between pairs of alleles at two loci (Charlesworth & Charlesworth, 2010, p. 373). The first question is whether this could be generated by the effect of random sampling of the 492 haploid genomes sequenced in their experimental population. Under the null hypothesis of no linkage disequilibrium (LD), an r^2 of 0.1 corresponds to a 1 df χ^2 of 49.2, for which $p = 2.31 \times 10^{-12}$, using the incomplete gamma function with parameter 0.5, which is equivalent to $0.5 \chi^2$ (<https://keisan.casio.com/exec/system/1180573447>). The expected number of SNPs with $r^2 \geq 0.1$ is thus approximately $2.31 \times 10^{-12} \times 7 \times 10^6 = 1.62 \times 10^{-5}$. Not surprisingly, therefore, this explanation can be ruled out. Note that the expected value of r^2 generated by random sampling in the absence of true LD is $1/492 \approx 0.002$, which is not far from the mean value of .004 for all pairs of unlinked SNPs reported by Gompert et al. (2022).

There appear to be at least six possible explanations for this unexpectedly large number of unlinked SNPs that are in fairly strong LD with *Mel-Stripe*:

1. There exist technical errors that result in spurious cases of LD or incorrect assignment of the locations of SNPs—for example, so that SNPs that are actually in the *Mel-Stripe* region are placed on other chromosomes. The quality control details needed to evaluate this possibility were not presented by the authors.
2. LD between neutral SNPs and the *Mel-Stripe* locus has been created by random genetic drift in a panmictic population over a long period of time. This seems improbable unless the effective population size is quite small, as the expected value of r^2 with no linkage is approximately $1/(2N_e)$ (Charlesworth & Charlesworth, 2010, p. 383), and the size of the *T. cristinae* population used in the experiment is said to be of the order of thousands of individuals, suggesting a very large effective population size (Gompert et al., 2022).
3. There has been very recent admixture from a genetically distinct population or populations, resulting in patches of LD with *Mel-Stripe* (Charlesworth & Charlesworth, 2010, p. 388). No structure/admixture modelling needed to evaluate this possibility appears to have been performed.
4. There has been a recent and severe bottleneck in population size, generating random LD of a much higher magnitude than expected under a constant population size (Charlesworth & Charlesworth, 2010, p. 389). As with point 3, these signatures may be detectable using standard demographic modelling approaches (reviewed in Beichman et al., 2018); again, such analyses appear not to have been performed.
5. The sample used in the experiment has captured an ongoing sweep involving very strong directional selection on *Mel-Stripe*; this seems implausible, given the evidence that the *Mel-Stripe* variants represent a long-standing balanced polymorphism (Lindtke et al., 2017).

6. There could be epistatic fitness interactions between the SNP loci and *Mel-Stripe*. This of course does not constitute “indirect selection” (i.e., genetic hitchhiking) of the type proposed by Gompert et al. (2022), but is perhaps what they have in mind when they refer to “polygenic selection.” However, it is stretching credulity that there could be tens of unlinked loci subject to very strong epistatic fitness interactions with *Mel-Stripe*, resulting in significant LD. Theoretical analyses of two-locus balanced polymorphisms have shown that substantial LD requires the measure of additive \times additive epistasis for fitness to considerably exceed the recombination frequency (Charlesworth & Charlesworth, 2010, pp. 420–425).

For example, in the simple symmetric two-locus fitness model of Lewontin and Kojima (1960), LD is maintained at equilibrium with free recombination only if $2 \leq e$, where e is the epistatic fitness parameter (fitnesses are here measured relative to the fitness of the double heterozygote). In this case, with equilibrium allele frequencies of 0.5 at both loci, $r^2 = 16D^2 = 1 - 2/e$. Very few convincing cases of LD maintained by epistatic selection among unlinked loci have been described. The classic case is that of the Australian grasshopper *Keyacris scurra* (formerly *Moraba scurra*), involving two inversion polymorphisms that show a consistent pattern of LD across multiple populations, and substantial deviations from Hardy–Weinberg frequencies that indicate strong viability selection (Turner, 1972). Even here, the magnitude of r^2 is small. In the sample that showed the highest value of D (i.e., Royalla B 1958), the data in table 3 of Turner (1972) give $D = 0.00116$ and $r^2 = 0.00349$.

In summary, the observation of many unlinked SNPs with substantial LD in *T. cristinae* seems to raise more questions than it answers, and cannot be taken as indicating widespread “indirect selection” without much more evidence, including a proper consideration of baseline expectations related to both technical (e.g., data quality) and evolutionary (e.g., population history) factors. Furthermore, even if these alternatives were to be ruled out by further analyses, genetic hitchhiking is neither a new nor poorly studied phenomenon.

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CONFLICT OF INTEREST

The authors declare that they have no conflicts of interest.

AUTHOR CONTRIBUTIONS

Both authors contributed equally to the writing of this article.

DATA AVAILABILITY STATEMENT

No new data were generated for this study.

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