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Magic traits, pleiotropy and effect sizes: a response to Haller *et al.*

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In our recent Review in *TREE* [1], we defined magic traits based on pleiotropy between divergent ecological adaptations and non-random mating. Haller *et al.* [2] imply doubt in the utility of this definition, concentrating their arguments on effect size (the contribution of a trait to the evolution of reproductive isolation, see [3]). They specifically make two points: (i) effect size is absent from the current definition of a magic trait; and (ii) magic traits of weak effect may be unimportant in speciation. We address each of these points in turn.

In general, definitions of biological phenomena are not conditioned on effect size, which would entail arbitrary cut-offs. For example, natural selection is defined as differences between individuals, based upon their traits, in viability or fecundity; this definition is not predicated upon such differences being large or even an important source of evolution in specific circumstances. Likewise, definitions of scientific concepts should not be affected by ease of measurement. Yet Haller *et al.* object that ‘distinguishing weakly divergent selection from the absence of selection is empirically difficult, making it hard to determine whether a trait is magic or non-magic’, and are concerned that it is empirically difficult to determine whether traits are pleiotropic. Natural selection itself is often hard to measure, but few would argue that ease of measurement should contribute to its definition (nor that the concept of natural selection is not useful as a result).

Can magic traits, defined by the presence of pleiotropy, be so weak as to be unimportant in speciation? We agree with Haller *et al.* that, under our definition, they can. For example, in our Review [1], we argue ‘it is very possible that some traits are “magic”; because they have the requisite pleiotropic effect but play a trivial role in speciation because of small effect sizes’. In the section ‘Effect size of magic traits’, we further elaborate upon the point that the importance of a magic trait in the speciation process depends upon both its contribution to a given component of pre-mating isolation and how much total reproductive isolation exists before the magic trait diverges; we conclude in our original Review that the importance of ‘magic traits with weak effects on late-evolving components of pre-mating isolation. . . might be trivial’.

Haller *et al.* object that such ‘trivial magic traits’ may be difficult to identify empirically, and that the distinction between them and non-magic traits is ‘largely irrelevant to many questions surrounding speciation in nature’. We caution that this conclusion is premature. Without knowing the actual distribution of effect sizes, it is too early to say which effect sizes are ‘important’ or ‘should be studied’. It may be the case that speciation often proceeds by the action of many genes of small effect sizes, so studying such genes will be important. Similarly, magic traits that are under weak divergent selection and/or play a small role in non-random mating might still have an important effect in speciation, perhaps because the timescale of speciation is long, or because they facilitate the divergence of other traits

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(see the discussion under ‘Interactions between magic and non-magic traits’ in [1]). Thus, identifying such traits might well pose an important challenge to empiricists.

In a similar vein, Haller *et al.* question the usefulness of distinguishing between magic traits and complexes of non-magic traits with tightly linked underlying genes (‘magic-trait mimics’). Their assumption seems to be that linkage and pleiotropy are equivalent in their capacity of facilitating speciation (and, hence, that our focus on pleiotropy is a reflection of ‘theoretical preoccupations with the genetics underlying traits’). This conclusion appears unfounded. Although we agree with Haller *et al.* that, in certain cases, non-magic traits may be just as important as magic ones (see the section ‘Can magic traits be mimicked by complexes of non-magic traits’ in [1]), theoretical studies clearly demonstrate the increased effectiveness of magic traits in driving speciation compared with complexes of non-magic traits under similar strengths of selection (e.g. [4,5]), illustrating the key importance of the presence or absence of pleiotropy.

Haller *et al.* make the interesting point that when selection varies spatially or temporally, traits may be magic in some situations but non-magic in others. Although we agree with this fact, it is not in any way unique to magic traits. Rather, the effects of spatio-temporal variation in selection apply to most aspects of speciation, whether the traits involved are magic or not. Any trait that is only sometimes under divergent selection will only be involved in the speciation process part of the time. It remains true that when a trait is acting as a magic trait, it will probably be a more efficient driver of speciation than when it is not.

Haller *et al.* conclude by stating that there is a gap that must be bridged between theoretical and empirical perspectives on magic traits, and that ‘the important...distinct-

tion is between traits expected to be of large effect size (whether magic or mimic) versus those expected to be of small effect size (whether trivial [magic] or non-magic)’. The fact that this conclusion effectively ignores the distinction between magic and non-magic traits altogether, derives, in our opinion, from a misinterpretation of ‘magic’ to refer to a trait that is necessarily important in speciation, versus one with the unique feature of direct involvement in both the selection and non-random mating components of the speciation process. We agree with Haller *et al.* that measurements of effect size are now required, but not that this should limit the utility of a definition of magic traits based on pleiotropy. A clear, unconditional, definition of magic traits will be of use to both theoreticians and empiricists alike.

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The quality of name-based species records in databases

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In a recent Letter to *TREE*, Huang and Qiao [1] propose a quicker way to boost the dissemination of species occurrence data to fill the generally perceived geographical and taxonomic gaps found in online biodiversity database aggregators, such as the Global Biodiversity Information Facility (GBIF) [2]. Following a previous paper by Whitlock [3], they suggest that researchers should be pressed to share their raw data, and that journals and editors should be convinced to make electronic submission of such data a prerequisite for publication. Basing their argument on the indisputable success of GenBank, they anticipate that, by adopting data-archiving policies, pub-

lishers would turn their repositories into major feeders of biodiversity data aggregators. Although we agree that such a scheme would certainly improve the geographical and taxonomic coverage of biodiversity records through electronic media, there is a point that deserves more thoughtful consideration: the quality control of archived and indexed species names. To put it simply, the core data of GenBank are sequences, and their quality control is mostly made downstream [4]. Sequences are mapped to scientific names (usually species names) by the Taxonomy Browser or Entrez. If a species has been inadequately determined by the submitter, the sequence itself remains useful and usable. Above all, sequences are comparable and replicable, regardless of the name associated with them.

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