

Author Correction: Speciation by hybridization in *Heliconius* butterflies

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In this Letter, there is an error in the analysis of data that affects some of the conclusions. The three main conclusions of the Letter were as follows. First, that the *Heliconius heurippa* wing pattern arose by hybridization between *H. cydno cordula* and *H. m. melpomene*, demonstrated by hybridization experiments. Second, that *H. heurippa* is a distinct species reproductively isolated from both *H. cydno cordula* and *H. m. melpomene*, demonstrated by patterns of genetic differentiation at multilocus microsatellite genotypes and by mate choice experiments

with live butterflies. Third, that mate choice on the basis of colour patterns explained a notable proportion of *H. heurippa* mating preference, such that hybridization led directly to both pre- and post-mating reproductive isolation in this species. It is this final conclusion that is affected by the error.

In the original Letter, the results of the wing model experiments are reported in Fig. 3a as the ‘Probability relative to controls’ (see Fig. 1a of this Amendment), whereas in fact the data plotted would be more correctly labelled as ‘Proportion of interactions with the heterospecific model’. Furthermore, the likelihood function was not corrected for the proportion of conspecific interactions, as previously reported¹ (and as reported in the Supplementary Information of the original Letter), but was instead similar to that later used by Merrill et al.². The null hypothesis (that is, no preference) would be 1 in the former, but 0.5 in the latter, which therefore changes the interpretation of the results. When we reanalyse the data with likelihoods based on the proportion of interactions with the heterospecific model (that is, in which 0 = a complete preference for the *H. heurippa* model, and 1 = a complete preference for the alternative model), the results map directly onto those shown in Fig. 3 of our original Letter (see left panels of Fig. 1b of this Amendment). However, there is no consistent statistical evidence from the data for a colour-based mate preference when the correction is applied (see right panels of Fig. 1b of this Amendment).

The implication of this re-analysis is that there is not good evidence for the key claim of the Letter that *H. heurippa* had a preference for the combined red and yellow hybrid wing phenotype. Furthermore, the inference that the colour pattern alone directly causes reproductive isolation is not supported. However, colour patterns could still have an important role in the reproductive isolation of *H. heurippa*, perhaps in combination with behavioural displays or chemical clues,

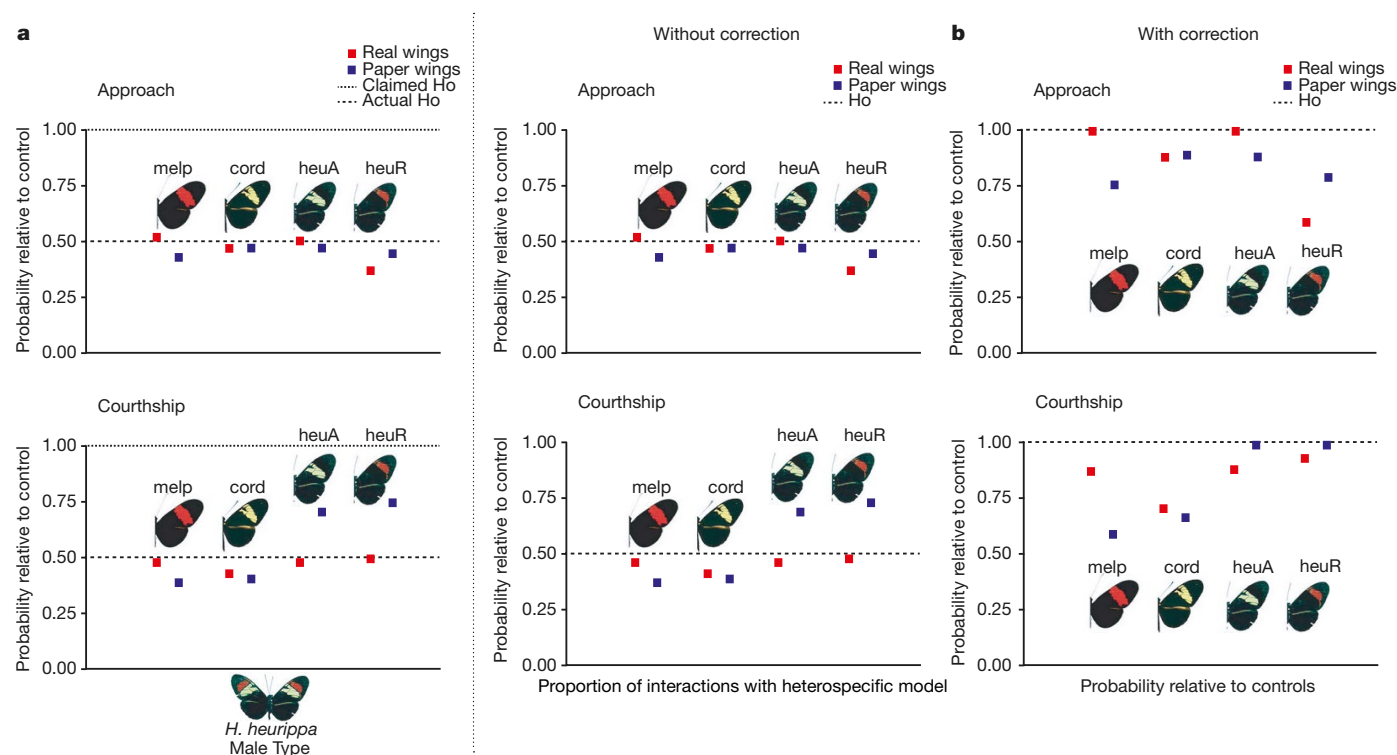


Fig. 1 | Reanalysis of the count data from Fig. 3 of the original Letter. a, This panel reproduces Fig. 3a of the original Letter for comparison. **b**, Re-analysis of the count data from Fig. 3 of the original Letter. Left, absolute probability of approach (top) or courtship (bottom) of the experimental model in which the null hypothesis would be 0.5. Right, probability of approach (top) or courtship (bottom) by *H. heurippa* males, with a correction applied to normalize

probabilities relative to the control model, in which the null hypothesis is equal to 1. In the original Letter, the data were calculated as in **b** (without correction, left panels) but were reported as if in **b** (with correction, right panels). Labels: melp: *H. m. melpomene*, cord: *H. cydno cordula*, heuA: *H. heurippa* with red band removed, heuR: *H. heurippa* with yellow band removed.

which cannot be mimicked with the type of mate choice experiments performed here. The evidence for a hybrid origin of the *H. heurippa* colour pattern and for partial reproductive isolation of *H. heurippa* from *H. cydno* and *H. melpomene* (from the no-choice and tetrad experiments) remains valid. In particular, the introgression of colour alleles from *H. melpomene* into the *H. cydno*/*H. timareta*/*H. heurippa* clade is now well established and supported by extensive genetic evidence^{1,3}. Our Letter was an early demonstration of this process, supported by hybridization experiments.

We thank Alex Hausmann and Richard Merrill for drawing attention to this issue. The original Letter has not been corrected.

1. The Heliconius Genome Consortium. Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. *Nature* **487**, 94–98 (2012).
2. Merrill, R. M., Van Schooten, B., Scott, J. A. & Jiggins, C. D. Pervasive genetic associations between traits causing reproductive isolation in *Heliconius* butterflies. *Proc. Biol. Sci.* **278**, 511–518 (2011).
3. Salazar, C. et al. Genetic evidence for hybrid trait speciation in *Heliconius* butterflies. *PLoS Genet.* **6**, e1000930 (2010).