

Ideas, tests and proofs. The value of hypotheses

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ABSTRACT

Hypotheses are derived from real data, and drive the discovery of new data. A paper in this issue illustrates how this will work in the future, with a real world example of hypothesis preceding experimental findings, and explaining them and expanding their implications.

Editorial

This issue of HyLS contains an example of the valuable role we hope our Journal can play. The Hypothetico-Deductive explanation of science says that hypothesis and experiment are intimately linked, with new hypotheses driving new experiment, new data driving the formulation of new hypotheses [1]. But most biological scientists, while paying lip-service to this idea, believe that data is the real driver. There is no theory underlying biology that has predictive power, unlike physics where the properties of planets can be predicted from their size and orbit, or chemistry where the properties of molecules can be predicted from their bonding structure (and vice versa). In biology, the argument goes, you just have to go and sequence the genome, measure the biodiversity, time the nerve impulses.

I have argued before that this is mistaken [2], and am delighted that this, our second issue of HyLS, illustrates the point. George Parris' paper [3] describes how chromosomal inversions can lead to a new species, effectively by reproductive isolation. He argues that some pericentric inversions will have minimal effects on the phenotype, but will dramatically reduce the fertility of the individual when mating with bearers of the normal karyotype. However if they inversion carrier mates with another carrier of the same inversion (or a very nearly identical one), then fertility will be near normal. Reproductive isolation has been achieved without geographic separation.

Now Kariminejad et al [4] report a very similar effect in humans, but with a balanced duplication and inversion. We cannot claim that we were responsible for Kariminejad et al's study, which has been running since before Hypotheses in the Life Sciences existed. But Parris' paper gives theoretical underpinning to

Kariminejad et al's observation, and suggests that such homozygous inversions may be more common than expected, and should be actively sought in other populations, especially inbred ones.

Does this example prove the 'meta-hypothesis' [1] that our journal is a valuable part of the scientific endeavour? It does not, for two reasons. Firstly, Parris [3] did not stimulate Kariminejad et al [4] to do their work, as is required by the classic 'Hypothetico-Deductive' description of science. Secondly, it is just one example. But this does illustrate that hypothesis is not merely about explaining what we know. This support for Parris' ideas may encourage others to investigate the other implications of the hypothesis, which has a substantial bearing on how we interpret evolution. And that has value.

References

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