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Hypotheses in the Life Science. A meta-hypothesis

William Bains

Rufus Scientific Ltd, 37 The Moor, Melbourn, Royston, Herts SG8 6ED, UK
EAPS, MIT, 77 Massachusetts Avenue, Cambridge, MA, 02139, USA
e-mail for correspondence: editor@hy-ls.org

ABSTRACT

Hypotheses in the Life Sciences seeks to offer a reviewed, rigorous, yet open-minded avenue for new hypotheses in the life sciences. As far as I know, this is something of a first. The journal will select papers by editorial board review, supplemented with outside peers, thus avoiding some of the inherent conservatism of conventional peer review while retaining the quality of the ideas we publish. As hypothesis generation and discussion is a central part of the scientific method, our hypothesis is that *Hypotheses in the life Sciences* will grow to become a valuable, widely read and widely cited part of the scientific process.

Why start a new journal?

Friends and colleagues alike asked me, when I told them that I was founding a new scientific journal, why I was doing it. It cannot be for the money: there is little money in independent publishing. It cannot be for the fame: it is our authors who get their names in print and their bibliographies enhanced by what we will do, not your editor. It cannot be for the sheer joy of typesetting. Why do it?

The first answer is historical, looking backwards to how we got here. That is a long and personal answer, and probably not that interesting to you. So I just will mention briefly the pioneering work of David Horrobin [1] and his successor Bruce Charlton [2] at Medical Hypotheses, and the short-lived spin-off that I helped to found [3, 4]: these provided a demonstration that there was a need for Hypotheses in the Life Sciences.

The second answer is looking towards where we are going. What function can another life science journal serve in a world where there are estimated to be 50 million articles published already [5], where the Science Citation Index adds nearly 15 articles *per minute* to the mass of published knowledge[1]? And if Hypotheses in the Life Sciences (HyLS) was just another journal adding to the pyramid of data that threatens to overwhelm even the most narrowly specialist discipline, there might indeed be little point in the journal.

But HyLS aims to be different, because we are not publishing data. We are publishing ideas. To the extent that scientists agree that there is such as thing as a 'method' of science, they usually agree that the hypothetico-deductive (H-D) process outlined by Karl Popper is a reasonable description of that method (e.g. ref 6). A scientist generates a hypothesis, often triggered by a new observation. The hypothesis has predictable consequences. The scientist tests those consequences, by experiment or observation. The resulting data support or refute the hypothesis, and lead to new hypotheses. The successive waves of hypothesis refine our view of the universe, bringing our models and theories closer to a practical, predictive description of reality.

So far, so good, and life science publishing is excellent at publishing the results of testing hypotheses, and at publishing that less structured exploration of life that is 'hypothesis-free' research – just looking to see what life is (e.g. ref 7). But the H-D method assumes that new ideas are also made widely available for anyone to test and refute, and here the life science literature is less permissive, because it is orientated towards data.

In fact, it is quite hard to get a new hypothesis published for another reason. The scientific literature is almost all peer reviewed. Peer review originated in the 17th century as a process of checking new ideas by people who had some idea of the subject matter. But it has evolved into a formalised process that is inherently biased towards saying 'no' to papers (See for example ref 8). How could it do otherwise, when there are over 200,000 life scientists, each of whom can type at 30 words a minute and many of whom are rewarded by the amount they publish? That means that the speculative, the innovative, and above all the concept that is not backed by lots of new, previously unpublished data has an increasingly hard time in getting published for others to read, understand, test and extend. In 1953 the peer referee system allowed publication of a paper that used other

[1] 7815862 articles in 2005 thru 2009. My thanks to Thomson Reuters Customer technical Support for these numbers

people's data to speculate on a new structural model of DNA [9]. I suspect that, were Watson and Crick to submit their short paper today, they would be told to go away and include some new experimental data to support their model, data that they were in no position to collect, but which others did collect, validating Watson and Crick's insight and launching an entire new science.

HyLS seeks to help add to the smooth running of the H-D process by providing a forum for new hypotheses, allowing good ideas about how life works to gain a wider readership, and hence be taken up, tested, refuted if wrong or developed if potentially correct. In line with this we use a carefully selected, expert editorial board as our principle peer group for review, not a random selection of over-worked scientists with a vested interest in saying 'no'. We will (and already have) rejected papers that are primarily about new data. We will insist that hypotheses have importance for a wide range of life sciences, not just one specialist research agenda. We will insist that they explicitly state how hypotheses can be tested, because testing a new hypothesis is also central to its value to science. And, of course, we insist on rigour and clarity.

What we do not insist on is that ideas are 'right'. We do not know if they are 'right', only future testing will show that. Trying to second-guess reality will bring us back to the inherent conservatism that says that ideas should only be considered when there is overwhelming data to support them. There is a strong argument that ideas that are incomplete, even ones that are wrong, play a valuable role in the scientific process, by allowing others to build on and then test the ideas [10]. After all, the structure proposed by Watson and Crick [9] was not 'right' in the sense of being correct in every detail. There is small but significant sequence-dependent variation in the Watson and Crick 'B-DNA' structure, as well as substantially different structures such as A-DNA, Z-DNA, triplex regions and other exotica in the DNA in real life [11]. This does not detract at all from the value of the 1953 paper.

Will our model of innovation-friendly publication add value to basic science? HyLS is a test of the hypothesis that our new journal will be valuable, enabling good ideas to be seen in a forum that makes substantial demands of quality and rigour in its papers (unlike the unrestrained speculation available in the blogosphere), and so is a genuine part of the quality scientific literature. I welcome our pioneer first authors, and look forward to scientists everywhere testing our idea, and helping to generate a positive outcome to our experiment.

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