The two complementary aspects of life history evolution, theory and experiment, are examined critically. Seven theoretical and five empirical sources of ambiguity are identified, and the reliability of life history data is assessed. The theory is not refined enough to make predictions testable by crucial experiments. That portion of the data that is reliable supports existing theory in only half the cases. [The SCT* and SSC* indicate that this paper has been cited in over 165 publications.]

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I began work on this paper in the spring of 1976 after moving down to the University of California at Berkeley from the Bodega Bay Marine Lab. As a postdoc, I had some time to think. In a previous paper1 I had reviewed the existing state of life history theory, and in my just-completed PhD I had tried to test some of that theory, but "ambiguities appeared in the interpretation of the results, some of them inherent in the theory, others in the observations. I could not decide which of several possible causal systems had produced the pattern I observed." Therefore I tried to locate the sources of ambiguity in the theory and assess critically the quality of the evidence available to test it.

The paper has often been cited by authors who refer to the criteria I drew up for an empirically sufficient study of life history evolution. Naturally, they authored papers in which the criteria cited were met. The idea of critically the quality of the evidence available seems to have been influential. One colleague told me that he recommended the idea as standard practice to graduate students doing the literature review for their PhD proposals. The notion is so straightforward that it must predate Aristotle by a millenium or two: the exercise of being subjected to a small dose of simple logic does not appear to have hurt the field.

Less attention has been paid to the theoretical ambiguities that I discussed. Only one of them has been cleared up definitively, but some progress has been made on all of them. The first remains the deepest and has become the focus of much continuing research: how to make appropriate simplifications in connecting genotype and phenotype in models of life history evolution. B. Charlesworth2 has reviewed an approach based on population genetics, H. Dingle and J.P. Hegmann3 have edited a book oriented towards quantitative genetics, and J. Koella and I4 have developed an approach based on reaction norms. The issue is not yet settled.

The second ambiguity, design constraints, has become a popular theme in evolutionary biology, not as the result of this paper, which is never cited in this regard, but because S.J. Gould and R.C. Lewontin5 made an issue of it two years later. The evolution of constraints and the development of methods for identifying them remains important. Wake and Roth are doing good work on it, and I have recently published a model and a review.6

The theoretical problem that has been settled is R&K-selection. This paper was one of the first to criticize it. Few people now use the term, but most agree that it was a good idea that played a useful role at the time.

This paper has been cited frequently because it, together with my earlier paper,1 reviewed a field that was just starting to explode. Such citations make it easy for other authors to indicate the state of the literature and make for more concise introductions. Equally good papers in fields that are not expanding do not get cited as frequently, nor do equally good papers that are written near the end of a literature explosion. There is a lot to be said for good timing, but I know of no way to predict in advance which field is about to take off. I was lucky.