

## Notes and Comments

### Adaptation to the Laboratory: Comments on Sgrò and Partridge

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Submitted October 24, 2000; Accepted May 31, 2001

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*Keywords:* laboratory adaptation, *Drosophila*, convergent evolution, genetic sampling effect.

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Understanding the processes of adaptation of wild populations to captivity (e.g., the laboratory) is an increasingly important issue, both in terms of general evolutionary questions and of conservation problems. In a recent article in *The American Naturalist*, Sgrò and Partridge (2000) present a study of the effects of laboratory adaptation in *Drosophila*. The authors compare laboratory populations of *Drosophila melanogaster* founded from the wild in three consecutive years. Their principal conclusion depends on an untested assumption, namely, that their latest founded population is an accurate representation of the initial states of the laboratory populations collected in previous years.

The rationale of this study is that differences between stocks can be attributed to the different number of generations spent in the laboratory, which indicates adaptation to the laboratory conditions. However, there is no way one can ascertain that the differences are due to laboratory adaptation and not to other causes. One possible source of differences is changes in the “natural population” from which flies were collected each time. We cannot discard the possibility that genetic changes occur in natural populations due to several sources of variation (e.g., Fontdevila 1989; Service 2000). The degree to which this may affect inferences from comparisons between populations founded at different times, even if from the same place, is unknown. Finally, genetic sampling effects of foundation

may play an important role in any differences between stocks, and there is no replication procedure that can avoid this problem since, in each new foundation, replicate populations are derived from one single sample. Thus, adopting methodologies used for standard laboratory evolutionary studies that are designed for established laboratory populations (see Rose et al. 1996) is inadequate here.

Despite these potential confounding sources of variation, Sgrò and Partridge (2000) interpret the differences between stocks founded in different years as an effect of how much time they spent in the laboratory. In other words, their analysis is based on the assumption that populations will converge given enough time. However, this is circular reasoning since demonstrating convergence would be essential for the aims of the study and cannot thus be used as a preliminary assumption.

Another problem is, at one extreme, the fact that the most recently founded population was only in its second generation when tested, which cannot rule out that the differences found relative to the other stocks are due to undesirable environmental effects (maternal and other; see Jenkins and Hoffmann 1994). At the other extreme, the two other stocks have already been maintained for more than 20 generations, making it possible that the main processes involved during laboratory adaptation have already occurred (Matos et al. 2000a, 2000b). This suggests caution in attributing the differences to laboratory adaptation.

Finally, we do not consider one of the ANOVA models useful, specifically the one-way ANOVA (which includes all stocks; tables 2, 9, and 12 in Sgrò and Partridge 2000) that is employed, as the authors state, to test for “effects of laboratory adaptation” (Sgrò and Partridge 2000, p. 342). Any indications of significance are difficult to interpret, given the heterogeneity of the stocks that differ in foundation and/or culture conditions.

What, then, is a correct design to tackle the problem of laboratory adaptation? Experimental evolution has to be studied by different means, depending on whether one’s expectation is divergent or convergent evolution. In the first case, a single test after a given number of generations of selection may give the basic information one needs (e.g.,

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degree of differentiation from the control ["ancestral"] population[s]). In the latter case, only through an analysis of evolutionary trajectories can one make inferences of the specific adaptive process involved. If populations with independent origin are used as source populations, it is not legitimate to causally associate the differences found among these populations with the number of generations in the novel environment (e.g., laboratory) and from there to the different degrees of local adaptation. The only test will thus be whether these populations converge through time in the laboratory to progressively more similar expressions of life-history traits.

With this in mind, we have been characterizing laboratory populations of *Drosophila subobscura* since foundation from the wild. In our first study, we compared a recently founded population with a population already in the laboratory for 24 generations, during the first 14 generations since foundation and then at a later generation. Convergence of several life-history traits was clear and was quite fast for early fecundity (see Matos et al. 2000a, 2000b). Though the design was weak in the absence of replicate populations (a problem already corrected in our ongoing research), the importance of defining an evolutionary trajectory was clear. We also found a strong suggestion that the first two or three generations are undesirable for comparisons because they give misleading indications of genetic differences between populations that are probably due to maternal effects or other environmental factors, such as contamination of culture medium with microorganisms brought from nature.

Finally, another problem with Sgrò and Partridge's (2000) article lies in its message of caution: "laboratory-adapted populations should be used for studies of life-history evolution with some circumspection" (p. 351). This idea is not new (Harshman and Hoffmann 2000), but the laboratory is just another environment to which populations adapt. If one is testing general evolutionary theories related to the potentialities expressed close to genetic equilibrium, such as the evolutionary theory of aging, the "peculiarities" of the laboratory environment, or of a given culture regime, are not problematic as long as populations have already adapted to it (Rose et al. 1996). Any laboratory regime, provided its characteristics are clear, can give information on the evolutionary potentialities of a population and thus be used to test general evolutionary theories. Thus, if populations maintained in discrete generations show a higher accumulation of mutations than

populations with overlapping generations, then this mechanism of aging is possible, a conclusion that is obviously relevant for studies of the genetic and evolutionary mechanisms underlying the evolution of aging. How much these results can be extrapolated to natural populations is another question, and it is one not soluble by comparing laboratory regimes and adjusting them one way or the other. This is not, however, the aim of laboratory evolutionary studies whose strong point is to study evolutionary potentialities.

Although the study of Sgrò and Partridge (2000) tackles an important, often-neglected issue in experimental evolutionary biology in general (and in studies using *Drosophila* as a model organism in particular), the lack of temporal dynamics in the data presented do not allow inferences about the evolutionary processes involved in the observed differences between the populations.

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