THE GENETIC ARCHITECTURE OF LIFE-HISTORY TRAITS IN A NATURAL POPULATION OF *TRIBOLIUM CASTANEUM*

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DECLARATION

I certify that the substance of this thesis has not already been submitted for any degree and is not currently being submitted for any other degree.

I certify that to the best of my knowledge any help received in preparing this thesis, and all sources used, have been acknowledged in this thesis.

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Abstract

The aim of this investigation was to study the nature of genetic constraints on life-history evolution in a natural population.

To identify possible constraints, estimates of variance and covariance components were obtained in the laboratory for a range of life-history characters in a population of *Tribolium castaneum* three generations after collection from the wild. Estimates were obtained by means of a diallel analysis. To test predictions about genetic constraints based upon the variance-covariance matrix, selection was conducted for duration of development in both directions for six generations followed by a phenotypic assay of all life-history traits in all lines.

After six generations of selection, there were significant differences between selected lines for both males and females for duration of development and growth rate, but no significant correlated responses in other characters. Some correlated responses, such as a decrease in late life egg production in slow developing lines approached significance and, if the selection program had been continued, may have become significant.

Both lack of genetic variation and negative genetic correlations between life-history traits can constrain response by a life-history trait to selection pressures.

It is unlikely that lack of genetic variation would constrain responses to selection of most life-history traits in this population as most exhibited low to moderate heritabilities. The exceptions were longevity and time to reach peak fecundity. These had virtually no heritable genetic variation but large amounts of non-additive genetic variation. This genetic architecture is suggestive that these traits had experienced strong directional selection and/or developmental buffering systems were suppressing their expression of additive genetic variation. Developmental buffering systems can be deregulated by stress and thus are not necessarily a long-term constaint on the ability of a trait to adapt to changes in the internal and/or external environment.

Although life-history traits were interrelated, the genetic correlations were generally low and should not constrain the response of individual life-history traits to short-term selection. Negative genetic correlations were found between some traits so that antagonistic pleiotropy could be important as a genetic constraint if selection is long-term. As a constraint, antagonistic pleiotropy also could be partially responsible for the maintenance of genetic variation in life-history traits.

Negative genetic correlations between reproduction and reproductive life-span are indicative of a "reproductive cost" which is probably the result of allocation of limited resources between reproduction and survival. This may be a universal constraint moulding the evolution of life-histories.

All fecundity indices were positively correlated but genetic correlations of less than unity and the decrease in late life egg production in slow developing lines suggest that the reproductive schedule is amenable to modification by selection.

Depression of late life fecundity in slow developing lines was not expected as late life fecundity had no heritable variation, and had low and insignificant positive correlations with duration of development. The depression may have been due to disruption of developmental processes as a result of selection for duration of development. It is possible that patterns of development characteristic of a taxon may restrict the range of future adaptations in that taxon. However, further investigation is needed before conclusions about this depression of fecundity can be drawn.

Experimental results do not support theories about the evolution and/or maintenance of senescence by the mechanisms of antagonistic pleiotropy between early and late life-history characters or the accumulation of deleterious mutations. Results do support the hypothesis that senescence is due to a running out of genetic program for internal repair and maintenance capabilities in organisms.

Whilst it is recognised that genetic variation and covariation are dependent upon environment, and thus genetic constraints may differ in different environments, studies which combine a quantitative genetic analysis of a population with a selection program carried out in a single environment are still useful. Firstly, they identify how the genetic variance-covariance matrix affects responses to selection in a specific environment. Secondly, they can help to identify possibly fundamental and universal constraints. Negative genetic correlations reflecting physiological trade-offs may be operational in all "realistic" environments. Studies would need to be repeated in a number of different environments to confirm the

identity of these universal genetic constraints.