

The University of Manitoba

AN EXAMINATION OF THE EFFICIENCY OF A REPEAT MATING DESIGN
FOR THE SEPARATION OF GENETIC AND ENVIRONMENTAL TRENDS IN
A SELECTION EXPERIMENT AND ITS RELATIVE
EFFICIENCY FOR THE GENERATION OF
RESPONSE TO SELECTION
IN MICE

By

Tsang Kay Cheung

A Thesis

Submitted to

The Faculty of Graduate Studies
in Partial Fulfillment of the Requirements
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ABSTRACT

AN EXAMINATION OF THE EFFICIENCY OF A REPEAT MATING DESIGN FOR THE SEPARATION OF GENETIC AND ENVIRONMENTAL TRENDS IN A SELECTION EXPERIMENT AND ITS RELATIVE EFFICIENCY FOR THE GENERATION OF RESPONSE TO SELECTION IN MICE

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The efficiency of a repeat mating design for the separation of genetic and environmental trends, and its effectiveness in achieving response to selection were observed during eight cycles of directional selection for large 12th day litter weight in mice. A control group was used to monitor the accuracy of the repeat mating group in estimating environmental trend. Two further groups under two different levels of mass selection were used to compare the relative success of the repeat mating group in achieving selection response.

From the 3rd cycle to the 8th cycle, the estimated genetic gain in 12th day litter weight in the

repeat mating group was 0.89 ± 0.25 gm per cycle. The selection response was lower than in M_2 mass selection group and higher than in the M_1 mass selection group. The estimate of environmental trend was -0.79 ± 0.78 gm per cycle which was in close agreement with the value of -0.88 ± 0.55 gm per cycle estimated from the control group.

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This thesis is dedicated to my parents in appreciation for their love and encouragement.

TABLE OF CONTENTS

	<u>Page</u>
ACKNOWLEDGEMENTS	ii
LIST OF TABLES	iv
LIST OF APPENDIXES	v
INTRODUCTION	1
REVIEW OF LITERATURE	2
MATERIALS AND METHODS	14
Breeding Stock	14
General Selection Criteria	14
Mating and Selection Scheme	15
Analysis of Data	20
RESULTS AND DISCUSSION	26
Response to Selection	26
Fertility and Litter Size	26
Estimates of Heritability	30
Estimates of Inbreeding Coefficient	32
Estimation of Genetic and Environmental Trends in the Repeat Mating Group	34
SUMMARY AND CONCLUSIONS	37
LITERATURE CITED	39
APPENDIX	42

LIST OF TABLES

		<u>Page</u>
Table 1.	Mating scheme of the repeat mating group.	17
Table 2.	Least square analysis with assumed data.	23
Table 3.	Generation means and standard deviations for 12th day litter weight of all groups for each of eight generations of selection.	27
Table 4.	The actual percent saved for breeding in each generation and the effective cumulated selection differential for groups M_1 and M_2 .	28
Table 5.	Average litter size and standard errors of all four groups for each of eight generations of selection.	29
Table 6.	Heritability estimates from sire-offspring regression for groups M_1 , M_2 and Control; and realized heritability estimates for groups M_1 , and M_2 .	31
Table 7.	Inbreeding coefficients for all groups in each generation.	33
Table 8.	Generation means and sire group means in each generation of the repeat mating group.	35

LIST OF APPENDIXES

	<u>Page</u>
Appendix 1. Response to selection for 12th day litter weight of the three groups measured as deviation from the control group.	42
Appendix 2. Regression of offspring on sire in control, M_1 and M_2 groups for all cycles, with the cycle effect removed.	43
Appendix 3. Computer program to calculate inbreeding coefficient.	44

INTRODUCTION

Quantitative geneticists have long been aware of the importance of an accurate separation of genetic and environmental trends in breeding programs and in selection experiments. Many methods have been developed to assess genetic and environmental trends, especially in the fields of poultry breeding and dairy cattle breeding. A repeat mating design has been proposed as a scheme to separate these trends and has received considerable theoretical treatment with regard to its advantages and efficiency. However, little or no major research work has been published where the repeat mating design has been subjected to an experimental test.

The present investigation was to examine the efficiency of the repeat mating design for the separation of genetic and environmental trends under directional selection for large 12th day litter weight in mice. Also of interest was the effectiveness of repeat mating under selection in achieving response to selection relative to two different intensities of mass selection.

REVIEW OF LITERATURE

The aim of artificial selection is to produce some change in the genetic structure of the population in question. The separation of observed change into its environmental and genetic components is an important part of the analysis of selection experiments or breeding programmes. Unless the environment can be maintained constant over the period of the experiment, a simple measure of genetic response using phenotypic change cannot be used. For some traits that are sensitive to environmental variation, a close to constant environment is not sufficient. Kojima and Kelleher (1963) reported that egg production in D. pseudoobscura showed marked fluctuations over a period of generations, even when the flies were maintained at constant temperature. Furthermore, except for laboratory animals, to provide a sufficiently constant environment for many generations is very difficult if not impossible.

Attempts have been made to compare different genotypes at the same time in the same environment. The use of control populations to provide material for the evaluation of the level of management and in monitoring the genetic improvement in selection programmes has proved its value. Control strains have been used extensively in laboratory investigations and in poultry breeding over a long period of time, but there have been few reports on

the genetic consistency of the control strains used. The first detailed analysis of one particular control flock over a short period was presented by Gowe et al. (1959a). Their objective was to describe the performance over six generations of a random bred control strain in poultry and to indicate the value of the strain in interpreting a selection experiment. The random-bred control strain of S.C. White Leghorns consisted of an average mating population of 47 males and 182 females in each of six generations. The effective number of parents per generation was estimated at 146 and there was no evidence of any significant change in the genetic value of the strain over the six generations when tested on six farms. The performance of the control strain was compared with that of two other strains on test in the same environment. Comparisons of the effects of selection on increased hen-housed egg production, survivor egg production, viability during fertility and hatchability measured in the two selected strains were made, based on the absolute trends in these flocks over the six generations and also on deviations from the performance of the control strain. The results indicated that this control strain could be used for the efficient separation of genetic and environmental effects.

Genetic changes in a control population may consist of both random drift and directional changes due to natural selection. From the point of view of genetic constancy, it is clear that a control population of

unlimited size is the ideal case. The practical task is to specify the mating design which will maximize efficiency in the sense that genetic drift is reduced to a minimum under the given circumstances of resources and labor. Gowe et al. (1959b) compared the theoretical efficiency of a pedigreed control population to a random bred control population in maintaining genetic constancy with care being taken that within the limit of the design each member of the population contributed equally to the next generation. With the same number of breeding parents in each generation for both kinds of control populations, genetic sampling in the pedigreed population was reduced to minimum and the effective number of parents was larger than in the random bred control population. It was concluded that the pedigreed control population was better than the random bred population in reducing the magnitude of genetic drift and was a more efficient control population for a selection programme.

Hill (1972), in discussing the design of control populations, has emphasized that efforts should be made to minimize genetic drift and has shown that if steps are taken to keep family size equal, both drift variance and possible directional selection effects are minimized. But the magnitude of the effects of natural selection and of genotype-environment interactions are difficult to quantify from theoretical arguments and estimates of their real importance in practical situations can only be obtained

from experimental analysis of field data.

Aside from laboratory animal research and poultry breeding, few selection programs with domestic animals can have a satisfactory control population in terms of size and design efficiency because of the prohibitive monetary expense involved. Even in poultry breeding, new mating designs with the purpose of separating genetic and environmental trends have been proposed in order to bypass the expense of maintaining control populations.

In breeding programs with farm animals, methods have been developed to estimate genetic and environmental trends based on the analysis of field records. The contemporary comparison procedure of Robertson and Rendel (1954), which compares all A.I. and non-A.I. first lactation daughters in the same herd-year-season, estimates the superiority of A.I. progeny over their non-A.I. contemporaries by means of least squares analysis of the field records. Van Vleck and Henderson (1961) modified this method to accommodate the estimation of genetic trend of the A.I. population by adding the seasonal estimates of contemporary comparison superiority to the estimates of trend in the non-A.I. population. Henderson et al. (1959) developed a maximum likelihood procedure to estimate genetic change in herds of species that have repeated records of production and are subject to culling. They showed that the classical least squares approach will give a biased estimate of environmental effect when culling is

practised. The statistical model provides estimates of both heritability and repeatability of the trait under analysis.

Smith (1962) proposed an analysis to estimate genetic change in a pig herd. The method depended upon the difference in the rate of change of performance in the population as a whole and in the successive progenies of individual sires. An estimate of genetic change from the regression of performance on time is given by twice the pooled within-sire regression on time of the difference between the population and individual sire means.

Burnside and Legates (1967) used records from full sisters and paternal half-sisters to estimate genetic trends in a population of Holstein-Friesians. All records were analyzed to obtain least-squares constants for year of calving. A weighted regression of these constants on years provided an estimate of the annual trend, genetic plus environmental. Full sisters were analyzed to obtain least-squares year constants adjusted for sire and dam effects and corrected for selection. Weighted regression of these constants on year indicated the environmental trend in the population, and comparison with the genetic plus the environmental trend provided an estimate of annual genetic trend. A second estimate of the annual genetic trend was obtained by comparing the over-all trend with one-half the genetic, plus the environmental trend estimated from records of paternal half-sisters adjusted

for sire effects. The authors reported a close agreement of estimates obtained by the two methods.

A formalized method for estimating environmental and genetic trends is the repeat mating design proposed primarily for poultry by Goodwin et al. (1960) and further elaborated by Giesbrecht and Kempthorne (1965). The terminology used is appropriate to poultry breeding but can be given general application. The plan of this design depends essentially on the use of matings which are repeated identically during two successive breeding seasons. Inter-year comparisons of progeny groups of the same generation measure environmental changes, and intra-year comparisons of progeny groups of two successive generations measure genetic changes.

Hickman (1958) designed a repeat mating system for use with dairy cattle on experimental farms. All virgin heifers and first lactation cows would be mated to young pedigree-selected bulls and all older cows would be mated to proven bulls. Bulls would be selected for use as proven sires at eight years of age and used as such for three years. As the same proven bulls would sire daughters from the same group of cows in successive years, the correlated array of genotypes over the two years would be the required subpopulations, and from them environmental differences in consecutive years, and age and genetic effects could be isolated.

Hickman and Freeman (1968) suggested that the

reports on repeat matings by Hickman (1958), Goodwin et al. (1960) and Giesbrecht and Kempthorne (1965) had included both male and female parents. Consequently, they were confronted with accounting for maternal effects. They proposed a design for dairy cattle selection with attempts to avoid confounding with maternal effects by repeating the use of only the male parents in a random fashion across all possible mates, to balance the maternal effects in comparisons of progeny of bull groups. Young bulls would be selected each year on pedigree performance using paternal half-sib and maternal information. After the progeny tests were completed, the bulls which sired the best progeny would be used to breed nominated cows which would become dams of a new group of young bulls. Such a group of young bulls would be introduced every year for two years' use, with each group being mated at random across all females except the nominated cows. The average difference in phenotype between daughters of successive bull groups provides an unbiased estimate of differences in genotype created by selection. If bulls are selected in the same direction each year, the average difference between successive bull groups is efficiently estimated by the regression of daughter performance on bull group number. Year effects can be simultaneously estimated by least squares analysis.

Krehbiel et al. (1969) used the repeat mating scheme proposed by Goodwin et al. (1960) to maintain a

control line of Montana No. 1 swine in order to monitor the effectiveness of reciprocal selection for performance of crosses between Montana No. 1 and Yorkshire swine. They reported that the repeat mating group was an adequate control population. The yearly environmental changes estimated from repeat matings in the control line were used to adjust the time trend to provide a better estimate of genetic improvement.

The few repeat mating schemes which have been developed have received considerable theoretical treatment, but no comprehensive research data have been published to verify experimentally the efficiency of a repeat mating design in estimating environmental and genetic trends. Whether the repeat mating group can replace the control group in practice in assessing environmental trend is still unclear. Also the effectiveness of the repeat mating group under selection in achieving response to selection has not been determined.

Growth of mammals during their suckling period is influenced by their own genes as well as by postnatal environmental influences, a portion of which would be due to the influence of the genotype of the dam. Twelve day litter weight in mice, as a preweaning trait, has received considerable attention in this regard. Falconer (1947) suggested that 12th day litter weight of nursing young may provide a useful measure of milk yield in dams. The sources of variation in 12th day litter weight were