Original article

On the use of animal models in the analysis of selection experiments[1]

Louis Ollivier

Station de génétique quantitative et appliquée,
Institut national de la recherche agronomique, 78352 Jouy-en-Josas cedex, France

Abstract – The use of an animal model in the analysis of selection experiments offers the theoretical advantage of accounting for changes occurring in the genetic parameters in the course of the experiments. Explicit estimators of realized heritability $\left(h_r^2\right)$ are derived in this paper for balanced one-generation selection designs. Expressions are given for the expectations and variances of the estimators in relation to the true heritability and for the sensitivity of the estimators to the prior value of heritability. Sensitivity is generally high, except for high values of the true heritability and/or extremely large family sizes. The uncertainty on heritability may, however, be taken into account in a context of Bayesian inference, which allows a simultaneous estimation of the initial heritability and of the response. On the other hand, animal model estimators, being dependent on the genetic model assumed, may not provide adequate measures of the actual responses. They also tend to overestimate the accuracy of genetic trend evaluations, since genetic drift is not properly accounted for. Animal models, however, provide a way of evaluating the effects of selection and limited population size in long-term selection experiments, and thus permit a check on the validity of the underlying infinitesimal additive genetic model. Some examples based on published results of long-term selection experiments on mice are discussed. © Inra/Elsevier, Paris

genetic evaluation / selection experiment / animal model BLUP / realized heritability

Résumé – Utilisation du modèle animal dans l'analyse des expériences de sélection. L'application du modèle animal à l'analyse des expériences de sélection permet en théorie une prise en compte de l'évolution des paramètres génétiques

---

[1] This paper is adapted from a contribution presented by the author at a Seminar of the Department of Animal Genetics of Inra: Utilisation du modèle animal pour l'analyse des expériences de sélection, in: Foulley J.L., Molénat M. (Eds.), Séminaire modèle animal. La Colle sur Loup (France), 26–29 September, 1994, pp. 37–45

au cours de l'expérience. Des estimateurs explicites de l'héritabilité réalisée h_r^2 sont présentés dans cet article pour le cas d'expériences de sélection sur une génération en dispositif équilibré. Des expressions sont données des espérances et des variances des estimateurs en fonction de l'héritabilité vraie, ainsi qu'une expression de la sensibilité des estimateurs à la valeur initiale de l'héritabilité. Cette sensibilité est généralement élevée, sauf pour des valeurs élevées de l'héritabilité vraie et/ou des tailles de famille très grandes. Cependant une méthode bayésienne d'inférence permet de s'affranchir de cette difficulté, en estimant simultanément la valeur initiale de l'héritabilité et la réponse. Par ailleurs, les estimateurs du modèle animal, parce que dépendants du modèle génétique supposé, ne fournissent pas toujours des mesures adéquates des réponses à la sélection. Ils tendent aussi à surestimer la précision des évolutions génétiques tracées, puisque la dérive génétique n'est pas bien prise en compte. Le modèle animal, en contrepartie, constitue une méthode d'évaluation des effets de la sélection et de la taille limitée des lignées dans les expériences de longue durée, et permet ainsi de tester la validité du modèle génétique additif infinitésimal sous-jacent. Quelques exemples basés sur des résultats de la littérature relatifs à des expériences de longue durée chez la souris sont discutés. © Inra/Elsevier, Paris

évaluation génétique / expérience de sélection / modèle animal BLUP / héritabilité réalisée

1. INTRODUCTION

One of the objectives of a selection experiment is to compare reality to theory, by checking whether the selection responses predicted are actually achieved. Use is made of the concept of realized heritability $\widehat{h}_r^2$, defined as the ratio of response (R) to selection differential (S) such that $h_r^2 = R/S$ (see Falconer [5]). This parameter (h_r^2) is in fact one element of a set of realized genetic parameters, which can be derived from a properly planned multitrait selection experiment. In farm animals with long generation intervals, selection experiments are generally carried out for a limited number of generations, and the main interest is to evaluate the effect of selection on the means of the selected populations. On the other hand, long-term selection experiments with laboratory animals have somewhat different purposes, which are essentially to assess the limits to selection and to evaluate the effect of selection on the genetic parameters. Most often, individual selection is applied, allowing an easy calculation of S and a direct measurement of R/S. Family and combined selection, however, may also be applied and h_r^2 is then a more complex function of R/S involving the corresponding index coefficients (e.g. see Pérez-Enciso and Toro [11]). With BLUP selection, no exact calculation of S for the selection criterion is possible, except in balanced designs, and realized heritability cannot be measured. Responses (R) are classically based on generation/line least-square estimators obtained in an experimental design properly controlling environmental differences between generations. However, responses may also be derived from individual breeding values. In the late 1970s it appeared that the BLUP method of evaluation could be taken to its 'logical conclusion', as noted by Thompson [16] in his review of sire evaluation, since genetic trends in dairy cattle using BLUP estimators began being presented at that time. In addition to the standard methods of analysis of selection experiments, essentially based on least-square estimators (see [8]), new methods based on mixed models were developed from then. Moving from sire models to animal

models offered additional advantages. As shown by Sorensen and Kennedy [13], the animal model has advantages in the estimation of selection response as well as in the study of the evolution of genetic variance. These two aspects will be considered in succession in this paper. A distinction will be made between inferences based on assumed prior values of the variances in the model and a more general approach integrating the uncertainty on those variances.

2. REALIZED HERITABILITY ESTIMATION IN ONE-GENERATION SELECTION EXPERIMENTS, ASSUMING PRIOR VALUES OF THE VARIANCES IN THE MODEL

As early as 1979, Thompson had pointed out that the responses derived from mixed models include information components based on the selection pressure applied. The estimator of R is then a function including S, which is not the case in the standard methods of analysis of selection experiments. The question explicitly put by Thompson [16] was whether "BLUP estimates of trend are just multiples of the selection differentials". By considering simple one-generation designs, analytical expressions of the weight of S in the estimation of R can be obtained, as will be shown below. Simple designs have previously been investigated by Thompson [17], who considered selection in one sex over several generations, and also by Sorensen and Johansson [12], who considered selection operating in both sexes.

2.1. Design 1: no control line

Though this situation has been fully addressed by Thompson [17], it is again summarized here for the sake of completeness, and the derivation of the estimator of $\widehat{h}_r^2$ is detailed in the Appendix. Using Thompson's notation, n unrelated males $(n \geq 2)$ are measured for the trait of interest in generation 1, out of which one is selected and leaves n progeny measured in generation 2. A pool of dams unrelated to the sires is assumed, in which pedigree information is ignored. In such a situation, the individual (animal) mixed model applied is:

$$y_{ij} = m_i + a_{ij} + e_{ij} \tag{1}$$

where y_{ij} is the value of the trait measured in generation i $(i = 1, 2)$ on the individual j $(j = 1, \ldots n)$, m_i the generation mean, a_{ij} the individual additive genetic value with variance σ_a^2, e_{ij} a random environmental effect with variance σ_e^2, and letting $h^2 = \sigma_a^2/(\sigma_a^2 + \sigma_e^2)$.

In this design, fixed effects are confounded with generation, and it was shown by Thompson [17] that the estimator of realized heritability is the prior value of h^2 assumed. The derivation presented in the Appendix may be extended to any balanced scheme implying selection of s sires leaving n offspring each. It has also been shown by Sorensen and Johansson [12] to hold when selection is in both sexes.

2.2. Design 2: control line

The situation considered here is the same as in design 1, with the addition of a very large pool of unrelated individuals of constant genetic merit, measured in both generations. This allows all measures to be expressed as deviations from a fixed control level. Environmental differences between generations are thus eliminated, and a common mean m may be taken in the model, which becomes:

$$y_{ij} = m + a_{ij} + e_{ij} \tag{2}$$

where y_{ij} is the trait value of individual j in generation i ($i = 1, 2; j = 1, \ldots n$) expressed as a deviation from the control, and a and e are defined as in model (1). As shown in the Appendix, model (2) yields the following estimator of realized heritability:

$$\widehat{h}_r^2 = \left(h^2 + 2\,k\,D/S\right)/(1 + k) \tag{3}$$

in which S is the selection differential, D the observed difference between generation means, and k a weighting factor such that:

$$k = 0.5\,h^2 \left[0.25(n - 1) + 1/\left(1 - h^2\right)\right] \tag{4}$$

A similar reasoning applies when selection operates in both sexes, one individual is selected out of n candidates in each sex, and the selected couple leaves a full-sib family of size $2n$. It can be shown that the weighting factor of D/S in equation (3) then becomes $k_f/\left(1 + k_f\right)$ with:

$$k_f = 0.5\,h^2 \left[(n - 1) + 1/2\left(1 - h^2\right)\right] \tag{5}$$

This situation has been considered by Sorensen and Johansson [12], who derived the proper weight, implicitly assuming $n = 2$. K in their notation equals $2\,k_f$. The above situations may easily be extended to sn unrelated candidates in generation 1, and s half-sib families of size n in generation 2, or s couples selected out of sn candidates of each sex and leaving s full-sib families of size $2n$, since the expressions (3), (4) and (5) are independent of s.

2.3. Design 3: divergent selection

The situation considered now is when the two extreme individuals are selected out of $2n$ unrelated candidates, and each of the selected individuals leaves n offspring, dam pedigree information being also ignored. Equation (1) then applies here, assuming $i = 1, 2$ and $j = 1, \ldots 2n$. As shown in the Appendix, the estimator of realized heritability is again:

$$\widehat{h}_r^2 = \left(h^2 + 2\,k\,D/S\right)/(1 + k) \tag{6}$$

in which S is the selection differential applied in generation 1, i.e. now the phenotypic difference between the two extremes, D is the observed difference in generation 2 between the two sire families, and k is a weighting factor such that:

$$k = 0.25\,h^2 \left[n + 3/\left(1 - h^2\right)\right] \tag{7}$$

When selection operates in both sexes, assuming the extremes to be selected out of n candidates in each sex, and assortatively mated to produce two full-sib families of size n, it can be shown that the weighting factor of D/S in equation (6) becomes $k_f/(1 + k_f)$, with:

$$k_f = 0.5\,h^2\left[n + 1/\left(1 - h^2\right)\right] \tag{8}$$

As with design 2, the situations can be extended to the case of $2sn$ unrelated candidates in generation 1 and $2s$ half-sib families of size n in generation 2, or sn candidates of each sex and $2s$ full-sib families of size n, since the expressions (6), (7) and (8) are also independent of s.

2.4. Statistical properties of the estimators of realized heritability: evaluation of the designs

In design 1, with discrete generations and no control, the estimator $\widehat{h}_r^2$ is strictly equal to the h^2 assumed in equation (1), and the response measured is strictly speaking a prediction, independent of the measures in generation 2 and of family size n. In designs 2 and 3, it can be seen that $\widehat{R}$ combines an a priori information $\left(0.5\,h^2S\right)$, in fact a multiple of the selection differential, and an a posteriori information (D), which is the observed response. The prior information dominates roughly in inverse proportion of h^2, as shown by the k values (4), (5), (7) and (8), which are increasing functions of h^2, as also noted by Sorensen and Johansson [12] for design 2. The statistical properties of the random variable $\widehat{h}_r^2$ in designs 2 and 3 will now be examined in order to evaluate more precisely the efficiencies of those designs.

The estimators (3) and (6) of $\widehat{h}_r^2$ have the following expectation, since $\mathrm{E}(D/S) = 0.5\,h_0^2$, h_0^2 being the true heritability, as opposed to the prior value h^2:

$$\mathrm{E}\left(\widehat{h}_r^2\right) = \left(h^2 + kh_0^2\right)/(1 + k) \tag{9}$$

As shown in *figure 1*, this function varies from 0 to h_0^2 when h^2 increases from 0 to 1, and goes through a maximum which can be obtained by setting the derivative of equation (9) equal to zero. It can be shown that this maximum is reached for $h^2 > h_0^2$, since the equation to solve may be written $h^2 = h_0^2 + (1 + k)/\left(\mathrm{d}k/\mathrm{d}h^2\right)$, and k and $\mathrm{d}k/\mathrm{d}h^2$ are both positive.

Equation (9) and *figure 1* clearly show how dependent the animal model estimators are upon the heritability assumed in the model. Excluding extreme deviations of h^2 from h_0^2, the estimators will generally increase with increasing value of h^2. The sensitivity of the design to the prior h^2 may be expressed as the slope of the curve defined in equation (9) at the value $h^2 = h_0^2$, which can be shown to be $1/(1 + k)$. The sensitivities of various designs for three values of h_0^2 are presented in *table I*. It can be seen that sensitivity varies from nearly 1, which means quasi-proportionality of $\widehat{h}_r^2$ to h^2, to nearly zero, a situation of independence of $\widehat{h}_r^2$ from h^2. However, low sensitivities can only be reached either for traits of high heritability or for very large family sizes. At equal family size, divergent selection (design 3) is generally less sensitive than
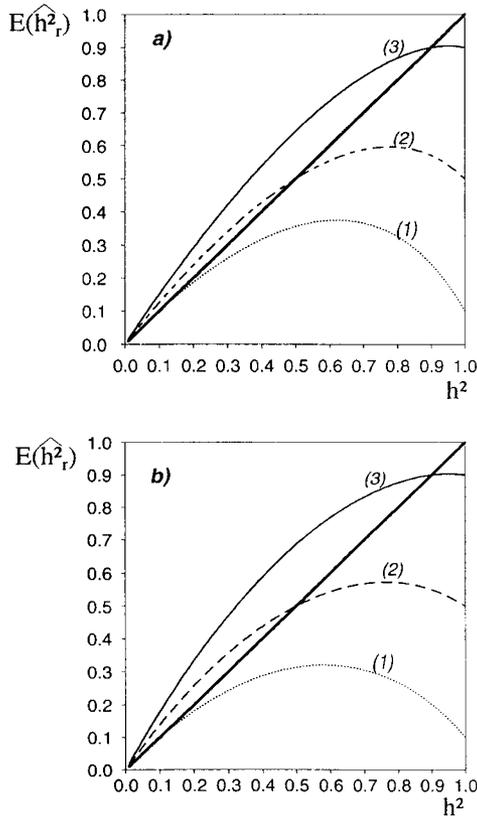
$E(\widehat{h^2}_r)$

Figure 1. Expected value of the estimator of realized heritability $\left(\widehat{h_r^2}\right)$ as a function of assumed heritability $\left(h^2\right)$ in two selection designs, for various values of true heritability $\left(h_0^2\right)$. a) Selected line and control, and half-sib family size $n = 2$; b) divergent selection, and half-sib family size $n = 1$. (1) $h_0^2 = 0.10$; (2) $h_0^2 = 0.50$; (3) $h_0^2 = 0.90$.

one-line selection with control (design 2). One sees also that the advantage of design 3 over design 2 increases with increasing heritability and/or larger family size. When selection operates in both sexes, similar patterns can be shown to hold.

The variance of the estimators (3) and (6) for given fixed values of S is:

$$\mathrm{V}\left(\widehat{h_r^2}\right) = [2k/S(1+k)]^2\, \mathrm{V}(D) \tag{10}$$

Given the assumptions underlying model (1) and further assuming $\sigma_a^2 + \sigma_e^2 = 1$ in both generations, it can be shown that in the general case of s or $2s$ sires selected in generation 1 and half-sib family size of n:

$$\mathrm{V}(D) = \left[2 + 0.25(n-5)h_0^2\right]/sn \ \ \text{or} \ \ \left[2 + 0.5(n-1)h_0^2\right]/sn \tag{11}$$

in designs 2 and 3, respectively.

Table I. Sensitivity[1] of the estimator of realized heritability $\left(\widehat{h}_r^2\right)$ to prior heritability $\left(h^2\right)$ for various values of true heritability $\left(h_0^2\right)$ and half-sib family size (n).

(h_0^2)	Design	n		
		2	10	100
0.10	2	0.94	0.86	0.44
	3	0.86	0.75	0.28
0.50	2	0.64	0.48	0.13
	3	0.50	0.32	0.07
0.90	2	0.18	0.15	0.06
	3	0.08	0.03	0.00

[1] Sensitivity is defined as $1/(1+k)$, k being given by equations (4) and (7) for designs 2 (control line) and 3 (divergent selection), respectively.

Equation (10) shows that the accuracy of estimation of $\widehat{h}_r^2$, in terms of the inverse of its standard error, is inversely proportional to the relative weight $k/(1 + k)$ given to the posterior information in this estimation. In designs yielding estimators very sensitive to prior heritability, i.e. with low heritability and small family size, animal model estimators of $\widehat{h}_r^2$ will be extremely accurate. It can also be seen that equation (11) does not include the drift variance associated with the limited effective size of the selected lines, and thus shows that the genetic drift variance is not properly accounted for in the animal model estimators. For instance, in the simple case of design 3 with $s = n = 1$, $V(D) = 2$ and does not include the drift variance due to an effective population size of $N = 4$ in each line, corresponding to one male and an infinite pool of unrelated females. Quite similarly, a strict application of least squares does not account for genetic drift either, but this effect may be incorporated into the variance of the estimators of realized heritability, through the procedures described by Hill [8].

3. INFERENCES FROM SELECTION EXPERIMENTS WHEN THE VARIANCES IN THE MODEL ARE UNKNOWN

The sensitivity of the estimators considered so far to prior values of h^2 is clearly the consequence of the uncertainty as to the real value of this parameter. The problem, however, has a conceptually simple solution when framed in a Bayesian setting, as shown by Sorensen et al. [15]. Inferences about selection responses can be made using the marginal posterior distribution of selection response, and the uncertainties about variance components are then taken into account by viewing those components as nuisance parameters.

The marginal posterior distributions can be obtained by Gibbs sampling, and probabilities that the response R lies between specified values can be computed. The same reasoning applies to variance components and h^2. In the simple designs considered in section 2, where S can be calculated, the posterior distribution of R/S could be obtained and compared to that of h^2. Inferences are influenced by the amount of data available and the assumed type of a

priori distribution of the variance components, as shown in the example in Sorensen et al. [15]. In this example h_r^2 cannot be obtained, since S cannot be easily calculated. But one can expect its properties to closely follow those of R, according to the amount of data and type of prior, i.e. the more data are available the less are the estimates of responses influenced by the choice of priors. And similarly for the variances of the estimate, they would be expected to be highly dependent on the type of prior, in addition to being larger than those obtained in the section 2 setting, since more uncertainty is taken into account.

4. EVOLUTION OF GENETIC VARIANCE IN SELECTION EXPERIMENTS OVER SEVERAL GENERATIONS

Moving from one cycle of selection, as considered above, to several successive cycles requires accounting for the effects of selection on the genetic variance. It is well known that selection induces linkage disequilibria tending to reduce the genetic variance, and leading to an asymptotic response lower than the response expected in the first generation [3]. In selected lines of limited size, an additional factor reducing the response is the decrease in genetic variance due to genetic drift, a decrease which itself depends on the selection criterion applied [18]. Consequently, the ratio R/S evaluated over several generations is not relevant, as it is expected to be systematically below the initial heritability. The animal model takes into account the two phenomena of variance reduction due to drift [13] and to the Bulmer effect [14]. This model, when applied to long-term selection experiments, thus yields unbiased estimates of selection responses over successive generations on the one hand, and provides an estimate of the initial genetic variance on the other, using the restricted maximum likelihood approach (REML: e.g. see [16]). A basic assumption of this approach is of course the additive genetic infinitesimal model.

Selection experiments have been analysed increasingly according to the animal model methodology, since Blair and Pollak [2] evaluated selection response in a seven-generation experiment on sheep, and suggested that mixed models could be used to estimate genetic trends when no control is available. One of the first applications to long-term selection experiments has been presented by Meyer and Hill [10], on 23 generations of selection for food intake in mice. In order to show the evolution of genetic variance, a two-step procedure of data splitting was implemented, first cumulating increasingly larger numbers of generations from the beginning of the experiment (analysis I), and then having separate groups of consecutive generations analysed independently (analysis II). As shown in *table II*, analysis I indicates that, as expected, standard realized heritability (R/S) decreases when the number of generations included increases, whereas the animal model heritability also decreases, which is contrary to expectation, since in theory the animal model estimates the initial genetic variance. Analysis II indeed reveals a marked reduction of genetic variance already at generation 8, and the effect is enhanced at generation 14. The authors could then safely conclude that 'selection for appetite in mice has reduced the genetic variance over and above the effects of inbreeding and selection', and that the infinitesimal model does not apply. Another conclusion to be drawn is that the animal model underestimates the initial heritability

and, consequently, responses are also underestimated initially, owing to the sensitivity of the estimator to prior heritability. A close examination of the graph of predicted values and phenotypic means over generations (in figure 2 of [10]) indeed seems to indicate a slightly larger observed divergence compared to the animal model prediction. In contrast, in another mouse selection experiment of similar duration, the animal model estimate of heritability over the whole experiment was found to be very close to the estimate obtained in the first seven generations, and, accordingly, the divergence predicted from the animal model was in good agreement with the actual phenotypic divergence observed [1].

Table II. Heritability estimates of food intake over variable numbers of generations of divergent selection in mice [10].

Generation subset	Analysis I R/S^1	$h^{2\ 2}$	Analysis II Generation subset	$h^{2\ 3}$
A	0.32	0.18	A$'$	0.23
A + B	0.14	0.13	B	0.11
A + B + C	0.13	0.10	C	0.06

A: generations 2–7 (A$'$: generations 5–7); B: generations 8–13; C: generations 14–23. [1] Realized heritability within full-sib families; [2] REML heritability within full-sib families; [3] overall REML heritability.

5. DISCUSSION AND CONCLUSIONS

The theoretical advantages of the mixed animal model in the analysis of selection experiments have been frequently emphasized. Compared to a simpler least-square analysis, the method allows one to better account for environmental effects and avoids the need for an experimental design with controls [2, 12, 14]. It is also well known that the estimates of selection response obtained via the animal model are dependent on the prior values of the genetic parameters [2, 12, 17]. As shown here, this dependency can be precisely evaluated in simple one-generation selection designs and the usual designs yield estimates of $\widehat{h}_r^2$ highly sensitive to the prior heritability in most cases (see *table I*). Such a conclusion can safely be extended to designs covering more generations, such as the repeat sire design investigated by Thompson [17] over three generations. The sensitivity of a design may also be evaluated a posteriori, by estimating responses with increasing values of the prior heritability, and in most cases responses have been shown to actually increase markedly when h^2 increases (see, for instance, [2] or [11]). A posteriori evaluations of responses with varying values of prior heritability should also be recommended in the more general case of field data. The sensitivity of the estimator to prior h^2 may be expected to be a decreasing function of the degree of overlap between generations, or of the degree of connectedness of the data. Obviously, when generations do not overlap the situation is that of design 1, with no control, and sensitivity is maximum.

In the absence of information on the true value of heritability, it was shown by Gianola et al. [6] that breeding values should be predicted using its REML estimate in the data. It was later shown that the problem of inferences about genetic change when heritability is unknown can be solved in a Bayesian setting [15]. It should be noted that the classical approach suggested by Gianola et al. [6] offers a good approximation to the full Bayesian method of Sorensen et al. [15] when the information about heritability in the experiment is large enough. The accuracy of BLUP evaluation has also been sometimes presented as an argument in favour of the method for the estimation of genetic trends. However, the prediction error variance of BLUP estimates is highly dependent on the weight given to the prior information, as equation (11) shows. A false impression of high accuracy will then be obtained in designs highly sensitive to prior genetic parameters. In addition, drift variance as a source of error between replicates is partially ignored, since the incidence matrix $\mathbf{Z}$ of individual genetic values and the relationship matrix $\mathbf{A}$ are considered as fixed. A common feature of the graphs showing genetic trends based on animal model evaluations of breeding values is the smoothing out of the between-generation fluctuations, in contrast with the highly irregular evolution of the phenotypic means (e.g. figure 1 of [2], or figure 2 of [10]). If a Bayesian approach is implemented, the choice of an appropriate prior distribution of heritability is an important issue to consider. As shown in the example simulated by Sorensen et al. [15], the variance of the posterior distribution of the selection response is considerably reduced when an informative prior is used. Another issue, quite distinct from the problems of statistical inference previously discussed, is the genetic model assumed. The additive infinitesimal model is implicit in models (1) and (2) and it is also the most generally used model in the analysis of long-term selection experiments. The responses estimated are clearly model dependent. In particular, ignoring dominance is known to lead to an overestimation of the responses. A simulation [9] has shown that for a trait showing 40 % additive genetic and 20 % dominance variance, the use of an additive animal model yielded a bias in the estimate of response over six generations which was 1.21 times the real response. Chevalet [4] has derived an expression for the bias expected in breeding value prediction when an additive model is applied in a dominance situation. In addition, the infinitesimal model cannot account for changes in gene frequency due to selection or mutational variance, which are likely to contribute substantially to changes in additive genetic variance. Heath et al. [7] have suggested an extension of the REML procedure to the estimation of changes in variance components over generations and they have shown that significant changes had occurred in their selected mouse lines.

In conclusion, the usefulness of the animal model approach for studying the evolution of genetic parameters in long-term selection experiments is now well documented. The model indeed provides a way of testing the adequacy of the genetic assumptions underlying the analysis of selection responses. As to genetic trends, the animal model, strictly speaking, only provides trends in breeding value predictions based on a specific genetic model. This dependency on the genetic model leads to questioning the adequacy of the animal model applied to evaluate genetic progress. It should be noted that the consequences of using a wrong genetic model for evaluating responses over several generations are expected to be different from the consequences on

breeding value predictions and selection efficiency. In breeding value predictions precision is more important than bias, as pointed out by Johansson et al. [9]. When responses are evaluated, the errors may be cumulative over generations, and create a sizeable bias. In other words, one may doubt that a proper evaluation of past events (such as genetic progress over a long period of time) can be safely based on a method whose aim essentially is to predict the future (such as breeding values needed to carry out selection decisions).

ACKNOWLEDGEMENTS

REFERENCES

[1] Beniwal B.K., Hasting I.M., Thompson R., Hill W.G., Estimation of changes in genetic parameters in selected lines of mice using REML with an animal model 1. Lean mass, Heredity 69 (1992) 352–360.

[2] Blair H.T., Pollak E.J., Estimation of genetic trend in a selected population with and without the use of a control population, J. Anim. Sci. 58 (1984) 878–886.

[3] Bulmer M.G., The effect of selection on genetic variability, Am. Nat. 105 (1971) 201–211.

[4] Chevalet C., Utilisation du modèle animal en présence d'effets génétiques non additifs, in: Foulley J.L., Molénat M. (Eds.) Séminaire modèle animal. La Colle sur Loup, 26–27 September 1994, Inra, Jouy-en-Josas, France, 1994, pp. 67–74.

[5] Falconer D.S., Introduction to Quantitative Genetics, 3rd ed., Longman, Harlow, UK, 1989.

[6] Gianola D., Foulley J.L., Fernando R., Prediction of breeding values when variances are unknown, Génét. Sél. Evol. 18 (1986) 485–498.

[7] Heath S.C., Bulfield G., Thompson R., Keightley P.D., Rates of change of genetic parameters of body weight in selected mouse lines, Genet. Res. 66 (1995) 19–25.

[8] Hill W.G., Estimation of realized heritabilities from selection experiments, Biometrics 28 (1972) 747–780.

[9] Johansson K., Kennedy B.W., Wilhemson M., Precision and bias of estimated genetic parameters in the presence of dominance and inbreeding, 5th World Congr. Genet. Appl. Livestock Prod. 18 (1994) 386–389.

[10] Meyer K., Hill W.G., Mixed model analysis of a selection experiment for food intake in mice, Genet. Res. 57 (1991) 71–81.

[11] Pérez-Enciso M., Toro M., Classical and mixed-model analysis of an index selection experiment for fecundity in Drosophila melanogaster, J. Anim. Sci. 70 (1992) 2673–2681.

[12] Sorensen D.A., Johansson K., Estimation of direct and correlated responses to selection using univariate animal models, J. Anim. Sci. 70 (1992) 2038–2044.

[13] Sorensen D.A., Kennedy B.W., The use of the relationship matrix to account for genetic drift variance in the analysis of genetic experiments, Theor. Appl. Genet. 66 (1983) 217–220.

[14] Sorensen D.A., Kennedy B.W., Estimation of response to selection using least-squares and mixed model methodology, J. Anim. Sci. 58 (1984) 1097–1106.

[15] Sorensen D.A., Wang C.S., Jensen J., Gianola D., Bayesian analysis of genetic change due to selection using Gibbs sampling, Genet. Sel. Evol. 26 (1994) 339–360.

[16] Thompson R., Sire evaluation, Biometrics 35 (1979) 339–353.

[17] Thompson R., Estimation of realized heritability in a selected population using mixed model methods, Genet. Sel. Evol. 18 (1986) 475–484.

[18] Verrier E., Colleau J.J., Foulley J.L., Long-term effects of selection based on the animal model BLUP in a finite population, Theor. Appl. Genet. 87 (1993) 446–454.

APPENDIX: Derivation of analytical expressions of realized heritabilities using animal models

A1. No control line

From equation (1), the following system of $2(1+n)$ equations is derived: see the approach in design I of [17], assuming one selected sire, $s = 1$, and a number of years $T = 2$. Letting y_{11} be the phenotypic value of the individual selected and letting y_1, y_2, a_1, a_2 represent the phenotypic and additive genetic mean values in generations 1 and 2, respectively, and putting $\alpha = (1 - h^2)/h^2$, the system is:

$$y_1 = m_1 + a_1 \tag{A1}$$

$$y_2 = m_2 + a_2 \tag{A2}$$

$$y_{11} = m_1 + (1 + \alpha + n\alpha/3)a_{11} - (2n\alpha/3)a_2 \tag{A3}$$

$$y_{1j} = m_1 + (1 + \alpha)a_{1j} \quad j = 2 \ldots n \tag{A4}$$

$$y_{2j} = m_2 - (2\alpha/3)a_{11} + (1 + 4\alpha/3)a_{2j} \quad j = 1 \ldots n \tag{A5}$$

From the equality $(A2) = \sum_j (A5)/n$ one obtains $a_2 = 0.5a_{11}$, and putting this value of a_2 into $(A1) = \left[(A3) + \sum_j (A4)\right]/n$ yields $a_1 = 0$, whence $m_1 = y_1$. By definition the selection differential is $S = y_{11} - y_1 = y_{11} - m_1$. From equation (A3), replacing a_2 by its value above, S may be expressed as a function of a_{11}, such as $S = (1 + \alpha)a_{11}$. As $a_1 = 0$, the selection response is $R = a_2 = 0.5a_{11}$. As $1 + \alpha = 1/h^2$, the estimator of R can be expressed as a function of S:

$$\widehat{R} = 0.5 h^2 S \tag{A6}$$

Since selection is only in one sex, the estimator of realized heritability $\left(h_r^2\right)$ is $2\widehat{R}/S$, i.e.:

$$\widehat{h}_r = h^2 \tag{A7}$$

A2. Control line

Replacing m_1 and m_2 by m in the previous system (A1)–(A5), the following system is obtained:

$$y_1 + y_2 = 2m + a_1 + a_2 \tag{A8}$$

$$y_1 = m + (1 + \alpha)a_1 + (\alpha/3)a_{11} - (2\alpha/3)\,a_2 \tag{A9}$$

$$y_2 = m - (2\alpha/3)a_{11} + (1 + 4\alpha/3)\,a_2 \tag{A10}$$

$$y_{11} = m + (1 + \alpha + n\alpha/3)a_{11} - (2n\,\alpha/3)\,a_2 \tag{A11}$$

From (A9) + (A10) + (A8) $= 0$, a_{11} may be expressed as $a_{11} = 3a_1 + 2\,a_2$. S, defined as in section A1, and $D = y_2 - y_1$ may also be expressed in terms of a_1 and a_2 in the following system:

$$0.5\,S = [1 + 0.5\,\alpha(n + 1)]\,a_1 + (1 + \alpha)\,a_2 \tag{A12}$$

$$D = -(1 + 4\,\alpha)\,a_1 + a_2 \tag{A13}$$

Solving (A12) and (A13) for a_1 and a_2 yields:

$$\hat{a}_1 = [0.5\,S - (1 + \alpha)\,D]\,/\Delta$$

$$\hat{a}_2 = \{(1 + 4\,\alpha)0.5\,S + [1 + \alpha(n + 1)/2]\,D\}/\Delta$$

with $\Delta = 2 + \alpha(n + 3)/2 + 4\,\alpha(1 + \alpha)$.

The estimator of $R = a_2 - a_1$ is:

$$\hat{R} = \hat{a}_2 - \hat{a}_1 = \{2\,\alpha\,S + [2 + \alpha(n + 3)/2]\,D\}/\Delta$$

If k is defined as the weight of D relative to that of $0.5\,h^2 S$ (i.e. $4\alpha/h^2$) in this estimator, $k = h^2[2 + \alpha(n + 3)/2]/4\alpha$, and $\hat{R}$ may be expressed as:

$$\hat{R} = (0.5\,h^2 S + kD)/(1 + k)$$

From this the estimator $(2\,\hat{R}/S)$ of h_r^2 given in equation (3) with the value of k in equation (4) is obtained.

A3. Divergent selection

Model (1) can account for this design, if one considers $2n$ individuals measured in each generation. Noting the symmetry in the equations for the two extreme (selected) individuals, y_{1h} and y_{1l}, and letting their respective progeny means be y_{2h} and y_{2l} and the corresponding additive genetic means in generation 2 be a_{2h} and a_{2l}, the following system is obtained:

$$y_{1h} = m_1 + (1 + \alpha + n\alpha/3)a_{1h} - (2\,n\alpha/3) + a_{2h} \qquad (A14)$$

$$y_{1l} = m_1 + (1 + \alpha + n\alpha/3)a_{11} - (2\,n\alpha/3)\,a_{2l} \qquad (A15)$$

$$y_{2h} = m_2 - (2\alpha/3)a_{1h} + (1 + 4\alpha/3)\,a_{2h} \qquad (A16)$$

$$y_{2l} = m_2 - (2\alpha/3)a_{2h} + (1 + 4\alpha/3)\,a_{2l} \qquad (A17)$$

S and D may be expressed as functions of $(a_{1h} - a_{1l})$ and $(a_{2h} - a_{2l})$ in the following system:

$$S = y_{1h} - y_{1l} = (1 + \alpha + n\alpha/3)(a_{1h} - a_{1l}) - (2n\alpha/3)(a_{2h} - a_{2l}) \quad (A18)$$

$$D = y_{2h} - y_{2l} = -(2\,\alpha/3)(a_{1h} - a_{1l}) + (1 + 4\,\alpha/3)(a_{2h} - a_{2l}) \qquad (A19)$$

Solving (A18) and (A19) for $(a_{2h} - a_{2l})$ yields the estimator of R:

$$\widehat{R} = a_{2h} - a_{2l} = [(2\,\alpha/3)S + (1 + \alpha + n\alpha/3)D] \,/\, [1 + \alpha + n\alpha/3 + 4\,\alpha(1 + \alpha)/3]$$

If k is again defined as the weight of D relative to that of $0.5\,h^2 S$ (i.e. $4\alpha/3h^2$) in this estimator, $k = 3h^2(1 + \alpha + n\alpha/3)/4\alpha$, and $\widehat{R}$ may be expressed as:

$$\widehat{R} = (0.5\,h^2 S + kD)/(1 + k)$$

From this, the value of $\widehat{h}_r^2$ given in equation (6) is derived with the value of k given in equation (7).