# Nonlinear heritabilities and curvilinear relationships: Genetic factors complicating selection for functional traits

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#### Abstract

Functional traits, especially fitness-related traits, may not always follow the pattern of inheritance commonly assumed by animal breeders (i.e. the infinitesimal model). Deviations from the infinitesimal model that produce nonlinear heritabilities and curvilinear genetic relationships between traits and their implications for breeding programmes are discussed.

Nonlinear heritability is reviewed in the context of reproductive fitness. The hypothesis of Gowe (1983) that the heritability of reproductive fitness is low in the upper 80 - 90 % of the phenotypic range and moderate for the lower 10 - 20 % of the range is supported by findings of short term divergent selection experiments with asymmetrical response. The conclusion that independent culling of a small proportion of the population with the lowest fitness prevents fitness decline whilst saving most of the selection pressure for economic traits is not fully supported by simulation studies.

A concept for estimating curvilinear genetic relationships between traits based on offspringparent polynomial regression is derived using a path model. It is shown that environmental effects dilute the curvilinearity of genetic relationships between traits very much so that even with rather extremely curved genotypic relationships, the phenotypic relationship may be almost linear. The method is used to estimate curvilinear relationships between milk yield and type traits. Only for some udder traits, significant curvilinearity is found in the offspring-parent regression.

It is concluded that use of standard linear selection index procedures to combine production and functional traits may be suboptimal and that work is needed in the areas of estimation of nonlinear genetic parameters and their adequate inclusion in multivariate selection.

#### 1. Introduction

Multivariate selection schemes in animal breeding are normally based on the additive infinitesimal model (Bulmer, 1985), the genetic parameters involved are heritabilities and genetic correlations. Functional traits, especially fitness traits do not fit very well into this framework as the proportion of additive variance in these traits is low and non-additive components of genetic variance play a bigger role (e.g. Fuerst and Sölkner, 1994). Also, the relationship between quantitative traits and fitness is likely to be nonlinear (fitness profiles; Falconer, 1982) and intermediate expressions of quantitative traits may often be optimal with respect to fitness. In the following we discuss a few deviations from the infinitesimal model that may be of importance when considering inclusion of functional traits into breeding programs.

### 2. Nonlinear heritabilities

Heritability may be defined as the ratio of genetic over phenotypic variance, as the square of the correlation between genotype and phenotype; and as regression of genotype on phenotype (Falconer, 1982). Only the last definition allows an extension of the concept of heritability towards nonlinearity.

## 2.1. Gowe's hypothesis

Gowe (1983) and Gowe et al. (1993) predicted that heritabilities of fitness traits were nonlinear, being close to zero in the upper 80 - 90 %, and moderate in the lower 10 - 20 % of the phenotypic range. This was attributed to segregation of low frequency deleterious recessive genes in mutation-selection balance. Under such a model, culling of a small proportion (10 - 20%) of the individuals with the lowest fitness was predicted to be successful in preventing a decline in reproductive fitness while maintaining most of the selection pressure on the other economic traits.

## 2.2. Tests of the hypothesis

There are three alternative ways to test the validity of the hypothesis of the existence of nonlinear heritabilites for fitness traits. The most direct one would be via offspring-parent regression. The second is to estimate the response to selection in direction of increased and decreased fitness. Asymmetrical response is expected in the presence of nonlinear heritability. The third way of testing the hypothesis is by evaluating it through the expected outcome, i.e. efficiency of culling a small proportion of individuals low in (reproductive) fitness to prevent a decline in fitness while putting selection pressure on other traits.

To our knowledge, nonlinearity of offspring-parent regression has not been tested for fitness traits. Reports on nonlinear offspring-parent regression are available for *Drosophila* experiments (Robertson, 1977; Salgado et al., 1989; Gifford and Barker, 1991; Gimelfarb and Willis, 1994), but traits are bristle number, weight and wing length.

The most convincing evidence to date for the existence of nonlinear heritability in fitness traits is a meta-analysis by Frankham (1990) where he compiled 30 published bidirectional selection experiments for reproductive fitness traits with Japanese quails, chicken, mice, *Tribolium* and *Drosophila*. In 24 of those 30 studies, significant asymmetry in the predicted direction was found. For studies reporting realized heritabilities, the means were 0.17 and 0.26 for lines selected for higher and lower reproductive fitness, respectively.

Independent culling for poor reproductive performance has been practised by Gowe et al. (1993) in a strain of poultry selected for egg production over many generations. No decline in hatchability and fertility was found in comparison to an unselected control. There was, however, no selected line without culling to confirm that fitness would have declined without culling. Frankham et al. (1988) reported a replicated selection experiment with *Drosophila melanogaster* with 3 lines: HO, selected for alcohol tolerance without culling for fitness, HS, a line selected for alcohol tolerance with culling of 20% of selected females on reproductive fitness, and C, an unselected control. After 25 generations, fitness was significantly lower in the HO lines than in the HS lines wheras HS lines did not differ significantly from C lines or the base population. Responses for alcohol tolerance were similar for HO and HS lines.

Computer simulations have been carried out trying to model the genetic mechanism described by Gowe (Gibson and Engstrom, 1995; Meuwissen et al., 1995) or to find genetic models that could explain the results found by Frankham et al. (Li and James, 1991, 1992). Results from these models generally show that by culling of 10 - 20 % of the animals for low fitness, some loss in gain for the selected production traits is to be expected and reproductive fitness is usually slightly but significantly reduced in comparison to unselected controls.

#### 2.3. Effect of nonlinear heritabilities on multivariate selection strategies

If heritabilities of functional traits are indeed nonlinear inclusion of such traits in a linear selection index is likely suboptimal. The selection strategy proposed by Gowe (1983) based on independent culling of a rather small proportion of individuals with poor reproductive fitness will be more efficient but may not be optimal either. Meuwissen et al. (1995) compare different selection strategies including restricted selection indices. They get different results depending on the genetic models imposed but there seems to be an overall advantage for a method they call "empirical restricted selection index". In this procedure, partial indices are constructed for production and reproduction and the relative weighting of these is changed each generation in a way that the average index for reproduction of selected animals conforms a preset value (i.e. initial average of reproduction). This is an indirect way of dealing with nonlinear heritablities in a linear selection index. Extension of selection index theory to indices nonlinear in the genetic parameters should be investigated as an alternative.

#### 3. Curvilinear genetic relationships between traits

The usual way of describing relationships between traits in quantitative genetics is by genetic correlations. This implies that these relationships are assumed to be linear (the correlation coefficient is a 'bilinear regression coefficient in standard measure'; Dickerson, 1969). Imputing linear relationships between traits may be a helpful simplification, but considering physiological limits it is unlikely that those are the rule in biology (Sölkner and James, 1994). This may be the case for quantitative traits under artificial selection (Moll et al. 1975) but will be especially true for the relationship between quantitative and fitness traits. Falconer (1982) describes the relationship between metric characters and fitness via "fitness profiles" and points out that many traits (e.g. body size traits in mice) may have an intermediate optimum in fitness. Hence, the assumption of a nonlinear relationship between traits should be a more adequate approach to describe the true state of the relationship between traits and provide a more factual insight how related traits will change under selection. A useful theory to evaluate nonlinear relationships on the genetic scale and their implications on selection has not yet been developed.

In the present paper, path analysis techniques (e.g., Wright 1968) are used to derive some formulae for estimation of a nonlinear genetic relationship between traits on the basis of a polynomial offspring-parent regression model of degree 2. By means of simulated data and the analysis of some dairy and type traits of the Austrian Simmental cattle population, problems of nonlinear relationships will be pointed out.

## 3.1. A method to evaluate curvilinear genetic relationships via offspring-parent regression

To describe a nonlinear phenotypical relationship between the variables y (dependent) and x (independent) the following quadratic regression model was used:

$$P_{y}' = b_{0} + b_{1}P_{x} + b_{2}P_{x^{1}} + \varepsilon$$
 (1)

with  $b_0$ ,  $b_1$  and  $b_2$  being intercept, regression coefficients for x and  $x^2$  and  $\varepsilon$  a random residual term. If  $P_x$  is centered (zero mean) and symmetrically distributed, the  $P_x$  and  $P_x^2$ , are uncorrelated so that the path coefficients  $b'_1$  and  $b'_2$  (see statistical path diagram, Fig. 1) can also be interpreted as correlation coefficients  $r(P'_y, P_x)$  and  $r(P'_y, P_x)$ , respectively.

Figure 1: Statistical path diagram

$$P'_{y} \underbrace{\begin{array}{c} b'_{2} \\ P'_{y} \\ b'_{1} \end{array}} P_{x}$$

Figure 2: Biometrical path model



In Fig. 2 the biometrical path model is shown, where  $A_x$  is the breeding value for X,  $A_y$  is that part of breeding value of Y which is independent of  $A_x$  and  $A_{x^2}$ ,  $A_y^{\bullet}$  is the genetic value of Y determined by  $A_y$ ,  $A_x$  and  $A_{x^2}$ ,  $a'_0$ ,  $a'_1$ , and  $a'_2$  are path coefficients and h denote the square roots of heritabilities (under normality  $E(h(x^2)) = h^2(x)$ ). From the path diagrams in Fig. 1 and 2 it can be seen that

$$b_1' = r(P_y', P_x) = h^*(y) \cdot 0.5 \cdot a_1' \cdot h(x)$$
<sup>(2)</sup>

$$b'_{2} = r(P'_{y}, P_{x^{2}}) = h^{*}(y) \cdot 0.25 \cdot a'_{2} \cdot h(x^{2})$$
(3)

and, following standard regression theory

$$b_1 = h^*(y) \cdot 0.5 \cdot a_1' \cdot h(x) \cdot \frac{\sigma_{P(y)}}{\sigma_{P(x)}}$$
(4)

$$b_{2} = = h^{*}(y) \cdot 0.25 \cdot a_{2}' \cdot h(x^{2}) \cdot \frac{\sigma_{p(y)}}{\sigma_{p(x^{2})}}$$
(5)

Solving equations (5) and (6) for  $a'_1$  and  $a'_2$ , respectively, we get

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$$a_{1}' = \frac{b_{1} \cdot \sigma_{p(x)}}{h^{*}(y) \cdot 0.5 \cdot h(x) \cdot \sigma_{p(y)}}$$

$$a_{2}' = \frac{b_{2} \cdot \sigma_{p(x^{1})}}{h^{*}(y) \cdot 0.25 \cdot h(x^{2}) \cdot \sigma_{p(y)}}$$
(6)
(7)

and for the genetic polynomial regression coefficients  $a_1$  and  $a_2$ 

$$\hat{a}_{1} = \frac{\hat{b}_{1} \cdot \sigma_{p(x)}}{h^{*}(y) \cdot 0.5 \cdot h(x) \cdot \sigma_{p(y)}} \cdot \frac{\sigma_{a(y)}}{\sigma_{a(x)}} = \frac{\hat{b}_{1} \cdot h^{*}(y)}{h^{*}(y) \cdot 0.5 \cdot h(x) \cdot h(x)} = \frac{\hat{b}_{1}}{0.5 \cdot h^{2}(x)}$$
(8)

$$\hat{a}_{2} = \frac{\hat{b}_{2} \cdot \sigma_{p(x^{2})}}{h^{*}(y) \cdot 0.25 \cdot h(x^{2}) \cdot \sigma_{p(y)}} \cdot \frac{\sigma_{a(y)}}{\sigma_{s(x^{2})}} = \frac{\hat{b}_{2} \cdot h^{*}(y)}{h^{*}(y) \cdot 0.25 \cdot h(x^{2}) \cdot h(x^{2})} = \frac{\hat{b}_{2}}{0.25 \cdot h^{4}(x)}$$
(9)

### 3.2. Example with simulated data

To demonstrate the usefulness of the derived formulae a sample of 10.000 parent-offspring pairs was generated by means of Monte Carlo technique following the biometrical path model given above. The following parameter values were used when simulating the data:  $h^{*2}(y) = 0.5$ ,  $h^2(x) = 0.3$  ( $\Rightarrow h^2(x^2) = 0.09$ ),  $r_{A_{p}^*,A_{z}} = 0.6$ ,  $r_{A_{p}^*,A_{z}^2} = -0.6$ ; all random variables  $(A_{p}, A_{x}, P_{x})$  are normally distributed with zero means.

Figure 3: Regression of a)  $A_y$  on  $A_x$  (genotypes within parents) and b)  $P'_y$  on  $P_x$  (phenotypes of offspring and parents)



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In Figure 3 the relationships are shown between genotypes of the same individual  $(A_x \text{ and } A_y)$ and between phenotypes of parents and their offspring  $(P_x \text{ and } P'_y)$ . Through diluting environmental effects and the effect of Mendelian segregation the relationship between the considered traits gets much looser (from  $R^2 = 0.72$  to  $R^2 = 0.013$ ) so that the expression of the phenotypic polynomial regression between offspring and parent is very weak. In other words this means that even if a phenotypic nonlinear relationship is very weak, the underlying genetic relationship may be quite strong.

## 3.3. A real-life example: milk yield and type traits in dairy cows

Norman et al. (1988) showed that the relationships between linear type traits and milk yield are often curvilinear. Consistent curvilinearity over breeds was found for fore udder attachment, suspensory ligament, udder depth, strength and dairy character.

Milk recording data of first lactation Austrian Simmental cows and the type trait classification data of their first lactating daughters were used, making the usual data checks. In total, 3750 mother-daughter records were used, analysing the relationships between milk yield, fat and protein percentage and the type traits height at withers, height of rump, depth of chest, width of pelvis, chest girth, length of barrel, udder attachment, fore udder, rear udder, teat placement, teat stature and the aggregate scores for udder, frame, shape and conformation. Residuals for 305-day-milk-yield, fat and protein percentage were predicted for mothers with calving year (1977-92) and calving month as fixed effects and age at first calving as covariable. Residuals for type traits were predicted for daughters with year of classification (1987-95), month of classification, time of classification (only for udder traits) and classifier as fixed effects, and age at first calving and stage of lactation as covariables. With the standardized residuals (mean=0, standard deviation=1) a quadratic regression analysis was conducted to get the phenotypic regression coefficients.

Significant phenotypic regression coefficients were only found between milk yield and the udder evaluation marks fore udder, teat placement and stature, udder attachment ( $P \le 0.10$ ) and aggregate score for udder. The genetic regression coefficients were calculated as described above, assuming a heritability for milk yield of 0.3. In figure 4 the relationships between milk yield and udder attachment, fore and rear udder are shown graphically As expected from the formulae and the example with simulated data, the transformation from offspring-parent to the genetic level produced a rather extreme curvilinearty for traits with significant offspring-parent quadratic regression coefficients. Although subjective scores are not a very good example when discussing possible correlated changes, the conclusions drawn from the curvilinear relationships will differ markedly from what may be predicted from a slightly positive linear relationship.

Figure 4: Phenotypic (full line) and genetic (dashed line) regression curves of udder attachment, fore and rear udder on milk yield (traits standardized)



## 4. Conclusions

Due to the genetic nature of functional, and especially of fitness traits, nonlinear heritabilities and curvilinear genetic relationships with other traits in the breeding goal might be expected. This has consequences for the multivariate selection strategies followed in breeding programmes. More work is clearly needed in the area of developing methods for estimating this type of heritablities and genetic relationships as well as for including such parameters in selection decisions in a formalized way. Given the large amount of data available for dain cattle, for example a son-sire regression for fertility traits (e.g. non-return rate) and test nonlinearity of such a regression via polynomial regression is quite straightforward. Other methods like Ablanalp's (1961) linear heritability estimates could also be used to test for nonlinear heritabilities using a broader data base. Extension of the linear selection index towards an index that is nonlinear in the genetic parameters should be investigated. Even if such an extension is feasible, the reliability of genetic parameters may become a limiting problem for successful application of such an index.

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