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IMPUTING CHARACTERISTIC VALUES OF AGRICULTURAL "SEED-STOCK"

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and
Division of Agriculture^{*}, West Texas State University, Canyon**Abstract**

Statistical methods of regression and mathematical (linear) programming are employed to combine principles of economics and genetics in a conceptual, multi-step, model of valuation for biotechnical change. The resulting model has the capacity to estimate the value of changes in specific characteristics for specific production environments, whether those changes are accomplished by traditional plant and animal breeding methods or by genetic engineering. The application of the model is illustrated with an example of commercial cow-calf production under conditions typical of the Texas Panhandle using a total of 32 breed groups.

KEY WORDS: Biotechnical change, characteristic economic values, regression, mathematical programming

1. Introduction

In recent years a significant portion of the agricultural research conducted at Land Grant Universities has included aspects of what is commonly referred to as "*Biotechnology*" (including aspects of gene mapping and recombinant DNA). In general, these studies are intended to accelerate the rate of genetic improvement (biological efficiency) in domestic plants and animals by making what might be referred to as "*cafeteria genetics*" commercially available.

For these results to be commercially adopted, and thus to be of any widespread value, the characteristics in question must have a positive economic value to producers. In this respect, recombinant DNA and other forms of cellular genetic research are no different from traditional plant and animal breeding. In each case the feasibility of a technology potentially resulting in genetic change is inadequate to assure its commercial adoption.

Under these conditions estimates of the relative economic values of alternative characteristics are essential to understanding a technology's potential for commercial adoption. Such an understanding is required if future biotechnical research efforts, especially those of an applied nature, are to be evaluated in light of their potential to attain the greatest possible rate of adoption and payoff from increasingly limited research funds.

2. Model Specification

Analyses of agricultural data typically involve two interrelated phases: 1) A conceptual phase in which the structural form of the (mathematical) model is specified; and 2) A computational phase in which the parameters of the model are actually estimated. While each phase potentially presents its own unique problems, agricultural research addressing commercial issues has become increasingly interdisciplinary in nature and, therefore, conceptually more complex. In the following we develop a mathematical model intended to facilitate

estimates of the relative economic values of genetically based characteristics in agricultural seed-stock. The interdisciplinary model is based upon underlying principles of agricultural economics and animal science that is, therefore, much more conceptual than computational in both emphasis and implementation.

2.1 Economic Values

Hazel (1943) argued that in multi-trait selection intended to improve more than one characteristic of seed-stock each characteristic should appropriately be weighted by its relative economic value. Melton et al (1979) and Ladd and Melton (1979) demonstrated that an appropriate interpretation of relative economic value can be obtained from the economic theory of the firm in which the firm is assumed to maximize profits derived from a biological production process governed by a technology frontier or production function in which at least one input (G) embodies the genetic characteristics (the animal or seed). For purposes of illustration, a single product (Y) firm is assumed. The implicit production function for one product and m inputs or factors of production (X) is

$$(1) \quad Y = f(X_1, X_2, \dots, X_i, \dots, X_m; G)$$

where

$$(2) \quad G = g(q_1, q_2, \dots, q_j, \dots, q_n)$$

is defined as the aggregate biological input and g is a linearly homogeneous function of the n qualitative characteristics embodied. Furthermore, q_j may be interpreted as the phenotypic expression of a characteristic determined by a combination of genetic (g) and random environmental (e_j) effects.

Producer profits to be maximized (π) may be represented as

$$\pi = PY - \sum_{i=1}^m w_i X_i - rG$$

where P and w_j are the fixed market prices of product and inputs, respectively, and r is the market price of G . The economic value of G may be represented as

$$\frac{d\pi}{dG} = \sum_{i=1}^m \left(P \frac{\partial f}{\partial X_i} - w_i \right) \frac{\partial X_i}{\partial G} + \left(P \frac{\partial f}{\partial G} - r \right) = \gamma$$

Thus, $r + \gamma$ is the maximum amount per unit a producer can afford to pay for increased G .

The maximum that can be paid for each observed (phenotypic) unit of a characteristic comprising G may be interpreted as the economic value of that characteristic. As an aggregate index, g is a homogeneous function. The economic value (r_j) can, therefore, be imputed by making use of Euler's Theorem, i.e.,

$$(3) \quad V = (r + \gamma)G = (r + \gamma) \sum_{j=1}^n \frac{\partial G}{\partial q_j} q_j = \sum_{j=1}^n r_j q_j$$

where

$$r_j = (r + \gamma) \frac{\partial G}{\partial q_j} = (r + \gamma) \alpha_j$$

and the effect of a change in a characteristic's level on the aggregate index (G) is a constant (α_j). The maximum market value of the animal or seed used in a commercial agricultural production process (V) should, therefore, equal the sum of the observed characteristics embodied in that seed-stock when each is weighted by its own economic value.

For the breeder, motivated by increasing the underlying genetic base (values) of seed-stock, the economic values of characteristics are slightly more obscure. Specifically, the function g is not necessarily linearly homogeneous in g_j . Due to the correlation between traits, a genetic increase in the level of one characteristic may result in phenotypic changes in several characteristics (Falconer, 1960) and the number of genotypes may actually be less than the number of phenotypes (i.e., a single genotype may control growth rates which are observed at different stages as different phenotypes; Dahm et al, 1983). Hence, a simple substitution of g_j for q_j in either equation (2) or (3) would be inappropriate. An estimate of genetic economic value (r_j^*) can, however, be derived based upon changes in aggregate value arising from changes in the genetic level of a characteristic and the relationships between phenotype and genotype (Falconer, 1960) as

$$(4) \quad r_j^* = \frac{dV}{dg_j} = \sum_{k=1}^m r_k \frac{\partial q_k}{\partial g_j}$$

where r_k is assumed to be constant with respect to genetic changes in characteristic levels. The value of a superior breeding animal or plant variety (line) may then be estimated as the net present economic value over the life of the genetic change up to infinity (Dahm, et al, 1983; Melton, 1980). Thus, unlike a commercial producer, a breeder must consider the value of a genetic change in not only the current animal or seed, but the phenotypic values of the progeny of that animal or seed throughout succeeding years and generations.

2.2 Analytical Model

A number of analytical problems become quickly apparent in the preceding economic model of characteristic values:

- Relationships between G and X_i are largely unclear in many agricultural production processes -- especially considering the large number of inputs employed in most agricultural production processes. This fact, coupled with the significant data requirements regarding input use, make the specification and estimation of equations (1) and (2) difficult at best.
- Neither V nor G is generally observed simultaneously with q_j . Experimental animals and crops, on which data are routinely collected regarding a multitude of traits, are not typically sold in the open market -- nor are they necessarily representative of those typically marketed. Conversely, limited characteristic data are available on the animals and crops routinely marketed. As such, the alternative of estimating equation (3) directly to obtain estimates of characteristic values (without the input data

required to estimate equations (1) and (2) first) becomes equally infeasible.

- The underlying genotypes of characteristics are not directly observable under currently technologies. Thus, even if the market and characteristic data necessary for estimation of either equations (1) and (2) or (3) were available, the estimation would still require correction for the attenuation of the estimated regression coefficients arising from the measurement error introduced by estimating g_j (Fuller, 1987).

Data could, in time, be collected to remedy these problems. The cost of such an effort would, however, be considerable. One would prefer, therefore, to make at least preliminary estimates of characteristic values based upon the abundance of secondary research data already in existence.

To accomplish this an alternative analysis is proposed based upon the properties of mathematical (linear) programming. For example, assume that $h=1, 2, \dots, p$ alternative breeds or crop varieties are identified in the literature or are commercially available. Denoting each of these as an alternative G_h , the problem for the commercial producer is to select the G_h that maximizes profits given the fixed resources of the firm (Z). A linear programming model of this situation is defined as

$$\max Z = \sum_{h=1}^p c_h N_h$$

subject to:

$$\sum_{h=1}^p a_{ih} N_h \leq b_i \quad i = 1, 2, \dots, m$$

$$N_h \geq 0 \quad \forall h$$

where N_h is the number of units (head, acre, etc.) of the h^{th} activity (representing G_h), c_h is the net revenue per unit of G_h , and a_{ih} is the technical coefficient relating the quantity of the limited input b_i required per unit of G_h .

For an optimal solution (Z^0) the relative economic value of each alternative breed or variety, say G_k , is

$$\frac{\Delta Z^0}{\Delta N_k} = \sum_h c_h \frac{\Delta N_h}{\Delta N_k} = z_k - c_k$$

= the shadow price of the k^{th} breed or variety (activity) at a zero level in the optimal solution.

Combining this result with those obtained previously in equation (3) when $r=0$ produces

$$(5) \quad z_k - c_k = \sum_h \sum_j \eta_{kh} \gamma_h \alpha_j q_{jh} = \sum_h \sum_j \eta_{kh} r_{jh} q_{jh}$$

where η_{kh} is the marginal rate of substitution of the k^{th} for the h^{th} breed or variety in the optimal solution. Hence, the shadow price or profit reduction associated with the marginal inclusion of the k^{th} breed or variety in the optimal solution is equal to the sum of the net changes in characteristic levels resulting from its inclusion when each characteristic is weighted by its own economic value.

In most solutions only a few breeds or varieties (typically one or two) will be optimal (at non zero levels) for any given resource base. All other breeds or varieties (at zero levels) in the solution will have negative shadow prices; i.e., their marginal inclusion will reduce profits from the optimal (Z^0). Thus, $z_k - c_k \leq 0$ for all k . Furthermore, the introduction of a non-optimal G_k will typically effect only the optimal (non-zero) activities of G_h . Hence, most $\eta_{kh} = 0$ (where $G_h = 0$) and $\eta_{kh} < 0$ iff $G_h > 0$.

Defining the matrices,

$$z' = [z_1 - c_1, z_2 - c_2, \dots, z_k - c_k, \dots, z_p - c_p]$$

$$\tilde{N} = \begin{bmatrix} 1 & \eta_{12} & \dots & \eta_{1p} & \dots & \eta_{1n} \\ \eta_{21} & 1 & \dots & \eta_{2k} & \dots & \eta_{2p} \\ & & \ddots & & & \\ \eta_{k1} & \eta_{k2} & \dots & \eta_{kk} = 1 & \dots & \eta_{kp} \\ & & & & \ddots & \\ \eta_{p1} & \eta_{p2} & \dots & \eta_{pk} & \dots & 1 \end{bmatrix}$$

$$\tilde{Q} = \begin{bmatrix} q_{11} & q_{12} & \dots & q_{1j} & \dots & q_{1n} \\ q_{21} & q_{22} & \dots & q_{2j} & \dots & q_{2n} \\ \vdots & & & & & \\ q_{k1} & q_{k2} & \dots & q_{kj} & \dots & q_{kn} \\ \vdots & & & & & \\ q_{p1} & q_{p2} & \dots & q_{pj} & \dots & q_{pn} \end{bmatrix}$$

and

$$\beta' = [\beta_1, \beta_2, \dots, \beta_j, \dots, \beta_n]$$

allows equation (5) to be rewritten in a rather familiar form,

$$(6) \quad z = \tilde{N}\tilde{Q}\beta.$$

In this form β can be easily interpreted as a vector of economic values for the n phenotypic characteristics comprising G relative to the resource base and prices defined for Z^0 . These values may rather easily be estimated by regressing $\tilde{N}\tilde{Q}$ on z using methods of least-squares. The underlying economic values for genotypic changes, more appropriate to

methodologies of genetic engineering, may then be estimated by differentiating phenotype with respect to each genotype and aggregating when weighted by the estimated economic values as shown in equation (4). An alternative unexplored herein, would be to employ any of several generalized least-squares or maximum likelihood methods of estimation to re-estimate (6) for genotypic levels in Q recognizing the bias of measurement error (Fuller, 1987).

3. Example: West Texas Cow-Calf Production

To illustrate the application of this model the breed group choice for a representative West Texas commercial cow-calf producer is considered. Resources defined for this producer (b_i) include 5000 acres of representative range (USDA/SCS, 1970), the forage nutrient production of metabolizable energy (ME) and digestible protein (DP) expected from that range in each of five alternative growing seasons of the year (NRC, 1984), and the annual quantity of operator labor and operating capital available. Base prices per unit of each class of livestock potentially marketed by this firm and of supplemental feeds provided in the linear programming model (c_i) were defined based upon an examination of 30 years of historical prices as those relative prices which a commercial producer might reasonably expect to face in the long-run.

Mean performance levels of 16 breed groups representing the cross of 16 breeds of sires with average Hereford-Angus cows were obtained from the Germ Plasm Evaluation study conducted at the U.S. Meat Animal Research Center, Clay Center, Nebraska (Cundiff et al, 1982; Cundiff et al, 1984; Cundiff et al, 1981; Smith et al, 1976; Green et al, 1991; and Jenkins et al, 1991). With an assumed heterosis level estimates were then derived for an additional 16 breed groups representing purebred cows of each breed of sire group. Hence, a total of 32 alternative possible breed groups were considered. Breed group means for all characteristics considered are shown in Table 1.

The technical coefficients relating input requirements to output levels (a_{ij}), especially with respect to breed dependent nutrient requirements, were derived from accepted relationships of animal science from each breed group. As a result, ME and DP requirements in the linear program vary with respect to the genetic ability for growth, weight, lactation, and reproductive performance of each breed group. In addition, the herd age distributions and optimal culling ages for each breed group were computed based upon the principles of optimal asset replacement (Melton, 1980). Details of the computations employed to obtain these technical coefficient estimates are reported in Melton et al (1993).

Optimal solutions to the linear programming model under "normal" weather conditions were utilized to compute shadow prices and marginal rates of substitution for each of the 32 breed groups as shown in Table 2. These shadow prices reflect marginal breed group values measured in terms of profit potential relative to the optimal breed group (Pinzgauer purebreds). Gross values for each breed group (V_i) could, therefore, be computed by adding a constant, the average profit per head of the optimal breed, to each shadow price. However, the addition of this constant will not effect the estimated regression coefficient values.

These data can be used to estimate the parameters of a model of the form shown in equation (6) including an intercept that is expected, *a priori*, to be non-significant based upon the specification of equation (3). Additionally, a high degree of multicollinearity is expected

between selected variables in Q . For example, birth weight is the difference between mature weight (A) and total weight gain (B). An additional model is therefore estimated in which certain non-significant variables believed to contribute to the multicollinearity are excluded from the estimation based on improvements in the Mean Square Error. Results of these estimations are summarized in Table 3.

Alternative means of correcting for multicollinearity (Greene, 1993) would reduce the standard error of the estimates at the expense of introducing an estimation bias. For the purposes of this analysis the bias was judged to be more detrimental than any loss of significance due to multicollinearity.

As expected the intercept, when included, is non-significant. In addition many post-weaning characteristics reflecting feedlot and/or carcass performance are also non-significant or have signs that are contrary to *a priori* expectations. This finding would tend to support the hypothesis that unless cow-calf producers, marketing calves at weaning, are differentially compensated for the post-weaning performance of their calves, little incentive exists to genetically improve these characteristics. Recent studies do not indicate the existence of such price differences (Schroeter et al, 1988). Thus, technologies leading to a genetic improvement in post-weaning feedlot performance or carcass quality will probably not be widely adopted nor yield an adequate return (measured in either public or private benefits) on the research dollars invested.

Additional information relative to direct genetic change, such as through genetic engineering, can be derived from these estimates, as indicated in equation (4). The change in the observed mean of a population due to a direct genetic change should be equivalent to the genetic change ($\partial q_k / \partial g_k = 1$). However, one may also expect the observed levels of other characteristics to change according to the genetic correlations between the characteristics (Falconer, 1960). Thus,

$$\frac{\partial q_j}{\partial q_k} = \frac{\partial q_j}{\partial g_j} \frac{\partial g_j}{\partial g_k} = (1) \frac{COV(g_j, g_k)}{V(g_k)}$$

The vector of economic values of a unit (animal or seed) marginal genetic change is, therefore,

$$R = \Sigma_g \beta$$

where Σ_g is a matrix of genetic regression coefficients (variances-covariances divided by the genetic variances),

$$\Sigma'_g = \begin{bmatrix} \frac{\sigma_{11}}{\sigma_{11}} & \frac{\sigma_{12}}{\sigma_{22}} & \dots & \frac{\sigma_{1k}}{\sigma_{kk}} & \dots & \frac{\sigma_{1n}}{\sigma_{nn}} \\ \frac{\sigma_{21}}{\sigma_{11}} & \frac{\sigma_{22}}{\sigma_{22}} & \dots & \frac{\sigma_{2k}}{\sigma_{kk}} & \dots & \frac{\sigma_{2n}}{\sigma_{nn}} \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ \frac{\sigma_{n1}}{\sigma_{11}} & \frac{\sigma_{n2}}{\sigma_{22}} & \dots & \frac{\sigma_{nk}}{\sigma_{kk}} & \dots & \frac{\sigma_{nn}}{\sigma_{nn}} \end{bmatrix}$$

The results for R are also summarized in Table 3 based upon the estimated matrix of genetic regression coefficients (developed from estimates of Woldehawariat et al (1977), Jenkins et al (1991) and the estimates of the authors) as shown in Table 4 (Σ_g).

These values indicate that, in general, a direct genetic change is worth as much as 6 times the change in phenotype. This is largely due to the correlated changes which are anticipated to accompany a change. At the same time, genetic changes in some characteristics may result in negative values, such as for slaughter weight or marbling score. Hence efforts at genetic engineering in these areas are not recommended. On the other hand, a direct genetic increase in average post-weaning rates of feed conversion has a very high value (over \$1750 per unit) even though its value for a phenotypic change is only \$270. Similarly, a genetic increase in average daily gain, due to its correlated effects, has a value of over \$500 per unit although the commercial cow-calf producer sees no direct value in its phenotypic expression.

4. Summary

Quite often statistics is viewed as an addendum to the scientific process: An after-the-fact method of analysis and hypothesis testing. However, as applied research become increasing interdisciplinary in nature, statistics and allied analytical and modeling methods may be critical to catalyzing the merger of two or more fields of study. In this study an example of that role is provided in which statistics and mathematical programming methods are employed to integrate theories of economics and breeding to estimate the economic value of a genetic change in individual characteristics of agricultural seed-stock. The resulting model is, therefore, quite conceptually, as opposed to computationally, sophisticated. It allows the commercial value of changes in a characteristic to be estimated from secondary data for specific production environments. As such, it is amenable to use by breeders, commercial producers, as well as researchers and research administrators involved in biotechnology.

To illustrate the application of the model, breed choices in commercial cow-calf production typical of West Texas were analyzed. The results indicate that a single breed is preferred (Pinzgauer purebred) under constant prices. Furthermore, the model illustrates, as expected, that in the absence of differential pricing of weaned calves to reflect post-weaning performance, cow-calf producers should put little if any value on post-weaning or carcass characteristics in their decisions.

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Table 1. Breed Group Means for Alternative Characteristics.

Breed Group	Angus	B. Swiss	Brahman	Charolais	Chianina	Gelbvieh	Hereford	Jersey	Limousin	M. Anjou	Pinzgauer	Red Poll	Sahiwal	Simmental	S. Devon	Tarentaise
PUREBREDS:																
Wean. Rate (WR)	82%	84%	85%	74%	85%	87%	82%	82%	78%	85%	83%	73%	90%	80%	84%	83%
Birth Wt. (BW)	38.20	42.70	34.80	44.00	45.80	41.40	38.20	32.00	39.60	46.70	42.30	40.90	28.60	42.30	42.70	39.60
12-hr Milk	2.70	4.70	5.30	2.20	2.70	4.60	2.70	5.50	2.20	2.90	4.40	4.00	4.80	4.60	3.10	4.30
Avg. Cow Wt. (CW)	544.10	560.10	585.80	655.30	666.80	592.50	544.10	405.40	547.40	663.30	534.10	497.00	440.60	589.00	580.50	521.70
Wean Wt. (WW)	170.50	186.60	229.60	167.20	174.60	188.10	188.30	132.60	146.80	185.40	235.60	141.30	187.30	185.20	172.90	215.50
Rate of Gain (ADG)	1.06	1.17	0.87	1.15	1.00	1.14	1.06	0.88	0.86	1.15	1.03	0.92	0.76	1.16	1.12	0.88
Gain/Mcal ME	0.13	0.11	0.10	0.12	0.09	0.11	0.13	0.12	0.10	0.11	0.12	0.10	0.10	0.12	0.12	0.11
Slaughter Wt. (SW)	430.80	556.10	552.40	601.00	684.60	621.50	430.80	385.50	564.60	577.60	485.60	413.90	460.10	603.10	491.40	507.60
Marb. Score	11.10	9.30	7.00	9.00	5.50	7.80	11.10	15.00	6.30	8.80	10.00	10.90	7.70	8.20	11.10	8.60
Retail Prod. (Ret %)	65.0%	70.5%	69.7%	75.0%	77.4%	71.1%	65.0%	63.4%	76.2%	71.9%	70.4%	65.6%	69.1%	73.5%	67.7%	71.1%
Mature Wt. (A)	498.60	514.20	562.00	575.30	643.60	546.10	475.00	328.00	501.20	631.90	518.80	496.60	437.90	497.30	498.60	507.10
T. Growth (B)	465.30	473.20	523.70	536.60	601.00	505.40	443.80	306.60	468.40	589.30	482.00	461.40	405.30	458.60	463.40	474.20
Grow. Rate (kx1000)	1.56	1.62	1.92	1.29	1.09	1.48	1.95	2.01	1.29	1.22	2.31	1.24	2.04	1.73	1.56	2.12
Lac. Const. (A ₁)	3.58	1.31	2.77	4.62	3.69	1.35	3.58	1.12	4.62	3.35	1.43	2.44	3.08	1.35	3.16	1.46
L. Rate (k ₁ x100)	1.59	2.01	1.21	1.58	1.58	1.99	1.59	2.01	1.58	1.58	1.99	1.59	1.21	1.99	1.59	1.99
Days of Gestation	284.00	285.00	291.70	287.00	287.50	286.30	284.00	282.90	289.20	285.40	286.00	285.20	294.00	287.30	286.70	287.10
CROSSBREDS:																
Wean. Rate (WR)	84%	85%	86%	80%	86%	87%	84%	84%	82%	86%	85%	79%	89%	83%	85%	85%
Birth Wt. (BW)	39.00	41.30	37.60	42.20	43.10	40.80	39.00	35.80	39.90	43.50	41.30	40.40	34.50	41.30	41.30	39.90
12-hr Milk	2.80	3.80	4.10	2.50	2.80	3.80	2.80	4.20	2.50	2.90	3.60	3.40	3.90	3.80	2.90	3.60
Cow Wt. (CW)	555.20	563.40	582.40	615.10	621.00	582.90	555.20	484.40	559.70	619.20	552.90	531.20	507.60	581.00	573.80	546.60
Wean Wt. (WW)	189.90	198.20	225.40	192.20	201.60	202.00	200.70	172.90	180.50	205.20	226.50	175.20	203.40	201.60	193.10	215.80
Rate of Gain (ADG)	1.11	1.16	1.02	1.16	1.08	1.15	1.11	1.01	1.01	1.16	1.09	1.04	0.96	1.16	1.14	1.02
Gain/Mcal ME	0.13	0.12	0.12	0.13	0.11	0.12	0.13	0.13	0.12	0.12	0.13	0.12	0.12	0.13	0.13	0.12
Slaughter Wt. (SW)	457.90	522.00	537.90	549.90	602.30	560.40	458.00	434.90	544.80	537.50	490.60	449.20	490.20	550.50	489.50	506.20
Marb. Score	11.30	10.40	9.30	10.30	8.50	9.70	11.30	13.30	8.90	10.20	10.80	11.20	9.70	9.90	11.30	10.10
Retail Prod. (Ret %)	66.3%	69.1%	69.4%	71.8%	73.0%	69.8%	66.3%	65.5%	72.4%	70.2%	69.4%	66.6%	69.1%	71.0%	67.7%	69.8%
Mature Wt. (A)	512.00	520.00	550.00	554.00	589.00	539.00	500.00	425.00	516.00	583.00	525.00	511.00	486.00	514.00	512.00	519.00
T. Growth (B)	478.00	482.00	513.00	517.00	550.00	501.00	467.00	397.00	482.00	544.00	489.00	476.00	452.00	477.00	477.00	485.00
Grow. Rate (kx1000)	1.75	1.78	1.98	1.62	1.52	1.71	1.94	1.98	1.62	1.58	2.14	1.58	2.01	1.84	1.75	2.04
Lac. Const. (A ₁)	3.20	1.87	2.61	3.55	3.20	1.87	3.20	1.68	3.55	3.05	1.94	2.60	2.80	1.87	3.00	1.96
L. Rate (k ₁ x100)	1.66	1.87	1.48	1.66	1.66	1.87	1.66	1.87	1.66	1.66	1.87	1.66	1.48	1.87	1.66	1.87
Days of Gestation	285.50	286.00	289.40	287.00	287.30	286.70	285.50	285.00	288.10	286.20	286.50	286.10	290.50	287.20	286.90	287.10

Table 2. Shadow Price and Marginal Rates of Substitution Relative to the Optimal Breed (Pinzgauer purebreds).

Breed of sire	Shadow Price (\$)		Marginal Rate of Substitution	
	Purebred	Crossbred	Purebred	Crossbred
Angus	-101.41	-60.92	-0.97	-0.98
Brown Swiss	-69.00	-52.78	-0.97	-0.98
Brahman	-14.81	-3.08	-1.04	-1.00
Charolais	-139.77	-85.70	-0.96	-0.98
Chianina	-89.74	-46.65	-1.00	-1.01
Gelbvieh	-59.73	-40.74	-1.01	-1.01
Hereford	-74.06	-52.06	-0.96	-0.99
Jersey	-118.44	-71.98	-0.84	-0.92
Limousin	-143.77	-87.81	-0.94	-0.97
Maine Anjou	-78.99	-41.72	-1.01	-1.01
Pinzgauer	0	-11.16	1.00	-1.01
Red Poll	-163.54	-105.32	-0.92	-0.96
Sahiwal	-35.46	-12.80	-0.98	-0.97
Simmental	-90.54	-55.86	-0.97	-0.99
South Devon	-92.77	-56.05	-0.98	-0.99
Tarentaise	-24.53	-24.64	-0.98	-1.00
Average	-81.04	-50.58		

Table 3. Economic Values of Alternative Characteristics for Phenotypic and Genotypic Change.

	Phenotypic				Genotypic	
	Overall		Min MSE		Overall	Min MSE
	Coeff.	t-Value	Coeff.	t-Value	Value	Value
Adj R ² / MSE	0.99	10.60	1.00	8.31		
d.f. error		15		20		
Intercept	-0.46	-0.17				
WR	423.49	12.26	411.20	19.43	1,170.64	1,105.34
BW	1.22	0.73	1.19	1.48	4.61	4.77
12-hr milk	4.45	0.61	3.22	1.50	18.30	13.52
CW	-0.26	-1.14	-0.26	-3.23	-0.15	-0.12
WW	1.88	7.33	1.89	9.57	3.07	2.29
ADG	28.49	0.33			879.05	522.79
Gain/Mcal	301.61	1.10	270.44	1.45	2,142.88	1,795.47
SW	0.06	0.55	0.11	2.87	-0.18	-0.03
Marbling	-1.61	-0.49			-28.88	-15.53
Ret %	72.35	0.53			465.62	249.72
A	-1.94	-0.73	-1.01	-1.64	0.05	0.08
B	2.02	0.72	1.04	1.67	0.17	0.15
k	-28.98	-1.37	-25.75	-1.87	-44.56	-33.16
A ₁	-2.04	-0.40			-11.04	-9.95
k ₁	-33.90	-1.72	-26.77	-2.60	-106.27	-103.02
Gestation	-1.25	-3.08	-1.26	-5.68	1.71	2.09

Table 4. Genetic Regression Coefficients for Alternative Characteristics.

	WR	BW	12 hr	CW	WW	ADG	Gain/M	SW	Marb	Ret %	A	B	k	Al	kl	Gest
Wean. Rate	1.00	-60.20	13.17	-35.25	302.44	-0.53	0.00	-148.57	0.00	0.00	-37.78	-35.90	-2.54	-11.47	-2.00	-32.32
Birth Wt.	0.00	1.00	-0.03	1.76	2.04	0.01	0.00	8.89	0.04	0.00	3.95	3.68	-0.01	0.00	0.00	0.16
12-hr Milk	0.01	-0.92	1.00	-16.06	2.76	0.00	0.00	-9.03	0.00	0.00	-22.96	-21.38	0.19	-1.26	-0.08	0.00
Cow Wt.	0.00	0.01	0.00	1.00	0.10	0.00	0.00	0.51	-0.01	0.00	0.97	0.90	0.00	0.00	0.00	0.00
Wean Wt.	0.00	0.11	0.00	1.66	0.79	0.00	0.00	2.21	-0.01	0.00	1.98	2.63	0.00	-0.02	0.00	0.07
Post-Wean ADG	-0.02	20.26	0.00	244.17	47.89	1.04	0.04	482.26	7.63	0.17	0.00	355.23	-1.13	0.00	0.00	-12.79
Gain/Mcal ME	0.00	-26.69	0.00	-390.63	720.64	5.02	1.00	-197.59	-25.13	1.87	-586.21	-556.93	2.82	0.00	0.00	-143.26
Slau. Wt.	0.00	0.03	0.00	0.56	0.14	0.00	0.00	0.79	-0.01	0.00	0.85	0.64	0.00	0.00	0.00	0.02
Marb. Score	0.00	0.14	0.00	-5.39	-0.92	0.02	0.00	-12.11	1.16	0.00	-4.62	-16.82	0.05	-0.02	0.00	-0.33
Retail Prod.	0.00	14.25	0.00	333.82	89.51	1.00	0.09	562.82	-10.74	1.00	393.60	509.92	1.81	1.09	-0.16	22.96
Mat. Wt. (A)	0.00	0.01	0.00	0.84	0.10	0.00	0.00	0.67	0.00	0.00	1.00	0.95	0.00	0.01	0.00	0.01
T. Growth (B)	0.00	0.01	0.00	0.87	0.15	0.00	0.00	0.56	-0.02	0.00	1.05	1.00	0.00	0.01	0.00	0.01
G. Rate	-0.02	-2.52	1.29	193.98	17.24	-0.19	0.00	140.16	3.57	0.05	-136.64	-126.99	1.00	-2.16	0.13	2.54
Lac. Const.	-0.01	0.00	-0.65	0.00	-6.59	0.00	0.00	0.00	-0.12	0.00	32.94	31.30	-0.17	1.00	-0.12	0.00
L. Rate	-0.05	0.00	-1.97	0.00	-22.64	0.00	0.00	0.00	0.85	-0.02	-198.00	-188.11	0.48	-5.50	1.00	0.00
Gest. (days)	0.00	0.25	0.00	0.00	1.87	-0.01	0.00	7.36	-0.14	0.00	5.85	5.55	0.02	0.00	0.00	1.00