# Selection Indices and Subindices for Improving Milk Yield Traits in Braunvieh Cattle

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## Abstract

*Milk production records of Braunvieh cows of Tirol region in Austria were used to construct different selection indices and subindices. Data on 46456 lactation records including 16569 paternal half-sisters representing 1556 sires were used to estimate the genetic and phenotypic variation and covariation of 305- day milk, fat and protein yield traits. Analysis was carried out using a mixed model including effects of year and month of calving, parity, days open, grazing region and interaction of year by parity (as fixed effects) and sires and cows-within-sires (as random effects). Seven indices of selection for improving yield traits of cows were constructed involving all combinations of two or three traits. Subindices were derived as if the three or two sources of information were used to select for just one trait, viz. to select for milk or fat or protein yield.*

*Large differences in index coefficients (b's) for protein yield against yields of milk or fat were observed. Rate of genetic progress in aggregate genotype decreased when protein yield was dropped and consequently, a considerable genetic improvement for cow productivity might be achieved through selection for protein yield. Milk yield contributed about 50% of the total economic-genetic gain while yields of fat plus protein contributed the remainder, 50%. Th expected economic-genetic gain per generation in yield traits was large in all of the indices and subindices constructed; estimates ranging between 414 to 424 kg for milk, 16.7 to 17.5 kg for fat and 14.1 to 15.2 kg for protein. Correlations between the index or subindex constructed and each individual trait in the aggregate genotype were relatively high and ranged from 0.62 to 0.74. A reduced index or subindex based on protein yield with either milk or fat yield could be practically applied efficiently to improve the productivity of Braunvieh cows under the local Austrian conditions.*

## Introduction

Selection programs in dairy cattle based on selection indices which employing measurements on milk, fat and protein have small economic-genetic advantage over indices employing measurements on milk and fat, but not protein (*Hanna and Cunningham, 1974; Anderson et al., 1978*). A UK report

*(CAS, 1978)* recommended that selection goals be changed to put greater emphasis on increased fat production. An examination of the situation in Canada *(McAllister, 1980)* showed 3% net deficit in butter production and 18% surplus in milk-protein production. The dairy industry in USA is currently concerned with the question of payment for the protein content of milk *(Mbah and Hargrove, 1982; de Jager and Kennedy, 1987)*. Technically, it is possible by selection to reduce the fat content and at the same time increase the protein content of milk *(Van Vleck, 1978; Kennedy, 1982)*. Such a breeding strategy would run counter to demands of the marketplace in Europe, at least as projected for other industrialized countries.

In the last ten years, the marketplace and economic situation in Europe and USA have been changed toward milk protein instead of fat. *Anderson et al. (1978)* and *Kuipers and Shook (1980)* found additional genetic gain in milk yield when protein yield was included in the selection index. The objectives of the present study were: (1) to construct a series of cow selection indices and subindices for improving yields of milk, fat and protein of Braunvieh cattle, and (2) to compare the effectiveness of selection indices and subindices with and without protein information.

## Material and Methods

### *Data and analysis*

Records of 46456 lactations for Braunvieh cows of Tirol province in Austria were collected over five consecutive calving years (1977 through 1981). Data were available on 16569 paternal half-sisters from 1559 sires. Details of the breeding policy and management followed for Braunvieh cattle in Austria were described by *Hartmann et al. (1986)*. Data of all lactations were analysed using the following mixed model:

$$Y_{ijklmnpq} = \mu + S_i + C_{ij} + A_k + B_l + P_m + D_n + G_p + (AP)_{km} + e_{ijklmnpq}$$

where: $Y_{ijklmnpq}$ denotes the performance of ijklmnpq lactation; $\mu$ = the overall mean; $S_i$ = the random effect of $i^{th}$ sire; $C_{ij}$ = the random effect of $J^{th}$ cow nested within sire; $A_k$ = the fixed effect of the $k^{th}$ year of calving (1977 through 1981); $B_l$ = the fixed effect of the $l^{th}$ month of calving (January .... December); $P_m$ = the fixed effect of $m^{th}$ parity (1 ..... 8); $D_n$ = the fixed effect of $n^{th}$ days-open class (60-89, 90-119, 120-149, 150-179 and $\geq$ 180 days); $G_p$ = the fixed effect of $p^{th}$ grazing region (Valley *vs* Alpage); $(AP)_{km}$ = the effect of the interaction between year and parity; and $e_{ijklmnpq}$ = a random deviation of $q^{th}$ lactation of $ij^{th}$ cow and assumed to be independently randomly distributed (O, $\sigma^2 e$).

Paternal half-sib analyses *(Harvey, 1977)* were performed in order to quantify the average genetic and phenotypic variation and covariation of 305-day yield traits of milk (MY), fat (FY) and protein (PY). Components of variance and covariance for sire ($\sigma^2$s), cows within sire ($\sigma^2$c:s) and remainder ($\sigma^2$e) were computed according to Method III of Henderson. Heritabilities were estimated for yield traits, across all lactations, as four times the intraclass correlation coefficient between sire groups: $h^2 = 4\sigma^2s / (\sigma^2s + \sigma^2c{:}s + \sigma^2e)$. Estimates of genetic and phenotypic correlation were obtained by computing techniques described by the LSML76 program of *Harvey (1977)*.

### *Relative economic values*

The production means in the present study for Braunvieh cows were 4294 kg milk with 3.98% fat and 3.12% protein. The base price in Austrian Schilling (OS) per kg of milk (3.98% fat and 3.12% protein) was calculated according to *WOM (1987)* as:

| | |
|---|---|
| 1.743 OS | for each kg of fat-free milk |
| + 2.468 OS | for 3.98% fat, where each point of fat equal to 0.62 OS, i.e. 3.98 x 0.62 = 2.468. |
| + 0.775 OS | for 1st grade quality of milk. |
| 4.986 OS | price per kg of milk |
| + 0.498 OS | for 10% of the price as taxes. |
| 5.484 OS | total base price per kg of milk. |

Costs of feeding, milk recording and fat-protein estimation were 0.051, 0.015 and 0.440 OS, respectively. Therefore, net price of one kg of milk (3.98% fat, 3.12% protein) paid to the Austrian farmers is 5.484 - 0.506 = 4.978 OS. According to prices of *WOM (1987)*, base price paid by dairy plants to the farmer for one kg of fat is 64.0 OS. Feed and manufacture costs of one kg of butterfat was 5.98 OS. Consequently, price paid to the farmer for one kg of fat is 64.0 - 5.98 = 58.02 OS. According to *Dommerholt and Wilmink (1986)*, the protein value in Central Europe is almost the same as that of fat and consequently, price of one kg of protein is also 58.02 OS. Hence, the relative economic values for yeilds of milk, fat and protein were set to be 4.978:58.02:58.02 or 1:11.7:11.7. However, several investigators (e.g. *Vandepitte and Hazel, 1977; Lin, 1978; Smith, 1983; Allan et al., 1985)* have concluded that the expected response and efficiency of index selection are not very sensitive to changes in the economic weights.

### *Construction of indices and subindices*

Seven selection indices and subindices for improving yields of milk, fat and protein were constructed according to procedures described by *Cunningham and Mahon (1977)*. The full matrix of heritabilities and phenotypic and genetic correlations used in construction are shown in Table 1. Studies in Europe on Braunvieh Cattle *(Schneeberger, 1981; Schneeberger and Hagger, 1984; Graml* *et al., 1987)* have shown similar heritabilities and correlations for yield traits.

**Table 1. Estimates of heritability (on diagonal) and phenotypic (above diagonal) and genetic (below diagonal) correlations used in construction of selection indices and subindices.**

| Variates+ | MY | FY | PY |
|---|---|---|---|
| MY | 0.50 ± 0.024 | 0.92 | 0.95 |
| FY | 0.95 ± 0.003 | 0.44 ± 0.022 | 0.91 |
| PY | 0.97 ± 0.002 | 0.96 ± 0.003 | 0.54 ± 0.025 |

+ where MY, FY and PY are 305-day milk, fat and protein yields, respectively.

The information required for constructing a cow genetic index was specified in the following four vectors and three matrices:

y : a vector of additive genetic values for $i^{th}$ yield traits included in the aggregate genotypic value.

a : a vector of constants representing the relative economic values of yield traits.

x : a vector of phenotypic measures for the n variables or sources of information to be included in the index (i.e. milk, fat and/or protein yields).

b : a vector of weighing factors to be used in the index (i.e. partial regression coefficients).

p : a squared nxn matrix of phenotypic variances-covariances of the three variables in $j^{th}$ variates.

G : a matrix of genotypic covariances between the n variables in $j^{th}$ variates and the $i^{th}$ traits in y.

C : a squared matrix of genotypic variances-covaraínces of y-traits.

The partial regression coefficients (b's) were computed as $b = p^{-1}Ga$ where $p^{-1}$ is the inverse of p (in matrix notation). Percentage of total economic-genetic gain accounted for by gain in each $i^{th}$ trait was computed according to *Cunningham (1970)* as $(b'G_i/b'Ga)\ (a_i)\ (100)$, where $a_i$ is the relative economic value of the $i^{th}$ trait. The correlation of the calculated index with the aggregate genotype was estimated as $r_{IH} = b'Ga/a'Ca$.

Data required for the construction of subindices were specified in the following matrices:

P : a nxn matrix of phenotypic variances-covariances of the n variates (i.e. milk, fat and protein yields).

G : a 3x1 matrix of genotypic covariances between the three variables in $j^{th}$ variates and $i^{th}$ trait (i.e. milk or fat or protein yield).

C : a scalar matrix of genotypic variance of $i^{th}$ trait.

The partial regression coefficients for subindices (b's) were computed as $b = p^{-1}G$. Correlation of subindex and $i^{th}$ trait was calculated as $r_{IX} = [(b'G_i)/C_{ii}]$, where $C_{ii}$ is the diagonal element of C.

## Results and Discussion

### *Selection indices*

For multi-trait selection, seven indices (I's) were constructed (Table 2). The design of the construction was so drawn that on one side there was an index (original index) with all the three variates (i.e. milk, fat and protein yields) which was assumed to be 100% efficient in the genetic sense and on the other side, one variate was dropped in an alternative way and a reduced index of two traits was obtained. The original index (I1) included three variates to be used for improving the aggregate genotype of the three traits while the main indices (I5 and I6 and I7) included three variates to be used for improving only two traits (i.e. milk-fat, milk-protein and fat-protein for I5, I6 and I7, respectively). The reduced indices (I2, I3 and I4) included only two traits to be used for improving all the three traits.

**Index coefficients.** The index coefficients (b's) for each of the seven indices constructed are shown in Table 2. These partial regression coefficients indicate the relative emphasis each trait should receive to maximise profitable genetic response and they are nearly similar to those obtained by *Mbah and Hargrove (1982)*. Values of b's for protein yield were greater than those of other variates in the different indices. This might be attributed to positive and high genetic correlations between this trait and yields of milk or fat (Table 1) which appeared in all indices. Also, a trait of high heritability (i.e. 0.54 for protein yield) in the index will have a high index weight, although this depends partly on what correlated traits are measured too. Procedures in Europe and USA have been developed for inclusion of correlated traits in an index for estimation of economic-genetic merit of sires of cows *(Cunningham, 1969; Anderson et al., 1978)*. In practice, the relative responses in the aggregate genotype are determined by the appropriate choice of selection index weights, i.e. b's obtained in the present study for yields of protein and milk would be advisable to be used in selection programs.

**Variates contribution.** The contribution of each variate to the index (V%) can be measured as the percentage reduction in overall rate of genetic progress which results if that variate is dropped *(Cunningham and Mahon, 1977)*. Estimates of V% (Table 2) indicate that including protein yield in selection programs of Braunvieh cattle offer more economic-genetic contribution over measures of milk and fat only. Some studies (e.g. *Hanna and Cunningham, 1974; Van Vleck, 1978; Kennedy, 1982)* indicated that measures of milk, fat and protein in dairy-cattle selection offer little economic contribution over

**Table 2. Selection indices (I's) for yield traits of Braunvieh cattle, value of each variate in index (V%), percentage of total gain attributable to each trait (H%) and expected genetic change per generation (EG) in each trait (kg).**

| | | Variates | | |
|---|---|---|---|---|
| Index | Item+ | Milk yield | Fat yield | Protein yield |
| I1 | b | 0.29 | -2.93 | 25.36 |
| | V% | 0.30 | 0.10 | 3.50 |
| | H% | 49.90 | 26.70 | 23.40 |
| | EG | 423.00 | 17.30 | 15.20 |
| | G% | 9.80 | 10.10 | 11.30 |
| I2 | b | 0.92 | 1.37 | |
| | V% | 7.00 | 0.00 | |
| | H% | 50.80 | 26.60 | 22.60 |
| | EG | 414.00 | 16.70 | 14.10 |
| | G% | 9.60 | 9.80 | 10.50 |
| I3 | b | 0.21 | | 24.11 |
| | V% | 0.20 | | 3.50 |
| | H% | 49.80 | 26.90 | 23.30 |
| | EG | 420.00 | 17.40 | 15.10 |
| | G% | 9.80 | 10.2 | 11.3 |
| I4 | b | | -0.63 | 30.65 |
| | V% | | 0.00 | 10.00 |
| | H% | 49.50 | 26.90 | 23.60 |
| | EG | 417.00 | 17.40 | 15.20 |
| | G% | 9.70 | 10.20 | 11.30 |
| I5 | b | 0.31 | -1.98 | 16.70 |
| | V% | 0.60 | 0.10 | 2.60 |
| | H% | 65.30 | 34.70 | |
| | EG | 423.00 | 17.30 | |
| | G% | 9.80 | 10.10 | |
| I6 | b | 0.31 | -4.50 | 18.40 |
| | V% | 0.7 | 0.50 | 3.40 |
| | H% | 68.3 | | 31.70 |
| | EG | 424.00 | | 15.10 |
| | G% | 9.90 | | 11.30 |
| I7 | b | 0.03 | 0.04 | 1.21 |
| | V% | 0.00 | 0.00 | 5.40 |
| | H% | | 53.40 | 46.60 |
| | EG | | 17.50 | 15.20 |
| | G% | | 10.20 | 11.30 |

+ where b = values of the coefficients of the index (i.e. partial regression coefficients), V% = percentage reduction in rate of genetic gain for aggregate genotype if variate is dropped, EG = expected genetic change in each trait in actual units of measurements (Kg) achieved by one standard deviation on the index, and G% = expected genetic change per generation in each trait as a percentage of the overall mean of the trait.

measures of milk and fat only. The low contribution of fat yield in all indices constructed may be due to the high genetic correlation between protein yield and yield of milk or fat (Table 1). However, effect of dropping of fat yield on index efficiency is negligible even though it is an economically important trait. Although relatively small differences existed in expected responses to an index including and excluding protein yield (Table 2), these differences would compound over generations *(Mbah and Hargrove, 1982)*. In addition, if there is a need for milk with high protein content, maintenance or improvement of that content can be achieved most effectively by using a reduced index including yields of protein and milk (i.e., I3 or I4).

**Total economic-genetic gain.** Percentage of total economic-genetic gain (H%) accounted for by gain in each trait are given in Table 2. These percentages for most indices constructed indicate that milk yield would contribute about 50% of the total economic-genetic gain of cow productivity, while yields of fat plus protein would contribute the remaining 50%. If selection emphasis is on milk and protien (I3 and I6) rather than fat, the economic-genetic responses would be expected to result in relatively large progress for all the three yields. Selection for yields of fat and protein (I4 and I7) with no emphasis on milk would also result in a relatively much larger economic-genetic change in aggregate genotype. *de Jager and Kennedy (1987)* reported that selection with equal economic values for fat and protein would result in lower expected responses in milk but higher responses in fat and protein in a descending order. As expected, the larger benefits (H%) attributable to protein selection (Table 2) occurred when protein yield was included in the index (i.e. all indices except I5). On economic balance, it could be stated that considerable expected genetic improvement for cow productivity of Braunvieh cattle might be achieved through selection for milk yield together with protein yield.

**Trait expected-gain.** The expected genetic gain (in actual units of measurements and as a percentage of the overall mean of the trait) per generation in each trait (i.e. milk or fat or protein) achieved by a selection differential of one standard deviation on the index are given in Table 2. The expected genetic change per generation (EG) ranged between 414 and 424 kg for milk, 16.7 and 17.5 kg for fat and 14.1 and 15.2 kg for protein, i.e. 9.6 to 9.9% for milk, 9.8 to 10.2% for fat and 10.5 to 11.3% for protein as a percentage of the respective overall mean of the trait. Selection indices including protein yield (all indices except I2) provide relatively large increases in yields of milk, fat and protein. On the contrary, *de Jager and Kennedy (1987)* found that expected responses from single-trait selection for yield traits were similar to those responses of selection based on an index which did not include protein. If one wished to obtain genetic gains in any yield trait similar to those possible from single-trait selection for any trait alone, then I3 and I4 would be recommended. From the genetic-point of view, gain in protein yield obtained from different indices constructed are relatively higher than those gain obtained for yields of milk or fat. Similarly, *Hanna and Cunningham (1974) and Van Vleck (1978)* reported that increasing the relative emphasis on yields of fat and protein would result in more genetic progress for yields of milk, fat and protein.

**Index-trait correlation.** Correlation between the indices constructed and each individual trait in the aggregate genotype ($r_{IX}$) are shown in Table 3. These correlations were high, all ranging between 0.67 and 0.74. Correlations between each cow index and protein yield was slightly higher than those between each index and milk or fat yield. However, these high correlations indicate that selection per generation on any cow index would actually lead to a high genetic gain in the productivity. By cow indices and sire evaluation, a high genetic gain in yield traits would be achieved as reported by *Kennedy (1982)*.

**Table 3. Index standard deviation (σx), correlation of index with total genotype ($r_{IH}$) and with each individual trait ($r_{IX}$) and the efficiency (RE) of different indices relative to the original index (I1).**

| Item | Index | | | | | | |
|---|---|---|---|---|---|---|---|
| | I1 | I2 | I3 | I4 | I5 | I6 | I7 |
| $\sigma I^*$ | 845.30 | 815.40 | 844.40 | 842.60 | 648.30 | 620.70 | 32.70 |
| $r_{IX1}$ | 00.72 | 00.71 | 00.72 | 00.71 | 00.72 | 00.72 | |
| $r_{IX2}$ | 00.70 | 00.67 | 00.70 | 00.70 | 00.70 | | 00.71 |
| $r_{IX3}$ | 00.73 | 00.68 | 00.73 | 00.74 | | 00.73 | 00.74 |
| $r_{IH}$ | 00.73 | 00.70 | 00.73 | 00.72 | 00.72 | 00.73 | 00.73 |
| RE to I1 | 100.00 | 96.40 | 99.90 | 96.70 | 99.20 | 100.00 | 100.00 |

* This is the value of economic-genetic gain in aggregate genotype achieved by one standard deviation on the index.

**Index accuracy.** The accuracy of an index is based on its correlation withthe aggregate genotype ($r_{IH}$) where the genetic gain from use of an index is directly proportional to $r_{IH}$. Relatively high values of $r_{IH}$'s for different indices were observed (around 0.7, Table 3). Indices not including protein yield (I2) showed somewhat less in accuracy (0.70 for I2 vs. 0.73 for I6 and I7) and consequently a reduced index including protein with either of milk or fat (I6 or I7) was the highest in accuracy. *de Jager and Kennedy (1987)* reported that including protein in the index lead to an increase in the accuracy of the sire breeding value. Many investigators (e.g. *Henderson and Quaas, 1976; Anderson et al., 1978; Everett et al., 1982)* reported that including a composite trait (e.g. fat-protein) in an index could increase the genetic gain of such trait and consequently increases the accuracy of the indices to be used for selection.

**Index efficiency.** The efficiency (RE) of different indices constructed relative to the original index (I1), are given in Table 3. Two-trait indices based on fat yield with either of milk (I2) or protein (I4) were of 96% as effective as the three-trait index (I1), while I3, I5, I6 and I7 were 100% as effective as the original index (I1). Selection index without fat is nearly as effective as the index that includes fat (I3 or I6) while the index without protein yield (I2) showed the lowest efficiency (96.4%). *Mbah and Hargrove (1982)* found that selection indices without protein yield was nearly as effective as indices that include protein. They also stated that indices based on yields of milk and fat only were 91 to 100% as effective as the indices included the three variates.

### *Selection subindices*

A series of subindices (SI' s) were constructed to maximise the gain in a specific trait and not the aggregate genotype. Each subindex was computed as if the three sources of information (i.e. three variates of milk, fat and protein yields) were to be used to select for just one trait, i.e. to select either for milk, fat or protein. All alternatives that cover all possible combinations of information available were obtained and listed in Table 4 along with other relevant parameters. The efficiencies of these subindices relative to the corresponding original subindex (SI1) were estimated as the ratio of the standard deviations of the two subindices *(Cunningham andMahon, 1977).*

**Reduction percentages.** It is shown in Table 4 that percentages of reduction (V%) in genetic gain by dropping milk yield from the different subindices constructed were small, i.e. milk yield contributed little in the subindices to be used to select for yields of fat or protein. Also, fat yield showed lower contribution in the subindices to be used to select for yields of milk or protein. For Braunvieh cattle and according to *Binet (1965) and Kennedy (1982)*, it is preferable not to use fat yield itself as selection criterion, but to use other measurable traits such protein yield (genetically correlated with fat yield) for the purpose of indirect selection for milk yield. On the other hand, protein yield showed a high contribution to the different subindices to be used to select for either of milk or fat yield (values of V% ranged between 1.6 to 13.5% as shown in Table 4). For such a case, a subindex that include protein yield (e.g. SI3 or SI4) are considered the most efficient subindices to be used to select for yields of milk or fat or protein.

**Genetic gain.** The magnitude of the expected genetic change (EG) in yields of milk or fat or protein was high in all the subindices used (Table 4); all estimates ranged from 416 to 425 kg for milk, 16.9 to 17.5 kg for fat and 14.1 to 15.3 kg for protein. These high estimates of expected gain are due to the modrate or high estimates of heritability and correlations for these traits as shown in Table 1.

**Relative efficiency.** The relative efficiency (RE) in genetic gain ,was also used to compare the present subindices (Table 4). The subindices (included

**Table 4. Selection subindices (SI's) for yield traits of Braunvieh cattle, value of each variate (VZ), expected genetic gain per generation in each trait (EG), correlation of subindex and each trait (r ) and the effiency (RE) of different subindices relative to the original subindex (SII).**

| + Item | SI1 | | | | | | SI2 | | | | | | SI3 | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | MY | | FY | | PY | | MY | | FY | | PY | | MY | | FY | | PY | |
| | b | v% | b | v% | b | v% | b | v% | b | v% | b | v% | b | v% | b | v% | b | v% |
| 1. Variates: | | | | | | | | | | | | | | | | | | |
| MY | 0.334 | 1.8 | -0.002 | 0.0 | -0.001 | 0.0 | 0.576 | 10.6 | 0.011 | 2.4 | 0.015 | 6.4 | 0.237 | 1.2 | 0.001 | 0.0 | -0.003 | 0.2 |
| FY | -3.506 | 0.7 | 0.118 | 0.4 | -0.073 | 0.2 | -1.865 | 0.2 | 0.209 | 1.6 | 0.040 | 0.1 | | | | | | |
| PY | 9.676 | 2.0 | 0.538 | 3.7 | 0.668 | 7.7 | | | | | | | 8.180 | 1.6 | 0.588 | 0.48 | 0.637 | 7.5278 |
| 2EF (kg) | 425 | 17.5 | 15.3 | 416 | 16.9 | 14.1 | 422 | 17.4 | 417 | | | | | | | | | |
| 3-r | 0.72 | 0.71 | 0.74 | 0.71 | 0.68 | 0.68 | 0.72 | 0.71 | 0.74 | | | | | | | | | |
| SIG | | | | | | | | | | | | | | | | | | |
| 4-RE to SI1 | 100 | 100 | 100 | 97.9 | 96.6 | 92.1 | 99.3 | 100 | 100 | | | | | | | | | |

| + Item | SI4 | | | | | | SI5 | | | | SI6 | | | | SI7 | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | MY | | FY | | PY | | MY | | FY | | PY | | MY | | FY | | PY | |
| | b | v% | b | v% | b | v% | b | v% | b | v% | b | v% | b | v% | b | v% | b | v% |
| 1. Variates: | | | | | | | | | | | | | | | | | | |
| MY | | | | | | | 0.334 | 1.8 | -0.002 | 0.0 | 0.333 | 1.8 | -0.001 | 0.0 | -0.002 | 0.0 | -0.001 | 0.00 |
| FY | -.837 | 0.1 | 0.101 | 0.4 | -0.085 | 0.4 | -3.506 | 0.7 | 0.118 | 0.4 | -3.506 | 0.7 | -0.073 | 0.2 | 0.118 | 0.4 | -0.073 | 0.2 |
| PY | 15.802 | 10.9 | 0.499 | 6.0 | 0.642 | 13.5 | 9.676 | 2.0 | 0.538 | 3.7 | 9.676 | 2.0 | 0.668 | 7.7 | 0.538 | 3.7 | 0.668 | 7.7 |
| 2-EG (kg) | 417 | | 17.5 | | 15.3 | | 425 | | 17.5 | | 425 | | 15.3 | | 17.5 | | 15.3 | |
| 3-r | 0.71 | | 0.71 | | 0.74 | | 0.72 | | 0.71 | | 0.72 | | 0.74 | | 0.71 | | 0.74 | |
| EIG | | | | | | | | | | | | | | | | | | |
| 4-RE to SI1 | 98.1 | | 100 | | 100 | | 100 | | 100 | | 100 | | 100 | | 100 | | | |

+ Where b = the coefficients of th esubindex (i.e. the partial regession coefficients), V% = Value of each variate in subindex (i.e. percentage reduction in rate of genetic gain for trait if variate is dropped, and EG = the value of the genetic gain in actual unit (kg) in each trait achieved by one standard deviation on the subindex.

protein yield) to be used for selection for just one trait (i.e. milk or protein or fat) permit 98.1 - 100% as much gain as could be made with the 1st subindex (SI1). Consequently, the subindex including protein yield with either of milk or fat may be useful in practice. These results are confirmed by the fact that the correlations of such subindices and each trait ($r_{sIG}$) showed generally stable values (0.71 or 0.72) and the expected genetic gain per generation in each trait (EG) were closely similar in magnitude (Table 4). However, changes in the efficiency of selection are more dependent on the genetic correlations among traits than on the phenotypic, but both affect the efficiency *(Smith, 1983)*. In the present study, genetic covariances between yield traits, used in calculations of subindices, showed that joint selection for milk, fat and protein would give larger expected responses for any yield trait than those genetic covariances obtained from other studies for different breeds of dairy cattle (e.g. *Kennedy, 1982; Mbah and Hargrove, 1982)*. The relative efficiency of SI2 decreased as protein yield was dropped (Table 4). Accordingly, SI2 is consideredthe least efficient subindex to be used to select for one trait. In practice, and as mentioned above, SI3 or SI4 might be considered the most accurate subindices, while SI2 was the lowest.

## Conclusion and Future Demands

From the practical and economic-genetic viewpoints, an index or subindex including protein yield with either of milk or fat yield is considered the best criterion for selection for the improvement of cow productivity of Braunvieh cattle under the local Austrian conditions. Information presented here indicates that it is technically possible through selection for protein yield to achieve near maximum gains in yields of milk and protein. Such a selection program for Braunvieh cattle would represent a marked departure from historic and current practices in dairy cattle selection, i.e. shifting from selection for fat content to selection for protein content. What then are future demands for milk constituents, and how should breeding programs in such breed of dairy cattle respond to them? This question was addressed recently by the Official Federation of Braunvieh-Cattle Breeders in Austria and by some other investigators in Central Europe (e.g. *Schneeberger, 1981; Schneeberger and Hagger, 1984; Graml et al., 1987)*. Thus, if the dairy industry is serious about improving the protein content of milk, testing and recording should be made on that trait. Consequently, our recommendation is either to stimulate demand for protein-rich-products (e.g. high-protein milk powder or skim milk) or to shift breeding goals in favor of high ratios of fat to protein.


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