

# Genetic Correlations Between Longevity and Conformation Traits in an Upgrading Dairy Cattle Population

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## ABSTRACT

Genetic correlations between longevity and conformation traits were estimated using data on Dutch Black and White cows born in 1978 (11,558 records), 1982 (39,252 records), and 1989 plus 1990 (58,864 records). Longevity traits considered were number of lactations, herd life, and stayabilities until 36 and 48 mo of age and their functional equivalents (i.e., the longevity traits corrected for production). For the 1989 plus 1990 data file, only stayabilities until 36 and 48 mo of age were considered. Conformation traits were rear legs set, front teat placement, udder depth, suspensory ligament, and subjective scores for udder, feet and legs, and type. Also investigated was a possible nonlinear relationship between conformation and longevity traits.

Genetic correlations between conformation and longevity traits differed between years of birth, mainly because farmers practiced large-scale upgrading with Holstein-Friesian bulls during the period considered, which caused a change in desired type. Therefore, the predictive value of conformation traits for longevity based on data from an upgrading population, might be limited. Estimates of genetic parameters should be based on the most recent data possible, and these parameters should be reestimated over time. From the 1989 plus 1990 data file, subjective scores for udder and feet and legs had the highest predictive values for functional longevity. Quadratic relationships between conformation and longevity traits did exist, but generally the linear relationships prevailed. (**Key words:** longevity, conformation, genetic parameters, nonlinearity)

**Abbreviation key:** AGE36 = stayability at 36 mo of age, AGE48 = stayability at 48 mo of age, F = functional (used as a prefix), HL = herd life, LSS = subjective score for feet and legs, MP = 305-d milk production during first lactation, NL = number of

lactations initiated, RL = rear legs set (side view), SL = suspensory ligament, TP = front teat placement, TSS = subjective score for type, UD = udder depth, USS = subjective score for udder.

## INTRODUCTION

Longevity is a trait of increasing importance in breeding programs. When lifetime performance is used to measure longevity of cows, the generation interval increases compared with a breeding program aimed solely at increased milk production. This prolonged generation interval causes a decrease in annual genetic progress (23). Using stayability traits as measures of longevity, the generation interval is likely to increase as well because, in practice, stayability is measured after the first lactation, at a minimum of 36 mo of age (6, 15, 30). An alternative would be the use of traits that are correlated to longevity and can be measured earlier. Burnside and Wilton (4) concluded that selection for longevity would be possible only with predictors of longevity that could be measured early in life and show genetic variation.

Conformation traits can be measured during the first lactation and have reasonable strong genetic correlations with longevity, especially conformation traits describing udder, feet and legs, and overall type (5, 17, 31). Functional longevity traits are a measurement of involuntary culling, as are conformation traits (4, 18).

The Dutch population of dairy cattle has been strongly influenced by the implementation of the quota system and large-scale crossbreeding with Holstein-Friesian bulls during the 1980s (32). These changes might affect the genetic correlations between longevity and conformation traits. The main objective of this study was to investigate the genetic relationship between longevity and conformation traits reflecting udder, feet and legs, and overall type, comparing these correlations for different years of birth to quantify the effect of intensive crossbreeding with Holstein-Friesian bulls.

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Some conformation traits might have an optimum value with regard to longevity. Several researchers (3, 5, 10) found significant quadratic regression coefficients when using conformation traits to explain longevity. In standard programs used for estimation of covariance components, only the linear part of a relationship between two traits is considered. A second objective of this paper was to investigate a possible nonlinear relationship between longevity and conformation traits.

## MATERIALS AND METHODS

### Materials

The Royal Dutch Cattle Syndicate (Nederlands Rundvee Syndicaat, Arnhem, The Netherlands) provided lactation and conformation records of Black and White cows (Dutch Friesian and Holstein-Friesian cows) born in 1978, 1982, and 1989 plus 1990. Three data files were created according to the year of birth. Cows in the data files had at least one test day for milk production, and sires were known. Cows born in 1978 and 1982 were known to be culled before the moment of data collection. All cows used in the analyses were classified for conformation during first lactation. Table 1 contains information on the data. Classification started in 1980, and the percentage of participating farmers increased rapidly to 42% in 1995 (21). The mean percentage of Holstein-Friesian genes increased substantially over the years of birth (6.1% in 1978 to 80.0% in 1989 plus 1990), showing the upgrading process during these years. The pedigree files of all three data files contained sire, maternal grandsire, paternal grandsire, and paternal great grandsire, if known.

### Traits

The chosen longevity traits included two lifetime traits: number of lactations initiated (**NL**) and days between birth and last test day or herd life (**HL**). In a previous study (32), these two lifetime traits converged best in bivariate analyses. Stayability until 36 mo of age (**AGE36**) was chosen as well. For the 1989 plus 1990 data file, stayability until 48 mo of age (**AGE48**) was included instead of lifetime traits NL and HL, because most cows in this data file did not have sufficient time to complete a lifetime record, but all cows had the opportunity to survive to at least 48 mo of age.

A second set of functional traits was analyzed in which each trait was precorrected for milk production in first lactation. For the 1978 and 1982 data files,

TABLE 1. Data characteristics.

Year of birth	Classified <sup>1</sup>	Cows	HF <sup>2</sup>	Sires
	(%)	(no.)	(%)	(no.)
1978	29	11,558	6.1	517
1982	36	39,252	38.3	762
1989 plus 1990	40	58,864	80.0	2469

<sup>1</sup>Approximate percentage of participating farmers in the conformation classification program in the year that the cows in the data files were classified.

<sup>2</sup>Mean percentage of Holstein-Friesian genes in data file.

this correction was performed by a linear regression of lactation value for the first lactation on each longevity trait. Lactation value is the net merit index used to compare phenotypic performances of cows within a herd for milk, fat, and protein production (standardized for lactation length, season of calving, and age at calving) (20). Farmers use lactation value as a management tool. For the 1989 plus 1990 data file, lactation values were not readily available. Instead of a lactation value, 305-d milk production (unadjusted) in the first lactation was used to precorrect longevity traits phenotypically to functional longevity traits, which are indicated by the prefix **F**.

The following definitions and abbreviations of conformation traits were used. Objectively scored conformation traits were set of rear legs (**RL**, side view), front teat placement (**TP**), udder depth (**UD**), and suspensory ligament (**SL**). Scoring was on a nine-point scale. A score of 1 for RL means steep legs, a 1 for TP means that the teat placement is wide, a 1 for UD means a deep udder, and a 1 for SL means a weak suspensory ligament. Conformation traits for udder (**USS**), feet and legs (**LSS**), and type (**TSS**) were scored subjectively from a 65 to 89 scale (20). Type in The Netherlands is scored as the milk potential of a cow and therefore may more closely resemble the US dairy character than the US type score. Also, 305-d milk production during first lactation (**MP**) was analyzed. Table 2 contains the abbreviations and definitions of all traits analyzed. Per data file, genetic correlations between longevity traits (both uncorrected and functional) and conformation traits and MP were estimated.

### Methods

Genetic correlations between longevity traits and conformation traits and milk production were estimated in bivariate runs using the VCE program for variance component estimation of Groeneveld (12).

The following model was used to analyze the 1978 and 1982 data files:

$$Y_{ijklm} = \text{herd}_i + \text{birthmo}_j + \text{HF}_k + \text{calvmo}_l + \text{sire}_m + e_{ijklm} \quad [1]$$

where

$Y_{ijklm}$  = observation on the longevity trait, conformation trait, or MP;  
 $\text{herd}_i$  = fixed effect of herd  $i$ ;  
 $\text{birthmo}_j$  = fixed effect of month of birth  $j$ ;  
 $\text{HF}_k$  = fixed effect of the Holstein-Friesian group  $k$ ;  
 $\text{calvmo}_l$  = fixed effect of month of last calving  $l$ ;  
 $\text{sire}_m$  = random effect of sire  $m$ ; and  
 $e_{ijklm}$  = random residual term.

The nine genetic groups were defined according to the percentage of Holstein-Friesian genes: 0, 12.5, 25, . . . , 100. If rounding was necessary, it occurred toward the breed of the sire. To account for seasonal effects, month of last calving was included in the model. Reasons for seasonal effects could be a desired calving pattern or differences in culling of cows on milk

production during the year as a consequence of the quota system. Because the quota year ends on April 1, cows that are culled in February or March might not have been culled if the quota had not been nearly met (8).

For the 1989 plus 1990 data file, the following model was used:

$$Y_{ijkl} = (\text{herd} \times \text{birthmo}_j) + \text{HF}_j + (\text{herd} \times \text{calvmo}_k) + \text{sire}_l + e_{ijkl} \quad [2]$$

where

$(\text{herd} \times \text{birthmo}_j)$  = fixed effect of the interaction between herd and month of birth, and  
 $(\text{herd} \times \text{calvmo}_k)$  = fixed effect of the interaction between herd and month of last calving.

The interaction terms were included in the model to enable consideration of the possibility that a certain farmer had problems not producing more than the quota allowed in one particular year but did not have these problems in the next year. For the 1978 and

TABLE 2. Mean estimated heritabilities<sup>1</sup> and mean sire variances<sup>1</sup> ( $\sigma_s^2$ ) of the traits analyzed.

Trait <sup>2</sup>	1978	1982	1989 plus 1990	
	$h^2$	$h^2$	$h^2$	$\sigma_s^2$
Uncorrected longevity				
NL	0.11	0.09	...	...
HL	0.13	0.10	...	...
AGE36	0.03	0.03	0.03	0.0007
AGE48	... <sup>3</sup>	...	0.03	0.0014
Functional longevity				
FNL	0.08	0.06	...	...
FHL	0.09	0.07	...	...
FAGE36	0.02	0.01	0.03	0.0005
FAGE48	...	...	0.02	0.0010
Objectively scored conformation				
RL	0.17	0.32	0.17	0.089
TP	0.32	0.43	0.35	0.224
UD	0.31	0.34	0.26	0.120
SL	0.27	0.20	0.25	0.148
Subjectively scored conformation				
USS	0.32	0.34	0.34	0.818
LSS	0.41	0.29	0.30	0.656
TSS	0.43	0.29	0.39	0.785
Production				
MP	0.41	0.43	0.46	0.090

<sup>1</sup>Averaged over bivariate analyses.

<sup>2</sup>NL = Number of lactations initiated, HL = herd life, AGE36 = stayability until 36 mo of age, AGE48 = stayability until 48 mo of age, F = functional (used as a prefix), RL = rear legs set (side view), TP = front teat placement, UD = udder depth, SL = suspensory ligament, USS = udder, LSS = feet and legs, TSS = type, and MP = 305-d milk production during first lactation ( $\times 1000$  kg).

<sup>3</sup>Not analyzed in this data file.

TABLE 3. Estimated genetic correlations between longevity traits, and conformation traits and milk production in the data file 1978.<sup>1</sup>

Trait <sup>2</sup>	NL	HL	AGE36	FNL	FHL	FAGE36
RL	-0.13	-0.10	-0.06	-0.24	-0.21	-0.14
TP	-0.05	-0.04	-0.16	0.08	0.08	0.07
UD	0.06	0.02	-0.16	0.44	0.39	0.35
SL	-0.03	-0.06	-0.34	0.12	0.08	-0.13
USS	0.10	0.00	0.01	0.23	0.24	0.22
LSS	0.13	0.15	0.11	0.20	0.24	0.15
TSS	-0.03	0.04	-0.07	0.07	0.16	0.18
MP	0.45	0.48	0.74	0.09	0.13	0.20

<sup>1</sup>Standard error of estimates ranged from 0.051 to 0.12.

<sup>2</sup>NL = Number of lactations initiated, HL = herd life, AGE36 = stayability until 36 mo of age, F = functional (used as a prefix); RL = rear legs set (side view), TP = front teat placement, UD = udder depth, SL = suspensory ligament, USS = subjective score and for udder, LSS = subjective score for feet and legs, TSS = subjective score for type, and MP = 305-d milk production in first lactation.

1982 data files, an interaction term could not be included because not enough data were available. The original 1989 plus 1990 data file (105,170 records) was edited so that each herd and birth month class contained at least two records.

Approximate standard errors of the estimates of genetic correlations were calculated using formulas 10.15 and 19.4 of Falconer (9). The PEST program (11) was used to estimate breeding values in univariate runs for the sires in the 1982 data file, using Model [1] and the mean heritability estimates from the bivariate analyses of longevity and conformation traits (Table 2). The estimated breeding values were used to check the genetic relationships between these traits for nonlinearity. Both the linear and the quadratic regression coefficients of each breeding value for a conformation trait on each breeding value for a longevity trait were calculated separately using the GLM procedure (25).

## RESULTS AND DISCUSSION

### Mean Heritabilities

In addition to the abbreviations and definitions of the traits, Table 2 contains the mean heritabilities and sire variances (only for the 1989 plus 1990 data file) from the bivariate analyses of conformation and longevity traits. Compared with results of a previous study (32), the heritabilities were similar. Data were selected to include only classified cows, but this edit hardly affected the heritability estimates for longevity traits.

### Genetic Correlations Between Longevity and Conformation Traits

Table 3 contains estimated genetic correlations between longevity traits, on the one hand, and confor-

mation traits and MP, on the other hand, based on the 1978 data file. The RL trait showed negative correlations with all longevity traits, although these correlations are stronger with functional (-0.14 to -0.24) than with uncorrected longevity traits (-0.06 to -0.13). Both TP and SL have slightly negative genetic correlations with uncorrected longevity traits, but slightly positive correlations with functional longevity traits, except for the correlation between SL and FAGE36, which equals -0.13. The genetic correlations of TP and SL with AGE36 are stronger than with the other longevity traits (-0.16 and -0.34, respectively). The trait UD shows inconsistent and rather weak genetic correlations with uncorrected longevity traits, but quite strong, positive, correlations with functional longevity traits (0.35 to 0.44).

The subjective traits (USS, LSS, and TSS) showed little or no genetic correlation with uncorrected longevity traits, although correlations with LSS were a bit higher. Genetic correlations between the subjective traits and functional longevity were generally stronger, and all were positive (0.07 to 0.24).

Genetic correlations between MP and uncorrected longevity traits were high (0.45 to 0.74). Functional longevity traits would be expected to have much lower correlations with MP, because these traits were corrected for lactation value of which milk production is an important component. The genetic correlations were 0.09 to 0.20; correlations were not equal to 0 because lactation value includes other traits as well and because correction was performed on the phenotypic level and within herds.

Table 4 contains estimated genetic correlations between longevity traits, on the one hand, and conformation traits and MP, on the other hand, based on the 1982 data file. Genetic correlations from this data file differed from those from the 1978 data file. The

TABLE 4. Estimated genetic correlations between longevity traits, and conformation traits and milk production in the data file 1982.<sup>1</sup>

Trait <sup>2</sup>	NL	HL	AGE36	FNL	FHL	FAGE36
RL	-0.05	-0.01	-0.01	-0.04	-0.01	-0.03
TP	0.07	0.07	-0.14	0.10	0.09	-0.15
UD	0.03	0.02	-0.30	0.09	0.07	-0.34
SL	0.09	0.13	0.14	0.07	0.12	0.17
USS	0.31	0.33	0.10	0.35	0.37	0.15
LSS	0.32	0.32	0.23	0.31	0.32	0.18
TSS	0.47	0.47	0.48	0.46	0.46	0.47
MP	0.39	0.44	0.80	0.33	0.39	0.84

<sup>1</sup>Standard error of estimates ranged from 0.015 to 0.067.

<sup>2</sup>NL = Number of lactations initiated, HL = herd life, AGE36 = stayability until 36 mo of age, FNL = functional number of lactations initiated, F = functional (used as a prefix), RL = rear legs set (side view), TP = front teat placement, UD = udder depth, SL = suspensory ligament, USS = subjective score for udder, LSS = subjective score for feet and legs, TSS = subjective score for type, and MP = 305-d milk production in first lactation.

trait UD was not strongly correlated genetically with functional longevity traits, except for the correlation with FAGE36, which was negative for 1982 (-0.34) but positive for the 1978 data file (0.35, Table 3). Also, the correlation between UD and AGE36 was relatively strong: -0.30, although this correlation might be partly caused by the negative genetic correlation between UD and MP (-0.38, not shown). The subjective scores USS, LSS, and TSS showed relatively strong (>0.3) genetic correlations with both uncorrected and functional longevity traits, except for the correlations between USS and LSS and between AGE36 and FAGE36 (0.10 to 0.23).

The correlation (0.80) between MP and AGE36 was very strong in the 1978 data file as well (0.74, Table 3), which is an indication that milk production is an important reason for culling during first lactation. This result was found in earlier, more specific references as well (13, 19, 28). Correlations between MP and uncorrected longevity traits were as high as in the 1978 data file (Table 3), but correlations between MP and functional traits stayed on the same high level, in contrast to the results from the 1978 data file.

These results indicate that correcting longevity traits for lactation value in the 1982 data file does not affect their relationships with conformation traits and milk production. In other words, lactation value was not the primary culling reason for these cows, and, thus, functional longevity traits are no longer measures of involuntary culling. The cows born in 1982 were in the middle of the upgrading process (Table 1). The original population of Dutch Friesian cows had deep udders. Crossing those cows with Holstein-Friesians decreased UD, so that, in the 1982 data file,

only weak correlations could be found between UD and functional longevity traits (because UD was no longer a trait of major concern), even though these correlations were strong in the 1978 data file. Crossbreeding with Holstein-Friesians meant in practice that farmers selected mainly on Holstein-Friesian genes instead of production, which explains why little difference exists between correlations with uncorrected and functional longevity traits in the 1982 data file. It also explains why genetic correlations between TSS and longevity traits are strong in this data file: during the period with intensive crossing with Holstein-Friesians, TSS was scored as Holstein-Friesian type, and farmers selected on Holstein-Friesian genes (A. Hamoen, Chief Inspector of the Royal Dutch Cattle Syndicate, 1996, personal communication).

The inclusion of the fixed effect of Holstein-Friesian group in the model might not have taken away the effect of selection on Holstein-Friesian genes, because the inclusion of Holstein-Friesian group in the model did not correct for the differences in competition to stay in the herd that cows experience depending on their percentage of Holstein-Friesian genes. In general, cows with low percentages of Holstein-Friesian genes had a higher risk of being culled, but this risk depended completely on the competitive herdmates. Including an effect for the interaction of herd and percentage of Holstein-Friesian genes might have partly accounted for this, but the only way to correct properly for this competition effect would be the use of survival analysis. This method not only makes use of censored records, but also corrects for fixed effects (e.g., herd) in a time-dependent way (8, 27). However, to make use of

TABLE 5. Estimated genetic correlations between longevity traits, and conformation traits and milk production in the data file 1989 plus 1990.<sup>1</sup>

Trait <sup>2</sup>	AGE36	AGE48	FAGE36	FAGE48
RL	0.10	-0.17	0.15	-0.14
TP	0.66	0.78	0.70	0.84
UD	0.32	0.56	0.50	0.74
SL	0.20	0.34	0.25	0.43
USS	0.70	0.82	0.78	0.93
LSS	0.22	0.39	0.20	0.43
TSS	0.37	0.62	0.05	0.21
MP	0.61	0.66	-0.04	-0.19

<sup>1</sup>Standard error of estimates ranged from 0.0072 to 0.050.

<sup>2</sup>AGE36, AGE48 = Stayabilities until 36 and 48 mo of age, respectively; F = functional (used as a prefix); RL = rear legs set (side view); TP = front teat placement; UD = udder depth; SL = suspensory ligament; USS = subjective score for udder; LSS = subjective score for feet and legs; TSS = subjective score for type; and MP = 305-d milk production in first lactation.

survival analysis, the data file analyzed must contain information on all cows that are present at a certain time. This situation does not hold for the data used in this study because only cows from a single year of birth were in each data file. Furthermore, the method does not allow estimation of covariances between traits.

To check whether the genetic correlations between longevity and conformation traits in the 1982 data file would equal those of the 1978 data file if only Dutch Friesian cows were analyzed, a subfile was made. Cows in this subfile were required to be in a herd that consisted only of cows with 25% or less Holstein-Friesian genes. In total, 3099 cows from the 1982 data file met this requirement. Genetic correlations between longevity and conformation traits were estimated using this subfile. Results were disappointing because many of the bivariate runs did not converge, and the remaining estimates were diverse and could not be interpreted. Reasons might be the very few data and the failure to consider cows with a higher percentage of Holstein-Friesian genes that entered the herd later and were competitors of the original Dutch Friesian cows.

Therefore, the 1989 plus 1990 data file was established and analyzed. The Black and White population was much more stable during this period. Genetic correlations between longevity and conformation traits from the 1989 plus 1990 data file are detailed in Table 5. In general, genetic correlations are positive and strong (0.05 to 0.93); correlations between conformation and functional longevity traits were stronger than between conformation and uncorrected longevity traits. However, the difference was not very

large, which may partially have been due to the correction of functional longevity traits for the absolute level of 305-d milk production in the first lactation instead of a within-herd measurement of production. Furthermore, it is unclear what effect a different model has on the genetic correlations. The correlations between AGE48 and RL, between FAGE48 and RL, between FAGE36 and MP, and between FAGE48 and MP were the only negative correlations (-0.17, -0.14, -0.04, and -0.19, respectively). The correlation between FAGE36 and LSS (0.20) was lower than that between AGE36 and LSS (0.22), which was the only case in which the genetic correlation between a functional longevity trait and a conformation trait was weaker than between an uncorrected longevity trait and a conformation trait. The relatively weak genetic correlations between longevity traits and RL and SL were found in the 1978 data file as well (Table 3). No strong correlations were found between longevity traits and TP in the 1978 or the 1982 data file (Tables 3 and 4, respectively). Especially USS has very strong correlations with FAGE36 and FAGE48 in the 1989 plus 1990 data file (0.78 and 0.93, respectively). The trait TSS has relatively weak correlations with functional longevity traits, as in the 1978 data file. This situation was found in literature reports as well, especially for grade herds (6, 7).

Table 6 contains the estimated genetic correlations among conformation traits and MP for the 1989 plus 1990 data file. The trait USS had relatively strong genetic correlations with the objectively scored udder traits (0.50 to 0.85), and LSS was correlated strongly with RL (-0.52). Correlations between TSS and the objectively scored udder traits and between USS and LSS ranged from 0.26 to 0.63. As expected, MP had a relatively strong genetic correlation with TSS (0.64) because classifiers score the milk potential of a cow with this trait.

In this study, conformation traits generally had stronger genetic correlations with functional traits than with uncorrected longevity traits. If, in The Netherlands, FAGE48 would be incorporated in the breeding goal, an index based on 60 daughters per sire and containing information on USS and LSS would give a reliability of 0.74, based on the results from the 1989 plus 1990 data file (Tables 5 and 6). Classifiers are capable of recognizing cows with a long potential herd life. Genetic correlations between conformation and longevity traits might indeed be influenced by the circumstances. When an index containing conformation traits is used to breed for functional longevity, estimates of genetic correlations and heritabilities should be based on the most recent

TABLE 6. Estimated genetic correlations among conformation traits in the data file 1989 plus 1990.<sup>1</sup>

Trait <sup>2</sup>	TP	UD	SL	USS	LSS	TSS	MP
RL	-0.16	0.10	0.08	-0.04	-0.52	-0.04	0.10
TP		0.45	0.43	0.85	0.33	0.36	0.08
UD			0.23	0.50	0.20	0.26	-0.16
SL				0.64	0.30	0.38	0.18
USS					0.56	0.63	0.25
LSS						0.47	0.19
TSS							0.64

<sup>1</sup>Standard errors of estimates ranged from 0.0076 to 0.033.

<sup>2</sup>RL = Rear legs set (side view), TP = front teat placement, UD = udder depth, SL = suspensory ligament, USS = subjective score for udder, LSS = subjective score for feet and legs, TSS = subjective score for type, and MP = 305-d milk production in first lactation.

data file possible and should be reestimated routinely. It is expected that the most recent data will more closely resemble the steady state. Reestimation of parameters is necessary either to adjust parameters if the population is still changing or to check whether the steady state has been reached already.

Compared with literature estimates, the estimates in this study of genetic correlations between conformation and longevity traits are high, especially for the 1989 plus 1990 data file. The strongest genetic correlation in this study was 0.93; in the literature, the strongest genetic correlations that were based on data from Holstein cows were usually not higher than 0.5 (1, 5, 17, 24, 26, 29).

Visscher and Goddard (31) found considerably stronger genetic correlations between stayability and conformation traits for Jerseys (around 0.8) than for Holsteins (around 0.3). Vukašinović et al. (33) found genetic correlations as high as 0.7 between conformation and longevity traits for Swiss Brown cows. In the literature, conformation and longevity traits were less correlated for Holstein cows than for cows of other breeds.

Rogers et al. (24) found that genetic correlations between conformation and stayability traits were weaker than the genetic correlations usually found between conformation and lifetime traits, the strongest being 0.36. However, Short and Lawlor (26) found no difference in correlations between conformation and lifetime traits or between conformation and stayability traits. In this study, only one stayability trait (AGE36) was considered in all three data files. In the 1978 data file (Table 3), AGE36 had some genetic correlations differing from those involving NL or HL. For instance, the correlation with UD was negative; for NL and HL, the correlation with UD was small but positive. Also, the correlation between AGE36 and MP was much higher than that between the other longevity traits and MP. In the correlations with TSS, however, HL was the only longevity trait with a positive sign. In the 1982 data file (Table 4),

AGE36 behaved differently from NL and HL at some points. Correlations between AGE36 and TP and between AGE36 and UD were negative, for instance, but correlations between NL and HL and between TP and UD were positive. Also in this data file, the genetic correlation between AGE36 and MP was higher than between NL or TP and MP. Genetic correlations between stayabilities and conformation traits and between lifetime and conformation traits differed partly because of the analysis of stayability traits using continuous models.

Dekkers et al. (5) found that 0.39 was the strongest of the genetic correlations between uncorrected longevity traits and conformation traits in registered herds; genetic correlations were lower between conformation traits and FHL in grade herds. Short and Lawlor (26) also found stronger genetic correlations between conformation and longevity traits for registered than for grade herds. Van Doormaal et al. (29) also found stronger genetic correlations between conformation and longevity traits for "breeders" than for "milkers". Even though they are not the same, it might be assumed that "breeders" are comparable with registered herds, and "milkers" with grade herds. In all three of these studies (5, 26, 29), for different breeding goals, different conformation traits were most important in determining longevity. In registered herds, traits such as dairy character, dairy form, final class, and general appearance were most important. In grade herds, traits such as UD, feet and legs, and mammary system were important, too. In the present study, because genetic correlations between the subjective scores for type and longevity traits was mostly relatively low, Dutch data could be compared with data from grade herds even though all cows were registered.

### Nonlinear Relationships

Because the REML estimates of the genetic correlations between longevity and conformation traits in

TABLE 7. Significance ( $P < 0.05$ ) of linear (L) and quadratic (Q) regression coefficients of sire breeding values of conformation traits on breeding values of longevity using the data file 1982.

Trait <sup>1</sup>	NL	HL	AGE36	FNL	FHL	FAGE36
RL	L			L	L	
TP						
UD		Q	L		Q	L
SL					L	
USS	L	L		L	L	
LSS	L + Q	L + Q	L	L + Q	L + Q	L
TSS	L + Q	L + Q	L	L + Q	L + Q	L
MP	L + Q	L	L + Q	L + Q	L + Q	L + Q

<sup>1</sup>NLC = Number of lactations initiated, HL = herd life, AGE36 = stayability until 36 mo of age, F = functional (used as a prefix), RL = rear legs set (side view), TP = front teat placement, UD = udder depth, SL = suspensory ligament, USS = subjective score for udder, LSS = subjective score for feet and legs, TSS = subjective score for type, and MP = 305-d milk production in first lactation.

the 1982 data file were different from expected, the estimated breeding values of the sires ( $n = 762$ ) from this data file were used to check for nonlinearity in the relationship between longevity and conformation traits. Table 7 indicates which conformation traits had significant ( $P < 0.05$ ) linear or quadratic (or both) regression coefficients when explaining longevity traits in a regression model containing only a mean, linear conformation trait effect, and quadratic conformation trait effect. Especially subjective conformation traits (USS, LSS, and TSS) and MP had significant nonlinear relationships with longevity traits, but the quadratic component was never significant when the linear was not significant. Only UD had significant quadratic relationships with HL and FHL when the linear relationships were not significant. Generally, conformation traits that have stronger genetic correlations with longevity (Table 4) also have significant regression coefficients.

Many other researchers (3, 10, 14, 22) have found significant quadratic regression coefficients when conformation traits are used to explain longevity, but Rogers et al. (24) found only significant linear coefficients. Dekkers et al. (5) found both significant quadratic and cubic regression coefficients. This study investigated only linear and quadratic regression coefficients. Brotherstone and Hill (2) found significant quadratic regression coefficients when survival was regressed on conformation scores phenotypically, but not when survival was regressed on estimated breeding values of sires for conformation traits. Those results conflict with results from this study, in which regression was on estimated breeding values and quadratic terms were significant.

Keller and Allaire (16) found that intermediate scores for conformation traits were associated with highest scores for survival traits. In the example in the present study of the relationship between FHL

and UD, both deep and shallow udders are related to a high FHL, which might cause a problem if FHL is incorporated in a breeding program. Deep udders are not desired, but, when breeding for FHL, UD will go to one of the two extremes. A solution would be the use of assortative mating.

## CONCLUSIONS

Conformation traits reflecting udder and feet and legs have stronger correlations with functional longevity traits than with uncorrected longevity traits. Care should be used with estimated correlations between conformation traits and longevity when those estimates are based on data from an upgrading population. The large-scale crossbreeding with Holstein-Friesians appears to have strongly influenced the desirability of a certain type of cow and decision-making policies for culling. For practical use in a breeding program, estimates of genetic correlation and heritabilities should be based on the most recent data possible and should be repeated over time. From the most recent data file analyzed in this study, it seems to be sufficient to put USS and LSS in a selection index when breeding for functional longevity in The Netherlands.

Nonlinear relationships between conformation and longevity traits exist, although hardly ever without simultaneous linear relationships. Only UD had a quadratic relationship with HL and FHL without a significant linear relationship.

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