

Genetic analysis of herd life and stayability in Danish Dairy Cattle

Pieter Bijma¹⁾ & Just Jensen²⁾

¹⁾ Department of Animal Breeding, Wageningen Institute of Animal Sciences, P.O. Box 338, 6700 AH, Wageningen, The Netherlands

²⁾ Danish Institute of Animal Science, Research Centre Foulum, Department of Breeding and Genetics, P.O. Box 39, DK-8830 Tjele, Denmark

Introduction

The herd life (HL) of a dairy cow is an expression of the farmers interest in keeping the cow in the herd. This interest is assumed to be governed mainly by economic reasons. In many breeding programs for dairy cattle various type traits, and traits related to disease incidence are used as early indicators of HL.

Production, obviously has an influence on HL. Dekkers (1993) presented a structured model for HL such that HL can be described as true herd life (THL) which is the observed herd life and functional herd life (FHL) which is THL corrected for the influence of production.

Other early measures of HL is stayability, i.e. survival to a certain time point either measured in age or in days in milk or in days after first calving (days in feed).

The purpose of this paper is to present genetic parameters of various measures of HL as well as for some early predictors of HL.

Materials and Methods

Traits

Data on milk production as well as pedigree and herd-information were extracted from the national database. From that information two types of survival traits were computed, either lifetime traits or stayability traits.

The lifetime traits were: HL = herd life = age at culling, DIF = days in feed = culling date - date of first calving, DIM = days in milk = DIF excluding dry periods. The stayability

traits were defined as a binary trait indicating whether the cow was alive at a certain age or after a certain length of productive life. The stayability traits defined in this study were: STAYHL36, 54, 84 = stayability (0-1) up to 36, 54 and 84 months of age, STAYDIF17, 30, 60 = stayability (0-1) up to 17, 30 and 60 months in feed, STAYDIM15, 25, 50 = stayability (0-1) up to 15, 25 and 50 months in milk. The last trait included was ECMPD1, the energy corrected milk production per day in the first lactation.

Data

Only animals that initiated their first lactation after July 1983 were considered, since earlier records did not contain total lactation yields. Further edits removed cows with a calving interval outside the range 270-600 d, cows sold alive to non-registered herds, cows exported, and cows with age at first calving outside the range 18-36 m. These rules are similar to rules used by e.g. Jairath et al. (1994).

The herd life of a cow obviously cannot be observed before the cow is culled. To avoid problems of censoring all cows were given opportunity to express HL. Following the suggestion of Jairath et al. (1994) we gave all cows 5 years of opportunity. Cows that initiated their first lactation less than 5 years before the final update of data or 5 years before the herd left the milk recording program had their records for HL, DIF and DIM set to missing.

For the stayability traits the opportunity time can be shorter. E.g. to express STAYHL54 all cows born 54 months before end of recording or final update can be included. Similar rules hold for STAYDIF and STAYDIM traits but here time must be computed from date of first calving.

The data contained information on three breeds, Danish Red (RD), Danish Friesian (DF) and Danish Jersey (DJ). Herd years were assigned as herd-year of first calving. For RD and DJ herd-years with less than 5 cows and sire groups with less than five daughters or with daughters in less than three herds were removed. For DF the limits were 10 cows per herd-year, 25 daughters per sire and daughters in at least 10 herd-years. Table 1 shows the number of records per year per breed. The records in later years will not have the HL and stayability traits due to lack of opportunity, so these records will only include production. Table 2 shows the number of records for each trait per breed.

Models

Two different sire models were used for the survival data. Model [1] for true survival that did not include production and model [2] for functional survival that included production as a covariable. All three breeds analyzed have imported genes from foreign populations. The effect of this was modelled as additive effects of population differences and heterosis effects due to dominance and additive by additive epistasis. All these effects were considered fixed in the model.

Model for functional survival:

$$y = HY + Y*SEAS + b_1*P + b_2*P^2 + b_3*P^3 + b_4*P^4 + b_5*P^5 + c_1*AGE + c_2*AGE^2 + ADD + DOM + EPIS + SIRE + e \quad [1]$$

Model for true survival:

$$y = HY + Y*SEAS + c_1*AGE + c_2*AGE^2 + ADD + DOM + EPIS + SIRE + e \quad [2]$$

where,

- y = observation for a survival trait
- HY = herd-year of first calving
- Y*SEAS = year*season of first calving
- P = relative production deviation from the herd-year mean
- AGE = age at first calving
- ADD = additive effect of gene imports as covariables
- DOM = dominance effects of gene imports as covariables
- EPIS = epistatic effects of gene imports as covariables
- SIRE = random effect of sire of cow
- e = random residual.

Model for milkproduction:

$$y = HY + Y*SEAS + d_1*AGE + d_2*AGE^2 + d_3*AGE^3 + ADD + DOM + EPIS + SIRE + e \quad [3]$$

All known relationships among sires due to male relationships were considered. Heritabilities were estimated from univariate analysis and correlations were estimated in bivariate analysis. All estimates were obtained by average information REML as described by Madsen et al. (1994) using the DMU package of Jensen & Madsen (1994).

Results and Discussion

Table 3 shows estimated heritabilities, by breed, for all traits analyzed. The estimates for the binary stayability traits were converted to an underlying normal scale.

The heritability estimates of the functional lifetime traits ranged from 0.048 to 0.076, with the estimates for DJ showing the lowest values. Dropping the correction for production increased the heritability to the range 0.072 to 0.112. The estimates are in general higher than estimates from Dutch data by Vollema & Groen (1994), but more in line with other literature estimates, e.g. Jairath et al., 1994, Klassen et al., 1992 and Van Raden & Klaaskate, 1993.

The heritability estimates for stayability traits are also shown in Table 3. The correction

to an underlying normal scale always increased the heritability estimates so they generally are larger than for the herd life traits. The estimates are also much higher than estimates obtained by Vollema & Groen, 1994, who on the most recent data obtained estimates from 0.021 to 0.092. The heritability of stayability on an underlying scale increases with increasing length of stayability. This is partly a function of the correction for the underlying scale since the correction gets relatively larger with increasing time, because the incidence of survivors gets lower.

Correlations

Estimates of phenotypic and genetic correlations are shown in Table 4 for RD and for a selected set of trait combinations only. Genetic correlations between all traits and functional DIM were very high except for STAYHL36 where the correlations were 0.83 and 0.78 for functional and true STAYHL36, respectively. The remaining correlations clearly show that stayability later than 36 m of age or stayability based on days in feed or days in milk can be used as indirect selection criteria for functional DIM.

Table 4 also shows correlations between herd life or stayability traits and production. The genetic correlations between true herd life/stayability traits and production were in the range 0.55 to 0.72 and those for the functional herd life or stayability traits were in the range 0.27 to 0.33. Correction for production clearly lowers the correlation but it seems that the genetic correlation between functional survival and production is positive.

Conclusions

- Estimated heritabilities of the lifetime traits are about 0.07 for functional traits and 0.10 for true traits.
- Estimated heritabilities of stayability traits are lower than those from life time traits.
- Estimated heritabilities are highest for

- the Danish Friesian, close to this for the Danish Red and lower for the Jersey.
- Genetic correlations between different measures of survival are high (>0.83), genetic correlations between true and functional lifetime traits are close to unity.
- Genetic correlations between production and survival are highest for true survival traits.
- No indication was found for a negative relationship between production and the ability to survive.
- Because of the high genetic correlation between stayability traits and DIM, stayability traits can be used as early predictors of DIM.

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Table 1 Total number of observations per breed per year

Breed/Year	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993
RD	12,891	22,052	20,765	22,934	20,833	21,211	20,471	19,395	18,560	18,798	18,307
DF	24,526	61,136	64,446	74,982	78,805	78,975	79,428	79,593	82,653	85,578	88,030
DJ	10,238	20,175	21,833	24,315	23,810	22,418	22,313	21,740	21,494	22,008	22,069

Table 2 Number of observations per trait per breed in the data used for the analyses

Trait / Breed	Danish Red	Danish Friesian	Danish Jersey
HL	127,349	426,193	131,690
DIF	127,349	426,193	131,690
DIM	127,349	426,193	131,690
STAYHL36	213,952	788,491	227,745
STAYHL54	186,850	665,283	193,578
STAYHL84	134,090	450,255	134,261
STAYDIF17	202,076	731,690	215,770
STAYDIF30	180,874	639,900	191,039
STAYDIF60	127,434	426,470	131,763
STAYDIM15	181,934	643,791	192,335
STAYDIM25	160,498	554,516	167,634
STAYDIM50	105,488	345,303	108,492
ECMPD1	216,428	798,152	232,953

Table 3 Heritability estimates for production and true and functional survival. Estimates for stayability traits are converted to normal underlying scale RD = Red Danish, DF = Danish Friesian, DJ = Danish Jersey

Trait	Functional			True		
	RD	DF	DJ	RD	DF	DJ
HL	0.067	0.072	0.048	0.095	0.108	0.072
DIF	0.067	0.068	0.048	0.095	0.104	0.072
DIM	0.071	0.076	0.052	0.100	0.112	0.076
STAYHL36	0.049	0.058	0.041	0.109	0.117	0.090
STAYHL54	0.078	0.076	0.051	0.106	0.114	0.076
STAYHL84	0.108	0.112	0.081	0.115	0.136	0.091
STAYDIF17	0.055	0.060	0.047	0.097	0.100	0.080
STAYDIF30	0.082	0.084	0.051	0.105	0.117	0.076
STAYDIF60	0.107	0.115	0.081	0.116	0.114	0.095
STAYDIM15	0.061	0.054	0.047	0.106	0.101	0.081
STAYDIM25	0.074	0.083	0.044	0.103	0.122	0.070
STAYDIM50	0.127	0.112	0.075	0.139	0.136	0.094
ECMPD1	-	-	-	0.214	0.268	0.216

Table 4 Genetic and phenotypic correlations among selected trait combinations for Danish Red

	Functional DIM		ECMPD1	
	genetic	phenotypic	genetic	phenotypic
Functional				
DIF	>0.99	0.99	-	-
STAYHL36	0.83	0.52	0.27	0.05
STAYHL54	0.99	0.76	-	-
STAYHL84	0.92	0.52	-	-
STAYDIF17	0.95	0.73	0.29	0.10
STAYDIF30	1.00	0.78	0.33	0.14
STAYDIF60	0.92	0.47	-	-
STAYDIM15	0.94	0.72	-	-
STAYDIM25	0.99	0.78	-	-
STAYDIM50	0.94	0.51	-	-
True				
DIF	>0.99	0.99	-	-
STAYHL36	0.78	0.55	0.72	0.33
STAYHL54	0.99	0.79	-	-
STAYHL84	0.91	0.52	-	-
STAYDIF17	0.93	0.75	0.69	0.34
STAYDIF30	0.99	0.79	0.55	0.27
STAYDIF60	0.92	0.47	-	-
STAYDIM15	0.93	0.74	-	-
STAYDIM25	0.98	0.80	-	-
STAYDIM50	0.92	0.51	-	-
DIM	-	-	0.63	0.42
ECMPD1	0.31	0.16	-	-