Phenotypic relationship between type and longevity in the Holstein breed

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Abstract

The relationship between type traits and longevity was studied in the French Holstein breed using a survival analysis model where the phenotypic value or the estimated genetic value of the cow for each type trait was included as a risk factor. This was done separately for two subpopulations (registered and non registered herds) and with or without adjustment for production traits, i.e., considering true or functional longevity.

For all herds, udder traits (and above all, udder depth) clearly influence length of productive life. There seems to be a more drastic voluntary culling on type traits in registered herds. The correction for production traits, as a way to approximate functional longevity, increases the importance of udder traits and decreases the weight of capacity traits. The same results were obtained when the phenotypic value of the cow for type was replaced by her EBV. The relationship between longevity and type traits is most often nonlinear, in particular for udder traits.

1. Introduction

The stayability of a cow in her herd is frequently conditioned by her morphology. Consequently, type traits are often presented as good predictors of longevity. Type scoring is usually performed during the first lactation, which brings an early information on survivability. To directly get reliable evaluations of sires on the longevity of their daughters, it is necessary to wait until a minimum number of daughters are dead and these evaluations may arrive too late to be useful in breeding programs. For all these reasons, it seems pertinent to combine in genetic evaluations, longevity information direct with indirect information on early predictors such as type traits. This requires a precise knowledge of the genetic relationship between type and longevity (see Larroque and Ducrocq, 1999). But for a proper choice of the type traits to be used as early predictors, it is interesting to more precisely assess the phenotypic impact of type traits on culling. This was studied in the French Holstein breed, focussing on two main aspects:

• <u>Is the risk of being culled due to poor type</u> characteristics the same in the whole French <u>Holstein population</u>?

In North America and some other countries, the fact that an animal belongs or not to the official herdbook has a strong effect on culling policy: registered cows are better valued on the speculative market because they may be sold for breeding purposes and not for commercial

production only. They are often kept longer in the herd (Dentine, 1987). They are less frequently voluntarily culled for low milk production and more frequently for substandard type. This fact explains why the analyses of the relationship between type and longevity are often performed separating the two (registered and grade) subpopulations (Short and Lawlor 1992: Brotherstone and Hill 1991; Dekkers et al. 1994). For registered cows, type traits regularly appear as a source of voluntary culling, similar to production traits, and no longer as a predictor of involuntary culling.

In France, herdbook associations were replaced by associations in charge of breed promotion (UPRAs: Unions de Promotion de la RAce). This is a more open system: breeders voluntarily subscribe to a service with systematic yearly visit for the type scoring of all first lactation cows. They can quit at any time. In other words, registration is on a herd basis, not on an animal basis and speculative business on registered animals is less intense.

However, registered herds are often elite herds and the two subpopulations (UPRA / NON UPRA) have never been compared with respect to the attitude towards culling on type traits.

• <u>Is the relationship between type traits and</u> <u>longevity linear?</u>

For some traits, this may be a reasonable assumption: the more extreme a type trait, the higher (or the lower) the culling risk. But for others, the relationship may be more complex: for example, some traits may have an intermediate optimum, with an increased culling risk when type score gets farther from this optimum; or a score above a certain threshold may be considered as satisfactory and then, the corresponding trait does not influence longevity at all, because it is no longer related to culling reasons.

These nonlinear relationships were mainly studied using regression methods (as in Dekkers et al. 1994). Another approach was applied by Ducrocq (1996, unpublished results) using survival analysis to assess the influence of type traits on longevity on registered and grade Holstein cows in the USA: the impact of the inclusion of each type trait to a survival model without any genetic component (no sire effect) was studied. The difference between results in the registered and grade population were striking. Also, intermediate optimum traits were found, for example on rump angle. Similar studies have been carried out in homogeneous populations (Dürr, 1997; Sölkner and Petschina, 1998; Vollema, 1998; Bunger and Swalve, 1998 (personal communication), Schneider, 1998)

To answer these two questions in the case of the French situation, the approach of Ducrocq (1996) was applied to the French Holstein data set and extended in several ways. In the study, three issues were combined:

1) The populations, distinguishing between registered (UPRA) herds and other herds;

2) the longevity traits, looking at "true longevity" (without correction for milk production) and "production adjusted longevity", as an approximation of functional longevity;

3) the way type traits are described in the model, as (adjusted) phenotype or as the animal EBV.

2. Material and method

Type data from Holstein cows scored between October 1992 and October 1997 was combined with survival information about all cows milk recorded in the same herds during the same period. All analyses were performed using the "Survival Kit-V3.0" (Ducrocq and Sölkner, 1998a).

2.1. Selection of herds

Registered (UPRA) herds were defined as herds with at least one systematic type classification of first lactation cows by UPRA technicians. For the others (NON UPRA), type scores originate from daughters of young sires (used for the first evaluation of these sires) as well as herdmates scored at the same time to define contemporary groups. This difference in the recording system lead to distinct selection criteria in the two subpopulations:

• The non registered (<u>NON UPRA</u>) file includes non registered herds of size > 20cows and with at least 10 type scored cows at a minimum of 4 distinct dates during the whole period. The type scored animals had to represent at least 18% of all animals in the herd. In total, 2165 herds were selected, with 209644 cows and 57092 type scored cows.

• The registered (<u>UPRA</u>) file contained data from registered herds of size > 20 cows, with at least 40 type scored cows in a minimum of 5 classification rounds during the whole period. 60% or more of the cows in the herd had to be classified. In total, this file included 1242 herds with 151741 cows, 104080 having type information.

2.2. Data

Longevity information: the measure used is length of productive life (LPL) defined as number of days since first calving. All records of animals calving before October 1st 1992 were left truncated. Those of animals still alive on October 1st 1997, or sold to other farms, were right-censored

<u>Type information</u>: for each type scored animal, the data for each trait were extracted from the routine multiple trait animal model evaluation and in particular:

- the cow's estimated breeding value \hat{g} ;

- the phenotype \hat{p} adjusted for systematic environmental effects (stage of lactation, age at first calving, herd-round-classifier effects). If \hat{r} represents the estimated residual of the linear model used in the evaluation, $\hat{p} = \hat{g} + \hat{r}$.

Because phenotypic scores have very different variabilities, they were expressed in the genetic standard deviation unit of each trait. Then, they were grouped into classes of equal width (0.2 genetic standard deviation), regrouping extreme categories. This standardisation resulted in 21 classes for estimated breeding values (from – $1.9\sigma_g$ to + $1.9\sigma_g$) and 41 classes for the phenotype (from – $3.9\sigma_g$ to + $3.9\sigma_g$). In contrast with the use of phenotypes or EBVs as continuous variables, this transformation into classes allows an analysis without any extra assumption on the form of the relationship between type traits and

longevity.

2.3. The reference model

The reference model for the analysis of LPL is similar to the one used for the genetic evaluation in France (Ducrocq and Sölkner, 1998b). In particular, the same environmental effects are incorporated, but no genetic (sire) component is included: this is necessary to avoid that the effect of \hat{p} or \hat{g} on culling risk be biased because part of it is accounted for by the sire effect.

In addition, a cow may have been culled before having the opportunity to be type scored. Culling may or may not have been caused by her type characteristics. For such a cow, the fact that she is not scored would apparently increase the culling risk. To check this, a indicator variable of "presence (=1) or absence (=0)" of type score was added to the reference model. The hazard function h(t) of a cow t days after her first calving is equal to: $h(t) = h_0(t) \exp\{\mathbf{x}'(t)\beta + \mathbf{z}'(t)\delta + p_s\}$ [1] where $h_0(t) = \lambda \rho(\lambda t)^{\rho-1}$ is the Weibull baseline hazard function (with $\rho = 2$). The exponential term includes:

• the (time-dependent) environmental effects **x**'(t) of the national evaluation model;

• the (time-dependent) effects \mathbf{z} '(t) of production traits (expressed as deviation to herd-year average). These effects are included as adjustment factors only for the approximate analysis of functional longevity. They are ignored for the true longevity analysis.

• p_s is the effect of presence / absence of type information. As some type traits were introduced after 1992, this effect is defined differently for each (group of) trait(s).

The phenotypic or the genetic effect of each type trait i is studied by adding to this reference model the effect m_i of each class. Then, the model is written:

$$h(t) = h_0(t) \exp\{x'(t)\beta + z'(t)\delta + p_s + m_i\}$$
 [2]

Systematic scoring of fore udder attachment and temperament is very recent in France. Few scored cows have been culled since then. This leads to a large inaccuracy of results.

3. Results

3.1. Effect of absence of type information

Whatever the population considered, the culling risk of a cow which was not type scored is significantly increased. The relative risk (RR), defined as $\exp\{\hat{p}_s\}$, represents the factor by which culling risk of cows not scored is increased (if RR>1) or decreased (if RR<1) with respect to a scored animal. This risk factor is 2.15 for the

registered (UPRA) population and only 1.17 for the non registered animals. These estimates are unchanged when a correction for production traits is added. In the UPRA population, all first lactation cows are classified and therefore, there is no sampling involved: it can be concluded that a cow without type information was voluntarily or involuntarily culled very early, before the yearly visit of the UPRA technician. Consequently, the effect of type on longevity that is obtained from the survival analysis is likely to underestimate the true effect. In the NON UPRA population, this phenomenon also exists, but since first lactation cows are not exhaustively classified, the sampling of herdmates for the type evaluation leads to an important "dilution" of the effect of absence of scoring.

3.2. Effect of type phenotype on longevity

Likelihood ratio tests comparing model [2] (full model) and model [1] (reduced model) reveal which types trait statistically influence true or functional longevity. Because all these test statistics have the same number of degrees of freedom (40), their magnitude also informs us on the relative importance of each trait. The contributions to the likelihood (x2) are displayed in figures 1 and 2 for the NON UPRA and UPRA populations respectively, and they can be compared to the 1% and 0.01% significance levels for a χ^2 test with 40 degrees of freedom.

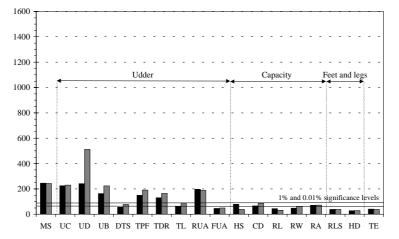
3.2.1. Comparison between UPRA and NON UPRA populations

Whether culling risk is adjusted or not for production traits, udder traits as well as milking speed are the most important traits. They are all significant at the 0.01% level, except teat distance (side) and for udder attachment in the NON UPRA population (it should be remembered however that data availability on fore udder attachment is too recent to be really informative). Clearly, the impact of these traits on longevity is much higher in the UPRA population. Also, all traits related to udder support (udder cleft, udder depth, udder balance and rear udder attachment) better explain culling risks differences than traits related to teat length and placement.

The effect of capacity traits on true longevity is significant in the UPRA population (although much less prominently than for udder traits) but not in the NON UPRA population.

Feet and legs traits (rear leg set and heel depth) have no significant effect on true longevity in the NON UPRA population and their impact is barely significant in the UPRA population.

Figure 1 : Contribution to the likelihood (x2) of adjusted <u>phenotype</u> for type traits on length of **productive life : NON UPRA data set** (without (in black) and with (in grey) correction for production)



MS: Milking speed; UC: Udder cleft; UD: Udder depth; UB: Udder Balance; DTS: Distance between teats, side; TPF: Teat placement front; TDR: Teat direction rear; TL: Teat length; RUA: Rear udder attachment; FUA: Fore udder attachment; HS: Height at sacrum; CD: Chest depth; RL: Rump length; RW: Rump width; RA: Rump angle; RLS: Rear leg set; HD: Heel depth; TE: Temperament.

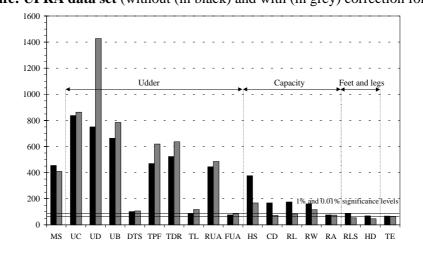


Figure 2: Contribution to the likelihood (x2) of adjusted <u>phenotype</u> for type traits on length of productive life: UPRA data set (without (in black) and with (in grey) correction for production)

Trait definition: as in figure 1

Temperament, as for fore udder attachment is penalised by a lack of information, due to its recent addition to the scoring table.

3.2.2. Comparison between true and functional longevity

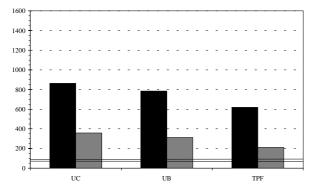
Overall, the importance of udder traits as an explanatory component of longevity is increased when production is corrected for. This is specially true for udder depth in both subpopulations: deep udders are more frequent among high yielding cows, which are less often voluntarily culled. As a result, the effect of udder depth is underestimated when production is not accounted for.

In contrast, for capacity traits, the inclusion of an adjustment for production decreases the importance of the traits (except for chest depth, rump width and rump angle among NON UPRA cows). These traits are considered as favourably correlated to milk production. Tall and deep cows often have higher production, which to some extent, protects them from voluntary culling. After correction, these traits do not contribute as much to longevity. However, they remain more important (significant) in the UPRA population. This may indicate a particular attitude of UPRA breeders towards capacity traits, with some voluntary culling on such traits.

3.2.3. Relative importance of udder depth

Udder traits seem all important. But knowing the large positive genetic correlations existing between udder depth and most of the other udder traits, one may wonder whether these latter traits appear significant only because they are correlated with udder depth. To check whether it is the case, each of these other udder traits was added to a model [2] which already includes udder depth. The contribution to the likelihood (x2) of the three most important ones is presented in figure 3 for functional longevity in the UPRA population

Figure 3: Contribution to the likelihood (x2) of some udder traits phenotypes for functional longevity when udder depth is excluded (in black) or already included (in grey) in the model (UPRA data set)

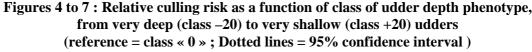


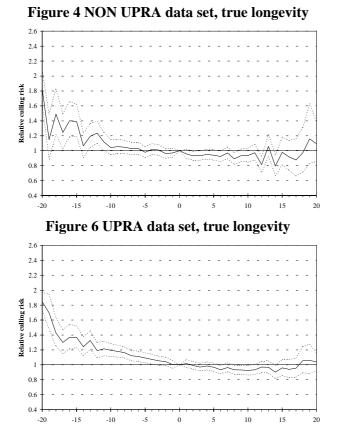
UC: Udder cleft; UB: Udder balance; TPF: Teat placement front

Udder cleft, udder balance and teat placement still contribute significantly to a change in culling risk, but their favourable relationship with udder depth (genetic correlations from 0.40 to 0.54) leads to a strong reduction of their impact after adjustment for udder depth.

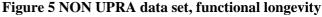
3.2.4. Estimates of relative risk

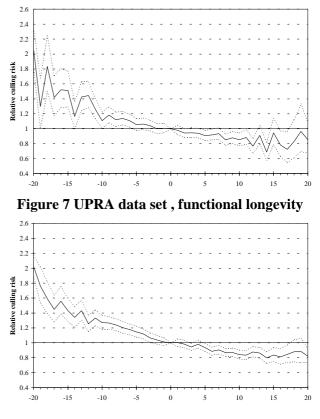
For each trait and each population and for both categories of longevity analysis, the relative risks $exp\{\hat{m}_i\}$ were plotted as function of the classes of adjusted phenotypic score (by step of $0.2\sigma_g$). Figures 4 to 7 present such plots for udder depth in the NON UPRA population (figures 4 and 5) and in the UPRA population (figures 6 and 7), for the true and functional longevity analyses, respectively. All estimates are compared to class "0" (0.1 to +0.1 σ_g).





As an illustration, take the phenotypic class "-8": it corresponds to scores adjusted for environmental effects between $-1.7 \sigma_g$ and $-1.5 \sigma_g$, i.e., raw values between -0.82 and -0.72 with respect





to the reference value ($\sigma_g = 0.4803$ for udder depth). In the NON UPRA population, the relative culling risk for an animal in this class is $\exp{\{\hat{m}_i\}}=1.05$ for true longevity and 1.12 for functional longevity. In the UPRA population, these values are higher: 1.16 for true longevity and 1.24 for functional longevity.

A 95% confidence interval for each estimate is also displayed on these figures. The rather erratic variations of estimates for extreme classes are due to a lower number of animals in each class, which results in a larger confidence interval.

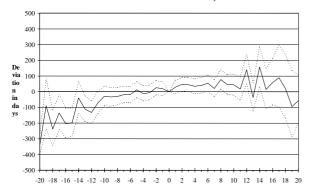
Again, it can be seen that udder depth is more important in the UPRA population and/or when production traits are adjusted for: then, the relative risk curves are somewhat steeper when udder depth gets worse.

3.2.5 Quantifying the effect of type traits on longevity

From these estimates m_i , it is possible to compute expected survival curves for animals with

Figure 8: change in expected length of life as a function of the class of udder depth phenotype : NON UPRA population

(Reference : class « 0 »; Dotted lines = 95% confidence interval)

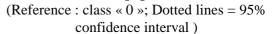


3.2.6 Form of the relationship between type traits and longevity

The previous curves show that the relationship between type traits and longevity is often nonlinear. To depict it more accurately, a weighted regression of the estimates $\hat{\beta}$ on classes of phenotype was performed. The weights were the inverse of the asymptotic error variances supplied by the "Survival Kit". Simultaneously, we checked that these approach gave almost identical results to a direct analysis treating phenotype (and its square, etc...) as a continuous covariate.

For all udder traits, quadratic terms were always significantly different from 0, whatever the population studied. For some traits, in particular teat placement front and teat direction rear, the cubic term was also significant, reflecting a different behaviour on the two extreme directions (for example a rather flat risk on one end). different phenotypes for type traits. These expected curves are the starting points for the calculation of more elaborate measures quantifying the effects of type on longevity. For example, figures 8 and 9 present the change in expected length of life of cows with different udder depth phenotypes. All calculations were done assuming a reference cow in average environmental conditions and with constant lactation length (305d) and calving interval (365d). These changes are expressed with respect to the average ("0") class. For example, a cow with udder depth scored in the "-8" class in an UPRA herd is expected to live 107 days less than a cow in class "0". The corresponding figure for a NON UPRA herd is 30 days. This reflects once more the larger importance of type in UPRA herds.

Figure 9: change in expected length of life as a function of the class of udder depth phenotype : UPRA population



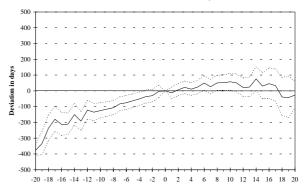
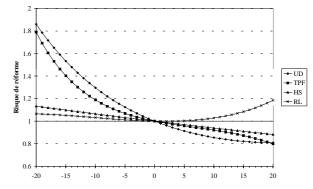


Figure 10: Relative culling risk as a function of phenotype, obtained after regression of $\hat{\beta}$ estimates on class of phenotype (UPRA population; functional longevity)



UD: Udder depth; TPF: teat placement front; HS: Height at sacrum; RL: Rump length

For capacity traits, a polynomial regression of $\hat{\beta}$ on classes of phenotype gave a poorer fit. Significant

quadratic terms were found in the UPRA population and only for true longevity in the NON UPRA herds. Even the linear coefficients were barely significant for Feet and legs. Smoother plots of relative risks as functions of phenotypes were obtained (figure 10)

3.3 Effect of type genotype on longevity

The same analysis as for phenotypes was performed replacing phenotype classes by genotype classes, based on the animal model EBVs of the scored animals. Figures 11 and 12 show the contribution to the likelihood of each trait, for the NON UPRA and UPRA populations, respectively. EBV classes seem to explain a larger part than phenotypic classes of the relationship between type and longevity. But overall, the same comments can be made:

• virtually all type traits are important in UPRA herds;

• udder traits and milking ease are important for longevity, whatever the population considered;

• capacity (size) traits do not influence longevity in the NON UPRA population and their importance is decreased in the UPRA population when production is adjusted for.

Figure 11 : Contribution to the likelihood (x2) of type traits <u>genotype</u> on length of productive life: NON UPRA population (without (in black) and with (in grey) correction for production)

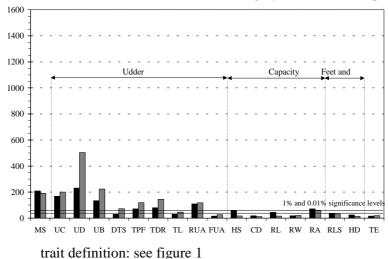
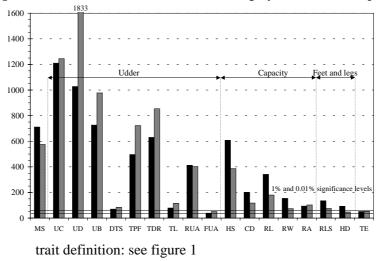


Figure 12 : Contribution to the likelihood (x2) of type traits <u>genotype</u> on length of productive life: UPRA population (without (in black) and with (in grey) correction for production)



4 Conclusion

These relatively detailed analyses of the relationships between type traits and longevity revealed differences between the two Holstein populations considered. These differences are not as pronounced as in the North American situation, for which for some traits, effects in opposite directions or of completely different orders of magnitude were found in the grade and registered populations (Ducrocq, 1996, unpublished results).

In the French situation, for all breeders, cows with a bad udder (in particular deep udder) are at a higher risk. But registered (UPRA) breeders appear more drastic in their culling practices on type. For them, capacity traits are also considered in culling decisions, even after accounting for production. The importance of these traits from a biological point of view seems difficult to justify. Therefore, it may be hypothesised that capacity traits are subject to voluntary culling in this population. Then, production adjusted longevity can no longer be considered as a good approximation of functional longevity, defined as the ability to delay involuntary culling. A direct consequence of this is that a correct estimation of genetic correlations as a tool to find early predictors of longevity should be based on the non registered (NON UPRA) data. Unfortunately, type information is often more scarce in this population.

The correction for production traits reveals some partly hidden relationships between type and longevity. This leads to an even higher contribution of udder traits and a reduction of the importance of traits positively correlated with production, such as some capacity traits.

As suspected, most type traits present a nonlinear relationship with longevity. This nonlinearity is more marked for udder traits. However, we did not find any trait with a clear intermediate optimum and quadratic or higher coefficients were relatively moderate: the computation of genetic correlations assuming linearity between genetic components of type and longevity should not be too much altered.

References

- Brotherstone, S. and Hill, W. G. 1991. Dairy herd life in relation to linear type traits and production.2. Genetic analyses for pedigree and non-pedigree. *Anim. Prod.* 53 : 289-297.
- Dekkers, J. C. M., Jairath, L. K. and Lawrence, B. H. 1994. Relationships between sire genetic

evaluations for conformation and functional herd life of daughters. *Journal of Dairy Science*, 77 : 844-854.

- Dentine, M. R., Mc Daniel B. T. and Norman, H. D. 1987. Comparison of culling rates, reasons for disposal, and yields for registered and grade Holstein cattle. *Journal of Dairy Science*, 70: 2616-2622.
- Ducrocq, V, 1997. Survival analysis, a statistical tool for longevity data. 48th Annual Meeting of the European Association for Animal Production; Vienna, Austria. 3:29.
- Ducrocq, V., and Sölkner, J. 1998a. «The Survival Kit V3.0», a package for large analyses of survival data. *Proc.* 6th World Congr. on Genet. *Appl. to Livest. Prod.*, Armidale, Australia 27: 447-448.
- Ducrocq, V and Sölkner, J 1998b. Implementation of a routine breeding value evaluation for longevity of dairy cows using survival analysis techniques. 6th World Cong. on Genet. Appl To Livest. Prod, Armidale, Australia 23 : 359-362.
- Dürr, J. W., 1997. Genetic and phenotypic studies on culling in Quebec Holstein cows. *PhD. Thesis*, Mc Gill Univ., Montreal, Canada.
- Larroque, H. and Ducrocq V., 1999. An indirect approach for the estimation of genetic correlations between longevity and other traits (these proceedings)
- Short, T. H. and Lawlor, T. J. 1992. Genetic parameters of conformation traits, milk yield, and herd life in Holsteins. *Journal of Dairy Science.*, 75 : 1987-1998.
- Sölkner J. and Petschina R., 1998. Relationship between type traits and longevity in Austrian Simmental. 49th Annual Meeting of the European Association for Animal Production, Warsaw, Poland, 4:177.
- Schneider, M.P., 1998. Effects of type traits on herd life in Holstein cows. *MSc. Thesis*, Mc Gill Univ., Montreal, Canada.
- Vollema, A. 1998. Selection for longevity in dairy cattle. *PhD. Thesis*, Animal Breeding and Genetics Group, Wageningen, The Netherlands.