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Reduced mortality and increased longevity in dairy cattle
Genetic analysis

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Introduction

One goal in the strategy of Danish Cattle has been to reduce calf and cow mortality to 5.5% and 3.5% by the end of 2013. In order to support this objective the project "Reduced mortality and increased longevity in dairy cattle" was initiated and one element of the project was to analysis if a genetic improvement of cow mortality would be possible.

For many years cow longevity has been part of the breeding objective in Denmark and breeding values for longevity are calculated routinely by NAV and incorporated in the Nordic Total Merit index, NTM. In the routine evaluation the definition of longevity is based on both voluntary and involuntary disposal.

If the genetic background is different for voluntary and involuntary culling the genetic evaluation could be improved by including the 2 traits separately. Besides, we know that the economic value of improved longevity due to decreased mortality is higher than of increased longevity due to less involuntary culling. The benefit of separate evaluation of involuntary and voluntary culling would be large.

NB: In this description voluntary culling is assumed to be the same as slaughtered cows and involuntary culling is assumed to be the dead cows

The current genetic evaluation of longevity

The current breeding value for longevity is estimated by evaluation of 5 traits

- Longevity after 1st lactation
- Longevity after 2nd lactation
- Longevity after 3rd lactation
- Longevity after 4th lactation
- Longevity after 5th lactation

Longevity are measured as days from 1st calving to culling (dead or slaughtered), but no lactation counts more than 365 days. If a calving interval is shorter than 365 days then the lactation count 365 days.

The official breeding value for longevity is: Longevity after 3rd lactation. The remaining 4 traits are used only as information traits in order to increase the reliability of the breeding value.

The genetic evaluation is made separately for Holstein, RDC and Jersey. Data from Finland, Sweden and Denmark are included and comprises cows born from 1985 and onward.

Data used

At the outset, the data used in this analysis was the same as used in the routine evaluation of longevity. This includes Danish, Swedish and Finnish data on Danish Holstein, RDC and Jersey born in 1985 and later. However in this analysis on Danish data was used.

For each breed and parity table 1 and 2 give a survey of the destiny of cows that calved in 2008 and in 2012. The main results are:

- Mortality in lowest in 1st lactation – and increasing with age/parity
- Holstein has the highest mortality and RDC the lowest
- The frequency of cows with unknown destiny is high in 2012 – mostly because they are still lactating. Eventually, some of these unknowns will die or be slaughtered.
- Mortality has decreased considerably from 2008 to 2012

Table 1. Destiny of cows calving in 2008

	HOL			RDC			JER		
	1st	2nd	>=3rd	1st	2nd	>=3rd	1st	2nd	>=3rd
Number	126,037	87,588	95,052	14,958	10,513	11,695	20,611	14,477	20,133
Pct survived	72.3	61.2	47.5	69.1	58.5	47.3	75.5	68.9	54.6
Pct unknown	0.2	0.1	0.1	0.2	0.1	0.0	0.3	0.1	0.1
Pct traded/moved	2.9	2.8	3.2	2.9	2.7	2.7	2.5	2.6	3.2
Pct slaghtered	20.2	30.4	40.0	24.6	34.8	43.1	18.6	24.3	33.5
Pct dead	4.3	5.5	9.2	3.2	3.9	6.8	3.2	4.0	8.6
Pct dead, total	6.1			4.5			5.4		

Table 2. Destiny of cows calving in 2012

	HOL			RDC			JER		
	1st	2nd	>=3rd	1st	2nd	>=3rd	1st	2nd	>=3rd
Number	136,857	97,875	108,921	14,293	10,519	11,172	23,317	17,708	23,483
Pct survived	69.7	61.5	46.5	68.3	59.6	45.3	72.5	67.0	53.5
Pct unknown	4.4	3.6	2.4	4.0	3.0	2.3	3.4	2.8	2.5
Pct traded/moved	4.5	3.2	3.0	3.3	2.3	3.0	3.1	3.1	3.6
Pct slaghtered	18.3	27.7	41.2	22.4	32.7	44.3	18.6	24.1	33.7
Pct dead	3.1	4.1	6.8	2.1	2.3	5.1	2.4	2.9	6.7
Pct dead, total	4.5			3.1			4.1		

In figure 1-3 more detailed results are shown for Holstein cows. The result behave “strange” for calving year 20013-14 because the destiny with respect to survival, culling, dead or trade is still unknown. The rate of morality has been increasing up to 2007-08 – but has been decreasing since then.

Figure 4 to figure 9 show addition detailed results for Holstein cows. The figures are shown in pairs. The first of the pair show distribution of dead, culled and traded in percent of the total number (dead + slaughtered + traded) and the second of pair show the distribution of dead, culled and traded at different stages of lactation.

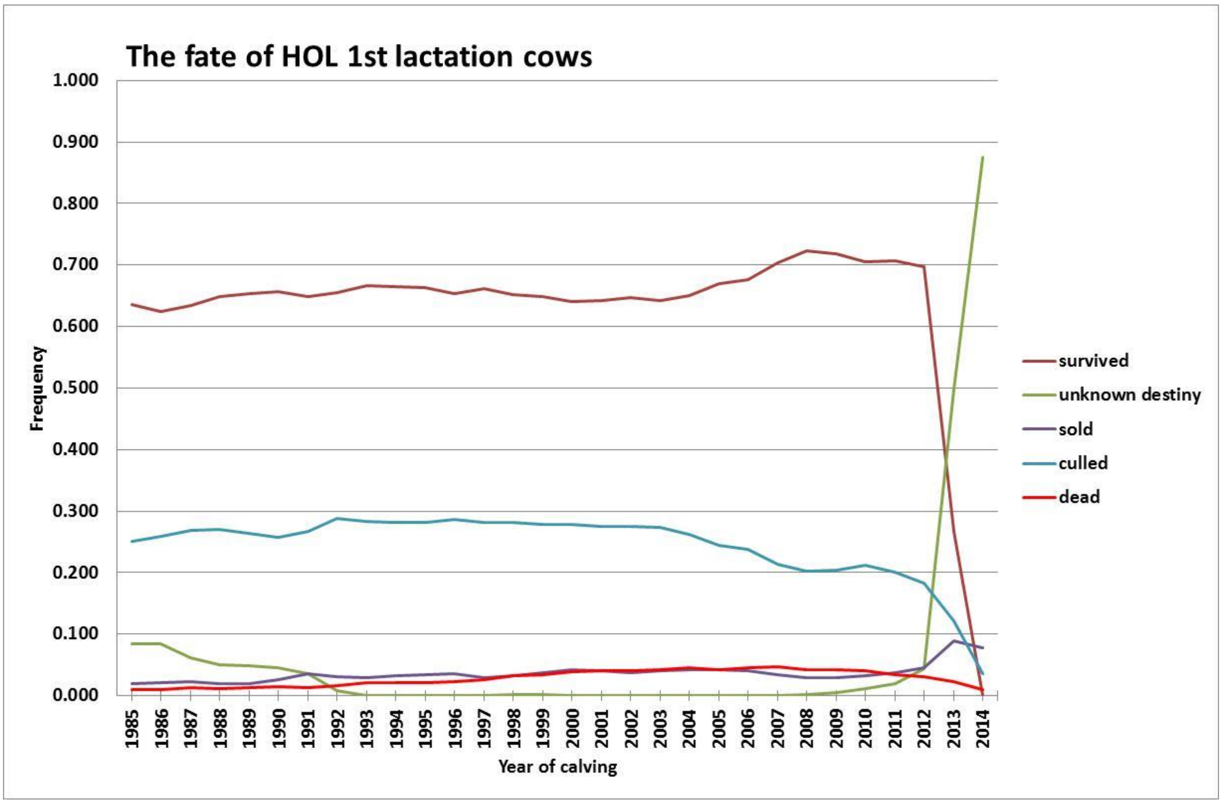

Figure 1. The destiny of 1st parity Holstein cows per year of calving

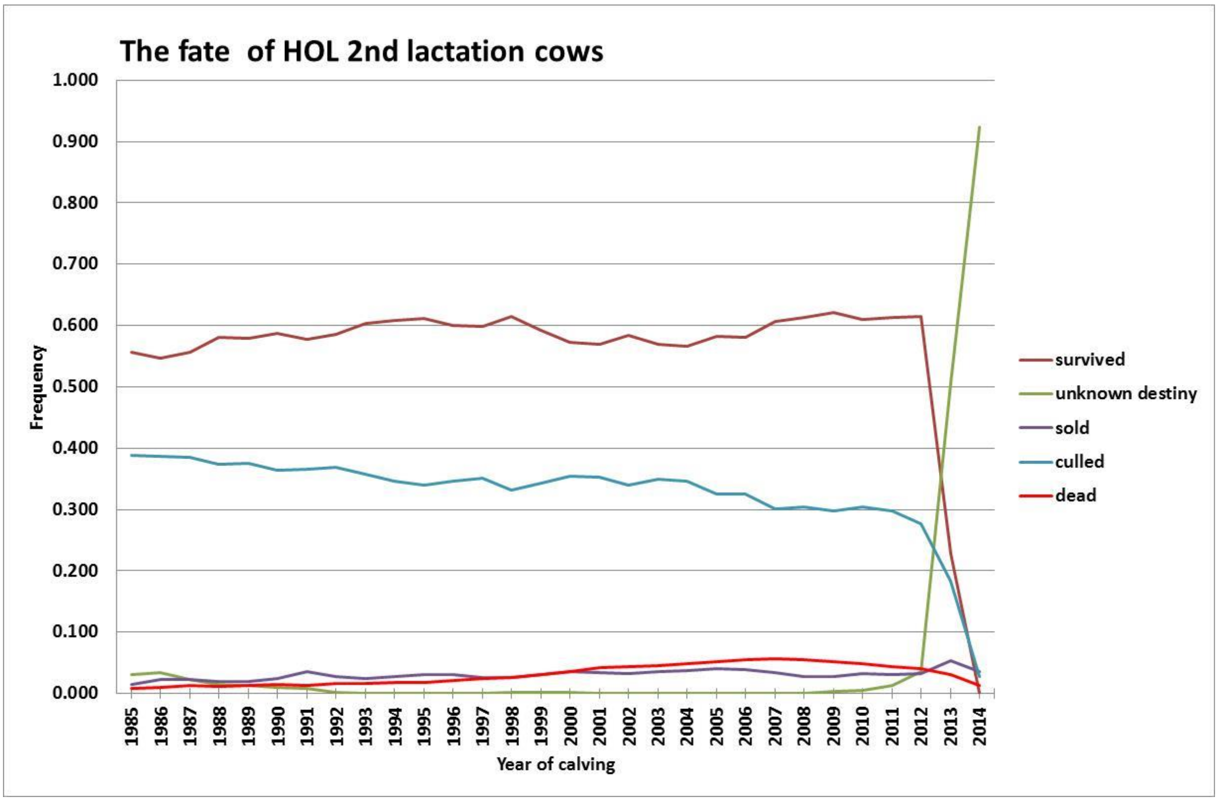

Figure 2. The destiny of 2nd parity Holstein cows per year of calving

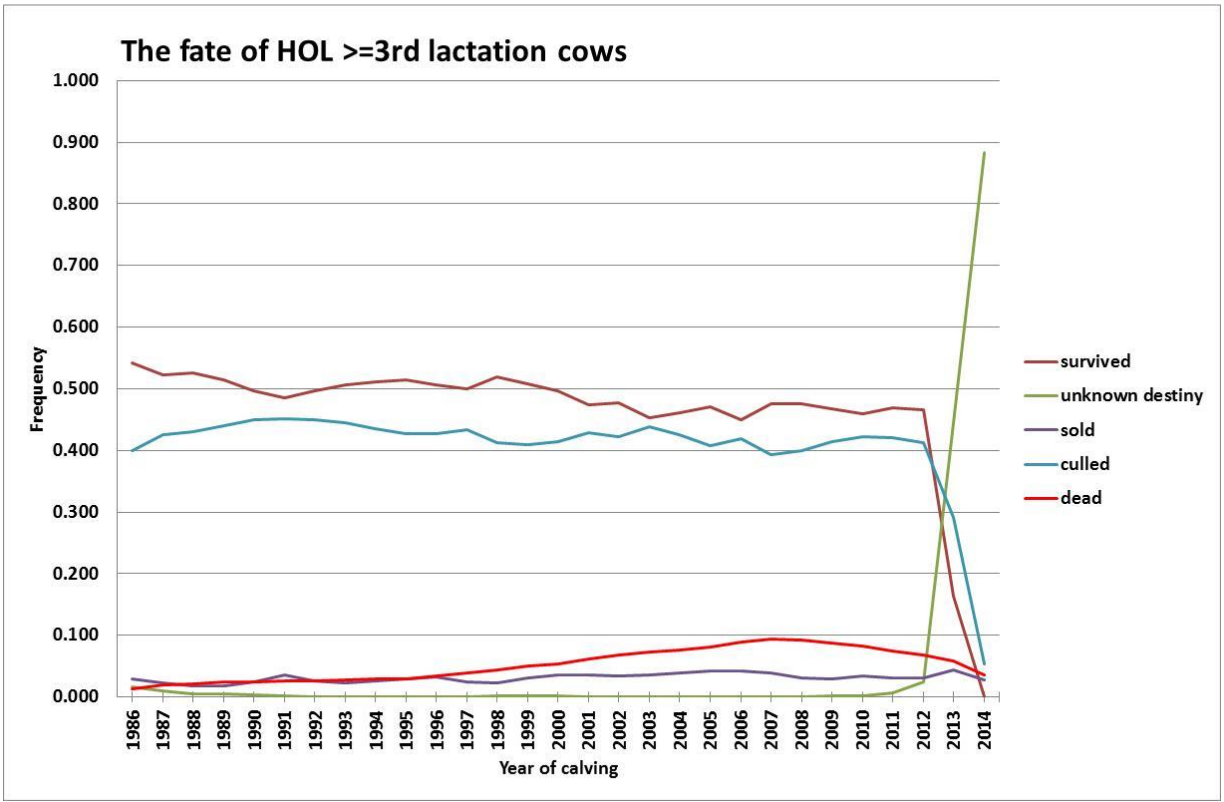

Figure 3. The destiny of 3rd parity Holstein cows per year of calving

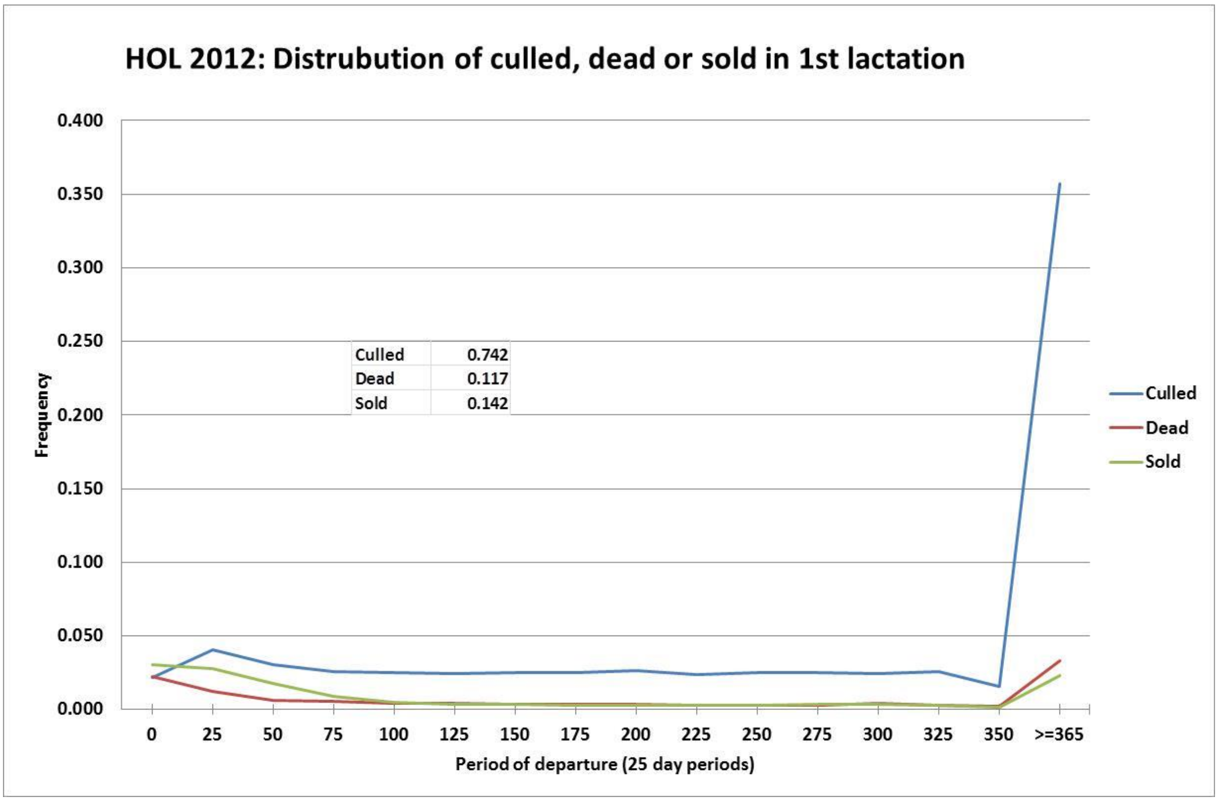

Figure 4. Distribution dead, culled or traded 1st parity Holstein cows relative to the total number

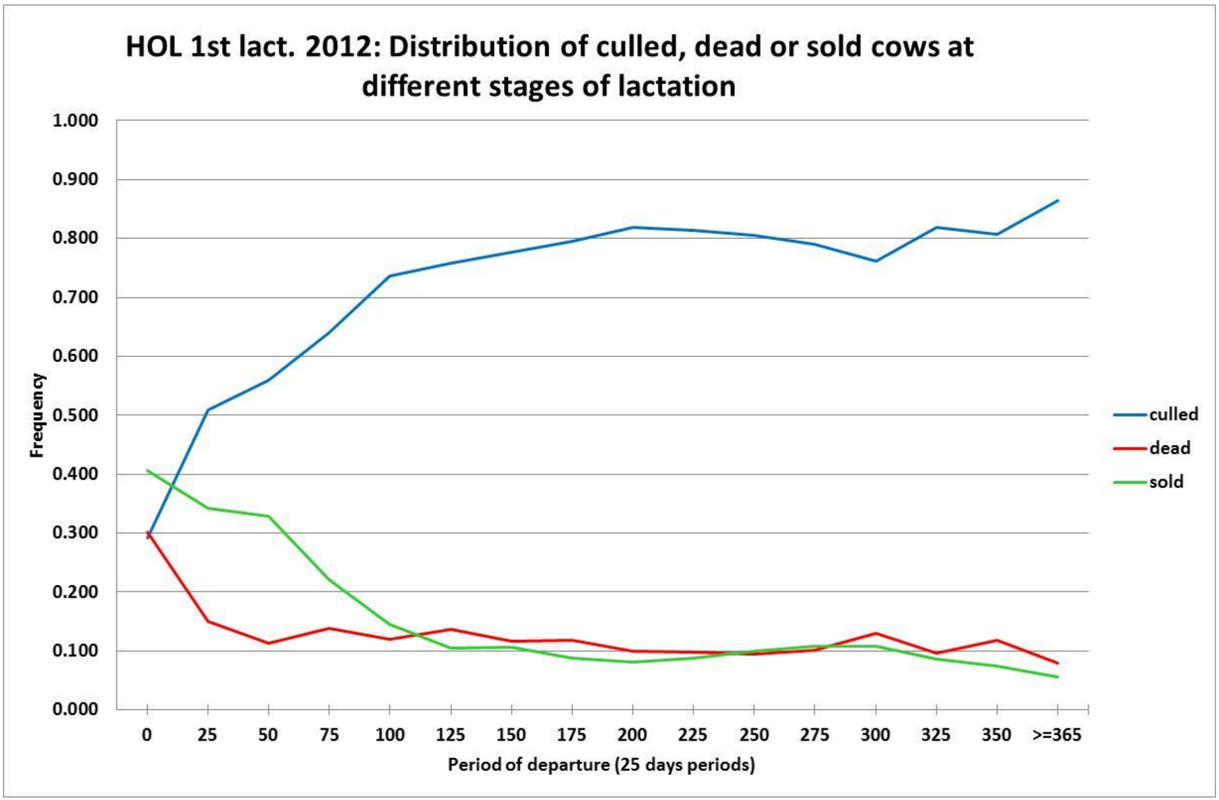

Figure 5. Distribution dead, culled or traded 1st parity Holstein cows at different stages of the lactation

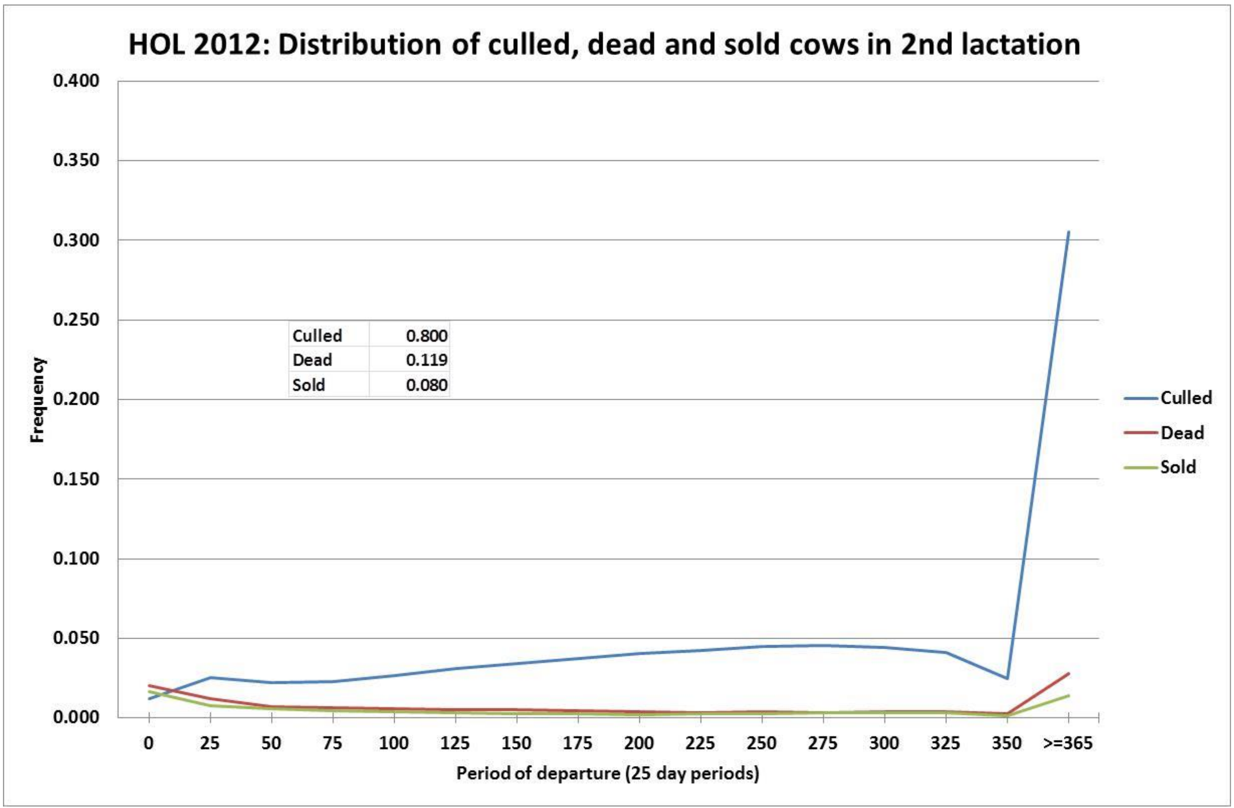

Figure 6. Distribution dead, culled or traded 2nd parity Holstein cows relative to the total number

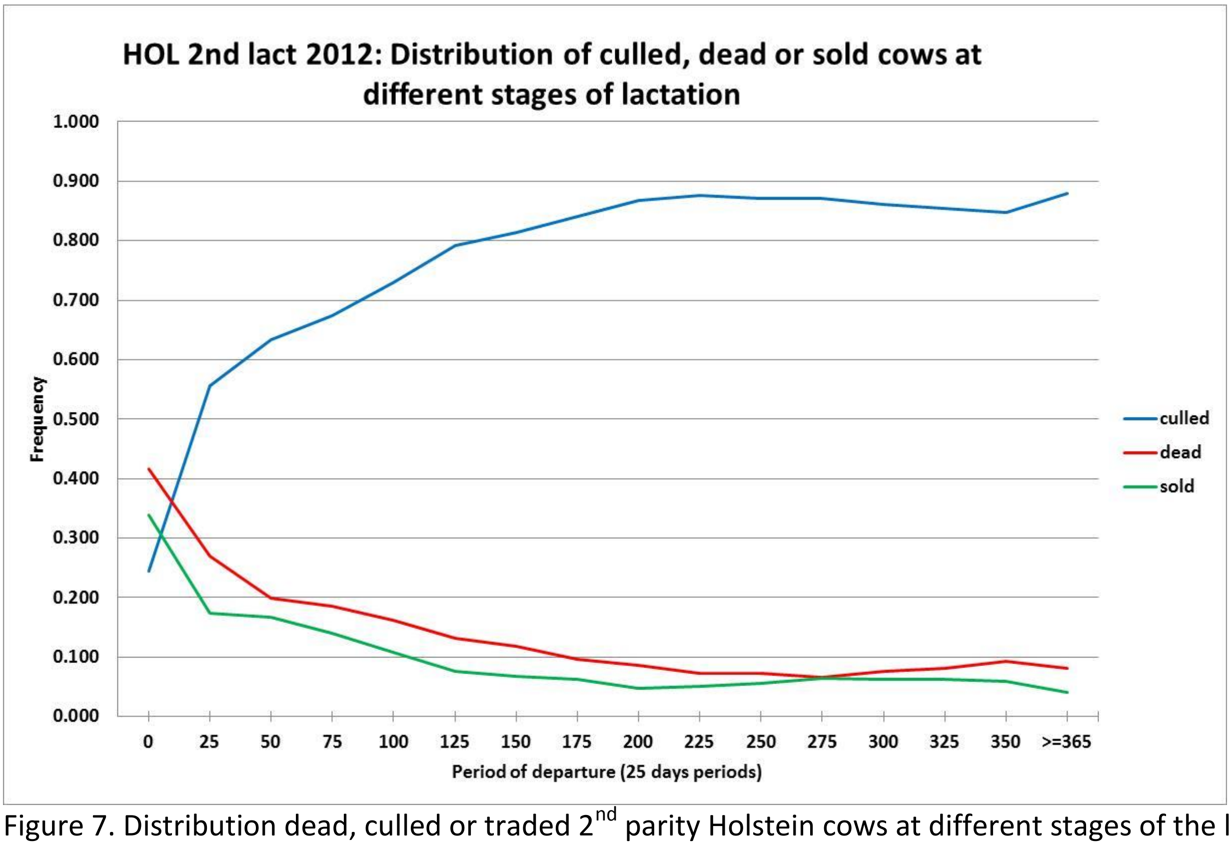

Figure 7. Distribution dead, culled or traded 2nd parity Holstein cows at different stages of the lactation

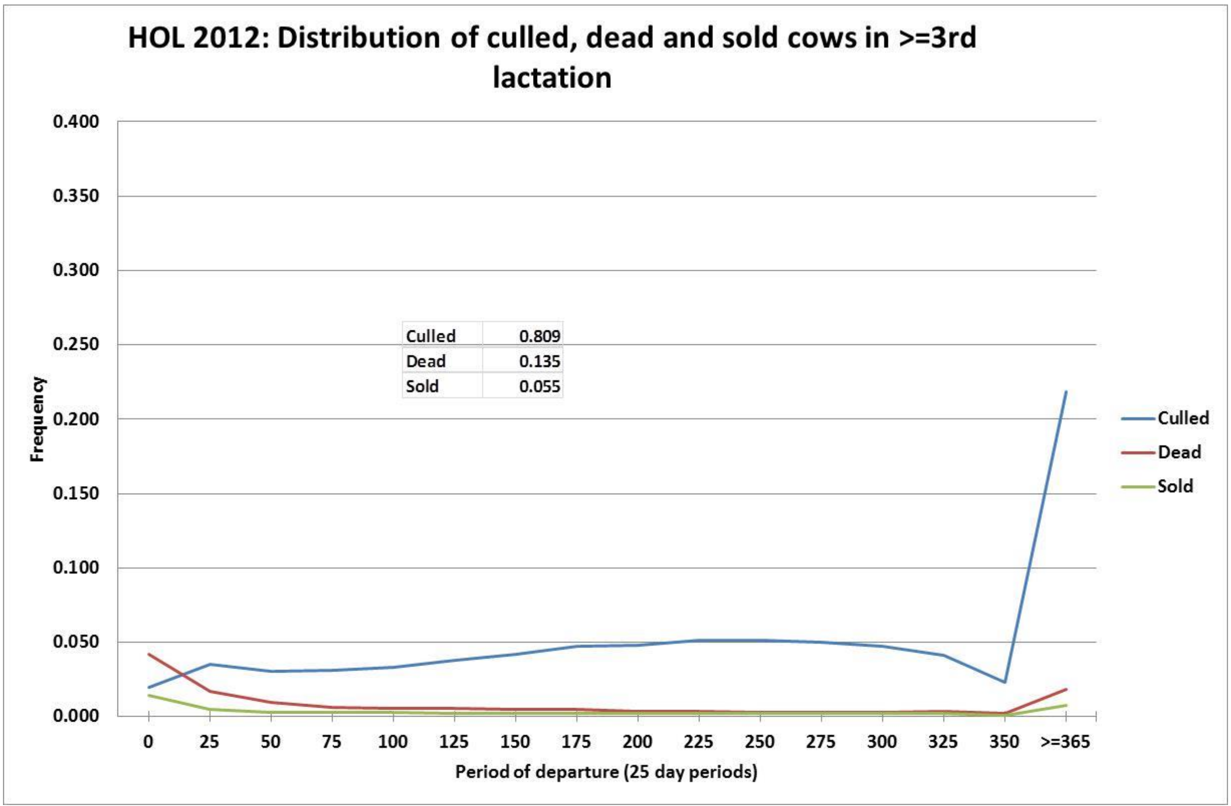

Figure 8. Distribution dead, culled or traded >=3rd parity Holstein cows relative to the total number

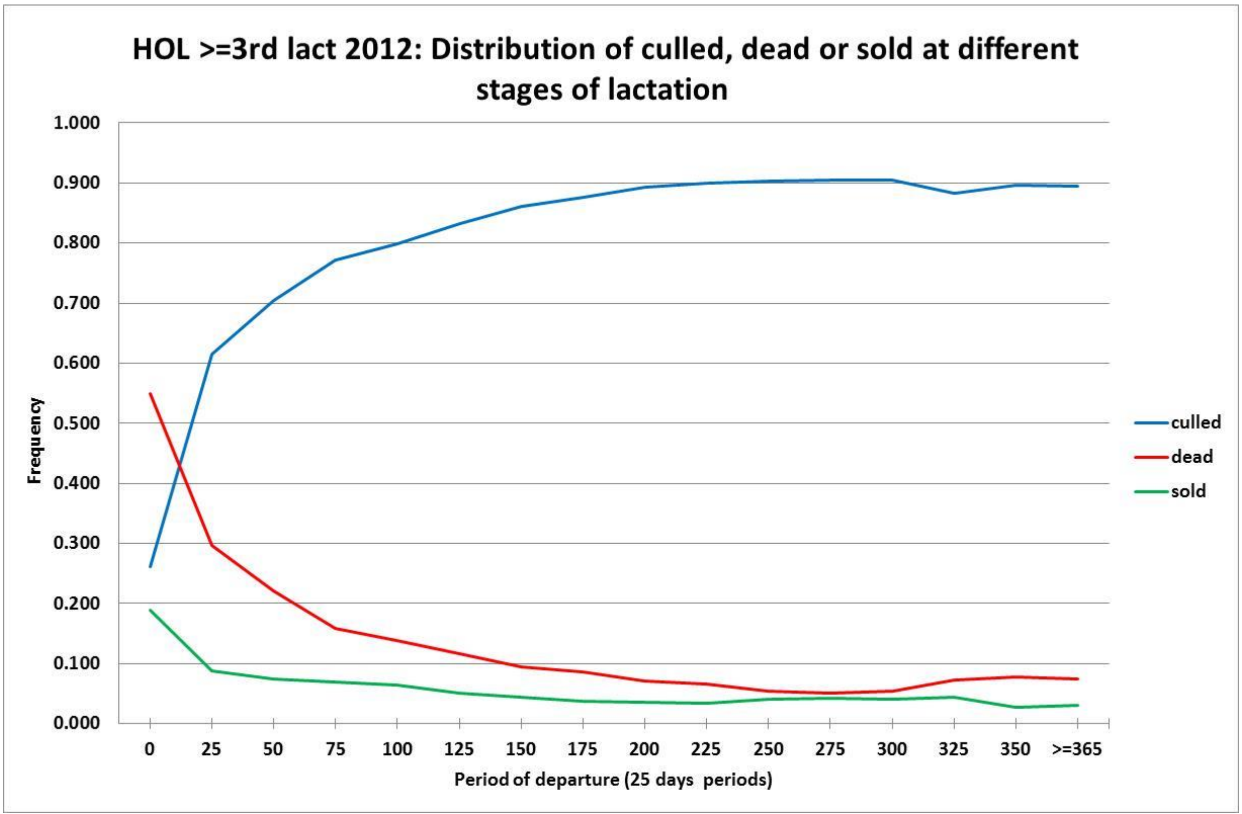

Figure 9. Distribution dead, culled or traded >=3rd parity Holstein cows at different stages of the lactation

Linear model adapted from the genetic evaluation of longevity

Alternative I

The most simple approach to this problem was to start with the routine evaluation of longevity and subdivide all 5 traits onto 2 traits: Longevity based on dead (and killed) cows and longevity based on slaughtered cows.

Longevity after xth lactation (C-longevity refer to longevity due to slaughter, D-longevity refer to longevity due to death and the subscript refer to trait number 1-5):

- Oppportunity period: Data is included if 1st calving is before date of data extraction – x * 365
- If the cow survive xth lactation then:
  - C-longevity$_x$ = x * 365
  - D-longevity$_x$ = x * 365
- If the cow do not survive xth lactation then:
  - If slaughtered:
    - C-longevity$_x$ = date of culling – date of 1st calving (max 365 days/lactation)
    - D-longevity$_x$ = .
  - If dead:
    - C-longevity$_x$ = .;
    - D-longevity$_x$ = date of culling - date of 1st calving (max 365 days/lactation)

Alternative II

Alternative II is very similar to alternative I, but it this alternative all traits are defined as binary traits:

Survival after xth lactation: (C-survival refer to survival due to slaughter, D-survival refer to survival due to death and the subscript refer to trait number 1-5):

- Oppportunity period: Data is included if 1st calving is before date of data extraction – x * 365
- If the cow survive xth lactation then:
  - C-survival$_x$ = 1
  - D-survival$_x$ = 1
- If the cow do not survive xth lactation then:
  - If slaughtered:
    - C-survival$_x$ = 0
    - D-survival$_x$ = .
  - If dead:
    - C-survival$_x$ = .;
    - D-survival$_x$ = 0

This alternative was tested because:

- The DMUAI runs for alternative I showed poor convergence properties. They were better for alternative II
- A second reason is that many cows are culled after day 365 (30-50%). The consequence is that a many of the cows has longevity records that are a multiple of 365 days. Therefore the similarity of the two alternatives is quite large.

Model for parameter estimation (JER)

C-survival = Proportion of DJ + DJxUSJ-heterosis + age at 1st calving + year x month 1st calving + herd x year 1st calving + sire

D-survival = Proportion of DJ + DJxUSJ-heterosis + age at 1st calving + year x month 1st calving+ herd x year 1st calving + sire

Type of effects

- Proportion of DJ: Regression
- DJxUSJ-heterosis: Regression
- Age at 1st calving: Fixed classes
- Year x month of 1st calving: Fixed
- Herd x year 1st of 1st calving: Fixed (or random)
- Sire: Random genetic effect

Problem in alternative I and II

Parameter estimation in both alternative I and II have one problem: The residual correlation between C-survival and D-survival (or C-longevity and D-longevity) will be based on observations where both C-survival and D-survival is defined. However, in that case C-survival and D-survival always have the same value (365 in alternative I and 1 in alternative II) and the estimate of the residual correlation will be 1.0.

The conclusion is that the model parameters for the relationships between C-survival and D-survival cannot be estimated with the trait definitions used in alternative I and II – unless some additional restrictions are applied.

Restrictions used

When relationship between C- and D-survival are included in the model, it is assumed that the residual correlation between C- and D-survival is 0. The herd x year is effect defined as random. For this (environmental) effect the correlation between C- and D-survival can be estimated.

Model versions

The 10 traits was first analysed in single trait analyses. Then three versions of a multi-trait model have been analysed:

- Version 1: 5-trait analysis within trait groups (D-longevity and C-longevity). The results for this version are – to some degree – comparable with the parameter estimates used in the routine evaluation.
- Version 2: Multi-trait analysis of all 10 traits. For this run the dataset should be reduced in order to run.

Results

I table 3 Jersey results for heritability are shown for C- and D-longevity (alternative I). I table 4 similar for C- and D-survival (alternative II) is shown.

The original estimates from 2009 of Jersey h^2 of longevity was 0.035, 0.051, 0.060, 0.063 and 0.064 for the five traits respectively (most comparable with version 1 results)

Table 3. Some estimates of model parameters for Jersey cow survival defined as a longevity (alternative I)

Trait	**no**	**Avg.**	**Single trait estimates**						**Multi trait estimates**	
			V(S)	**V(HY)**	**V(R)**	**SD(G)**	**SD(E)**	**h^2**	**Ver. 1**	**Ver. 2**
C-long$_1$	**1**	335	70	75	6023	*17*	*77*	**0.046**	0.027	0.036
C-long$_2$	**2**	578	709	642	44526	*53*	*207*	**0.062**	0.029	0.051
C-long$_3$	**3**	735	2190	1880	120772	*94*	*341*	**0.070**	0.034	0.061
C-long$_4$	**4**	826	4178	3324	211872	*129*	*450*	**0.076**	0.038	0.068
C-long$_5$	**5**	872	6019	4653	291981	*155*	*528*	**0.080**	0.041	0.073
D-long$_1$	**6**	359	3	18	1763	*4*	*42*	**0.007**	0.007	0.008
D-long$_2$	**7**	698	82	206	14995	*18*	*121*	**0.022**	0.016	0.017
D-long$_3$	**8**	994	861	956	59784	*59*	*239*	**0.057**	0.028	0.028
D-long$_4$	**9**	1208	4107	3084	159398	*128*	*384*	**0.100**	0.041	0.039
D-long$_5$	**10**	1307	10486	7146	308184	*205*	*526*	**0.132**	0.051	0.050

Table 4. Some estimates of model parameters for Jersey survival – defined as binary traits (alternative II)

Trait	**no**	**p**	**Single trait estimates**						**Multi trait estimates**	
			100 * V(S)	**100* V(HY)**	**V(R)**	**SD(G)**	**SD(E)**	**h^2**	**Ver. 1**	**Ver. 2**
C-sur$_1$	**1**	**0.76**	*0.170*	*0.211*	0.172	*0.082*	*0.412*	**0.039**	0.035	0.038
C-sur$_2$	**2**	**0.53**	*0.316*	*0.283*	0.235	*0.112*	*0.478*	**0.053**	0.050	0.062
C-sur$_3$	**3**	**0.34**	*0.315*	*0.221*	0.212	*0.112*	*0.453*	**0.058**	0.059	0.070
C-sur$_4$	**4**	**0.20**	*0.144*	*0.644*	0.154	*0.076*	*0.395*	**0.036**	0.054	0.066
C-sur$_5$	**5**	**0.11**	*0.092*	*0.090*	0.093	*0.061*	*0.301*	**0.039**	0.046	0.059
D-sur$_1$	**6**	**0.97**	*0.005*	*0.031*	0.030	*0.014*	*0.174*	**0.007**	0.008	0.011
D-sur$_2$	**7**	**0.92**	*0.047*	*0.078*	0.072	*0.044*	*0.266*	**0.026**	0.018	0.027
D-sur$_3$	**8**	**0.82**	*0.160*	*0.122*	0.132	*0.080*	*0.356*	**0.048**	0.026	0.031
D-sur$_4$	**9**	**0.68**	*0.388*	*0.215*	0.184	*0.125*	*0.416*	**0.082**	0.036	0.045
D-sur$_5$	**10**	**0.50**	*0.495*	*0.353*	0.197	*0.141*	*0.427*	**0.098**	0.040	0.052

Notes: p for culled cows = survived/(survived + culled)), p for dead cows = survived/(survived + dead))

In table 5 genetic and environmental correlations are shown for model version 1 (within trait group correlations). The environmental variances and covariances include HY-variances. For C-survival the correlations are quite similar to those used in the routine evaluation. The correlation between the D-survival traits are very high (higher than between the C-survival traits)

In table 6 the results from the version 2 model are shown.

- The environmental correlations within the 2 traits groups are very similar to those estimated within trait groups estimates separately (table 5).
- The environmental correlations between C-survival and D-survival are close to 0.

- Also the genetic correlations between the C-survival traits are similar to those estimated in Version 1, the within traits group estimates.
- Between the D-survival traits the genetic correlations were lower than I version 1 (within trait group estimates).
- The genetic correlations between C-survival and D-survival are between 0.64 and 0.83 – the highest correlations are between corresponding traits, eg C-survival$_3$ and D-survival$_3$.

Table 5. Estimates of correlations from the alternative II version 1 model. (within trait group analysis). Genetic correlations are above diagonal and environmental correlations below diagonal

		C-sur$_1$	C-sur$_2$	C-sur$_3$	C-sur$_4$	C-sur$_5$	D-sur$_1$	D-sur$_2$	D-sur$_3$	D-sur$_4$	D-sur$_5$
	Traitno	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
C-sur$_1$	1		0.97	**0.90**	0.83	**0.77**					
C-sur$_2$	2	0.58		0.98	0.94	0.90					
C-sur$_3$	3	**0.40**	0.68		0.99	**0.97**					
C-sur$_4$	4	0.28	0.48	0.71		0.99					
C-sur$_5$	5	**0.20**	0.34	0.50	0.72						
D-sur$_1$	6							1.00	**0.98**	0.95	**0.91**
D-sur$_2$	7						0.66		0.99	0.97	0.94
D-sur$_3$	8						**0.45**	0.69		0.99	**0.98**
D-sur$_4$	9						0.34	0.51	0.74		0.99
D-sur$_5$	10						**0.27**	0.41	**0.59**	0.80	

Table 6. Estimates of correlations from the alternative II, version 2 of the model. Genetic correlations are above diagonal and environmental correlations below diagonal

		C-sur$_1$	C-sur$_2$	C-sur$_3$	C-sur$_4$	C-sur$_5$	D-sur$_1$	D-sur$_2$	D-sur$_3$	D-sur$_4$	D-sur$_5$
	Traitno	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
C-sur$_1$	1		**0.97**	**0.90**	**0.84**	**0.78**	**0.74**	**0.71**	**0.70**	**0.66**	**0.64**
C-sur$_2$	2	0.59		**0.98**	**0.94**	**0.90**	**0.79**	**0.79**	**0.80**	**0.77**	**0.75**
C-sur$_3$	3	0.40	0.68		**0.99**	**0.96**	**0.76**	**0.77**	**0.82**	**0.80**	**0.79**
C-sur$_4$	4	0.28	0.47	0.70		**0.99**	**0.74**	**0.76**	**0.82**	**0.82**	**0.81**
C-sur$_5$	5	0.20	0.33	0.49	0.71		**0.71**	**0.75**	**0.81**	**0.82**	**0.83**
D-sur$_1$	6	0.00	-0.01	-0.02	-0.01	-0.02		**0.98**	**0.96**	**0.93**	**0.88**
D-sur$_2$	7	-0.01	-0.02	-0.03	-0.02	-0.02	0.65		**0.72**	**0.72**	**0.89**
D-sur$_3$	8	-0.02	-0.02	-0.03	-0.02	-0.02	0.45	0.69		**0.73**	**0.91**
D-sur$_4$	9	-0.02	-0.03	-0.04	-0.03	-0.03	0.33	0.51	0.74		**0.92**
D-sur$_5$	10	-0.02	-0.03	-0.04	-0.03	-0.03	0.26	0.40	0.59	0.80	