NAV longevity evaluation
Data edit, model development and validation

Jørn Pedersen
Jan-Åke Eriksson, Minna Toivonen, Jukka Pösö, Ulrik Sander Nielsen, Gert Pedersen Aamand

Content

Introduction

The dairy cattle breeds in Sweden, Finland and Denmark have for many years evaluated longevity. The Danish and Finnish evaluations are quite similar and calculated by "Survival Kit", a French evaluation system based on a Weibull frailty model (reference). In both countries the so-called "functional longevity" is published, i.e. the longevity is corrected for effect of yield level. Sweden has used a linear evaluation of survival up to 4th lactation in a multi trait model that includes survival to 2nd and 3rd lactation as information trait (all 3 are binary traits evaluated in a linear model). Correction for milk production is not included in the model, i.e. it is the so-called "productive longevity".

When the NTM was introduced in NAV in 2008 a common evaluation of longevity had not yet been developed and therefore an average of longevity indexes from the three countries has been used in the calculation of NTM.

This was not a satisfactory solution and a project on development of common NAV-longevity index started in the autumn of 2008. At the outset of the project there was an evaluation of the following problems related to longevity.

Functional or productive longevity

It has been decided that NAV should evaluate longevity as productive longevity and not as functional longevity. Correction for other traits such as yield, fertility or mastitis should not be included

Type of model

The "real" survival models are theoretically the best type of models and should be able to utilize data most effective. Longevity is usually the last index to obtain a proper accuracy and the last index to be published. Therefore this quality is quite important. However, the edb programs available for survival models were very inflexible and resource demanding with respect to computer size and computing time

The linear models are more easy to use, much more flexible with respect to definition of model and multiple trait evaluation is possible. The drawback is that there are very strict requirement on input data. Therefore accurate breeding value is not available before late in the sire's life.

The result of this evaluation at the outset of the project was that we should focus on development of linear model for the following 5 traits:

- Days from 1st calving to end of 1st lactation – including at maximum 365 days in 1st lactation
- Days from 1st calving to end of 2nd lactation – including at maximum 365 days per lactation
- Days from 1st calving to end of 3rd lactation – including at maximum 365 days per lactation
- Days from 1st calving to end of 4th lactation – including at maximum 365 days per lactation
- Days from 1st calving to end of 5th lactation – including at maximum 365 days per lactation

Other basic decision

- Separate evaluation for three breed groups: RDC, HOL, JER
- DRH and FIC: DRH included in HOL and FIC in RDC evaluation

- In Finland RDC included in HOL-evaluation – and HOL included in RDC-evaluation
- Same genetic parameters across countries – if possible
- An animal model should be used, possible
- The model should include random Herd x year – and fixed herd x time period effects, if possible

Data description

General edit of input data

The data delivered from each country consists on data on all calvings and cullings from:

- Denmark: From 1985 and onward
- Sweden: 1982 and onward. However some Swedish data are missing in the very first years. Therefore it was decide to delete data on Swedish cows starting their 1st lactation before 1985
- Finland: Data from 1988 (?) and onward.

The data received are edited and checked in various ways. Table 1 shown then number of records deleted from original files. There

1. The files received include all parities. However only parity 1 to 5 are used for the final definition of longevity traits
2. Calving date below limit: The limits are 1.1.1985 for DNK and SWE and 1.1.1988 for FIN
3. It is required that the all cows included start with parity 1 – and that the following parities are sequential. However, if the first 3 parities are in correct sequence only the following parities are deleted, but the culling date and culling reason are of cause assumed to be unknown.
4. In Denmark unknown birth dates was relatively common in data from before 1997
5. The limits on age at 1st calving applied are: 450 to 1280 days

Table 1. Edit of data received from Denmark, Finland and Sweden (Aug 2010)

	Origin of data		
	DNK	FIN	SWE
Received records, number of calvings (1)	14,298,758	8,673,327	8,086,418
	Deleted records		
Missing parity number	1,218	0	0
No herd identification	786	4,441	0
Calving date below limit (2)	0	2,352,864	299,186
Double parity number	0	352	0
Parity number not sequential (3)	2,593,679	624,096	336,953
Calving dates not sequential	123	47	0
Calving date after extraction date	3	0	0
Logic culling data	0	0	0
Not in NAV pedigree file	530	2	1,495
No birth date (4)	137,110	0	0
Too low or too high calving age (5)	57,976	11,587	37
	Remaining records		
	11,507,333	5,679,938	7,448,747
	Subdivision according to breed		
RDC	1,243,488	4,167,494	3,994,156
HOL	7,737,082	1,453,716	3,329,740
JER	1,555,822	0	49,265
RED(DNK) or FIC(FIN)	120,655	58,728	0
Other/Unknown/Crosses	850,286	0	75,586

Note: These data can be used for a further edit toward both the survival model and the linear model

Edit for the linear longevity model
Table 2 show the outcome of the next step of the editing procedure for the linear longevity model. This includes:

- Merging of data into the predefined evaluation groups
- Deletion of records after a herd change (assuming culling date and culling reason unknown)
- Deletion of events after 5th parity
- Definition of the 5 linear longevity traits where an important factor is the definition opportunity periods

Table 2. Edit of data for the linear longevity model (Aug 2010)

	Evaluation group		
	RDC	HOL	JER
DNK data	1,243,488	7,737,082	1,555,822
SWE data	3,994,156	3,329,740	49,265
FIN HOL data	1,453,716	1,453,716	0
FIN RDC data	4,167,494	4,167,494	0
DNK RED data	0	120,655	0
FIN FIC data	58,728	0	0
Total	10,917,582	16,808,687	1,605,087
	After edit for herd changes		
Final number of parities	10,634,967	16,327,113	1,532,034
Final number of cows	4,151,164	6,799,801	622,800
	Number of cows after edit for opportunity period		
1Y-longevity	3,455,611	5,833,372	518,621
2Y-longevity	3,144,048	5,326,560	469,765
3Y-longevity	2,852,267	4,866,868	426,427
4Y-longevity	2,581,540	4,436,088	386,824
5Y-longevity	2,336,268	4,030,734	349,883
	Average of input data		
1Y-longevity	331.9	329.5	329.6
2Y-longevity	575.5	558.1	553.5
3Y-longevity	733.8	698.7	696.1
4Y-longevity	825.3	776.8	782.4
5Y-longevity	873.6	816.5	832.3

Definition of opportunity periods

The purpose of the opportunity periods are to ensure that all cows of same age have had the opportunity to present a record. The definition of opportunity period is based on "newest date" in data. For most cows "newest date" is date of data extraction, but for cows in herds that have closed down at some point in time the newest date must be defined otherwise.

The definition of "newest date" is:

- Herds still operation: Date of data extraction
- Herds closed down:
  - 2 years prior to the date of last 1st calving is the basis. A 2 year period is chosen because the closed down of a herd in many cases is a decision made long time before the actual closing, and because this decision will affect the culling practices
  - The 2 year period do not apply for herds where the last 1st calving is within the latest 2 years. For herd that has closed down within the last 2 years it is not possible to define a special "newest date".

Then no data are included with a 1st calving later than

- 1 year longevity(1Y) : "Newest date" – 365
- 2 year longevity(2Y) : "Newest date" – 365 * 2
- 3 year longevity(3Y) : "Newest date" – 365 * 3
- 4 year longevity(4Y) : "Newest date" – 365 * 4
- 5 year longevity(5Y) : "Newest date" – 365 * 5

Definition of longevity traits

- 1 year longevity(1Y):
  - 1st lactation:
    - Distance from 1st calving to culling
    - 365 days if the cow is culled after 1st lactation

- 2 year longevity(2Y): Sum of
  - 1st lactation:
    - Distance from 1st calving to culling
    - 365 days if the cow is culled after 1st lactation
  - 2nd lactation:
    - 0 if the cow is culled before 2nd
    - Distance from 2nd calving to culling
    - 365 if the cow is culled after 2nd

- 3 year longevity(3Y): Sum of
  - 1st lactation:
    - Distance from 1st calving to culling
    - 365 days if the cow is culled after 1st lactation
  - 2nd lactation:
    - 0 if the cow is culled before 2nd
    - Distance from 2nd calving to culling
    - 365 if the cow is culled after 2nd
  - 3rd lactation:

    - 0 if the cow is culled before 3rd
    - Distance from 3rd calving to culling
    - 365 if the cow is culled after 3rd

- 4 year longevity(4Y): Sum of
  - 1st lactation:
    - Distance from 1st calving to culling
    - 365 days if the cow is culled after 1st lactation
  - 2nd lactation:
    - 0 if the cow is culled before 2nd
    - Distance from 2nd calving to culling
    - 365 if the cow is culled after 2nd
  - 3rd lactation:
    - 0 if the cow is culled before 3rd
    - Distance from 3rd calving to culling
    - 365 if the cow is culled after 3rd
  - 4th lactation:
    - 0 if the cow is culled before 4th
    - Distance from 4th calving to culling
    - 365 if the cow is culled after 4th

- 5 year longevity(5Y): Sum of
  - 1st lactation:
    - Distance from 1st calving to culling
    - 365 if the cow is culled after 1st lactation
  - 2nd lactation:
    - 0 if the cow is culled before 2nd
    - Distance from 2nd calving to culling
    - 365 if the cow is culled after 2nd
  - 3rd lactation:
    - 0 if the cow is culled before 3rd
    - Distance from 3rd calving to culling
    - 365 if the cow is culled after 3rd
  - 4th lactation:
    - 0 if the cow is culled before 4th
    - Distance from 4th calving to culling
    - 365 if the cow is culled after 4th
  - 5th lactation:
    - 0 if the cow is culled before 5th
    - Distance from 5th calving to culling
    - 365 if the cow is culled after 5th

Statistics on input data

Table 3, 4 and 5 show the number of records (cows) included in the August 2010 evaluation. Over years the total number has been reduced by 30%, 20% and 10% for Jersey, RDC and Holstein, respectively, such that number of new records per year is 21.000 for Jersey, 140.000 for the RDC evaluation and 260.000 for the Holstein evaluation.

I figure 1, 2 and 3 are shown the development in average 1Y-, 3Y- and 5Y-longevity input data (not the same as total longevity). Simple linear regression analyses of input on year of 1st calving are shown in table 6. It demonstrated a negative development in longevity in both Finnish RDC and HOL. In Swedish data there has be a positive development for 1Y-, 2Y- and 3Y longevity, whereas 4Y- and 5Y-longevity has decreased most in HOL. In Danish RDC and HOL the development has generally been positive, mostly in RDC. In Danish Jersey the development has been mostly negative.

Table 3. Number of cows included in RDC evaluation of longevity (Aug 2010)

Year of 1st calving	DNK	FIN	SWE	FIN FIC	FIN HOL	Total
1985	29,250		70,683			99,933
1986	31,108		71,571			102,679
1987	28,424		70,821			99,245
1988	28,028	65,190	70,811	923	15,447	180,399
1989	26,942	69,072	72,296	897	16,760	185,967
1990	26,593	71,526	69,980	877	17,982	186,958
1991	25,966	71,064	64,224	835	18,413	180,502
1992	24,999	73,134	65,199	860	19,246	183,438
1993	23,715	71,393	62,173	837	20,277	178,395
1994	23,401	72,648	62,140	835	20,589	179,613
1995	22,774	72,473	62,479	934	21,569	180,229
1996	21,602	72,452	62,870	935	22,361	180,220
1997	21,577	74,173	60,796	991	23,352	180,889
1998	21,213	72,988	61,362	1,089	24,043	180,695
1999	21,520	70,126	58,643	1,008	23,849	175,146
2000	21,019	69,119	57,579	1,151	24,764	173,632
2001	19,414	73,560	57,099	1,106	27,804	178,983
2002	18,484	69,072	54,687	1,112	27,384	170,739
2003	18,462	66,924	55,044	1,023	27,234	168,687
2004	17,705	65,294	52,641	1,020	28,619	165,279
2005	16,358	61,713	50,559	1,076	28,154	157,860
2006	16,346	58,946	50,559	966	28,075	154,892
2007	15,436	56,567	46,190	1,000	28,292	147,485
2008	14,904	55,030	45,483	1,131	29,029	145,577
2009	15,020	51,774	42,506	958	28,327	138,585
2010	6,339	21,730	15,833	398	12,788	57,088

However, we cannot expect that these results for raw average of input data are reflected in the breeding values. The average of input data are not expected to change very much even if breeding value for longevity is improved, because improved genetic level of longevity will in practise give room for in a stronger selection – In “model-terms” it means that the environmental factors become more harsh.

If we apply a strong genetic selection on longevity and obtain a positive genetic trend then we must expect a corresponding negative environmental trend, because the phenotypic level will remain fairly constant. *(Except if the improved genetic level results in a stronger selection among heifers – or more intense use of sexed seemen/crossing with beef breeds)*

Table 4. Number of cows included in HOL evaluation of longevity (Aug 2010)

Year of 1st calving	DNK	FIN	SWE	DRH	FIN RDC	Total
1985	121,921		46,739	2,020		170,680
1986	131,573		47,400	2,031		181,004
1987	132,746		48,639	1,943		183,328
1988	133,466	15,446	50,188	1,993	65,187	266,280
1989	133,352	16,760	51,229	2,017	69,072	272,430
1990	134,406	17,982	51,420	1,949	71,526	277,283
1991	136,110	18,413	47,862	2,080	71,063	275,528
1992	134,374	19,245	50,001	1,936	73,132	278,688
1993	130,764	20,277	48,173	1,924	71,392	272,530
1994	129,532	20,589	50,187	1,906	72,647	274,861
1995	127,943	21,569	51,508	1,904	72,472	275,396
1996	129,365	22,360	52,346	2,029	72,448	278,548
1997	135,557	23,350	53,141	2,023	74,172	288,243
1998	133,040	24,043	55,360	2,105	72,988	287,536
1999	138,036	23,849	54,757	2,428	70,126	289,196
2000	141,285	24,763	54,518	2,428	69,119	292,113
2001	137,376	27,804	54,876	2,286	73,560	295,902
2002	136,037	27,384	53,973	2,217	69,072	288,683
2003	136,046	27,234	53,736	2,214	66,924	286,154
2004	134,232	28,618	54,250	2,244	65,294	284,638
2005	128,032	28,154	52,049	2,121	61,713	272,069
2006	128,680	28,075	53,649	2,254	58,946	271,604
2007	122,685	28,292	50,806	2,404	56,567	260,754
2008	125,700	29,029	51,605	2,102	55,030	263,466
2009	126,910	28,326	48,823	2,201	51,772	258,032
2010	55,141	12,788	19,519	896	21,730	110,074

Table 5. Number of cows included in JER evaluation of longevity (Aug 2010)

Year of 1st calving	DNK	SWE	Total
1985	28,289	1,064	29,353
1986	29,614	1,136	30,750
1987	28,915	1,126	30,041
1988	27,407	1,230	28,637
1989	27,087	1,194	28,281
1990	26,948	1,123	28,071
1991	26,203	847	27,050
1992	25,264	812	26,076
1993	23,961	618	24,579
1994	22,643	511	23,154
1995	22,728	496	23,224
1996	22,980	484	23,464
1997	23,509	528	24,037
1998	23,111	519	23,630
1999	23,369	513	23,882
2000	22,529	536	23,065
2001	23,059	555	23,614
2002	21,368	521	21,889
2003	20,141	568	20,709
2004	20,567	586	21,153
2005	19,610	568	20,178
2006	19,890	644	20,534
2007	19,183	605	19,788
2008	20,522	584	21,106
2009	20,612	615	21,227
2010	9,182	222	9,404

Table 6. Linear regression of linear longevity input data on year of 1st calving (see also figure 1, 2 and 3)

	Linear regression: Days/year				
	1Y-longevity	2Y-longevity	3Y-longevity	4Y-longevity	5Y-longevity
RDC DNK	-0.20	0.64	1.54	2.48	3.14
RDC FIN	-0.03	-0.88	-2.90	-5.32	-7.44
RDC SWE	0.29	0.54	-0.31	-1.72	-3.55
HOL DNK	0.10	0.95	1.22	1.24	1.22
HOL FIN	0.17	-0.61	-2.42	-4.68	-6.29
HOL SWE	0.88	1.54	0.96	-0.34	-1.54
JER DNK	-0.25	0.27	0.06	-0.68	-1.42
JER SWE	0.45	1.77	2.75	4.10	3.87

Figure 1. RDC average of input data for longevity evaluation of 1Y-, 3Y- and 5Y-longevity

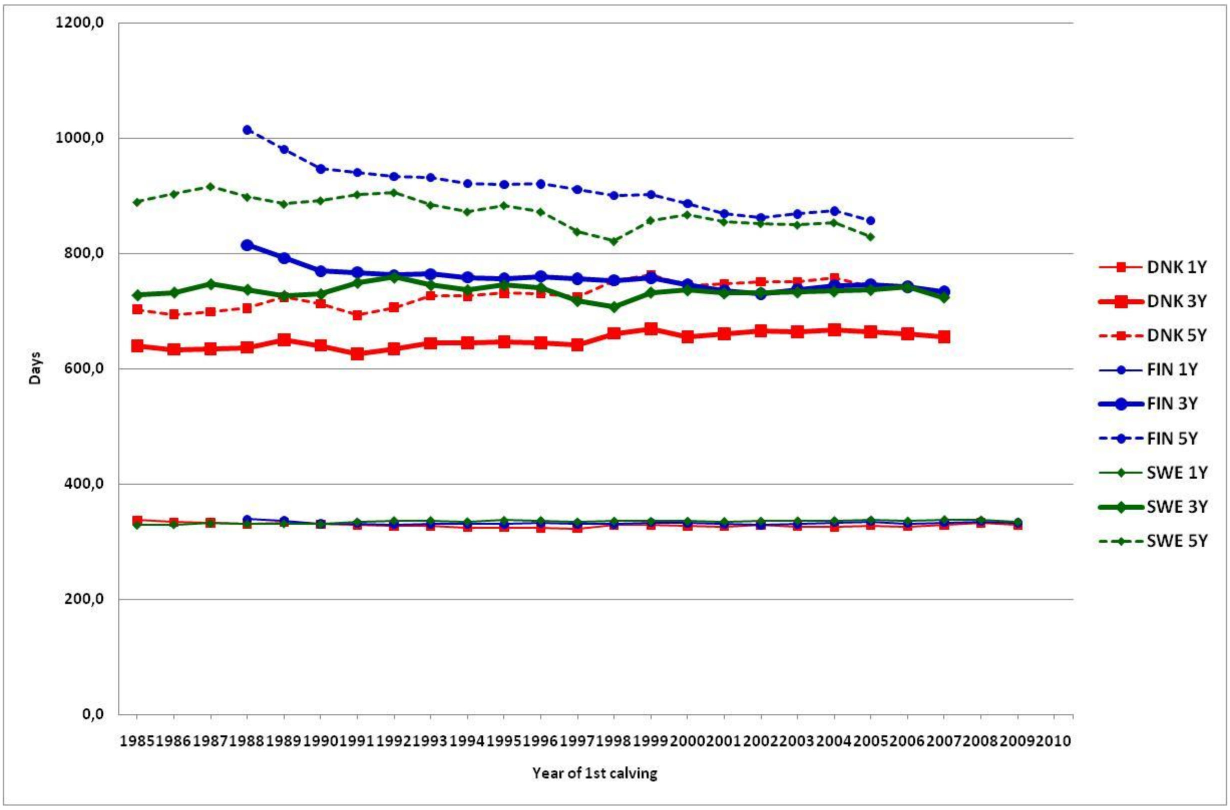


Figure 2. HOL average of input data for longevity evaluation of 1Y-, 3Y- and 5Y-longevity

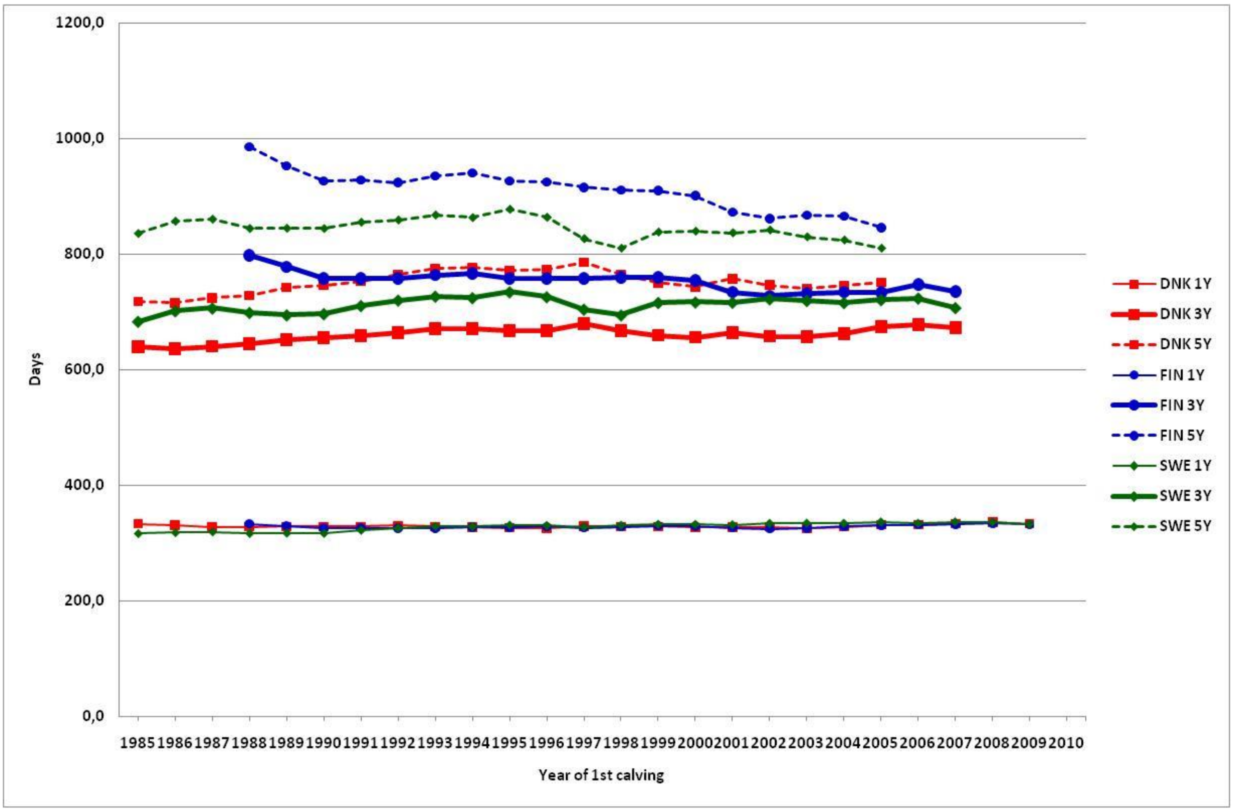
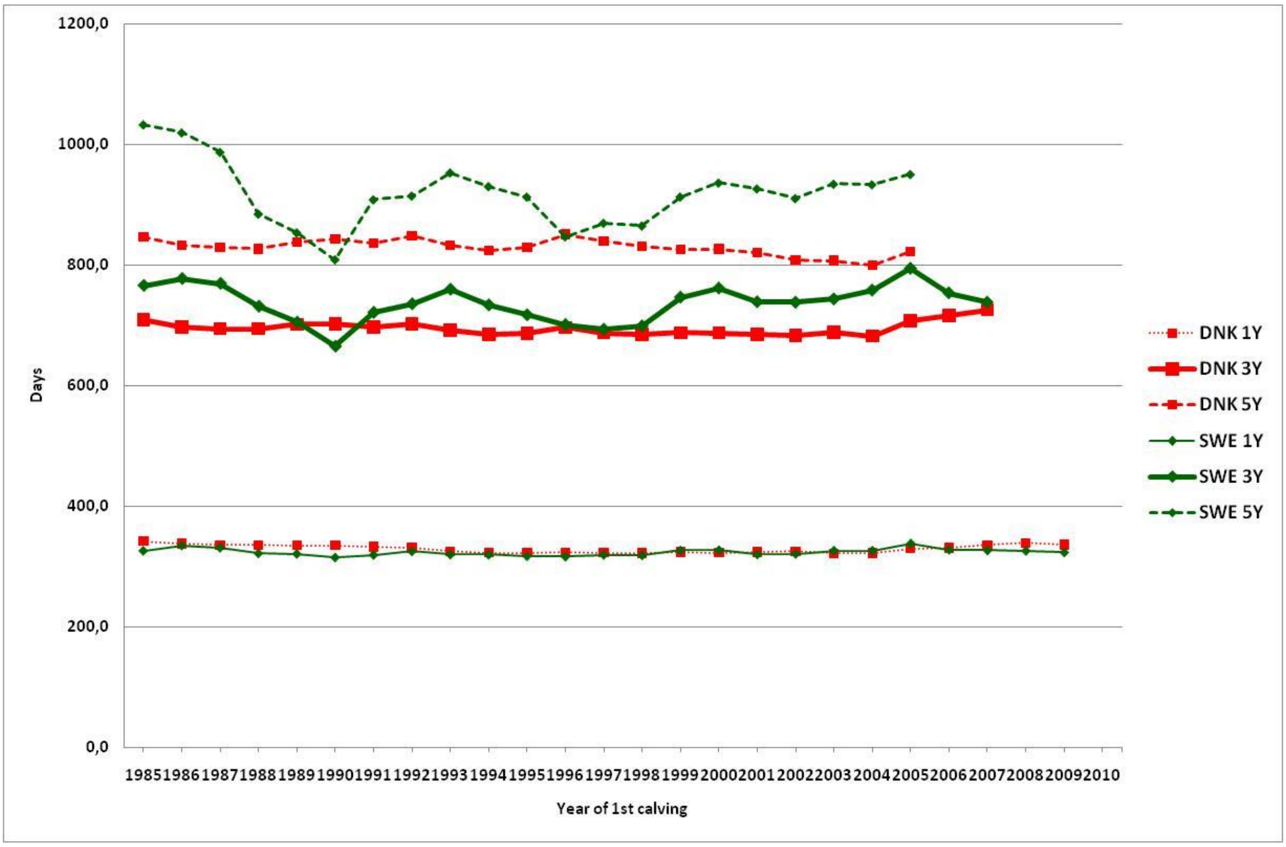


Figure 2. JER average of input data for longevity evaluation of 1Y-, 3Y- and 5Y-longevity



Model for linear longevity

The evaluation model developed is an animal model with multi-trait evaluation of the 5 linear longevity traits

The effects of the model are:

- Age at 1st calving (fixed effect)
- Year x month of 1st calving (fixed effect)
- Herd x 5-year period (fixed effect)
- Regression on heterozygoty (fixed effects)
    - RDC: rdm x abs, rdm x hf, abs x hf, rdm x nor, abs x nor, cay x nor, hf x nor, srb x fay, srb x nrf, fay x fic, total holstein
    - HOL: bw x hf, rw x hf, hol x rdc, tothet
    - JER: jer x usj
- Genetic groups modelled as phantom parent groups (random effect)
- Herd x year of 1st calving (random effect)
- Cow (random genetic effect)

The pedigree file

The pedigree of cows included was traced as far back as possible in the NAV-pedigree file – and pruned such that only ancestors that had more progeny-lines with data was included.

Random parameters (environmental and genetic variances and covariances)

Here come a number of tables

Genetic parameters for the 5 longevity traits were estimated

- Sire models are used
- Multi-trait with all 5 traits included
- Using data on every third herd (DNK HOL much less – FIN RDM every fifth).

The results on genetic and environmental parameters are shown in table 7 – 12.
In general the genetic parameters (heritabilities, genetic and environmental correlations) are very similar across breeds and countries. Therefore it was concluded that the genetic parameter could be merged.

Table 7. RDC estimates of genetic parameters of longevity. h^2 on diagonal. Genetic correlations above diagonal. Environmental correlations below diagonal

	1 year long.	2 year long.	3 year long.	4 year long.	5 year long.
	SWE RDC				
1 year longevity	**0.026**	0.962	0.921	0.888	0.864
2 year longevity	0.793	**0.040**	0.989	0.970	0.954
3 year longevity	0.657	0.929	**0.051**	0.995	0.987
4 year longevity	0.579	0.850	0.967	**0.059**	0.998
5 year longevity	0.535	0.796	0.924	0.984	**0.065**
Genetic SD	**12.9**	**42.2**	**75.4**	**104.5**	**124.8**
Environmental SD	79.3	206.8	326.6	416.9	474.9
	FIN RDC				
1 year longevity	**0.024**	0.968	0.922	0.885	0.856
2 year longevity	0.914	**0.034**	0.987	0.965	0.945
3 year longevity	0.802	0.942	**0.047**	0.995	0.985
4 year longevity	0.718	0.866	0.968	**0.058**	0.998
5 year longevity	0.666	0.811	0.926	0.984	**0.065**
Genetic SD	**18.2**	**46.5**	**81.5**	**113.6**	**136.2**
Environmental SD	117.0	248.7	366.7	457.4	517.8
	DNK RDC				
1 year longevity	**0.048**	0.948	0.898	0.866	0.849
2 year longevity	0.768	**0.074**	0.989	0.974	0.964
3 year longevity	0.634	0.932	**0.087**	0.996	0.992
4 year longevity	0.567	0.865	0.974	**0.094**	0.999
5 year longevity	0.535	0.826	0.944	0.990	**0.096**
Genetic SD	**19.3**	**58.8**	**95.3**	**119.3**	**131.5**
Environmental SD	85.6	208.2	308.3	371.1	403.8
	Across country parameters				
1 year longevity	**0.029**	0.946	0.902	0.869	0.843
2 year longevity	0.839	**0.044**	0.978	0.957	0.938
3 year longevity	0.711	0.924	**0.057**	0.984	0.975
4 year longevity	0.632	0.847	0.958	**0.066**	0.988
5 year longevity	0.585	0.794	0.915	0.974	**0.072**
Genetic SD	**17**	**48**	**83**	**113**	**133**
Environmental SD	97	225	340	425	479

Table 8. HOL Estimates of genetic parameters of longevity. h^2 on diagonal. Genetic correlations above diagonal. Environmental correlations below diagonal

	1 year long.	2 year long.	3 year long.	4 year long.	5 year long.
			SWE HOL		
1 year longevity	**0.034**	0.963	0.919	0.889	0.871
2 year longevity	0.813	**0.053**	0.989	0.972	0.959
3 year longevity	0.682	0.932	**0.066**	0.996	0.989
4 year longevity	0.606	0.857	0.969	**0.074**	0.998
5 year longevity	0.562	0.806	0.928	0.985	**0.079**
Genetic SD	**16.8**	**51.5**	**88.7**	**118.9**	**139.8**
Environmental SD	89.6	217.3	333.7	420.2	476.0
			FIN HOL		
1 year longevity	**0.041**	0.982	0.954	0.932	0.918
2 year longevity	0.927	**0.054**	0.992	0.979	0.969
3 year longevity	0.820	0.943	**0.073**	0.996	0.991
4 year longevity	0.737	0.868	0.969	**0.087**	0.999
5 year longevity	0.684	0.814	0.926	0.984	**0.095**
Genetic SD	**25.4**	**60.6**	**102.4**	**139.4**	**165.3**
Environmental SD	123.0	252.8	365.9	452.1	509.3
			DNK HOL		
1 year longevity	**0.035**	0.934	0.875	0.841	0.818
2 year longevity	0.765	**0.051**	0.986	0.969	0.955
3 year longevity	0.629	0.930	**0.060**	0.996	0.990
4 year longevity	0.558	0.858	0.971	**0.066**	0.999
5 year longevity	0.521	0.813	0.936	0.987	**0.068**
Genetic SD	**16.5**	**49.2**	**81.3**	**105.4**	**118.7**
Environmental SD	86.5	212.5	321.4	396.0	440.2
			Across country parameters		
1 year longevity	**0.035**	0.944	0.891	0.858	0.836
2 year longevity	0.777	**0.052**	0.987	0.969	0.955
3 year longevity	0.640	0.929	**0.062**	0.996	0.989
4 year longevity	0.566	0.853	0.969	**0.069**	0.998
5 year longevity	0.525	0.803	0.930	0.986	**0.072**
Genetic SD	**17**	**50**	**84**	**110**	**126**
Environmental SD	88	214	326	404	452

Table 9. JER estimates of genetic parameters of longevity. h^2 on diagonal. Genetic correlations above diagonal. Environmental correlations below diagonal

	1 year long.	2 year long.	3 year long.	4 year long.	5 year long.
			DNK JER		
1 year longevity	**0.035**	0.967	0.937	0.916	0.902
2 year longevity	0.783	**0.051**	0.993	0.981	0.971
3 year longevity	0.646	0.935	**0.060**	0.997	0.991
4 year longevity	0.569	0.861	0.971	**0.063**	0.998
5 year longevity	0.524	0.807	0.930	0.985	**0.064**
Genetic SD	**16.4**	**49.5**	**83.4**	**109.1**	**126.5**
Environmental SD	86.0	213.5	330.7	421.0	483.3

Table 10. RDC HxY-parameters. On diagonal V(HxY)/V(Total), off diagonals correlations

	1Y-longevity	2Y-longevity	3Y-longevity	4Y-longevity	5Y-longevity
1Y-longevity	**0.021**				
2Y-longevity	0.824	**0.023**			
3Y-longevity	0.717	0.953	**0.020**		
4Y-longevity	0.652	0.903	0.973	**0.017**	
5Y-longevity	0.605	0.857	0.939	0.978	**0.016**
SD of HxY	14	35	50	58	63

Table 11. HOL HxY-parameters. On diagonal V(HxY)/V(Total), off diagonals correlations

	1Y-longevity	2Y-longevity	3Y-longevity	4Y-longevity	5Y-longevity
1Y-longevity	**0.031**				
2Y-longevity	0.842	**0.030**			
3Y-longevity	0.721	0.960	**0.027**		
4Y-longevity	0.657	0.911	0.985	**0.024**	
5Y-longevity	0.625	0.879	0.964	0.994	**0.022**
SD of HxY	16	39	56	65	70

Table 12. JER HxY-parameters. On diagonal V(HxY)/V(Total), off diagonals correlations

	1Y-longevity	2Y-longevity	3Y-longevity	4Y-longevity	5Y-longevity
1Y-longevity	**0.028**				
2Y-longevity	0.829	**0.031**			
3Y-longevity	0.707	0.948	**0.028**		
4Y-longevity	0.639	0.895	0.974	**0.025**	
5Y-longevity	0.595	0.854	0.947	0.982	**0.023**
SD of HxY	15	39	58	70	77

Reliabilities

The reliability was calculated using the APAX-program by the Tiers and Meyer approach (reference). Table 13-15 show some relation between number of daughters and the reliability (r_{AI}^2)

Table 13. RDC Average number of daughters included and r_{AI}^2 depending of birth year

		No of daughters included			
Birth year	No of sires	1Y longevity	2Y longevity	3Y longevity	r_{AI}^2
DNK					
2000	39	214.3	87.7	69.4	65.4
2001	38	87.1	79.5	77.3	63.3
2002	47	91.9	88.4	65.3	62.3
2003	44	79.7	55.0	2.3	52.6
2004	44	52.0	1.7	0.0	40.4
2005	25	0.4	0.0	0.0	29.1
2006	0	-	-	-	-
FIN					
2000	136	367.1	211.0	167.3	78.1
2001	128	170.6	147.7	142.4	72.6
2002	94	161.4	156.6	106.6	70.9
2003	121	145.6	111.1	5.1	63.4
2004	106	125.1	8.7	0.0	52.3
2005	110	17.4	0.0	0.0	32.5
2006	9	0.0	0.0	0.0	28.4
SWE					
2000	96	215.3	157.5	151.0	74.9
2001	84	148.3	137.6	132.8	71.8
2002	76	162.4	156.1	113.3	71.9
2003	73	166.1	115.4	9.6	64.7
2004	76	115.2	9.3	0.0	50.8
2005	73	6.3	0.0	0.0	29.9
2006	7	0.0	0.0	0.0	27.7

Table 14. HOL Average number of daughters included and r_{AI}^2 depending of birth year

		No of daughters included			
Birth year	No of sires	1Y longevity	2Y longevity	3Y longevity	r_{AI}^2
			DNK		
2000	319	138.6	85.1	76.1	66.1
2001	332	111.0	80.3	77.1	65.3
2002	291	104.8	101.3	83.0	66.7
2003	264	116.2	86.8	6.6	62.0
2004	245	92.3	3.6	0.0	48.7
2005	229	6.4	0.0	0.0	30.3
2006	35	0.0	0.0	0.0	26.5
			FIN		
2000	46	196.5	132.7	124.0	73.1
2001	63	169.6	153.0	147.3	74.6
2002	46	167.5	161.7	99.9	73.3
2003	44	163.0	119.9	2.7	66.6
2004	39	172.4	12.1	0.0	58.1
2005	46	19.0	0.0	0.0	32.8
2006	6	0.0	0.0	0.0	26.5
			SWE		
2000	87	246.2	110.5	103.6	68.5
2001	100	122.1	113.9	108.2	66.2
2002	93	137.2	128.4	85.1	68.5
2003	74	137.1	90.6	3.7	63.7
2004	90	83.2	5.0	0.0	46.5
2005	59	5.5	0.0	0.0	29.9
2006	4	0.0	0.0	0.0	27.8

Table 15. JER Average number of daughters included and r_{AI}^2 depending of birth year

Birth year	No of sires	No of daughters included 1Y longevity	2Y longevity	3Y longevity	r_{AI}^2
			DNK		
2000	71	135.0	88.7	67.2	63.9
2001	50	99.1	72.4	70.9	63.1
2002	55	87.7	84.6	71.9	63.4
2003	54	87.3	74.0	10.2	58.7
2004	48	91.3	7.9	0.0	51.5
2005	45	11.6	0.0	0.0	31.8
2006	6	0.0	0.0	0.0	28.5

Calculation of longevity index

The conversion of the original estimates of breeding values to indexed are a 2 step procedure: Standardization of the variance and standardization of the average

Standardization of the variance

- Standardization of the variance such that the standard deviation of a predetermined group of sire is 10.
- In NAV the predetermined groups is currently sires born 1997-98.
- This standardization is normally fixed for a longer period of time

Table 16 shows the standardization factors used for the new longevity index – and for the other traits included in the evaluation. These factors is fairly similar to the standardization factors used for the current longevity index

Table 16. Standard deviation (SD) of original estimates of breeding values.

	SD of original EBVs(days) EBV days in 10 index units			**EBV days in 1 index unit**		
	RDC	**HOL**	**JER**	**RDC**	**HOL**	**JER**
1Y-longevity	11.5	12.5	13.4	1.15	1.25	1.34
2Y-longevity	37.0	41.5	40.9	3.70	4.15	4.09
3Y-longevity	**67.5**	**72.4**	**71.2**	**6.75**	**7.24**	**7.12**
4Y-longevity	94.3	96.4	95.9	9.43	9.64	9.59
5Y-longevity	112.9	111.0	113.9	11.29	11.10	11.39

Standardization of the average

- Standardization of the average such that a predetermined group of animal (the base) have average index of 100.
- In NAV it has been generally decided to publish all indexes on a cow base. It is also decided that the cow base should cows born in the period 3 to up 5 years prior to the evaluation date.
- This standardization is made at every evaluation – the base is rolling

Publication

The only trait published is the trait "Days from 1st calving to end of 3rd lactation", the trait that have been denoted 3Y-longevity.

The sire will get official longevity index if reliability is equal to or larger than 50. The consequence is that

- Some sires will have official longevity index when they are 5 - 5½ years old
- Most sires will have official longevity index when they are 5½ - 6 years old
- In general, the new longevity will be published 0-6 prior to current longevity index.

Economic value of the new longevity
The basic economic value of longevity has not changed. In the project on economic value of the NTM-index the value of longevity was estimate to:

- 0.38 € per day in RDC
- 0.51 € per day in HOL
- 0.40 € per day in Jersey

However the accuracy of the new longevity index might change – and therefore the standard deviation of the new index might change:

- 1 index unit in RDC include 6.75 days
- 1 index unit in HOL include 7.24 days
- 1 index unit in JER include 7.12 days

In the current model a large part of the economic value are redistributed to five other traits (Fertility, Udder Health, Other Diseases, Feet&Legs, Udder Conformation), because the economic model that was used, did not take into account the value of reduced culling when the value of these 5 traits were estimated.

Therefore the basic economic values of longevity calculated in the NTM-project were:

- RDC: Value reduced by 70%: Used value 0.38 * (1 – 0.70) = 0.114 € per day
- HOL: Value reduced by 70%: Used value 0.51 * (1 – 0.70) = 0.153 € per day
- JER: Value reduced by 50%: Used value 0.40 * (1 – 0.50) = 0.200 € per day

Using these reduced values with the new standardization factors give the following economic values of longevity:

- RDC: 6.75 days/index unit * 0.114 €/day = 0.77 €/index unit
- HOL: 7.24 days/index unit * 0.153 €/day = 1.11 €/index unit
- JER: 7.12 days/index unit * 0.200 €/day = 1.42 €/index unit

The value of longevity is redistributed from longevity to the other traits because the economic model that was used, did not take into account the value of reduced culling when the value of these other traits were estimated.

In perfect system the economic values for each trait should include value of reduced culling and the longevity EBV should be corrected for the effect of these traits (a residual longevity). Because the system is not perfect we can choose to:

- Redistribute the value from longevity to the other traits
- Use the value of longevity directly without redistribution

In general the EBVs of the other traits are estimated with larger reliability and earlier that the EBV of longevity. Therefore it was seen as an advantage to redistribute the value of longevity.

The same argument can be used for redistribution of value to yield – but we can for other reasons also chose to stay with the current system without doing any violations with respect to double counting

The question is now: Should we change anything at this stage? – We are not in the process of revising economic values, so maybe we should just do the adjustments that are justified/necessary by the change in standardization of the index

The redistribution problem really belong to a more general revision of the economic values

Comparison with current longevity index

Three factors causes changes in index

- Model change. The effect best evaluated by correlations between the current and the new longevity index (correlations within birth year).
- However, high correlations do not imply that the changes in indexes are small. Change in index could be caused by a general difference in level due to the change from a sire base to a cow base
- The change in index level could also be due to differences in genetic trends. If there are differences in genetic trend the changes would be largest for the older sires (because we the younger group sires have an average close 100 for both in the current system and for the new system)

Correlations within birth year

The model has been changed drastically: For DNK and FIN there are both a change from a survival model to a linear model – and a change from functional to productive longevity. On paper, the change in the SWE part of the model might seen smaller, but evaluated on the correlation between current and the new longevity the change is just as large as in DNK and FIN.

In all three countries the correlation between the current and the new longevity is somewhere between 0.80 and 0.90 for SWE and FIN sires and even lower for DNK sires. That indicates that there will be some re-ranking of the sires (of same age)

Figure 4. RDC correlations between new longevity index (Aug 2010) and old NAV-longevity (May 2010)

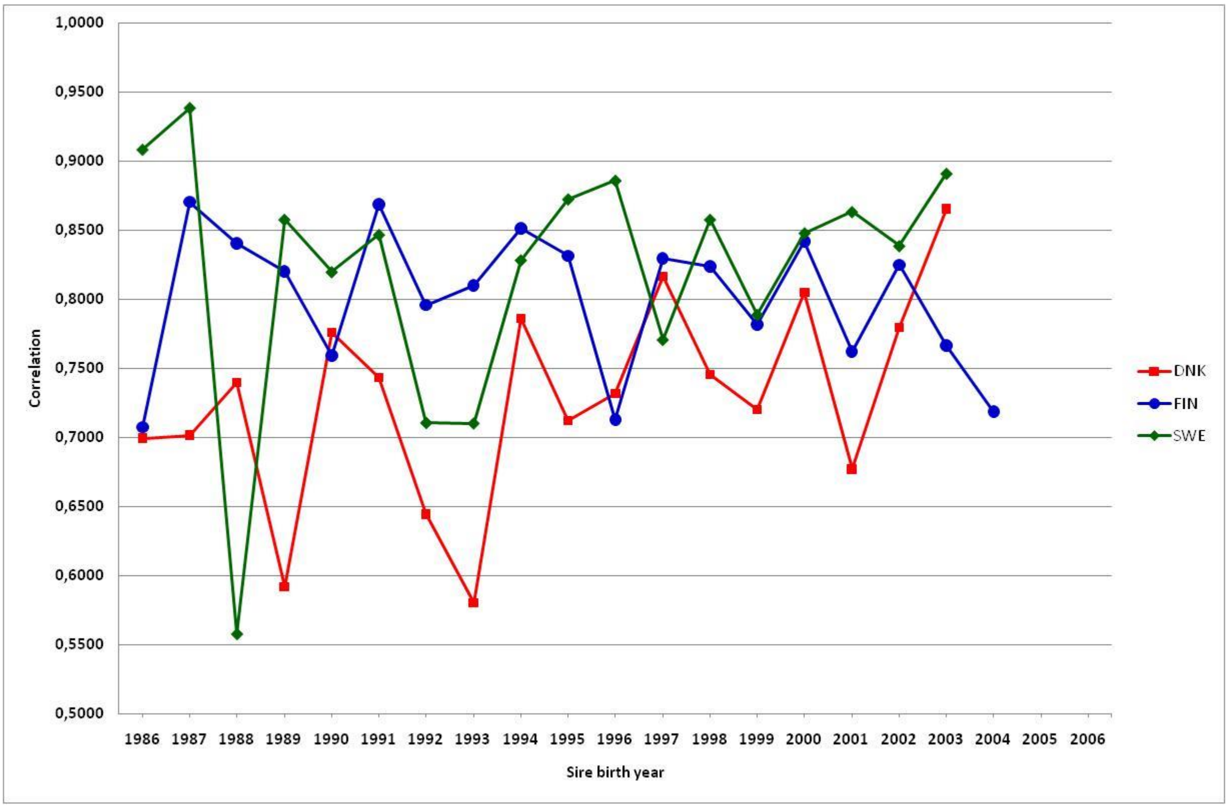


Figure 5. HOL correlations between new longevity index (Aug 2010) and old NAV-longevity (May 2010)

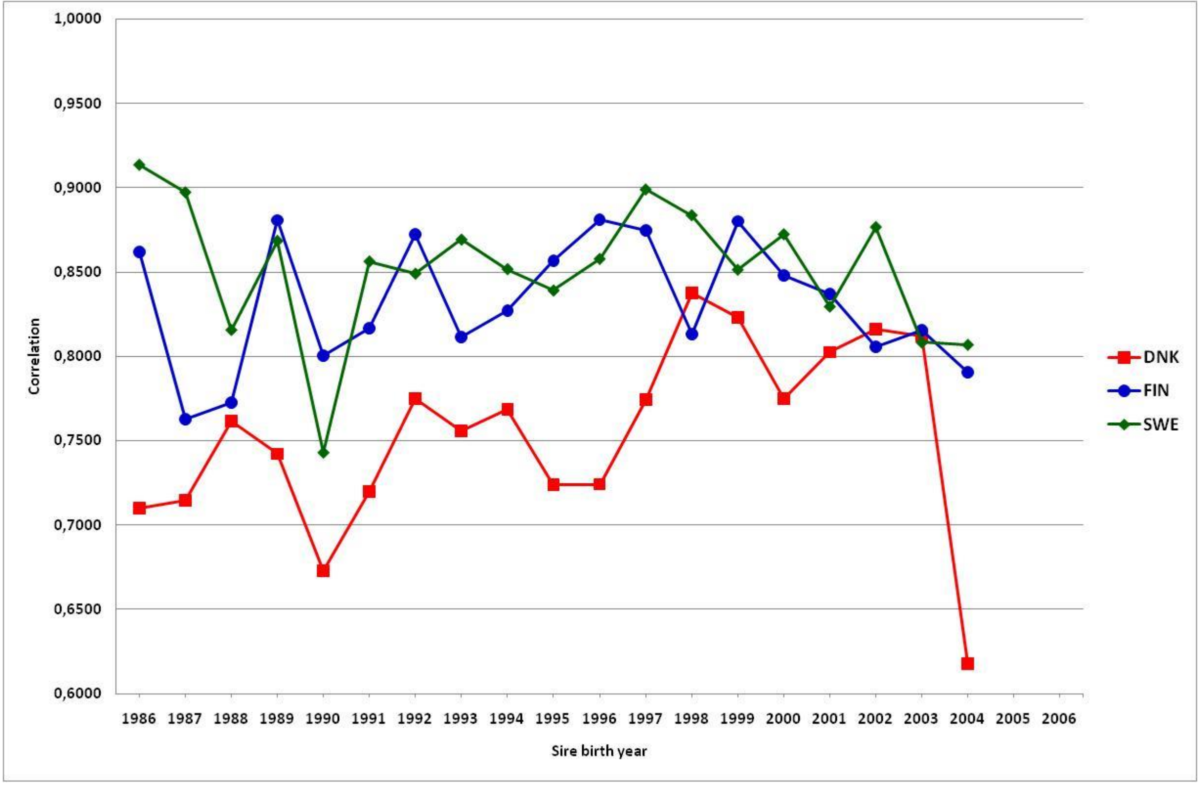
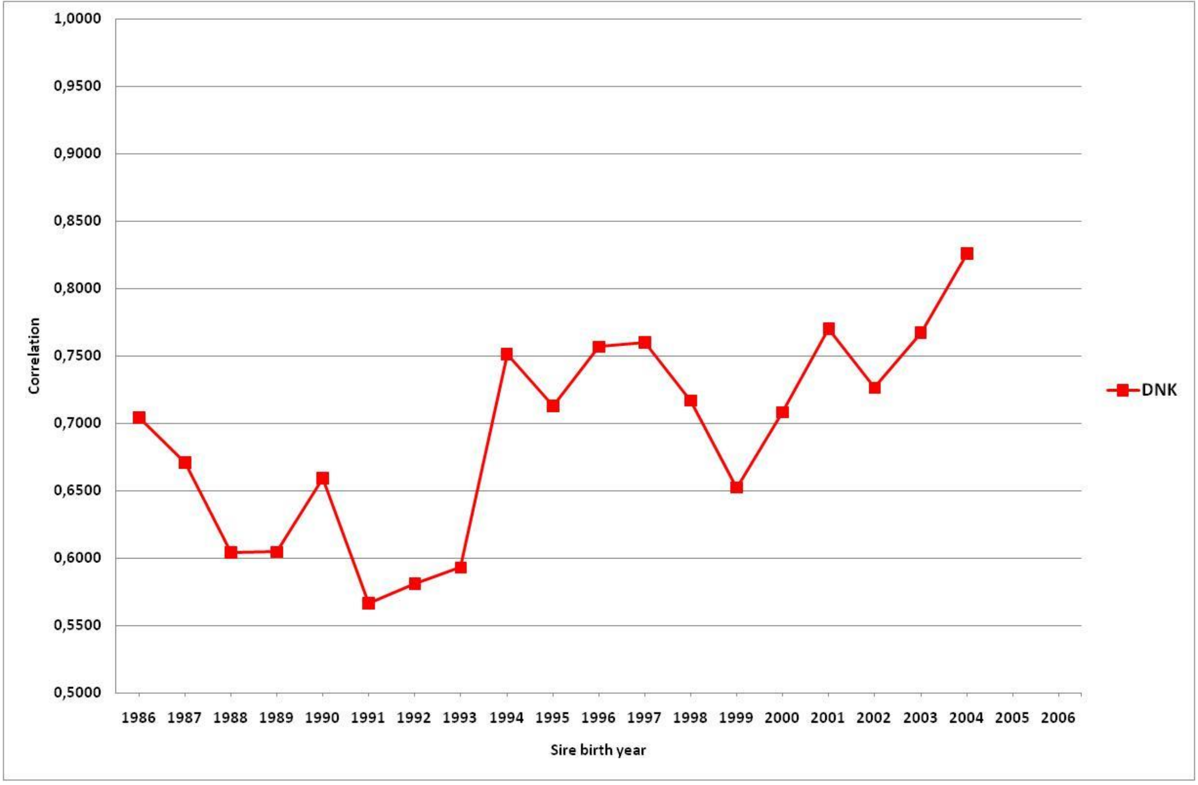


Figure 6. JER correlations between new longevity index (Aug 2010) and old NAV-longevity (May 2010)



Sire base and cow base

Especially in Holstein and Jersey the differences is quite large. The change from a sire base to a cow base will decrease the average level by:

- RDC: ÷2.0 index units
- HOL: ÷6.5 index units
- JER: ÷5.7 index units

Besides, the change from a nation base to a common NAV base might also have a small impact on average change in indexes.

Trend differences

The figures below show the genetic trends of the current and the new longevity index. There is a tremendous difference in trends and give very large index change for the older sires (more details). For the youngest sires the difference between the new and the current longevity most reflect the difference between the sire and the cow base. For the older sire the effect of trend differences are added.

Figure 7. RDC sire trends for new longevity index (Aug 2010) and old NAV-longevity (May 2010)

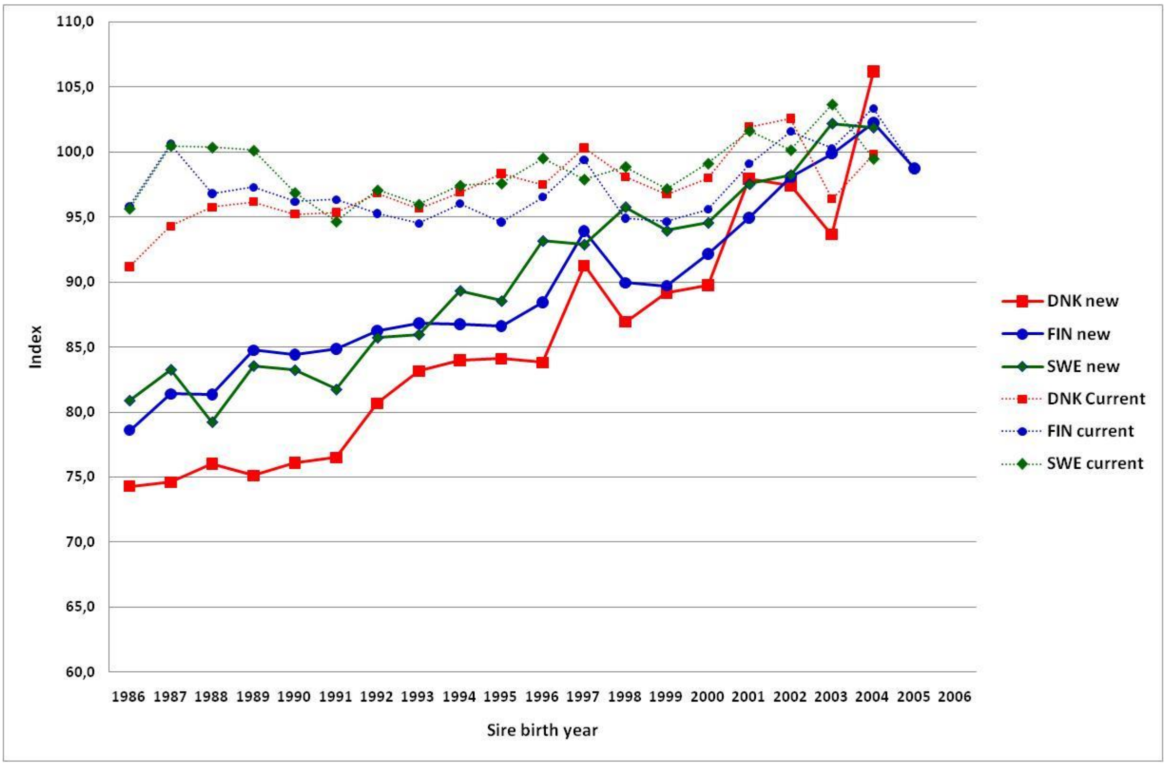


Figure 8. HOL sire trends for new longevity index (Aug 2010) and old NAV-longevity (May 2010)

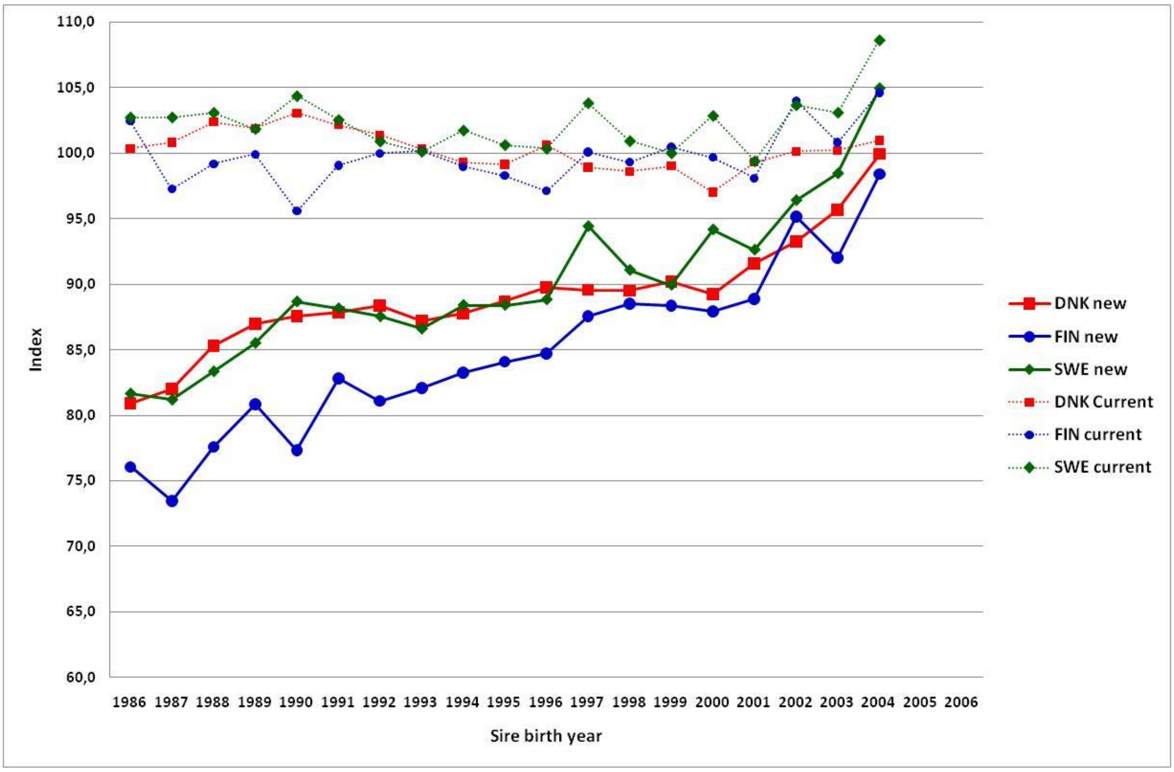


Figure 9. JER sire trends for new longevity index (Aug 2010) and old NAV-longevity (May 2010)