

# Feasibility of MACE for Longevity for Colored Breeds

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## Abstract

International genetic evaluation for longevity for colored breeds were studied and found feasible. 9, 7, 5, and 4 countries participated in the pilot study for direct longevity for AYS, JER, GUE, and BSW, respectively, and average genetic correlations of 0.56, 0.51, 0.69, and 0.77 were obtained. The moderate genetic correlations within breed as well as the difference in average correlations may be caused by differences in national evaluation models, heritabilities, trait definitions, and culling strategies. Product moment correlations between international breeding values for direct longevity and udder health, udder depth, foot angle and overall conformation also showed differences in correlations between traits across breeds.

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## Introduction

International genetic evaluation of longevity traits for Holsteins has been shown to be feasible (Van der Linde & De Jong, 2002; Jakobsen, 2003; Van der Linde & De Jong, 2003). However, breed differences in genotype-environment interactions for longevity traits may exist and the aim of this study was to investigate feasibility of MACE for longevity for colored breeds. Firstly, across country genetic correlations were estimated. Secondly, product moment correlations were obtained between international breeding values for direct longevity and other internationally evaluated traits within each country.

## Material and Methods

### Data

Data for direct longevity for colored breeds were delivered by Australia (AUS), Canada (CAN), Germany-Austria (DEA), Germany (DEU), Denmark (DNK), Finland (FIN), Great Britain (GBR), The Netherlands (NLD), New Zealand (NZL), Sweden (SWE), and The United States of America (USA). Number of breeds for the test run and the pilot study, as well as a summary of features of national models is shown in Table 10. Number of common bulls and number of common bulls in  $\frac{3}{4}$  sib families as well as number of records in well connected subset are shown in Tables 1, 3, 5, and 7 for Ayrshire (AYS), Jersey (JER), Guernsey (GUE), and Brown Swiss (BSW),

respectively. Simmental data were submitted from DEA and NLD, but due to poor links correlations were found to end up anywhere between -1 and 1. Therefore, no results are shown for Simmental. Also JER data were submitted from DEU but due to very few bulls (34 bulls with evaluations) unbelievable negative correlations (-0.49 and -0.33) were obtained between DEU and AUS and between DEU and NZL. Therefore, correlations for Jersey were re-estimated but without German data included. Correlations were obtained without a requirement of validated genetic trend.

### Methods

The Holstein-USA MACE software (Klei, 1998; Klei & Weigel, 1998) was used to obtain the across country genetic correlations. Minimum phantom group size was set to 30.

## Results and Discussion

Genetic correlations are shown in Tables 2, 4, 6, and 8 for AYS, JER, GUE, and BSW, respectively. Average genetic correlations were 0.56, 0.51, 0.69, and 0.77 for AYS, JER, GUE, and BSW, respectively. In comparison, genetic correlations for the Holstein breed was on average 0.64 (unpublished results). Average genetic correlations across breeds are not directly comparable due to difference in number of countries submitting data for different breeds. Genetic correlations close to zero were obtained between NZL and CAN, GBR, and

USA for AYS, and between AUS and DNK, NLD for JER. The reasons for these very low correlations are unknown. For AYS, some countries do have poor links to some of the other countries. A solution of use of HOL priors as performed for AYS conformation (Mark *et al.*, 2003) can be speculated. However, a comparison to genetic links between countries

participating in international genetic evaluation for somatic cell count (Interbull, 2004) and direct longevity showed equally good links. Therefore, if trait definitions for longevity differ between populations, use of HOL correlations as informative prior to estimate AYS correlations may impose a false correlation structure.

**Table 1.** Ayrshire breed. Number of common bulls below diagonal, number of common bulls in  $\frac{3}{4}$  sib families above diagonal, and number of records in well connected subset in diagonal.

	AUS	CAN	DEU	DNK	FIN	GBR	NZL	SWE	USA
AUS	224	64	7	22	16	41	96	59	37
CAN	65	212	3	2	10	38	56	10	103
DEU	6	3	30	13	13	0	4	19	0
DNK	21	2	13	68	6	0	5	20	0
FIN	15	10	12	6	214	4	59	59	7
GBR	57	40	0	0	3	93	44	4	24
NZL	114	56	4	4	64	53	226	27	35
SWE	60	9	15	17	42	4	24	225	4
USA	36	83	0	0	7	21	37	4	144

**Table 2.** Ayrshire breed. Genetic correlations for direct longevity. Minimum (Min), maximum (Max), and average (Avr) correlations are shown in the three bottom rows.

	AUS	CAN	DEU	DNK	FIN	GBR	NZL	SWE	USA
AUS		0.39	0.85	0.64	0.69	0.12	0.54	0.46	0.48
CAN			0.49	0.81	0.62	0.58	0.08	0.90	0.89
DEU				0.74	0.75	0.44	0.76	0.71	0.37
DNK					0.78	0.79	0.19	0.88	0.71
FIN						0.56	0.52	0.61	0.70
GBR							0.03	0.73	0.37
NZL								0.29	-0.01
SWE									0.64
USA									
Min	0.12	0.08	0.37	0.19	0.52	0.03	-0.01	0.29	-0.01
Max	0.85	0.90	0.85	0.88	0.78	0.79	0.76	0.90	0.89
Avr	0.52	0.60	0.64	0.69	0.65	0.45	0.30	0.65	0.52

**Table 3.** Jersey breed. Number of common bulls below diagonal, number of common bulls in  $\frac{3}{4}$  sib families above diagonal, and number of records in well connected subset in diagonal.

	AUS	CAN	DNK	GBR	NLD	NZL	USA
AUS	555	80	63	62	34	253	179
CAN	89	166	33	50	16	65	93
DNK	39	25	284	47	43	75	71
GBR	71	54	42	114	28	61	47
NLD	30	18	38	28	67	40	34
NZL	292	74	50	62	35	678	156
USA	183	97	47	53	39	194	1129

**Table 4.** Jersey breed. Genetic correlations for direct longevity. Minimum (Min), maximum (Max), and average (Avr) correlations are shown in the three bottom rows.

	AUS	CAN	DNK	GBR	NLD	NZL	USA
AUS		0.33	0.09	0.17	0.06	0.60	0.70
CAN			0.71	0.46	0.84	0.37	0.71
DNK				0.76	0.94	0.53	0.42
GBR					0.58	0.55	0.50
NLD						0.38	0.47
NZL							0.61
USA							
Min	0.06	0.33	0.09	0.17	0.06	0.37	0.42
Max	0.70	0.84	0.94	0.76	0.94	0.61	0.71
Avr	0.33	0.57	0.58	0.50	0.55	0.51	0.57

**Table 5.** Guernsey breed. Number of common bulls below diagonal, number of common bulls in  $\frac{3}{4}$  sib families above diagonal, and number of records in well connected subset in diagonal.

	AUS	CAN	GBR	NZL	USA
AUS	97	39	29	31	40
CAN	43	74	16	18	48
GBR	37	15	69	18	37
NZL	34	16	17	53	28
USA	34	36	36	27	228

**Table 6.** Guernsey breed. Genetic correlations for direct longevity. Minimum (Min), maximum (Max), and average (Avr) correlations are shown in the three bottom rows.

	AUS	CAN	GBR	NZL	USA
AUS		0.69	0.50	0.91	0.34
CAN			0.95	0.89	0.68
GBR				0.74	0.79
NZL					0.41
USA					
Min	0.34	0.68	0.50	0.41	0.34
Max	0.91	0.95	0.95	0.91	0.79
Avr	0.61	0.80	0.75	0.74	0.56

**Table 7.** Brown Swiss breed. Number of common bulls below diagonal, number of common bulls in  $\frac{3}{4}$  sib families above diagonal, and number of records in well connected subset in diagonal.

	CAN	DEA	NLD	USA
CAN	71	53	18	59
DEA	45	513	38	218
NLD	15	28	52	42
USA	51	224	36	405

**Table 8.** Brown Swiss breed. Genetic correlations for direct longevity. Minimum (Min), maximum (Max), and average (Avr) correlations are shown in the three bottom rows.

	CAN	DEA	NLD	USA
CAN		0.89	0.84	0.83
DEA			0.58	0.51
NLD				0.98
USA				
Min	0.83	0.51	0.58	0.51
Max	0.89	0.89	0.98	0.98
Avr	0.85	0.66	0.80	0.77

Product moment correlations between within country international breeding values for direct longevity and birth year, milk yield, fat yield, protein yield, udder health, udder depth, foot angle, and overall conformation are shown in Table 9. Correlations between longevity and yield traits were much higher for countries that do not correct for yield than for those that do. Correlations between longevity and birth year followed a similar pattern, indicating that yield adjustments affect genetic trend. Similar observations were reported for the Holstein breed in an earlier study (Powell & VanRaden, 2003).

Correlations between longevity and udder health were rather similar for all countries for AYS, BSW, and GUE, while correlations for JER differed across countries. This indicates that culling due to udder health may vary more for JER than for the other breeds.

Correlations between longevity and udder depth differed across countries within breeds, but within countries across breeds these correlations were very similar. Correlations between longevity and foot angle were similar across countries for JER and GUE, whereas these correlations varied for AYS and BSW. Correlations between longevity and overall conformation were similar across countries for GUE, and apart from NLD and DNK also very similar for BSW and JER. In summary, some breed differences exist in correlations between longevity and conformation traits.

For AUS, product moment correlations for the JER breed seem to be slightly different than for AYS and GUE. A zero correlation was obtained between longevity and udder health for JER, whereas the correlation was 0.40 and 0.35 for AYS and GUE, respectively. The opposite was seen for the correlation to overall conformation, where the correlation was 0.19 and 0.60 for AYS and JER, respectively. These correlations indicate a population difference in trait definition within country. A similar picture was observed for CAN and the USA, where JER was the breed with lowest correlation to udder health. However, the genetic correlations for longevity between these countries were as high as 0.68 (GUE) and 0.89 (AYS) between CAN and USA, whereas correlations were in the range from 0.33 to 0.69 between AUS and CAN, and from 0.34 to 0.70 between AUS and USA. A comparison of correlations between AUS, CAN, NZL, and USA showed larger correlations between countries within breeds for hemispheroid country pairs of AUS-NZL and CAN-USA. These observations also indicate a larger degree of harmonization of trait definition within hemisphere. Culling reasons in seasonal grazing systems may differ from culling reasons in year-round production systems.

A comparison of the correlations for JER and AYS in GBR and DNK show very similar correlation to other traits. Also, looking at ge-

netic correlations between GBR and DNK for AYS (Table 1) and Jersey (Table 3) shows correlations of 0.79 and 0.76, respectively. A correlation of a similar magnitude (0.72) was obtained between GBR and DNK for the Holstein breed (unpublished results). So for these two countries, trait definitions across breeds within country seem to be very similar. Although statistical models differed between these two countries (Table 11) models were consistent within country.

## Conclusion

Moderate genetic correlations were obtained for direct longevity for the colored breeds. There seem to be population differences both within and across countries. These differences can be due to differences in national evaluation models, heritabilities, trait definitions, and culling strategies. Product moment correlations between traits within country were different across breeds within country. This also indicates a breed difference in trait definition.

Even though we may expect to see a similar correlation structure across breeds for longevity as we have seen for e.g. production traits we may actually convince ourselves that we to a certain extent are working with a trait that is determined of a number of other traits, by the interaction between those traits, and by statistical correction for yield. Also, farmers culling decisions are very much determined by climatic and political circumstances. In summary, if we can accept that correlations between country pairs differ across breeds, international genetic evaluation for direct longevity is feasible also for colored breeds.

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**Table 9.** Product moment correlations for colored breeds between within country international breeding values for direct longevity (Pilot study March 2004) and birth year, milk yield, fat yield, protein yield, udder health, udder depth, foot angle, and overall conformation from February routine evaluation (2004).

CNT	Breed	Birth Year	Milk Yield	Fat Yield	Protein Yield	Udder Health	Udder Depth	Foot Angle	Overall Conformation
AUS	AYS	0.26	0.66	0.72	0.72	0.40	0.06	0.09	0.19
AUS	GUE	0.30	0.40	0.52	0.49	0.35	.	.	.
AUS	JER	0.69	0.77	0.70	0.82	-0.04	0.02	0.12	0.60
CAN	AYS	0.20	0.23	0.18	0.18	0.35	0.31	0.26	0.38
CAN	GUE	0.26	-0.06	0.31	0.05	0.52	0.23	0.11	-0.11
CAN	BSW	0.14	0.37	0.20	0.18	0.31	0.31	0.05	0.29
CAN	JER	0.10	0.23	0.03	0.13	0.17	0.15	0.19	0.25
DEA	BSW	-0.04	-0.02	-0.14	-0.10	.	0.28	0.05	.
DEU	AYS	0.16	0.23	0.23	0.21	0.41	.	.	.
DNK	AYS	0.39	0.22	0.20	0.27	0.30	0.38	0.02	-0.01
DNK	JER	-0.09	-0.24	-0.13	-0.21	0.39	0.41	0.15	-0.21
FIN	AYS	0.02	-0.06	-0.15	-0.10	0.39	0.40	-0.11	.
GBR	AYS	0.03	-0.09	0.03	-0.04	0.28	0.33	0.25	0.18
GBR	GUE	-0.01	-0.24	-0.07	-0.21	0.63	0.46	-0.01	-0.02
GBR	JER	0.17	-0.02	0.14	0.05	0.28	0.45	0.24	0.18
NLD	BSW	-0.13	0.18	0.25	0.12	0.37	0.04	-0.21	-0.13
NLD	JER	0.39	0.61	0.27	0.55	-0.47	.	.	.
NZL	AYS	0.21	0.11	0.31	0.25	.	.	.	0.05
NZL	GUE	0.39	0.60	0.57	0.54	.	.	.	.
NZL	JER	0.37	0.22	0.66	0.47	.	.	.	0.11
SWE	AYS	0.38	0.42	0.38	0.43	0.21	0.21	0.14	0.25
USA	AYS	0.29	0.36	0.28	0.27	0.32	0.38	0.13	0.17
USA	GUE	0.27	0.26	0.43	0.37	0.37	0.28	0.06	-0.04
USA	BSW	0.33	0.47	0.40	0.41	0.43	0.20	0.28	0.32
USA	JER	0.44	0.51	0.46	0.54	0.08	0.13	0.23	0.43

**Table 10.** Country (CNT), national evaluation models, official trait, data inclusion in national model, breeds for March test and pilot run, heritability ( $h^2$ ), correction for milk production, and trait definition for countries participating in the longevity test run or longevity pilot run for direct longevity in March 2004.

CNT	Model	Official Trait	Data Inclusion	Breeds	$h^2$	Correc- tion for milk prod.	Trait Definition
AUS	AM-REP-BLUP	Comb.	From 1975	HOL, AYS, GUE, JER	0.025	No	Probability of surviving from one year to the next (is this calendar year or lactation or are these equal). Up to seven years after first calving.
CAN	AM-MT-BLUP	Comb.	From 1980 (year of first calving)	HOL, AYS, GUE, JER, BSW	0.091	Yes	Survival in the first three lactations
CHE	Survival Ana.	Comb.	Lactations starting 1 <sup>st</sup> of January 1980	HOL	0.1385	Yes	Productive life span of cow in months
DEA	Survival Ana.	Comb.	Since 1979	BSW, (SIM)	0.120	Yes	Functional length of productive life
DEU	Survival Ana.	Comb.	From 1985	HOL, AYS	0.180	Yes	Functional herd life
DNK	Survival Ana.	Direct	Cows calved after 1984	HOL, AYS, JER	0.117	Yes	Risk of involuntary culling
DNR	Survival Ana.	Direct	Cows calved after 1984	RHOL	0.117	Yes	Risk of involuntary culling
ESP	Survival Ana.	Comb.	Cows calving since 1986	HOL	0.105	Yes	Productive life span of cow
FIN	Survival Ana.	Direct	From 1.1.1980 onwards	AYS	0.120	Yes	Stayability from 1 <sup>st</sup> calving
FRA	Survival Ana.	Direct	Cows calved after Dec. 1 <sup>st</sup> 1984	HOL	0.157	Yes	Productive life
GBR	AM-MT-BLUP	Comb.	Cows born since 1986	HOL, AYS, JER, GUE	0.060	Yes	Lifespan
IRL	AM-MT-BLUP	Comb.	Cows calving since 1971	HOL	0.030	Yes	Reappearance in subsequent lactation
ISR	Single trait AM	Direct	Cows calving since 1985	HOL	0.110	No	Days from first calving to max. exit at 2922 days. For cows still milking exit date is predicted.
ITA	Survival Ana.	Comb.	Cows calved since 1980	HOL	0.097	Yes	Risk of involuntary culling during a cow's lifetime
NLD	Survival Ana.	Direct &Comb.	Cows in production since Jan. 1 <sup>st</sup> . 1988	HOL, BSW, JER	0.066	Yes	Risk of involuntary culling during a cow's lifetime
NZL	AM-BLUP	Direct		HOL, AYS, GUE, JER	0.072	No	Herd life
SWE	SM-MT-BLUP	Direct	From 1984	HOL, AYS	0.060	No	Survival rate 4th calving
USA	ST-BLUP-AM	Comb.	Cows calving from 1960	HOL, AYS, JER,BSW, GUE	0.085	No	Productive life. Time in the milking herd before removal by voluntary culling, involuntary culling, or death. Calculated in months of milk in each lactation, summed across lactations, with full credit for complete records and partial credit for short records.