



Institutionen för husdjursgenetik

Predicting Swedish breeding values for Danish dairy bulls

by

Anja Johansson

Handledare:

Hossein Jorjani, Freddy Fikse ; HGEN

Bengt Lindhé, Hans Stålhammar ; Svensk Avel

Examensarbete 274

2005

Examensarbete ingår som en obligatorisk del i utbildningen och syftar till att under handledning ge de studerande träning i att självständigt och på ett vetenskapligt sätt lösa en uppgift. Föreliggande uppsats är således ett elevarbete och dess innehåll, resultat och slutsatser bör bedömas mot denna bakgrund.



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Agrovoc: Dairy cattle, selection index, multiple regression

Other: Conversion equation, genetic evaluation

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Notice:

Review of literature and collection of data for this MSc dissertation, as well as all the data analyses, were done between 2001 and 2002. However, because of some highly unusual set of circumstances publication of this MSc dissertation has been delayed for a long time. Therefore, some of the reported (material and) values, e.g. heritability estimates, are out of date. Interested readers are encouraged to look for the latest estimates in the Interbull's web site at www.interbull.org.

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ABSTRACT

Progress in dairy cattle breeding is facilitated by good methods to calculate estimated breeding value (EBV) from several countries. It is now possible to exchange genetic material across countries. In 1983 Interbull was formed with the intention to increase the transparency of national genetic evaluation systems in the member countries to facilitate the across-country evaluations. Today, Interbull publishes results of routine evaluations for production, conformation traits, udder health longevity and calving traits.

The objective of this study was to extend the method of conversion of breeding values from single trait to multiple traits. Bulls with EBVs in both Sweden and Denmark were used for the conversions.

A data set containing the information on bulls with evaluations in both Sweden and Denmark was used for this study. The Swedish information included EBVs for bulls, their effective number of daughters and the heritabilities used for different traits. The Danish information included EBVs for bulls together with their corresponding reliabilities. The bulls were born 1986 or later. The common bulls originated from seven countries: Sweden, Denmark, the Netherlands, Germany, France, the United States and Canada.

To find the Danish traits best suited for conversion the traits with correlation of EBVs significantly different from zero were used.

Three different methods of converting Danish traits that showed high genetic correlation with corresponding Swedish EBV were performed and a converted total merit index (C_TMI) were calculated for each of the methods.

The first method was the Wilmink method (Wilmink et al., 1986). One Danish trait was used for calculation of a converted Swedish EBV which in turn was multiplied by the economic weights used in calculation of the Swedish total merit index (TMI) to calculate a converted TMI ($C_TMI_{Wilmink}$).

One alternative to the Wilmink method was to use two or more Danish traits for calculation of converted breeding values for each of the Swedish traits and then combining these into the Swedish TMI ($C_TMI_{indirect\ reg}$).

Another alternative to the Wilmink method was to use two or more Danish traits for direct computation of a converted Swedish TMI ($C_TMI_{direct\ reg}$).

The bulls were ranked in three different Top 20 lists. Correlations between the three different methods were calculated, both for all bulls in the material and for the Top 20 bulls. For the Top 20 bulls the best correlation was observed for $C_TMI_{Wilmink}$ and $C_TMI_{indirect\ reg}$. The same procedure performed for all bulls in the material gave the best correlation for $C_TMI_{direct\ reg}$ and $C_TMI_{indirect\ reg}$.

INTRODUCTION

The fast progress in the reproduction techniques for dairy cattle with, for example, the use of artificial insemination (AI) and embryo transfer is most meaningful when they are combined with methods to calculate estimated breeding values (EBV) from several countries. It is necessary for the farmers and others in charge of breeding that they are able to make an accurate selection decision. Direct comparison of EBVs from one country to another is not possible for several reasons: a) differences in expression of national genetic evaluations; b) traits of interest in one country may not be evaluated in other countries; c) not all countries use the same evaluation model; and d) there might be genotype by environment interaction. In 1983 Interbull was formed with the intention, among other things, to co-ordinate the breeding evaluation in member countries and to facilitate the across country evaluations. Today, Interbull publishes results of routine evaluations for production, conformation, udder health, longevity and calving traits.

In Sweden a large number of functional traits are evaluated since these have a large influence on costs of production. Unfortunately, not all of the traits of interest in Sweden have a direct equivalent in other countries and it is not obvious which method should be used for calculation of a Swedish total merit index (TMI) for foreign bulls, should these bulls lack the evaluation in Sweden. The Swedish TMI value, which is a linear combination of 11 sub-indices, is the basis of the most important selection decisions at all levels of the dairy industry in Sweden and it is of great interest to find accurate methods to estimate a Swedish TMI for foreign bulls until they have nationally estimated breeding value (NBV) for all traits in the Swedish TMI.

The objective of this study was to compare three different methods of conversions of breeding values. The three methods were:

- 1) **Single trait conversion**, the so-called Wilmink method, to calculate converted Swedish breeding values, which in turn were multiplied by the Swedish economic weights to calculate a converted TMI (C_TMI_{Wilmink}).
- 2) **Indirect multi-trait conversion** where several Danish traits were regressed on each of the Swedish sub-indices. The converted breeding values for the Swedish sub-indices were then combined into a converted TMI ($C_TMI_{\text{indirect reg}}$).
- 3) **Direct multi-trait conversion** where several Danish traits used earlier were regressed directly on Swedish TMI. All traits with high correlation to any of the Swedish EBVs were initially used for regression on the Swedish TMI. The combination of traits that resulted in a high adjusted R^2 was used for direct calculation of a converted TMI ($C_TMI_{\text{direct reg}}$).

In order to compare these three methods the results of Danish and Swedish genetic evaluation are used as an example. The methods can be used for many other purposes.

CONVERSIONS OF BREEDING VALUES

There are several possible methods of calculating EBVs for foreign bulls. One is by using conversion equations, a simple, cheap method that allows only pair wise comparisons. An EBV from the exporting country is converted to an EBV in the importing country by the equation:

$$EBV_{imp} = a + b \times EBV_{exp} \quad [1]$$

a = the difference in base between the two countries (intercept)

b = the conversion coefficient (slope)

This method has successfully been used in many countries. However, estimation of a - and b -values assumes random use of the bulls in both countries. If not, the estimates might be biased and give either an over- or under-estimate of the bulls' converted breeding value. When estimating the a and b coefficients or breeding values the data set must contain data from most recent official evaluation. The bulls should be born within a 10-year period counted from the youngest bull with reliable proofs. At least 20 bulls with daughters in at least 20 herds and a repeatability of 75% or more in both countries are needed for an accurate estimate (Interbull, 1990).

Nowadays, compared to 1980's and 1990's, evaluation results from a larger number of traits are available. Therefore, it would be interesting to use multiple trait regression method, i.e. to regress more than one trait from the exporting country to one trait in the importing country.

Multiple trait regression implies that several of the traits in the exporting country are regressed on one trait or a TMI sub-index or the TMI in the importing country.

DAIRY CATTLE BREEDING IN SWEDEN

BREEDING ORGANISATION

The Swedish breeding goals are high producing cows and low production costs, giving the producer an overall good economy. Functional traits such as fertility, disease resistance and functional conformation are important to reduce the costs for the producer. The Swedish Dairy Association, Svensk Mjölk, decides the breeding goal. The Swedish Dairy Association is a farmer co-operative organization formed by dairy companies, AI-companies and animal services co-operatives.

In Sweden there were 417 000 dairy cows in June 2002. The Swedish milk recording system included 85%, or 354 799 of all cows. The average herd size was 40 cows. The most common breeds are Swedish Red and White (SRB) and Swedish Holstein (SLB), which comprise 47.1% and 47.4% of the recorded cows respectively. Production figures are presented in Table 1

Table 1

Information about the dairy breeds in Sweden 2002 (Svensk Mjök, 2003-12-04).

Breed	Number of recorded, pure-bred cows	Average yield	
		milk, kg	fat + protein, kg
Swedish Red and White (SRB)	166 995	8 427	649
Swedish Holstein (SLB)	168 183	9 234	667
Swedish Polled Cattle (SKB)	1 797	5 653	446
Jersey (SJB)	1 786	6 132	583

GENETIC SELECTION PROCEDURES FOR SWEDISH HOLSTEINS

Svensk Avel, the only AI organisation carrying out a domestic breeding program for dairy cattle, buys approximately 120 bull calves every year. These are selected on pedigree and dam's performance. Additionally about 40 bull calves are produced by embryo transfer for progeny testing. The young bulls are kept together and performance tested on daily gain and growth. Between 60-70 young bulls, 12-16 months old, are selected for progeny testing. The aim is to get 130 daughters tested. This requires about 1300 doses from each bull. The bulls are kept waiting while the daughters' results are evaluated. Every year 3-4 bulls will be approved as elite bulls (Hans Stålhammar, personal communication).

GENETIC EVALUATION PROCEDURES

The Swedish Dairy Association is responsible for the official milk recording and performs national genetic evaluations for a large number of traits. Breeding values are expressed on a relative scale with mean 100 and defined to make high values desirable. Genetic standard deviation is standardised to 7 for all traits. Genetic base is defined as a rolling average of the last three years of tested bulls (Svensk Mjök, 2001).

Total Merit Index

The Swedish total merit index (TMI), calculated for bulls and cows, comprises a large number of sub-indices. The TMI values are the basis of the most important selection decisions at all levels of the dairy industry. For Holstein bulls the TMI is calculated from eleven sub-indices, as described in Table 2. Heritabilities of individual traits used in any sub-index will be presented separately. However; heritabilities used for the most important traits are summarized in Table 5.

Table 2

TMI-indices included in TMI and their economic weights (Svensk Mjök, 2001).

Index	Economic weight for Swedish Holstein bulls.
Yield index	1.000
Beef index	0.200
Daughter fertility	0.350
Calving performance - sire	0.100
Calving performance – MGS	0.300
Mastitis resistance	0.400
Resistance to other diseases	0.100
Udder	0.400
Legs	0.300
Temperament	0.100
Residual stayability	0.200

Yield sub-index

Breeding values calculated for the milk production traits are based on 305 days milk recording from lactations longer than 100 days in the first lactation. Records on culled cows are extended from 46 days. Data from 1983 and onwards are included. A single-trait animal model is used. The model includes, among other things, age at first calving, calving month and number of days open.

From the official milk recording system recordings of milk (kg), fat and protein yield (kg), are used to calculate the TMI sub-index for milk production traits (TMI_{yield}) (Interbull, 2000):

$$TMI_{\text{yield}} = -0.2(EBV_{\text{milk}} - 100) + 1.05(EBV_{\text{protein}} - 100) + 0.2(EBV_{\text{fat}} - 100) + 100 \quad [2]$$

The breeding values are published 4 times per year and criteria for official publication are 15 daughters in lactation and 15 completed 305 days lactations or alternatively an effective number of daughters of 40.

Beef sub-index

Breeding values for beef production traits are calculated using information on carcass gain and carcass classification from the slaughterhouses. Bull calves slaughtered between 365 and 850 days of age are used in the evaluation of carcass gain. Carcass classification is scored according to the EUROP system. Data from 1985 are included. A single-trait sire model including effects of herd-year-season, month of birth and month of slaughter is used. A minimum of 15 effective sons are required for official publication and the breeding values are published twice a year (Interbull, 1996).

$$TMI_{\text{beef}} = 0.85 \times EBV_{\text{carcass gain}} + 0.55 \times EBV_{\text{carcass classification}} \quad [3]$$

Daughter fertility sub-index

The daughter fertility index (TMI_{DF}) combines the breeding values for fertility disorder (EBV_{FD}) with the breeding value for daughter fertility (EBV_{DF}). The EBV_{DF} in its turn is a combination of number of inseminations per period (NINS), calving to first insemination (CFI) between 20 and 230 days and heat strength (HS). Cows with more than 7 inseminations, heat synchronized or moved within the period are excluded from the genetic evaluations. The traits are observed on first lactation cows inseminated between 12 and 27 months, heifers calving between 22 and 36 months and 2nd lactation cows. A sire model, including effects of herd-year- season, month-year and breed is used. The TMI_{DF} is published twice a year for bulls with at least 69 effective daughters.

Table 3

Heritabilities estimated for the traits in the TMI_{DF} (Svensk Mjöl, 2001).

	Trait	h^2
Heifer traits	NINS	0.025
	HS heifer	0.020
Cow traits	NINS 1 st lact	0.050
	NINS 2 nd lact	0.040
	CFI 1 st lact	0.040
	CFI 2 nd lact	0.030
	HS 1 st lact	0.020
	HS 2 nd lact	0.025

Calculation of TMI_{DF} (Interbull, 1996) is as follows:

$$\begin{aligned} EBV_{DF} = & - 959 \times EBV_{NINS \text{ heifer}} - 725 \times EBV_{NINS \text{ 1st lact.}} - 841 \times EBV_{NINS \text{ 2nd lact}} \\ & - 632 \times EBV_{HS \text{ heifer}} - 452 \times EBV_{HS \text{ 1st lact}} - 524 \times EBV_{HS \text{ 2nd lact}} \\ & - 8.5 \times EBV_{CFI \text{ 1st lact}} - 18.3 \times EBV_{CFI \text{ 2nd lact}} \end{aligned} \quad [4]$$

$$TMI_{DF} = 0.80 \times EBV_{DF} + 0.35 \times EBV_{FD} \quad (\text{Svensk Mjöl, 2001}) \quad [5]$$

Calving performance sub-index as sire and as maternal grand sire

The TMI sub-indices for calving performance for sires and maternal grandsires (TMI_{sire} and TMI_{mgs}) include calving difficulty (CD) and stillbirths (SB). Farmers score these traits and report when the bull is sire or maternal grandsire (MGS) of the calf. Calves that are born dead or died within 24 hours after birth are considered stillborn and twins are excluded. Calvings that require assistance from veterinarian or two persons pulling the calf out are considered as difficult. A sire model, including the fixed effects of herd-year, year-calving month, sex of calf, breed of dam, calving age, sire and MGS of calf, is used. Calves of unknown sex are randomly distributed as 70% males and 30% females (Interbull, 1996).

The two TMI sub-indices are calculated separately according to equations set up by the Swedish Dairy Association and published twice a year for bulls with more than 100 registered calvings.

The TMI_{sire} for calving performance as sire of the calf is calculated as:

$$0.70 \times EBV_{SBsire} + 0.45 \times EBV_{CDsire} \quad [6]$$

The TMI_{mgs} for calving performance as maternal grand sire of the calf is calculated as:

$$0.70 \times EBV_{SBmgs} + 0.40 \times EBV_{CDmgs} \quad [7]$$

Sub-index for Resistance to mastitis

The sub-index for mastitis resistance (TMI_{MR}) consists of the EBV for clinical mastitis and for somatic cell count (SCC) in first lactation. Veterinarians report presence of clinical mastitis or data are registered from culling reports. Cows with diagnosed mastitis during first lactation are registered. The two traits are evaluated separately and then weighed together. The genetic correlation between the traits is estimated to be 0.70, and the economic weight of SCC is set to 0. Therefore, the SCC is only used to increase the accuracy of the prediction of clinical mastitis resistance (Svensk Mjolk, 2001). The sire model used considers herd-year-season, calving month, calving age and breed of dam. The criterion for official publication is at least 70 effective daughters and the index is published twice a year (Interbull, 1996).

Sub-index for Resistance to other diseases

The TMI sub-index for resistance to other diseases (TMI_{OD}) comprises resistance to other diseases than mastitis or fertility disorders and is scored as no treatment (0) or treatment (1) from 10 days before to 150 days after first calving. Recorded diseases are ketosis, retained placenta, paresis, teat injuries, leg and foot diseases, infectious and metabolic disorders reported by veterinarians or culling reports. The evaluation procedure is the same as for resistance to mastitis (Svensk Mjolk, 2001).

Sub-indices for Conformation and workability traits

Conformation and workability traits are scored on a linear 1-9 point scale on first lactation cows 30 to 270 days after calving. Employees from the animal service companies perform the classifications. The cow must be between 21 and 36 months of age when the calf is born for the record to be included. The traits front teat placement, teat length, floor to udder distance, and stature are also measured in centimetres. Individual traits and their heritabilities are presented in Table 4. Note that only some of the presented traits for “leg” and “udder” are included in the corresponding sub-indices.

A single trait animal model is used, the effects of classifier-year, calving age, month, stage of lactation (8 classes) and hours post milking (for udder traits) are considered in the model (Svensk Mjolk, 2001).

Table 4

Used heritabilities for the conformation and workability traits (Svensk Mjöl, 2001).

Trait	h^2	Trait	h^2
<i>Body</i>		<i>Udder</i>	
Dairyness	0.350	Udder balance	0.200
Strength	0.200	Udder oedema	0.150
Body depth	0.300	Extra teats	0.300
Rump width	0.300	Fore udder attachment	0.300
Rump angle	0.350	Rear udder height	0.350
Topline	0.250	Rear udder width	0.350
Body remarks	0.100	Suspensory ligament	0.150
		Udder depth	0.200
<i>Legs</i>		Teat placement	0.200
Rear leg set	0.200	Teat length	0.300
Legs rear view	0.200	Udder remarks	0.100
Foot angle	0.200		
Hock quality	0.200	<i>Workability</i>	
Leg remarks	0.100	Milking speed	0.250
Weak pasterns	0.100	Leakage	0.100
Straight pasterns	0.150	Temperament	0.150
Skeleton	0.300	Temperament as heifer	0.150
<i>Measured</i>			
Teat length, cm	0.350		
Front teat distance, cm	0.350		
Teat to floor, cm	0.350		

Sub-index for Residual survival

The sub-index for residual survival describes the daughters' ability to survive the second lactation. Three traits are defined as surviving the first lactation, surviving 150 days of second lactation and surviving second lactation and are scored as dead or alive. Probabilities of surviving the designated time are computed for cows that are alive at the time of evaluation. A single trait sire model, including the effects of herd-year-season, calving month, calving age, breed of dam and sire of cow, is used. Data since 1982 are included (Eriksson, 2000).

Included in the TMI is residual survival (TMI_{SRES}) until end of second lactation. Residual survival is adjusted for the effects of traits that influence stayability and are already included in the TMI.

$$TMI_{SRES} = EBV_{\text{survival}} - 0.25 \times TMI_{\text{yield}} - 0.19 \times TMI_{\text{DF}} - 0.10 \times TMI_{\text{sire}} - 0.05 \times TMI_{\text{MGS}} - 0.30 \times TMI_{\text{MR}} - 0.11 \times TMI_{\text{OD}} \quad [8]$$

Table 5

Heritabilities used for some traits in the TMI (Svensk Mjölkk & Eriksson, 2000).

Trait	h ²	Trait	h ²
Milk, kg	0.250		
Fat, kg	0.250	Days open 1 st lactation	0.040
Protein, kg	0.250	2 nd lactation	0.030
Fat, %	0.500	Stillborn, %	0.020
Protein, %	0.500	Difficult calvings, %	0.020
Carcass gain, g	0.330	Clinical mastitis	0.020
Carcass classification, %.	0.300	SCC	0.080
NINS heifer	0.025	Fertility disorders	0.020
NINS 1 st lactation	0.050	Other diseases	0.020
NINS 2 nd lactation	0.040	Survive 1 st lactation	0.020
Heat strength heifer	0.020	1 st + 150 days	0.020
1 st lactation	0.020	2 nd lactation	0.020
2 nd lactation	0.025		

DAIRY CATTLE BREEDING IN DENMARK

BREEDING ORGANISATION

The Danish breeding goal is to maximise the profits by optimising the genetic progress. The model, called the "Scandinavian profile", takes into account not only production traits but also focuses on cost savings through lower incidence of mastitis as well as improved fertility and functional traits like milking speed and conformation. The TMI, called S-index in Denmark, for bulls summarises all the main EBVs according to their economic weights (<http://www.cattle.dk/Raceforeninger/diverse/service.htm>).

Danish breeding goal is based on milk records, performance tests and recorded data of fertility, calving ability, conformation and health. There are recordings from more than 85% of all Danish dairy cattle (Dansire, 2001).

The most common dairy breeds present in Denmark are Danish Holsteins, Danish Jerseys and Red Danish Dairy Breed. In 1999 the tested population averaged 7828, 5471 and 7161 kg milk for Holsteins, Jerseys and Red Danish Dairy Breed, respectively (Table 6). The average fat yield varied from 301 to 327 kg and the protein yield varied from 224 to 264 kg. The average herd size was 61 cows.

Table 6Three main dairy breeds in Denmark in 1999 and some recorded results of production (<http://www.cattle.dk/Raceforeninger/diverse/CATTLE.htm>).

Breed	Number of recorded, pure-bred cows	Average yield		
		milk, kg	fat, kg	protein, kg
Danish Holsteins	403 544	7 828	325	264
Danish Jerseys	71 879	5 471	327	224
Red Danish Dairy Breed	55 480	7 161	301	256

Denmark was the first country in the world to use artificial insemination as a tool in cattle breeding (<http://www.cattle.dk/Raceforeninger/diverse/service.htm>). The Danish Holstein Association handles the interests related to Danish Holstein cattle in close co-operation with the Danish AI-centres.

BREEDING PROGRAM FOR DANISH HOLSTEINS

Six AI-societies co-operate in The Federation of Danish AI-societies (<http://www.cattle.dk/Raceforeninger/diverse/Service.htm>). All of the societies have their own bull station (Dansire, 2001).

Each year about 500 selected bull calves are bought by the AI-societies. Between the ages of 12 and 18 months, 300 of those are reserved at an AI-centre where they produce semen for 800 test-doses and 3000 doses for storage. The AI-societies co-operate in the progeny testing of the young bulls. The young bulls wait while the different recordings on their offspring are made. Criteria for approval are a TMI above 109. The result is about 8 selected new bulls after 57 months. Two of the new bulls will be recommended as sires of sons.

NATIONAL GENETIC EVALUATION PROCEDURES

On national level “The National Committee on Danish Cattle Husbandry” is the highest authority on dairy cattle breeding. The committee is responsible for official milk recording and national breeding evaluation. The milk recording routines follow the regulations of The International Committee for Animal Recording (ICAR). Breeding values are expressed on a relative scale with mean 100 and defined to make high values desirable. Genetic base is defined as a rolling average of the last five years of tested bulls (Dansire, 2001).

Total Merit Index

In Denmark different traits are summarized into ten sub-indices, which in turn are combined with each other in a TMI according to their different economic weights. The economic weights used for Danish Holstein are presented in Table 8. The Danish TMI is calculated eight times per year. Heritabilities for some traits in the TMI are presented in Table 7.

Table 7

Heritabilities used for the traits in the Danish TMI (Årsstatistik-Avl, 1999-2000).

Trait	h ²	Trait	h ²
Milk	0.300	Size, (1 st)	0.040
Fat	0.300	Vitality, (later)	0.010
Protein	0.300	Calving ease, (later)	0.030
Carcass weight	0.160	Size, (later)	0.040
Carcass classification	0.290	Mastitis I	0.040
NR 56 (heifer)	0.008	Mastitis II	0.050
IFL (heifer)	0.016	Mastitis III	0.050
NR 56 (cow)	0.010	Mastitis IV	0.050
CFI (cow)	0.070	SCC	0.110
IFL (cow)	0.020	Dairy form	0.260
Vitality, (1 st)	0.040	Fore udder attachment	0.240
Calving ease, (1 st)	0.070	Udder depth	0.330

Table 8

The composition of TMI, the EBVs are expressed as indices with a mean of 100 (Årsstatistik-Avl, 1999-2000).

Sub-index	Economic weight for Danish Holstein
Y-index (yield)	0.800
I-index (growth, muscle area)	0.050
Daughter fertility index	0.250
Calving index	0.180
Mammary health index	0.420
Body index	0.200
Feet and legs index	0.360
Mammary system index	0.400
Milking speed index	0.140
Temperament index	0.040

Yield sub-index

The sub-index for milk production (TMI_{yield}) is published eight times per year for all bulls with enough information to give 60% reliability (Interbull, 2000). The breeding values are based on 305 days milk recording from the first three lactations. The evaluation is based on recordings from the official milk recording. Incomplete lactations are included if they have lasted more than 45 days and been recorded twice. The TMI_{yield} consists of three traits, milk yield (M), fat yield (F), and protein yield (P). A single breed, single trait animal model is used including information on all cows with their first lactation starting after January 1st 1982. The model includes management group, calving year-month-period, calving age-lactation-period, and previous calving interval-lactation-period. The heritability used for the TMI_{yield} is 0.30 for milk, fat and protein yields. The TMI_{yield} is constructed with economic weights corresponding to the breeding goal. For Danish Holsteins the composition of TMI_{yield} is (Årsstatistik-Avl, 1999-2000):

$$TMI_{yield} = 100 + (-0.125 \times (EBV_M - 100) + 0.375 \times (EBV_F - 100) + 0.750 \times (EBV_P - 100))$$

[9]

Sub-index for beef production (I-index)

The sub-index for beef production traits (TMI_{beef}) includes data from the slaughter industry from slaughtered bull calves with a slaughtered weight between 140 and 320 kg. Information on carcass gain and carcass classification according to the EUROP system is collected. The calf must be between 210 and 540 days old when slaughtered and not moved from the herd after 90 days of age.

The TMI_{beef} is based on two traits, growth and muscle area. A multiple trait, sire model is used. Fixed effects in the model are herd-birth year, season-year of birth, age of dam, slaughter season-age-year, multiple birth, breed and heterosis. Heritabilities used are 0.16 for carcass weight and 0.29 for carcass classification. Different weights are used for different breeds in the calculation of TMI_{beef} , according to the breeding goal. For Danish Holstein the composition of the TMI_{beef} is:

$$TMI_{\text{beef}} = 16.04 \times EBV_{\text{growth}} + 245 \times EBV_{\text{muscle area}} \quad [10]$$

The TMI_{beef} is published four times per year and the minimum reliability required for official publication is 50%.

Daughter fertility sub-index

The female fertility sub-index, $TMI_{\text{fertility}}$, is a standardised sub-index of TMI that combines five female fertility traits (Årsstatistik-Av1, 1999-2000). The trait “non-return rate after 56 days” (NR56) is recorded as re-inseminated or not (1/0). Insemination period (IFL) is the interval, in days, from first to last insemination. NR56 and IFL are recorded both on heifers (h) and on cows (c). The interval, in days, from calving to first insemination (CFI) is recorded on cows (Interbull, 1996).

The estimation of breeding values is based on fertility records registered since 1985 (Dansire, 2001). Insemination information is collected from the AI service and the information on calving data from the milk recording system. Information from all lactations is included. The breeding values are estimated with a multiple trait sire model for heifer and cow traits separately. The model includes the effects of heterosis, herd-year, age at calving (age at first insemination for heifers), and calving season-year (Interbull, 1996).

The breeding values are estimated four times per year. The minimum reliability required for official publication is 35%. The total TMI-index for female fertility is calculated (Interbull, 1996) as:

$$TMI_{\text{fertility}} = 100 + (0.61 \times EBV_{\text{NR56(h)}} - 5.30 \times EBV_{\text{IFL(h)}} + 1.32 \times EBV_{\text{NR56(c)}} - 13.50 \times EBV_{\text{IFL(c)}} - 13.50 \times EBV_{\text{CFI}}) / 24 \quad [11]$$

Calving sub-index

Information on all calvings is collected from the milk recording system. Recorded traits are vitality of the calf, calving ease and size of the calf. The traits are recorded separately for first calving and later calvings. Vitality is defined as an all or none trait where a calf born dead or

dead within 24 hours after birth is scored 0. Calving ease and size are scored from 1 to 4 where 1 is used for an easy calving and a small calf and 4 is used for a very difficult calving (assisted by a veterinarian) and a big calf.

The sub-index for calving (TMI_{calving}) is a value describing the ability of daughters of sires to give birth to live born calves and to have easy calving (maternal traits). The EBV_{birth} is an index describing the ability of sires to breed easy born and live born calves (direct traits). All traits are evaluated simultaneously with a multi trait sire model. The model includes the effects of herd-year, season-year, age of calf-region, and sex of calf-region.

Only TMI_{calving} is included in the TMI, the birth performance traits are combined in to the EBV_{birth} that is used for selection of sires for heifer inseminations (Pedersen *et al.*, 1995). The recorded traits are weighed together with different economic weights. In the EBV_{birth} only vitality and calving ease have economic weights due to the focus on heifer calvings (Dansire, 2001).

The TMI_{calving} is calculated as (Interbull, 1996):

$$TMI_{\text{calving}} = 100 + ((850 \times EBV_{\text{vitality1st}} + 165 \times EBV_{\text{ease 1st}} + 12.25 EBV_{\text{size1st}} + 1225 \times EBV_{\text{vitality later}} + 135 \times EBV_{\text{ease later}} + 10 \times EBV_{\text{size later}}) / 17) \quad [12]$$

Udder health sub-index

A new, improved sub-index for udder health (TMI_{UH}) was introduced in Denmark in March 2000. The information about mastitis in different periods is treated as four different traits (see Table 9). Somatic cell count (SCC) in the period 10-180 days after calving in the first parity and three conformation traits (dairy form, fore udder support and udder depth) are used in TMI_{UH} (Sander Nielsen *et al.*, 2000).

Table 9

Mastitis in four different periods are recorded and used in the sub-index $TMI_{\text{udder health}}$.

	Period of registration
1 st parity (I)	10 days before calving until 50 days after calving
1 st parity (II)	10 days before calving until 305 days after calving
2 nd parity (III)	10 days before calving until 100 days after calving
3 rd parity (IV)	10 days before calving until 100 days after calving

Data from the Danish health recording system are used. Veterinarians and farmers report the data since 1990 (Sander Nielsen *et al.*, 2000). The statistical model used is a multiple trait sire model. The model includes the effects of herd-year-season, year-month and calving age (in first parity) (Dansire, 2001). The EBVs for mastitis are summarised in the TMI_{UH} . Each of the four EBVs has the same economic weight in the TMI sub-index. The TMI_{UH} is calculated four times a year and is published if the reliability is 40% or higher (Årsstatistik-Av1, 1999-2000).

Sub-indices for conformation and workability traits

The linear type traits registered on cows in first lactation, presented in Table 10, are used together with a score on milking speed and temperament when calculating the sub-indices for conformation and workability traits (Årsstatistik-Av1, 1999-2000). The evaluation model is a single trait animal model that includes the effects of season-year-classifier, months from calving, month of calving, age at calving and herd-year-season (Dansire, 2001).

Table 10

Used heritabilities and economic weights (W) for the conformation and workability traits.

Trait	h^2	W	Trait	h^2	W
<i>Body</i>			<i>Mammary system</i>		
Stature	0.600	0.100	Fore udder attachment	0.240	0.140
Body depth	0.310	0.170	Rear udder width	0.220	0.140
Chest width	0.180	0.120	Udder cleft	0.190	0.140
Dairy form	0.310	0.200	Udder depth	0.360	0.140
Top line	0.160	0.120	Teat length	0.410	0.070
Rump width	0.270	0.100	Teat thickness	0.310	0.050
Rump angle	0.320	0.070	Teat placement (front)	0.400	0.200
Code for rump disorder	0.100	0.120	Codes for teat disorder	0.120	0.120
<i>Feet and legs</i>			Milking speed	0.260	0.140
Rear legs, side view	0.230	0.100	Temperament	0.130	0.040
Rear legs, rear view	0.130	0.250			
Hock quality	0.180	0.200			
Bone quality	0.280	0.100			
Foot angle	0.130	0.350			

Sub-index for other health traits

Danish index for other health traits (EBV_{health}) was not yet included in the Danish TMI when the data used in the present study was acquired. The index includes reproductive- digestive- and feet / leg diseases in the period 10 days before calving to 100 days after calving in first, second and third parity.

MATERIAL AND METHODS

MATERIAL

To reduce the risk of receiving inaccurate conversion equations the data set contained data from most recent official proofs. The bulls were born within a 10-year period counted from the youngest bull with reliable proofs. At least 20 bulls with daughters in at least 20 herds and a repeatability of 75% or more in both countries were used as the bull selection criteria. This was recommended by Interbull (Interbull, 1990).

The material used was the results of the Swedish national genetic evaluations from May 2001 for Holstein bulls used in Sweden, in form of national breeding values (NBV). The Swedish

material was completed with NBVs for Swedish bulls used in Denmark. After edits the Swedish material contained 430 bulls and information on the number of effective daughters, or sons, for the sub-indices.

The material from Denmark contained Danish NBVs from April 2001 for all Holstein bulls used in Denmark. The Danish material contained breeding values, reliabilities (REL) for the sub-indices and number of effective daughters for the conformation and workability traits.

A merged dataset was created, including Swedish NBVs, number of effective daughters in Sweden and the reliabilities calculated from the number of effective sons and daughters for different traits (see equation [14]), together with Danish NBVs and their corresponding reliabilities. All bulls were born 1986 or later. The common bulls in the merged data set originated from seven countries: Sweden, Denmark, the Netherlands, Germany, France, the USA and Canada. The total number of bulls with breeding values in both countries was small, only 64 bulls were found totally. The number of common bulls for the traits with the same name or definition was even smaller. The number of bulls with EBVs in both Sweden and Denmark varied between traits. There were 35 Danish traits included in this study.

METHODS

All statistical calculations were performed with the statistical software SAS (SAS Institute Inc. Cary, NC, USA).

To find the Danish traits best suited for conversion to each Swedish EBV the Pearson product-moment correlation (r_p) between NBVs in Sweden and Denmark was computed. The traits with r_p value significantly different from zero were used. Genetic correlations were estimated for these traits by the Calo-method, as described by Blanchard *et al.* (1983):

$$r_g = r_p \times \frac{\sqrt{(\sum REL_{swe} \times \sum REL_{dk})}}{\sum (REL_{swe} \times REL_{dk})} \quad [13]$$

r_g = the genetic correlation between traits

r_p = the Pearson correlation between traits

REL_{swe} = the reliability of the breeding value for the Swedish trait

REL_{dk} = the reliability of the breeding value for the Danish trait

The Swedish material contained no information about reliabilities of the breeding values but information on the effective number of recorded offspring for the different sub-indices. The Swedish reliabilities were approximated as (Blanchard *et al.*, 1983, Calo *et al.*, 1973):

$$REL_{swe} = \frac{n_{swe}}{n_{swe} + (\sigma_e^2 / \sigma_s^2)} \quad [14]$$

n_{swe} = the effective number of recorded offspring in Sweden

$$\sigma_e^2 / \sigma_s^2 = \text{the ratio of error to sire variance} = \frac{4 - h^2}{h^2} \quad [15]$$

The Wilmink method

The Wilmink method (Wilmink *et al.*, 1986) was used for the conversion of the Danish traits that showed high genetic correlation with corresponding Swedish TMI sub-index. The equation below [16], was initially sanctioned by the International Dairy Federation (IDF):

$$CBV_{swe} = a + (b \times EBV_{dk}) \quad [16]$$

CBV = converted breeding value

a = the difference in base between the two countries (intercept)

b = the conversion coefficient (slope)

Wilmink *et al.* (1986) suggested to use the reliability in the importing country to adjust the EBVs in the exporting country, the breeding value of exporting country is expressed as a deviation from mean and multiplied by the Swedish reliability:

$$EBV_{dk}^* = (EBV_{dk} - \overline{EBV_{dk}}) \times REL_{swe} \quad [17]$$

A b -value is estimated with:

$$EBV_{swe} = a + (b^* \times EBV_{dk}^*) + \varepsilon \quad [18]$$

The estimated a -values adjusts for differences in genetic levels, the difference of mean breeding value after the breeding value from Denmark has been rescaled by the conversion coefficient (b):

$$a^* = (\overline{EBV_{swe}}) - b \times (\overline{EBV_{dk}}) \quad [19]$$

Finally, converted values for different Swedish TMI sub-indices were calculated. The converted Swedish TMI sub-indices were multiplied with the economic weight used when calculating Swedish TMI.

Multiple regression

Considering the availability of national genetic evaluation for a larger number of traits it is natural to extend single trait conversion method to multiple traits, e.g. calculate Swedish EBVs by using more than one Danish trait. Two different approaches were used:

Indirect multi-trait conversion: A converted breeding value (CBV) for each Swedish TMI sub-index was calculated by the extension of the single trait conversion, as recommended by the International Dairy Federation (IDF, 1981), to two or more traits. For this purpose the Danish traits with an r_p value higher than 0.3 ($p < 0.05$) were regressed on each of the Swedish TMI sub-indices. Several combinations of Danish traits were evaluated to find the best match for each Swedish TMI sub-index. The aim was to maximize the value of the adjusted R^2 .

$$CBV = a + (b_1 \times EBV_{dk,1}) + (b_2 \times EBV_{dk,2}) + \dots + (b_n \times EBV_{dk,n}) \quad [20]$$

The converted TMI sub-indices were combined to a converted TMI ($C_TMI_{indirect\ reg.}$) with the economic weights used for calculation of Swedish TMI presented earlier.

Direct multi-trait conversion: As above, with the exception that the Danish traits were directly used for calculation of a converted Swedish TMI ($C_TMI_{direct\ reg.}$).

$$C_TMI_{direct\ reg.} = a + (b_1 \times EBV_{dk,1}) + (b_2 \times EBV_{dk,2}) + \dots + (b_n \times EBV_{dk,n}) \quad [21]$$

RESULTS AND DISCUSSION

CORRELATIONS AND COMMON BULLS

Milk index

The Danish TMI_{yield} , index for other health traits, fat yield and teat thickness showed high correlation with the Swedish TMI_{yield} and were used for conversion. Almost all of the common bulls had corresponding breeding values for milk production in both countries, the correlation between indices was very high, as expected, and is presented in Table 11. A negative correlation between Swedish TMI_{yield} and Danish index for other health traits (not included in TMI) were found.

Table 11

Number of common bulls, estimated genetic correlation and level of significance for correlations ($Pr > F$) for Danish traits used for conversion to the Swedish TMI_{yield} .

Trait	Number of common bulls	Genetic correlation	$Pr > F$
TMI_{yield}	60	0.917	<0.0001
Index for other health traits	47	-0.420	0.0194
Fat yield	60	0.678	<0.0001
Teat thickness	44	0.423	0.0102

Beef index

Since this sub-index is evaluated in a similar way in both countries higher correlations would have been expected if it had been possible to compare the traits directly. However, in the material used for the calculations there were no reliabilities presented for the Danish beef-production traits, therefore the Danish TMI_{beef} could not be used. The traits best corresponding to Swedish TMI_{beef} were the Danish protein yield, stature and teat length. Correlations and significance levels are presented in Table 12.

Table 12

Number of common bulls, estimated genetic correlation and level of significance for correlations ($Pr > F$) for Danish traits used for conversion to the Swedish TMI_{beef} .

Trait	Number of common bulls	Genetic correlation	$Pr > F$
Protein yield	53	0.350	0.0472
Stature	48	0.415	0.0205

Daughter fertility index

The traits used to estimate Swedish TMI_{DF} was Danish $TMI_{fertility}$ and the conformation trait chest width. There were 48 and 54 common bulls respectively. Table 13 shows the genetic correlation and significance level of the correlations. The correlation between Swedish and Danish daughter fertility index was rather low, 0.373.

Table 13

Number of common bulls, estimated genetic correlation and level of significance for correlations ($Pr>F$) for Danish traits used for conversion to the Swedish TMI_{DF} .

Trait	Number of common bulls	Genetic correlation	$Pr>F$
$TMI_{fertility}$	48	0.373	0.0274
Chest width	54	0.501	0.0031

The reason for the relatively low correlations may be explained as follows: There is only one common trait used for calculation of the sub-indices for daughter fertility, Swedish TMI_{DF} and Danish $TMI_{fertility}$, in the two countries. The Danish TMI -index is based on non-return rate in 56 days (NR56), insemination period and calving to first insemination (CFI). In Sweden the traits fertility disorder incidence, number of inseminations per period (NINS), heat strength and CFI are combined. Both countries record data from heifers. In Sweden information on cows in first and second parity are used and in Denmark records from cows in all parities are registered. There are discussions whether traits measured in different parities are the same trait or not since they might be regulated by different sets of genes (Roth *et al.*, 1998. Roxström *et al.*, 2001).

Calving performance index – Sire and MGS

The Danish traits used for conversion to the Swedish TMI_{sire} were birth performance traits, index for other health traits, fat yield, fat percent and the conformation trait teat length.

It seems, as if the maternal calving performance traits have no influence on the direct traits.

Table 14

Number of common bulls, estimated genetic correlation and level of significance for correlations ($Pr>F$) for Danish traits used for conversion to the Swedish TMI_{sire} .

Trait	Number of common bulls	Genetic correlation	$Pr>F$
Birth performance traits	44	0.552	0.0018
Index for other health traits	43	0.443	0.0314
Fat yield	56	0.405	0.0263
Fat percent	41	0.452	0.0162
Teat length	42	-0.419	0.0353

The Danish traits best corresponding to the Swedish TMI_{mgs} were the Danish $TMI_{calving}$, birth performance traits and index for other health traits. Some conformation traits also showed high correlation: rump width and front teat placement. Table 14 present the number of common bulls, genetic correlation and level of significance for these correlations.

Table 15

Number of common bulls, estimated genetic correlation and level of significance for correlations ($Pr>F$) for Danish traits used for conversion to the Swedish TMI_{MGS}

Trait	Number of common bulls	Genetic correlation	$Pr>F$
$TMI_{calving}$	52	0.471	0.0067
Birth performance traits	47	0.372	0.0343
Index for other health traits	46	0.517	0.0078
Rump width	56	0.438	0.0156
Teat front placement	44	0.420	0.0172

The Danish $TMI_{calving}$ describes maternal traits; the daughters' ability to give birth to live born calves and to have easy calvings. The birth performance traits consists of direct traits, predicting the bulls' ability to breed easy born and live born calves. Calving ease and live born calves are registered in both countries and the Danish breeding value is also based on the size of the calf. In Denmark records from heifers are evaluated separately. Since Swedish TMI_{MGS} describes maternal traits, the Danish $TMI_{calving}$ would have been expected to show the highest correlation to Swedish TMI_{MGS} .

Resistance to mastitis

The traits used for conversion to Swedish TMI_{MR} were the Danish $TMI_{udder\ health}$, stayability and the conformation traits teat length and udder depth. The correlations were generally high but the number of common bulls was low for all of the traits, as seen in Table 16.

Table 16

Number of common bulls, estimated genetic correlation and level of significance for correlations ($Pr>F$) for Danish traits used for conversion to the Swedish TMI_{MR} .

Trait	Number of common bulls	Genetic correlation	$Pr>F$
$TMI_{udder\ health}$	48	0.518	0.0035
Stayability	43	0.594	0.0015
Teat length	48	0.834	0.0023
Udder depth	46	0.457	0.0169

In Sweden only information of SCC and clinical mastitis from first lactation cows are registered in the TMI_{MR} . The Danish TMI_{UH} combines some udder conformation traits with SCC and incidence of mastitis from four different periods (first to third parity). The correlation between mastitis resistance and stayability might be explained since presence of mastitis is one of the most customary reasons for culling in dairy cattle.

Index for survival

When estimating conversion equations for the Swedish TMI_{SRES} the Danish traits fat percent, rump width and rear legs – side view were used. Correlations were rather high, as shown in Table 17, but might be rather coincidental since the Danish breeding values corresponding to Swedish survival are difficult to explain biologically.

Table 17

Number of common bulls, estimated genetic correlation and level of significance for correlations ($Pr>F$) for Danish traits used for conversion to the Swedish TMI_{SRES} .

Trait	Number of common bulls	Genetic correlation	$Pr>F$
Fat percent	45	-0.419	0.0317
Rump width	57	0.569	0.0028
Rear legs - side view	55	-0.555	0.0036

Resistance to other diseases

The Danish traits best correlated to the Swedish TMI_{OD} were EBV_{health} , TMI_{yield} , fat percent and temperament. Information on correlations and number of common bulls are given in Table 18. A strong correlation between the Swedish TMI_{OD} and Danish index for other health traits was found. Negative genetic correlations between disease resistance and temperament or TMI_{yield} were observed.

Table 18

Number of common bulls, estimated genetic correlation and level of significance for correlations ($Pr>F$) for Danish traits used for conversion to the Swedish TMI_{OD} .

Trait	Number of common bulls	Genetic correlation	$Pr>F$
Index for other health traits	47	0.784	<0.0001
TMI_{yield}	60	-0.384	0.0356
Fat percent	45	0.415	0.0277
Temperament	43	-0.428	0.0297

Danish index for other health traits (EBV_{health}) is, as mentioned earlier, not yet included in the Danish TMI. The index includes reproductive- digestive- and feet / leg diseases in the period 10 days before calving to 100 days after calving in first, second and third parity.

The corresponding Swedish TMI_{OD} contains records on presence of diseases as ketosis, retained placenta, paresis, teat injuries, leg and foot diseases, and infectious and metabolic disorders.

CONVERTED TMI

THE WILMINK METHOD

For each of the Swedish TMI sub-indices the Danish trait with the highest correlation was used to calculate conversion factors using the Wilmink method. No converted TMI sub-indices were calculated for the Swedish leg, udder and temperament. Table 19 summarizes the results.

Table 19

Conversion factors obtained from the use of the Wilmink method for eight Swedish sub-indices together with the Pearson product moment correlation (p-corr) and the genetic (Calo type) correlations (g-corr).

Swedish TMI-index	Danish trait	p-corr	g-corr	a-value	b-value
TMI _{yield}	TMI _{yield}	0.87	0.92	-23.12	1.26
TMI _{beef}	Stature	0.33	0.41	98.92	2.17
TMI _{DF}	Chest width	0.39	0.50	95.16	2.25
TMI _{sire}	Birth performance traits	0.46	0.55	76.17	0.24
TMI _{MGS}	Index for other health tr.	0.39	0.52	47.22	0.51
TMI _{MR}	Udder depth	0.65	0.83	101.40	3.82
TMI _{OD}	Index for other health tr.	0.56	0.78	55.29	0.43
TMI _{SRES}	Rump width	0.39	0.57	104.78	2.73

Values for the converted Swedish TMI ($C_TMI_{Wilmink}$), based on the above conversion factors, are presented in Table 21.

MULTIPLE REGRESSION

For the calculation of the $C_TMI_{direct\ reg.}$ the Danish traits used were sub-indices for fertility, yield, udder health and fat yield, the index for other health traits, stayability, fat percent, chest width, teat length, teat thickness, teat front placement and temperament. The adjusted R^2 value in this analysis was 0.91 ($P < 0.0001$).

For the calculation of the $C_TMI_{indirect\ reg.}$ The Danish traits were used: TMI_{yield}, TMI_{fertility}, TMI_{udder health}, TMI_{calving}, index for other health traits, fat yield, fat percent, protein yield, teat thickness, teat length, teat front placement, chest width, rump width, rear legs, side view, stayability and temperament.

Results for $C_TMI_{indirect\ reg.}$ and $C_TMI_{direct\ reg.}$ are presented in Table 20.

Table 20

The Danish traits used for conversion to Swedish EBVs with multiple regression.

Swedish TMI Sub-index	Danish trait	p-corr	a-value	b-value	Adj R-Sq	Pr>F
TMI _{yield}			6.88		0.83	<0.0001
	TMI _{yield}	0.87		1.52		
	Index for other health tr.	-0.34		-0.21		
	Fat yield	0.54		-0.35		
	Teat thickness	0.38		0.87		
TMI _{beef}			65.33		0.15	0.0156
	Protein yield	0.27		0.33		
	Teat length	-0.34		-1.91		
TMI _{DF}			76.01		0.19	0.0037
	TMI _{fertility}	0.32		0.20		
	Chest width	0.39		2.18		
TMI _{sire}			-20.21		0.78	<0.0001
	Birth performance traits	0.46		0.86		
	Index for other health tr.	0.33		0.06		
	Fat yield	0.30		0.26		
	Fat percent	0.37		-1.26		
	Teat length	-0.33		-0.90		
TMI _{MGS}			-42.66		0.75	<0.0001
	TMI _{calving}	0.37		0.78		
	Birth performance traits	0.31		0.35		
	Index for other health tr.	0.39		0.26		
	Rump width	0.32		1.23		
	Teat front placement	0.36		1.88		
TMI _{MR}			9.45		0.59	<0.0001
	TMI _{udder health}	0.41		0.50		
	Stayability	0.47		0.40		
	Teat length	0.35		1.63		
TMI _{OD}			22.36		0.45	<0.0001
	Index for other health tr.	0.56		0.54		
	TMI _{yield}	-0.27		0.22		
	Fat percent	0.33		2.30		
	Temperament	-0.33		-1.00		
TMI _{SRES}			104.30		0.33	0.0005
	Fat percent	-0.32		-5.89		
	Rump width	0.39		2.36		
	Rear legs, side view	-0.39		-2.60		

The three different C_TMI values for the Top 20 bulls are given in Table 21. Pair wise comparison of the Top 20 bulls shows that there is little difference between C_TMI_{Wilink} and C_TMI_{indirect reg.} (there are 16 bulls in common between them). However, C_TMI_{direct reg.} is different from the other two methods, reflected in the number of bulls in common between C_TMI_{direct reg.} and C_TMI_{Wilink} (13 bulls) and C_TMI_{indirect reg.} (14 bulls).

Table 21

Top twenty bulls when TMI is converted with the Wilmink procedure and with two different multiple regression methods, A and B respectively.

rank	WILMINK METHOD	C_TMI Wilmink	Indirect multiple regression	C_TMI indirect reg.	Direct multiple regression	C_TMI direct reg.
1	Zan Royal	20	Lord Lily	17	S Rudolf	58
2	Lord Lily	16	B Patron	16	L Merv	47
3	East Cash	16	Ked Juror	16	Zan Royal	46
4	Dannix	16	Esquimau	12	Pit	46
5	B Patron	13	B Mountain	12	Blacky	40
6	Ked Juror	13	Caro Amos	12	M Storm	40
7	S Rudolf	10	A Oscar	11	B Patron	20
8	Esquimau	10	T Burma	11	Caro Amos	20
9	M Bellwood	9	East Cash	11	HMT Tegl	17
10	Häradsköp	9	M Bellwood	10	B Mountain	16
11	A Oscar	9	Dannix	9	M Bellwood	15
12	S-B Mascot	8	Lasso	8	Lord Lily	13
13	B Mountain	8	Blacky	8	L Merrill	12
14	HJ Vogd	7	Häradsköp	7	Häradsköp	12
15	Lasso	6	O B Cubby	6	Ernlo	12
16	T Burma	6	HMT Tegl	6	A Oscar	12
17	Caro Amos	5	S-B Mascot	6	Ked Juror	9
18	Besne Buck	4	Ernlo	5	T Burma	9
19	O B Cubby	4	H Lutenant	5	Esquimau	8
20	M Aerostar	4	M Aerostar	5	Lasso	7

Correlations between the three different methods were calculated, both for all bulls in the material and for Top 20 bulls. The result is presented in Tables 22 and 23. Correlation between Top 20 bulls indicates the same pattern as the pair wise comparison, the highest correlation was observed for C_TMI_{Wilmink} and $C_TMI_{\text{indirect reg.}}$, 0.593. The same procedure performed for all bulls in the material gave the correlation 0.812 for $C_TMI_{\text{direct reg.}}$ and $C_TMI_{\text{indirect reg.}}$.

Table 22

Correlations between the three different methods performed on the Top 20 bulls.

	C_TMI_{Wilmink}	$C_TMI_{\text{direct reg.}}$
C_TMI_{Wilmink}	1	0.398
$C_TMI_{\text{direct reg.}}$	0.398	1
$C_TMI_{\text{indirect reg.}}$	0.593	-0.121

Table 23

Correlations between the three different methods performed on all bulls with converted TMI in the material.

	C_TMI_{Wilmink}	$C_TMI_{\text{direct reg.}}$
C_TMI_{Wilmink}	1	0.635
$C_TMI_{\text{direct reg.}}$	0.635	1
$C_TMI_{\text{indirect reg.}}$	0.765	0.812

FINAL DISCUSSION

A working group of Interbull (Interbull, 1990) has studied various conversion methods and one of the suggested methods was the so-called Wilmink method (Wilmink *et al.*, 1986); which was used for this work. There are, however, some limitations counted for this method (e.g. Powell & Sieber, 1992). 1) An insufficient number of bulls with progeny in several countries, 2) Instability of conversion equations over time caused by changes in the group of bulls used to develop the equations, 3) No possibility for re-ranking of bulls across countries if genotype by environment interaction is present, and 4) Reduced accuracy of prediction for elite bulls, the bulls of most interest in breeding programs. The last limitation is of special concern since these bulls are generally 5 to 15 years older than the bulls currently used for breeding. Because of intense selection the genetic merit of present elite bulls may be higher than the mean of the older bulls that were used for development of the conversion equations (Weigel, 1997). To reduce the risk of calculating inaccurate conversion equations the used data set contained data from most recent official proofs are often used, but it is not clear how large is the lag.

Despite the fact that several of the traits are recorded in similar ways in Sweden and Denmark the estimated genetic correlations between Swedish and Danish traits were much lower than expected. One possible explanation might be existence of few bulls in the Danish material. Nonetheless, the comparison of methods and the differences of the converted TMI is still of interest.

The $C_TMI_{direct\ reg}$ values for the top 20 bulls had a standard deviation of 7.15, while the corresponding values for $C_TMI_{indirect\ reg}$ was 3.45. These values pertain to a selected group of bulls and are not directly comparable with the usual standardized standard deviation of 7.0 for the RBV values in Sweden. However, the higher variance for $C_TMI_{direct\ reg}$ gives a better tool for selection since the differences in ranking of bulls becomes more obvious. The high correlation and variance for the direct conversion method could also be caused by correlations between the eleven traits used for the conversion. The used traits were sub-indices for fertility, yield, udder health and the EBV for fat, the sub-index for other health traits, stayability, fat percent, chest width, teat length, teat thickness, teat front placement and temperament. It might be possible to get a more accurate result if only one among strong correlated traits are included in the model.

Correlations calculated on the different C_TMIs between Top 20 bulls and all bulls in the material did not follow the same pattern. For Top 20 bulls the highest correlation was found between $C_TMI_{Wilmink}$ and $C_TMI_{indirect\ reg}$ while for all bulls in the highest correlation was observed for $C_TMI_{direct\ reg}$ and $C_TMI_{indirect\ reg}$. One explanation for this might be that no special consideration was given to bulls with missing data when the multiple regressions were performed. These bulls received very low $TMIs$ in both multiple regression models. Since the $C_TMI_{Wilmink}$ includes fewer traits the error is smaller and the correlation to the other two methods weaker when all bulls are compared. The correlation received between the C_TMIs in this group is probably the most correct, because the bulls on the Top 20 list have less missing data since these bulls are already famous and frequently used as sires in both countries.

This work has shown that it is possible to estimate a Swedish TMI for foreign bulls long before they have NBVs for all traits in the Swedish TMI. Nowadays evaluation results from a larger number of traits are available. Therefore, until a direct international genetic evaluation

for TMI (or all its constituent traits) through Interbull becomes available, it should be feasible to use multiple regression method to calculate the Swedish TMI for foreign bulls.

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PERSONAL COMMUNICATION

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