Sveriges lantbruksuniversitet
Swedish University of Agricultural Sciences

Department of Animal Breeding and Genetics

International Genomic Evaluation of Brown Swiss and Holstein Dairy Cattle

– Multi-trait vs. Single-trait Approach

Mohammed Sallam

Master´s thesis • 30.0 hp credits
Interbull Center
Uppsala, Sweden. 2020

International Genomic Evaluation of Brown Swiss and Holstein Dairy Cattle Multi-trait vs. Single-trait Approach

Mohammed Sallam

Supervisor:	Erling Strandberg, Swedish University of Agricultural Sciences, Department of Animal Breeding and Genetics
Assistant supervisor:	Haifa Benhajali, Swedish University of Agricultural Sciences, Department of Animal Breeding and Genetics, Interbull Center
Examiner:	Dirk-Jan De Koning, Swedish University of Agricultural Sciences, Department of Animal Breeding and Genetics

Credits:	30.0 hp credits
Level:	Second cycle, A2E
Course title:	Independent project in Animal Science
Course code:	EX0870
Course coordinating department:	Department of Animal Breeding and Genetics
Place of publication:	Uppsala, Sweden.
Year of publication:	2020
Cover picture:	-
Online publication:	https://stud.epsilon.slu.se
Keywords:	***Genotype-based international genomic evaluation, single trait, multi-trait, reliability, MACE proofs, national proofs, selection index , Brown Swiss, Holstein, Gene by environment interaction***

Swedish University of Agricultural Sciences
Faculty of Veterinary Medicine and Animal Science
Department of Animal Breeding and Genetics
Interbull Center

Sammanfattning/Abstract

International genomic evaluation for Brown Swiss population known as InterGenomics, was officially launched in 2011 by Interbull Center in Uppsala, Sweden. The routine evaluation is currently carried out using a single-trait approach where estimated breeding value from multi-trait across countries evaluation (MACE EBV) are used as a dependent variable and genetic correlations are assumed to be equal to one between countries. The current study is exploring a multi-trait approach as an alternative to the routine one. This approach uses the estimated breeding value (EBV) from the national genetic evaluations as a dependent variable and make use of the genetic correlations estimated between countries as well. In this study, we compared reliability from both approaches for Brown Swiss (BSW) and Holstein (HOL) dairy cattle in traits with different heritabilities. Findings show that single-trait approach resulted in higher reliability than multi-trait approach. There were some cases where multi-trait approach showed a small gain in evaluations variance for traits where heritability and genetic correlations were low. Further work may be required to check the extent of bias that could exist in both approaches.

Keywords: *genotype-based international genomic evaluation, single trait, multi-trait, reliability, MACE proofs, national proofs, selection index , Brown Swiss, Holstein, Gene by environment interaction*

Innehållsförteckning/Table of contents

Tabellförteckning/List of tables

Figurförteckning/List of figures

Förkortningar/Abbreviations

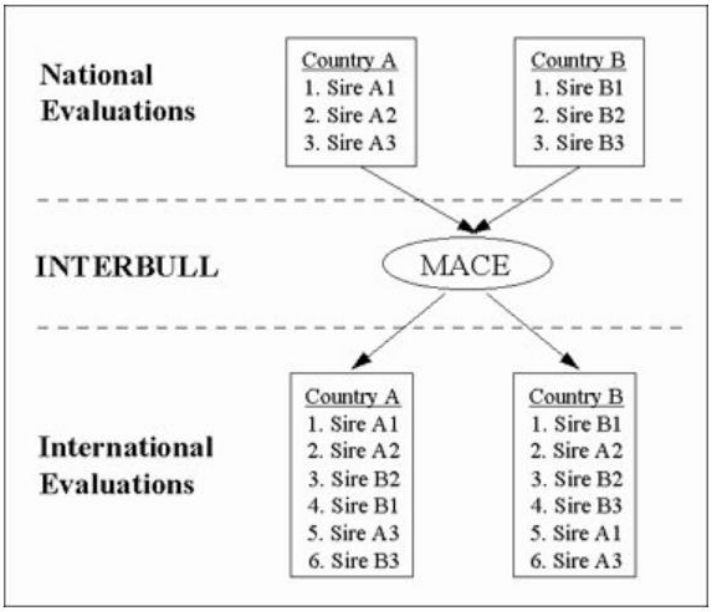
BLUP	Best linear unbiased prediction
BSW	Brown Swiss population
Cand.	Candidate bulls
cc1	Lactating cow ability to conceive (1)
cc2	Lactating cow ability to conceive (2)
DE	Daughter equivalent
DGV	Direct genomic value
EBV	Estimated breeding value
GEBV	Genomically enhanced estimated breeding value
h^2	Heritability
HOL	Holstein population
IG	Intergenomics
Int	Interval trait
Interbull	International Bull Evaluation Service, *interbull.org*
MACE	Multi-trait across countries evaluation
MGS	Maternal grandsire
MT	Multi-trait approache
PA	Parent average
Pro	Protein trait
Ref.	Reference bulls
REL	Reliability
SD	Standard deviation
SNP	Single-nucleotide polymorphism
ST	Single-trait approache
TBV	True breeding value

1 Introduction and Aims

National and international traditional genetic evaluation

The basic aim of genetic evaluation procedures is to rank animals for breeding purposes. Genetic evaluations are performed at two levels; national within country and international across countries. The evaluation at national level helps to make choices of which domestic bull to use for artificial insemination within the national breeding programme. The evaluation at international level helps to make accurate choices of which foreign bull or semen to import from different countries. In a certain country, an imported bull may or may not perform better than a domestic bull. Technically, the international genetic evaluation is achieved through what is called MACE; Multi-trait Across Countries Evaluation that was proposed by Schaeffer (Schaeffer, 1994). MACE is routinely performed by Interbull Center in Uppsala, Sweden, to provide breeding values for a bull, for example from a country X, on scale of each country participating in MACE, and update the national breeding value of this bull on the scale of country X as well (see Figure 1). The MACE breeding value reliability is expected to be higher than national breeding value reliability of bull A if the bull A has daughters in any of other countries participating in MACE. Thus, MACE could provide more reliable breeding values than the national evaluation on the same country scale.

Figure 1 MACE process by Interbull Center (interbull.org)



Traditional and genomic evaluation

Traditional genetic evaluation of dairy cattle uses information on phenotypes and pedigree to predict breeding values. By the development of genotyping technology, information on genomics is used to enhance the genetic evaluation in dairy industry. The power of genomic-based prediction (referred to as genomic evaluation) is to predict the breeding value for candidates without own phenotype records at an early stage of their life, which is essential for shortening generation intervals and achieving genetic gain in dairy populations in shorter time. Since the genomic evaluation is able to estimate breeding values for candidates without own phenotype, the accuracy in genomic evaluation is an issue to consider (Goddard and Hayes, 2009)

National and international genomic evaluation

The accuracy expected from genomic evaluation depends on several factors (Goddard and Hayes, 2009), one of those being the size of the reference population. The reference population consists of individuals that have both genomic and phenotypic information, whereas candidates are individuals that have only genomic information without phenotypic information. The larger the reference population, the more accurate and efficient the genomic predictions are (Goddard and Hayes, 2009; Liu et al., 2011). At national level, genomic evaluation can be performed successfully if

the national reference population size is big enough within the country, but in practise, some foreign bulls are added to that national reference population for more accurate/efficient genomic evaluation. Also a common reference population could be used in genomic evaluation for two or more of closely related countries, for example United States of America and Canada in North America or Denmark, Finland and Sweden in Northern Europe. Therefore, the term national genomic evaluation may not be fully precise as information used in is not exactly limited to "within-country information".

At Interbull international level, two scenarios are suggested based on the information approved by countries to be shared. Usually, countries with large dairy population (as the major situation in HOL breed) accept to share GEBVs but not genotypes, then Genomic MACE (GMACE) method can be used in similar way to MACE method to provide Genomic EBVs (or Genomically enhanced breeding values, GEBVs) on scales of countries participating in GMACE. On the other hand, countries with small dairy populations (as the situation in BSW breed and countries with small HOL populations) accept to share genotypes, then a genotype-based international genomic evaluation can be used (VanRaden and Sullivan, 2010). It is important to mention that both GMACE and MACE could be viewed as calculation of breeding values on the different country scales more than real evaluation as the inputs in both MACE and GMACE are already evaluations at national level in MACE or semi-national level in GMACE.

Genomic evaluation for countries with small reference populations

The situation in BSW and for countries with small HOL dairy populations is that countries can not achieve large enough a reference population size to obtain the accuracy that makes genomic evaluation an efficient tool. That is why the Interbull Genomics Task Force (Banos et al., 2009) envisaged a potential scenario for pooling genotypes from different countries for building a common reference population, based on which the Interbull Centre would perform genotype-based international genomic evaluation on their behalf. With larger common reference population, genomic evaluation accuracy/reliability can be improved, and this was the basic idea leading to the introduction of the InterGenomics service (IG) by Interbull Center. This is a genotype-based international genomic evaluation service for countries with small reference dairy population, where participating countries share their genotypes (VanRaden and Sullivan, 2010). InterGenomics was officially launched for BSW dairy population in 2011, and since 2017, several proposed studies are running to develop IG for HOL dairy population as a service for countries with small HOL dairy populations. One observation is that the main countries that are contributing

to the world BSW dairy population are already participants in the routine IG-BSW, whereas the main countries that are contributing to the world HOL dairy population are not participants in the proposed IG-HOL.This implies that for the proposed IG-HOL, using only national phenotypes (not real phenotypes but alternatively de-regressed national EBV) as input into the genotype-based international genomic evaluation will cause the loss of lots of information that would come from the big countries through MACE if we use de-regressed MACE EBV instead. Additionally, the absence of the big (exporting) countries can also result in a lack of connectedness between the participating countries.

Approaches of genotype-based international genomic evaluation

The approaches suggested for genotype-based international genomic evaluation are based on the availability of data. If both genotypes and phenotypes are available a single-step approach (Legarra et al., 2014) may be a good choice in case that other computational issues related to the single-step approach have been solved. However, the situation for dairy cattle is that countries do not share phenotypes. Therefore, the basic multi-step approach (VanRaden, 2008; VanRaden et al., 2009) is used, based on de-regressed proofs (EBVs) (Garrick et al., 2009) as an alternative to real phenotypes. Two possible de-regressed proofs are suggested to be used as dependent variable in genotype-based international genomic evaluation (IG) : 1) national de-regressed proofs or 2) MACE de-regressed proofs. As mentioned above the MACE proof is expected to be more reliable than the national proof. In addition, the size of reference population is expected to be larger when using the MACE proofs as dependent variable. Then, using the MACE proofs could provide a better (more accurate) genomic prediction. However, use of MACE proofs as dependent variable restricted the approaches into only single-trait (ST) approach, with no possibility to use genetic correlation again via multi-trait (MT) approach, in order to avoid information double counting since the de-regressed MACE proofs are basically obtained through a multi-trait frame work utilizing genetic correlations. On the other hand, even if the national proofs are less accurate, using these as a dependent variable provides a possibility to make use of genetic correlations (across countries) as well via a multi-trait (MT) approach. Shifting the approach from ST to MT leads to shifting the assumption about genetic correlation between countries from being equal one in ST to be equal an estimated correlation values (less than one) in MT. The genetic correlations equal 1 via ST that assumes the same trait in all countries ignoring the potential impact of gene by environment interaction, that may be inccorrect assumption especially if the actual genetic correlations between countries are low, which is the case for: 1) almost all trait-country combinations participate in

the proposed IG-HOL, and 2) Some trait-country combinations participate in the routine IG-BSW. Thus, use of MT (with assumption that trait is not the same in all countries) may provide more reliability. Use of MT have been shown to provide more reliable genomic prediction than ST in simulated data studies (Calus and Veerkamp, 2011; Guo et al., 2014; Jia and Jannink, 2012; VanRaden and Sullivan, 2010). Which approach, ST or MT approach, that would provide the most reliable GEBV for trait-country combinations of different heritabilities in two dairy populations, Brown Swiss and Holstein, is not known. To the best of our knowledge there are no studies performing a comparison like this with real data.

Aims of the study

The aims of this study were to 1) check the workflow required to run a multi-trait genomic evaluation for three different traits in two breeds, Brown Swiss and Holstein, based on real data; 2) study changes in the reliability of the calculated genomic breeding values by shifting the approach from single trait to multi-trait.

2 Data

In single-trait (ST) approach, the estimated breeding values obtained from multi-trait across countries evaluations (MACE) were: 1) de-regressed and then used as a dependent response variable of reference bulls; 2) used for calculation of parent averages by sire-dam method for candidate bulls:

$$PA = (EBV\ sire + EBV\ dam) * 0.5$$

$$PA\ reliability = (EBV sire\ reliability\ + EBV dam\ reliability) * 0.25$$

In multi-trait model (MT), the estimated breeding values obtained from national evaluations were: 1) de-regressed and then used as a dependent response variable of reference bulls; 2) used for calculation of parent averages by sire-maternal grand sire method for candidate bulls , not sire-dam method since the national proofs for dams are not available:

$$PA = 0.5 * EBV sire + 0.25 * EBV maternal\ grand\ sire$$

$$PA\ reliability = 0.25 * (EBV sire\ reliability + (0.25 * EBV\ maternal\ grand\ sire\ reliability))$$

The same pedigree has been used in both approaches with size equal to 25,919 and 91,874 in HOL and BSW, respectively. Genotypes were obtained from the May 2018 IG-HOL proposed run and the April 2019 IG-BSW routine run. The same genotyped animals were used for both approaches : 7,173 and 34,093 in HOL and BSW, respectively. Each genotyped bull was assigned as either a reference (Ref.) or a candidate (Cand.) bull. A bull was assigned to be a reference bull only if the bull had been genotyped with available breeding value obtained by MACE in ST or national evaluation in MT. Bulls were assigned to be candidate if the bull had been only genotyped. The number of reference bulls in single-trait approach was, as expected, larger than in multi-trait approach (Tables 1 and 2). Both approaches used the same heritability, submitted by countries to Interbull MACE runs April 2018

and April 2019 for HOL and BSW breed, respectively (Tables 3 and 4). The genetic correlations that were used for MT approach were obtained from the April 2018 and April 2019 MACE runs for HOL and BSW breed, respectively. Data of three traits were tested by both ST and MT for each breed. For BSW breed, protein yield (pro), interval from calving to conception (cc1), and calving interval (int). For HOL breed; pro, cc2 and int were used. Interbull definition of fertility traits (cc1, cc2 and int) plus each country definition are mentioned in Table 5. Pro trait can be described as a high heritability trait with high genetic correlations between countries, whereas cc1, cc2 and int are low heritability traits, and the genetic correlations for cc1 and cc2 are a bit lower than genetic correlations for int (*see Appendix A tables for correlations between countries*).

Table 1 Number of reference and candidate bulls in ST and MT for each trait in BSW

				Genotyped bulls	
Breed	Trait	h²	Approach	Ref.	Cand.
BSW	pro: milk protein yield trait	High	ST	7490	26603
			MT	7128	26965
			MT-ST	-362	362
BSW	cc1: lactating cow ability to conceive (1)	Low	ST	5833	28260
			MT	5450	28643
			MT-ST	-383	383
BSW	int : calving interval trait	Low	ST	5177	28916
			MT	4897	29196
			MT-ST	-280	280

h²=Heritability, Ref = Reference bulls, Cand = Candidate bulls

Table 2 Number of reference and candidate bulls in ST and MT for each trait in HOL

				Genotyped bulls	
Breed	Trait	h²	Approach	Ref.	Cand.
HOL	pro: milk protein trait	High	ST	3142	4031
			MT	2603	4570
			MT-ST	-539	539
HOL	cc2: lactating cow ability to conceive (2)	Low	ST	2652	4521
			MT	1783	5390
			MT-ST	-869	869
HOL	int: calving interval trait	Low	ST	1552	5621
			MT	651	6522
			MT-ST	-901	901

h²=Heritability, Ref. = Reference bulls, Cand. = Candidate bulls

Table 3 Heritability per country for each trait in BSW population

		Country						
Breed	Trait	A	B	C	D	E	F	G
BSW	pro	0.250	0.340	0.387	0.300	0.180	0.259	0.200
	cc1	0.027	0.018	0.012	0.020	-	-	0.016
	int	0.045	-	0.049	-	0.060	-	0.014

Table 4 Heritability per country for each trait in HOL population

		Country							
Breed	Trait	H	I	J	K	L	F	M	N
HOL	Pro	0.199	0.450	0.414	0.240	0.220	0.207	0.303	0.185
	cc2	-	0.012	0.067	-	-	-	0.050	0.040
	Int	-	0.012	-	-	-	-	0.050	0.040

Table 5 Definitions of fertility traits; Interbull's definition and countries' definitions

Trait Code	Interbull's definition / Countries' definitions			Definition date
cc1	Interbull		Lactating cow's ability to conceive (1), expressed as a rate trait. Traits like conception rate (CR) and non-return rate (NR, preferably NR56) will be considered for this trait group.	Aug. 2007
	Country	A	NR=Non Return Rate after 56 Days in cows(NRR), %	Apr. 2019
		B	NR=Non Return Rate after 56 Days (NRR), %	Apr. 2019
		C	NR=Cows' Non Return Rate after 56 days	Apr. 2019
		D	CR=Cows' Conception rate (binary trait)	Apr. 2019
		G	CR=Conception rate (cow)	Apr. 2019
cc2	Interbull		Lactating cow's ability to conceive (2), expressed as an interval trait. The interval first insemination-conception (FC) or interval first-last insemination (FL) will be considered for this trait group. As an alternative, number of inseminations (NI) can be submitted. In the abscence of any of these traits, a measure of interval calving-conception such as days open (DO), or calving interval (CI) can be submitted.	Aug. 2007
	Country	I	CI=Calving interval	Apr. 2018
		J	CR=Inverse of the number of inseminations to conception (%)	Apr. 2018
		M	Days open expressed as Daughter Pregnancy Rate	Apr. 2018
		N	CI=Calving Interval	Apr. 2018
int	Interbull		Lactating cow's measurements of (I)nterval (T)raits calving-conception, such as days open (DO) and calving interval (CI)	Aug. 2007
	Country	A	DO=Days open	Apr. 2019

C	DO=Days open (days)	Apr. 2019
G	DP=Daughter Pregnancy Rate	Apr. 2019
E	DO=days open (days)	Apr. 2019
I	CI=Calving interval	Apr. 2018
M	Days open expressed as Daughter Pregnancy Rate	Apr. 2018
N	CI=Calving Interval	Apr. 2018

3 Methodology

3.1 Genotypes

Countries participating in IG share genotypes using different SNP-Chips and densities. The shared genotypes have been pooled using a reference map containing 55,172 SNPs. The SNPs of the common reference map, which are not in the original chips have been set to missing. Duplicate genotypes (within and across countries) were removed keeping only the genotype with fewer missing SNPs. Consistency of SNPs across sire-son parentage has been checked on both autosomes and sex-chromosome; pedigree-based relationships have been removed (i.e. sire set to be missing) for sire-son with more than 600 conflicts. SNPs with sire-son parentage conflicts larger than 200 have been set to missing for these individuals. Imputation of missing markers was performed. After the imputation, SNP quality control was performed. The SNPs with missing frequency higher than 10% were discarded from the evaluation. Moreover, only SNPs with frequencies of both homozygotes and heterozygous above zero were included in the evaluation.

3.2 Statistical approach to compute GEBV

From a computational aspect, the main difference between ST and MT is that MT makes use of genetic correlation between traits (countries) estimated by Interbull center. Then, MT fits more traits (countries) simultaneously per run, whereas ST fits only one country per run and assume that the genetic correlations between coun-

tries are equal to one. This means we need X runs by ST approach to perfom evaluations for X countries, but only one run by MT approach to perfom evaluations for the same X countries.
Both ST and MT statistical approaches in the current study are based on multi-step genomic evaluation approach (VanRaden, 2008; VanRaden et al., 2009) as following:

A) SNP marker effects are estimated from reference bulls via "Bayes-A SNP-BLUP" which fits also a residual polygenic effect.

$$y = \mu + Zg + Wu + e$$

$-\ y$ is n × 1 vector of de-regressed MACE proofs in ST or n × t matrix of de-regressed national proofs in MT, where n is the number of reference individuals and t is the number of traits. Input data will be used later on this text to refer to this (y) either being vector or matrix.
$-$ μ is the general mean.
$-\ Z$ is m × 1 design matrix containing regression coefficients on m markers in ST or m × t in MT, where t is the number of traits.
$-\ g$ is m × 1 vector of marker effects in ST or m × t matrix in MT.The same set of 45,473 SNP markers was used in both approaches.
$-\ W$ is p × 1 design matrix in ST that relates records to animals where p number of animals in the pedigree, or p × t design matrix in MT.
$-\ u$ is p × 1 vector of polygenic effect in ST or p × t matrix in MT, consider the weight of polygenic effect=0.1
$-\ e$ is n × 1 vector containing the adjusted reliability of the MACE de-regressed proofs in ST or n × t diagonal matrix with diagonals equal the adjusted reliability of the national de-regressed proof in MT.

About the estimation of marker effects
Both approaches assume that 90% of variance in dependent response variable (y) is explained by the marker effects and the rest is explained by individual polygenic effect. Both approaches assume that each marker represents quantitative trait loci and each marker has an effect and those effects are assumed to have a heavy-tailed prior distribution referred to as "Bayes A prior" proposed by (VanRaden, 2008), which makes the estimation of allele effects non-linear.
The variance of the polygenic effect is assumed to be the variance explained by pedigree relationships. The variance of the error is assumed to be the adjusted reliability of values in response variable. Both approaches fit the unknown parent groups to account for selection in the data.

B) Direct genomic values (DGV) are obtained as summation of allele effects for both references and candidates bulls plus the associated estimated polygenic effect.

$DGV = Z\hat{g} + \hat{u}$

$-\ Z$ as defined above, $\hat{g}$ and $\hat{u}$ are estimates of g and u as defined above.

C) Combination of the obtained DGV with traditional genetic evaluation results via a selection index method to obtain the combined estimated breeding values referred to as GEBVs.

Combining DGV with traditional EBV is required to make full use of all available information to improve the reliability. Candidate bulls are expected to benefit from combining process more than reference bulls because the input data (y) reliabilities of reference bulls are already high. To understand the importance of the combining process for candidates, please recall that candidate bulls have neither own nor progeny records. Then, their estimated breeding values came from their ancestors i.e. the parent average (PA). Furthermore, not all of their sires or maternal grand sires and none of their dams have been genotyped. Therefore, the PA for those candidate bulls is assumed to be partitioned into two parts. The first part is a genomic term represented by DGV coming from genotyped ancestors. The second part is non-genomic traditional term represented by traditional PA, coming from non-genotyped ancestors. Then: *Traditional PA from non-genotyped ancestors = traditional PA from all ancestors minus traditional PA from genotyped ancestors*. This traditional PA from genotyped ancestors is also the reflection of overlapping information between genotyped and non-genotyped ancestors information that is required to be calculated and accounted for within the combination process in order to avoid information double counting.

To calculate traditional PA and its associated reliability from genotyped ancestors, a traditional BLUP (either being single-trait BLUP in ST or multi-trait BLUP in MT) using traditional pedigree relationship matrix **A** is computed, excluding observations of non-genotyped ancestors, i.e. using only observations of genotyped ancestors. This is referred to as subset terms; subset-EBV and subset-REL.

By obtaining subset-REL, the extent of information overlapping (covariances) between 3 terms (DGV, subset and traditional) for each animal can be obtained, then selection index (SI) theory is used to combine those 3 terms. First step of SI is to calculate the index weight for each of the three terms supposed to combine. The

index weights derived from the reliabilites(DGV REL, Subset REL and Traditional REL) not the estimated breeding values(DGV, Subset-EBV and Traditional-EBV) since reliabilities are basically the quantification of information used for estimating each of the breeding values, using the following formula (VanRaden, 2001):

$b = c' \ V^{-1}$

Where b here is a column vector of index weights for each of the three terms supposed to combine i.e. a column vector contains: DGV term weight ($b1$), subset term weight ($b2$) and traditional term weight ($b3$). c' is a transpose vector of the covariance between each of the 3 reliabilities and the corresponding true breeding reliabilities which is equal to the diagonals of V matrix i.e. c is a row vector contains: DGV REL, subset REL and traditional REL. V^{-1} is the inverted variance-covariance matrix of these 3 RELs.

Then, the second step is to do the combining itself using weights ($\boldsymbol{b}_s$) calculated above, the combined breeding value (GEBV) computed for each animal by the following formula: $\text{GEBV} = b' \, c'$, which is by the same formula, and for simplicity sake, equal to:

$GEBV = b1 * DGV + b2 * subsetEBV + b3 * traditionalEBV.$

By a similar formula, the reliability of GEBV computed using the same weights $\boldsymbol{b}_s$, as following:

$GEBV\ REL = b1 * DGV\ REL + b2 * subset\ REL + b3 * traditional\ REL.$

3.3 Reliability of evaluation

Approximation instead of inversion

In large scale routine genomic or genetic evaluations, it is computationally difficult to calculate the reliability of the breeding values by inversion of the left-hand side of the mixed model equations. Therefore, the reliability of evaluation is often approximated. Consequently, the sets of equations that are used for the evaluation are not necessarily the same equations as those used for reliability approximation.

Approximation of reliability in the current study was done as follows:

Three reliabilities; DGV REL, Subset REL and Traditional REL are approximated separately, then the 3 RELs of each animal were weighted and combined through selection index approach to get the final GEBV REL as mentioned before:

$GEBV\ REL = b1 * DGV\ REL + b2 * subset\ REL + b3 * traditional\ REL.$

The methods used to obtain (approximate) each of the 3 RELs are explained as the following:

1) DGV REL; refers to the approximated reliability of the DGV, recall that DGV in the current study is obtained as sum of marker effects + polygenic effect, then two reliabilities are required to be approximated; A) reliability of the estimated "sum of marker effects" and, B) reliability of the estimated "polygenic effect". Both A and B are calculated on daughter eqivalent (DE) terms (*see* VanRaden and Wiggans (1991) *for details about the concept of DE*), then added to each other, then the result of the addition is converted into REL terms by the formula: REL= Daughter Equivalent /(1.0+ Daughter Equivalent)

A) The daughter equivalent (DE) of the estimated "sum of marker effects" is approximated by one of the methods suggested by VanRaden and Sullivan (2010), the one that is used in the current study is a simple method that requires neither genomic relationship matrix nor its inversion, as it simply assumes one constant value of DE for all animals for the same trait as the following formula:
Sum-of-marker-effect-DE for each trait =
[(Σ RELpta-RELpa) /DEdivisor] * [(4-h^2)/h^2], where "RELpta-RELpa" is the product of subtracting parent average reliability from EBV reliability, DEdivisor is the number of high reliability bulls needed to obtain 50% genomic reliability, and a larger DEdivisor is needed for breeds with greater effective population size. DEdivisor is breed specific value and equals 120,000 in the current study for both BSW and HOL breed. This method does not account for the number of close relatives that are genotyped. However, it seems a good strategy in case we want to avoid G-matrix construction and inversion.

B) The daughter equivalent (DE) of the estimated "polygenic effect" for each bull is calculated based on the subset-REL (will be fully explained next paragraph) by the following formula:
Polygenic-effect-DE for each bull = subsetREL/ (1.0 - subsetREL)

2) Subset REL; the reliability of subset-EBV
A Traditional BLUP evaluation (either being single-trait in ST or multi-trait in MT) was performed using the traditional relationship matrix plus performance records (de-regressed MACE proofs in ST or de-regressed national proofs in MT) of only genotyped animals to obtain subset-EBV. It is described as subset because it uses only performance records of a subset of bulls who are genotyped, excluding records of non-genotyped bulls. Then, Subset-REL is approximated using the 3×3 method of (Misztal and Wiggans, 1988) where daughter equivalents from parents, progeny,

and own records summed in an iterative process using starting values for reliability from previous evaluation.

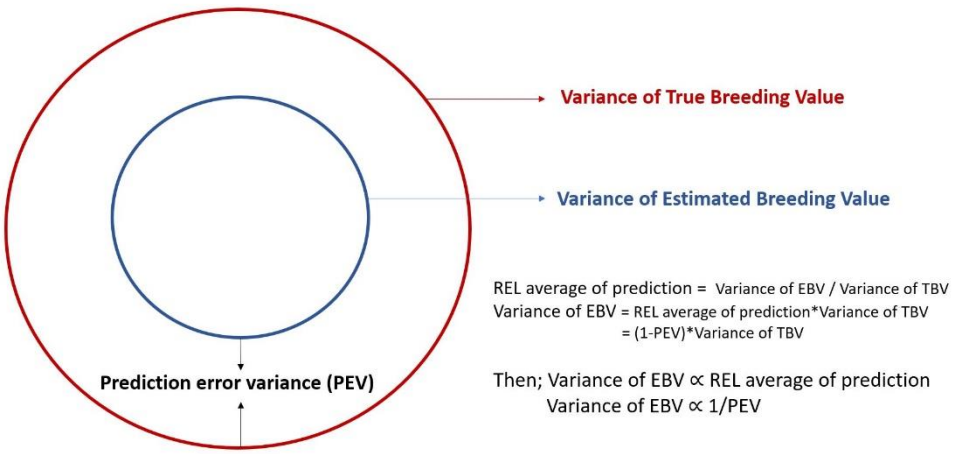
3) Traditional REL; the reliability of traditional-EBV
The traditional-EBV and traditional-REL are basically from traditional complete BLUP evaluation; MACE process performed by Interbull Center in ST and national evaluation performed by each country in MT, "complete" here means an evaluation using performance records of all bulls, both genotyped and non-genotyped.

Weighting rules
Before computing the weights (selection index coefficients) associated with the three REL terms, some rules have been applied to check consistency between values supposed to combine in order to compute appropriate weighting. The subset-REL should be the lowest. If either DGV-REL or traditional-REL is the lowest, the lowest REL and its associated EBV is forced to be equal to subset-REL and its associated EBV, respectively. In addition, if subset-REL was not the lowest, the weights are forced to be one, zero and zero for DGV, subset and traditional terms, respectively. Subset information (subset REL) is the proxy of the overlapping between genomic, subset and traditional information available for each animal, and if this overlapping is greater than traditional information, the latter is seen as valueless information to be combined with genomic information. Being subset information greater than genomic information is unlogic and indicate incorrect approximation of DGV reliability.

4 Results

The genomically enhanced estimated breeding value (GEBV) in the current study is the result of combining three estimated breeding values for each bull: genomic value (DGV) and the other two traditional non-genomic values (subset-EBV and traditional-EBV). Since the variance of the estimated breeding value is directly proportional to reliability average of prediction(Figure 2), and in order to check the consistency between predictions' variance and predictions' reliability, the reliability average and standard deviation of : DGVs, subset-EBVs, traditional-EBVs, and GEBVs calculated for all bulls, and for reference and candidate bulls separately for each breed-trait-country combination from both ST and MT approaches. Differences between ST predictions' standard deviation and MT predictions' standard deviation have been calculated in addition to differences between the corresponding predictions' reliability averages.

Figure 2 Relationship between between predictions' variance and predictions' reliability



DGV and GEBV

Single trait approach resulted higher standard deviation and reliability average than MT approach for direct genomic value DGV, in all breed-trait-country combinations except in few cases where the direct genomic values' SD (but not the corresponding reliability averages) differences were in favour of MT approach (Figure 3 for BSW and Figure 4 for HOL).

The differences between ST and MT approaches for both GEBV standard deviation and GEBV reliability average have the same pattern as the pattern in DGV differences (for SD and REL averages) in all breed-trait-country combinations except some cases in HOL breed where GEBV SD (but not DGV SD) obtained from MT exceed those obtained from ST (Figures 4 for BSW and 6 for HOL).

Subset and traditional terms

In order to check consistency between subset and traditional terms within each approach separately as a kind of within-approach checks, "subset-EBV SD minus traditional EBV SD" and "subset-EBV REL average minus traditional EBV REL average" have been calculated in each approach separately before and after applying weighting rules(Figures 7-8 for ST and 9-10 for MT).

In ST approach in all breed-trait-country combinations, for reference bulls, both subset-EBV SD and subset-EBV REL averages were higher than traditional-EBV SD and traditional-EBV REL averages, respectively, before applying of weighting rules (Figure 7) and equal to each other after applying weighting rules (Figure 8). For candidate bulls, subset-EBV SD was higher than traditional-EBV SD whereas subset-EBV REL was lower than traditional-EBV REL both before (Figure 7) and after (Figure 8) applying the weighting rules.

In MT approach in almost all breed-trait-country combinations (see Figure 9-10), for both reference and candidate bulls, subset-EBV SD and subset-EBV REL average were higher than traditional-EBV SD and traditional-EBV REL average, respectively, before applying of weighting rules (Figure 9) and equal to each other after applying weighting rules (Figure 10).

Common reference bulls' inputs and outputs

For common reference bulls i.e. bulls were assigned as reference bulls in both MT and ST approaches, the SD and REL averages of their data input (y), DGV and GEBV, in each approach have been calculated in addition to SD and REL averages of their national and MACE proofs as well (Tables 6-7)

Figure 4 Direct genomic value standard deviation differences (top panel), reliability average differences (middle panel) and correlations (bottom panel) between ST & MT in BSW population for all bulls, candidate bulls and reference bulls for all combinations of trait (cc1, int and pro) and country code.

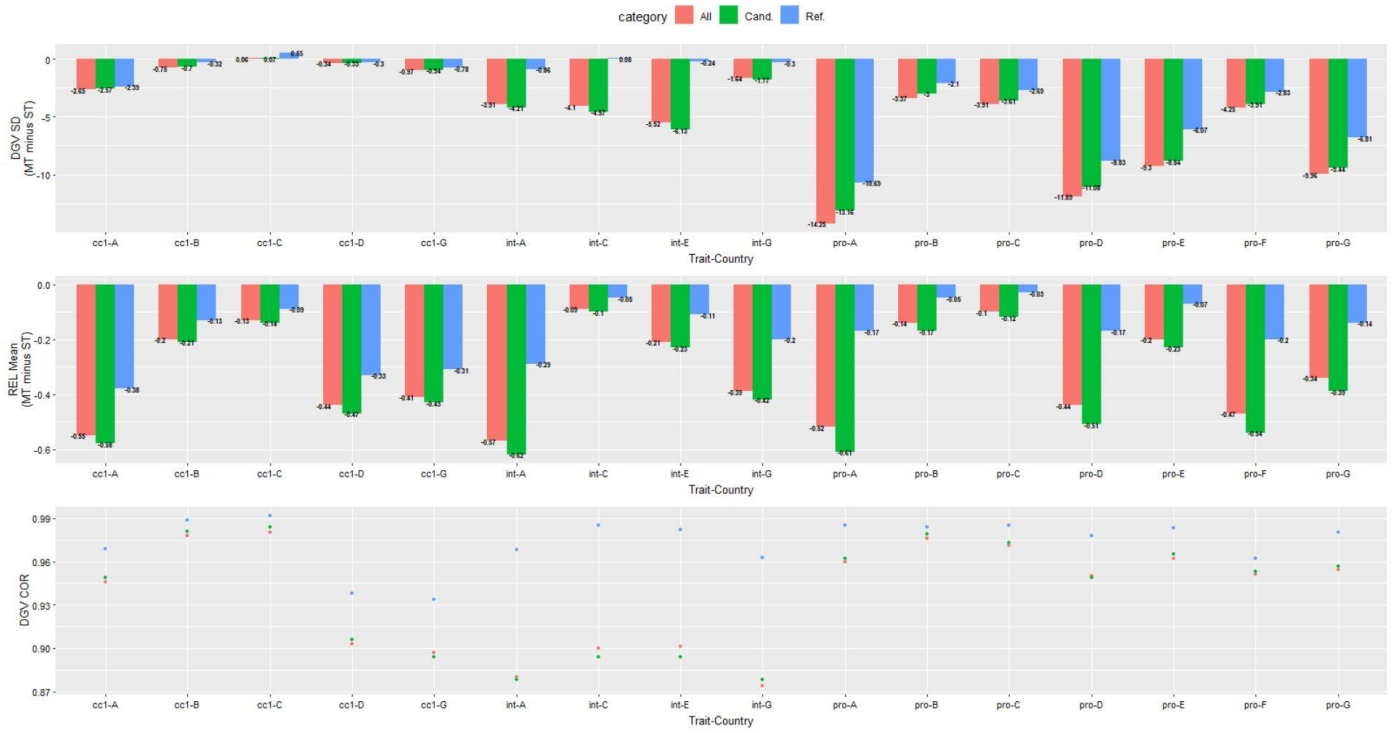


Figure 3 Genomic estimated breeding value standard deviation differences (top panel), reliability average differences (middle panel) and correlations (bottom panel) between ST & MT in BSW population for all bulls, candidate bulls and reference bulls for all combinations of trait (cc1, int and pro) and country code

Figure 5 Direct genomic value standard deviation differences (top panel), reliability average differences (middle panel) and correlations (bottom panel) between ST & MT in HOL population for all bulls, candidate bulls and reference bulls for all combinations of trait (cc1, int and pro) and country code

Figure 6 Genomic estimated breeding value standard deviation differences (top panel), reliability average differences (middle panel) and correlations (bottom panel) between ST & MT in HOL population for all bulls, candidate bulls and reference bulls for all combinationsof trait (cc1, int and pro) and country code

Figure 7 Subset-EBV and traditional-EBV standard deviation (top panel) and reliability average (bottom panel) differences before applying weighting rules for breeds-trait-country combination in ST approach

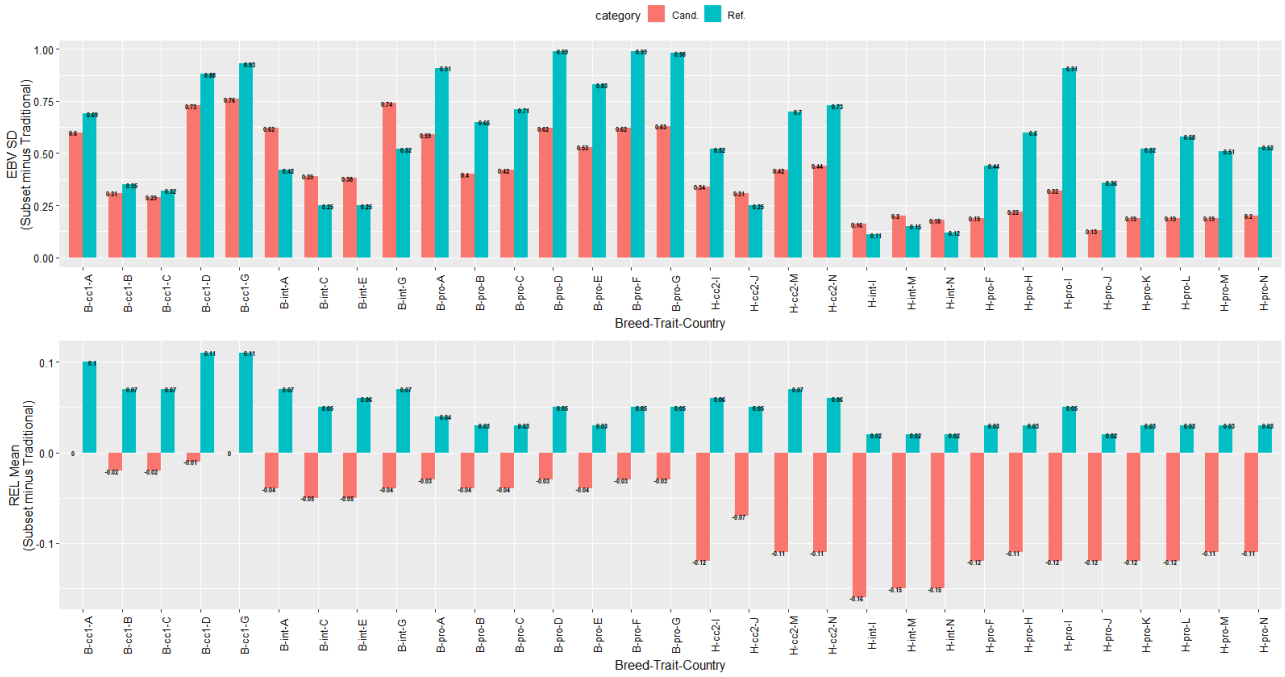


Figure 8 Subset-EBV and traditional-EBV standard deviation (top panel) and reliability average (bottom panel) differences after applying weighting rules for breeds-trait-country combination in ST approach

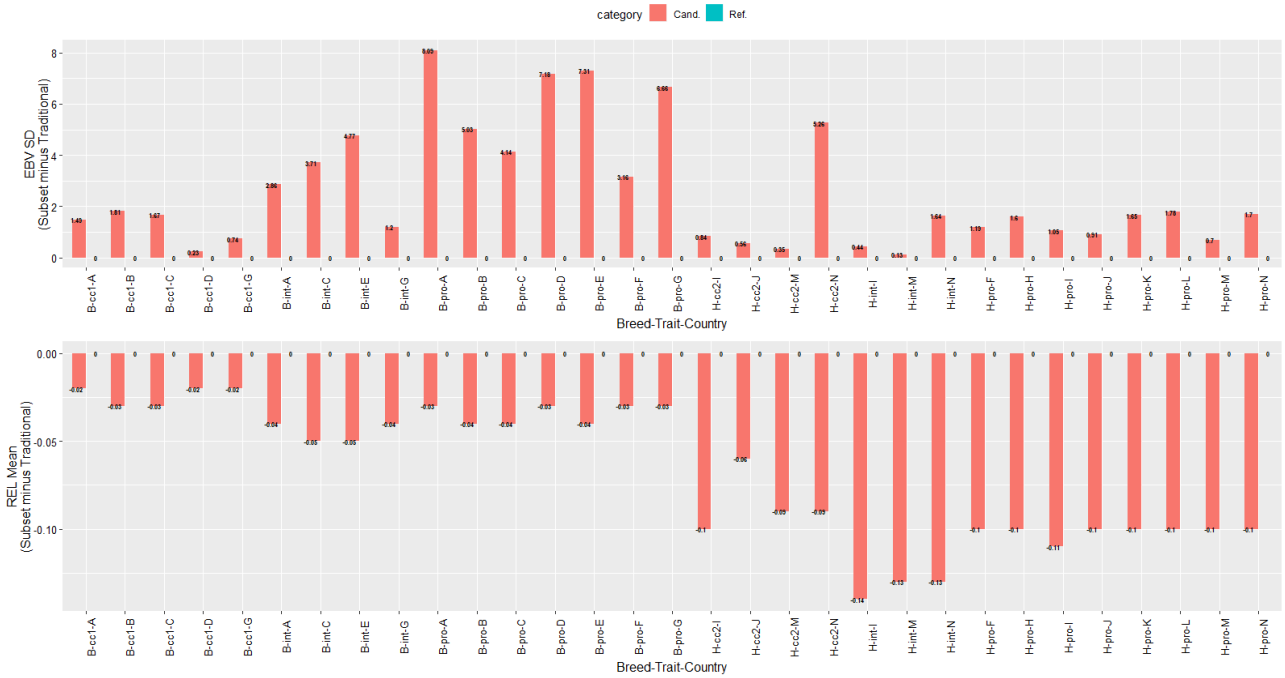


Figure 9 Subset-EBV and traditional-EBV standard deviation (top panel) and reliability average (bottom panel) differences before applying weighting rules for breeds-trait-country combination in MT approach

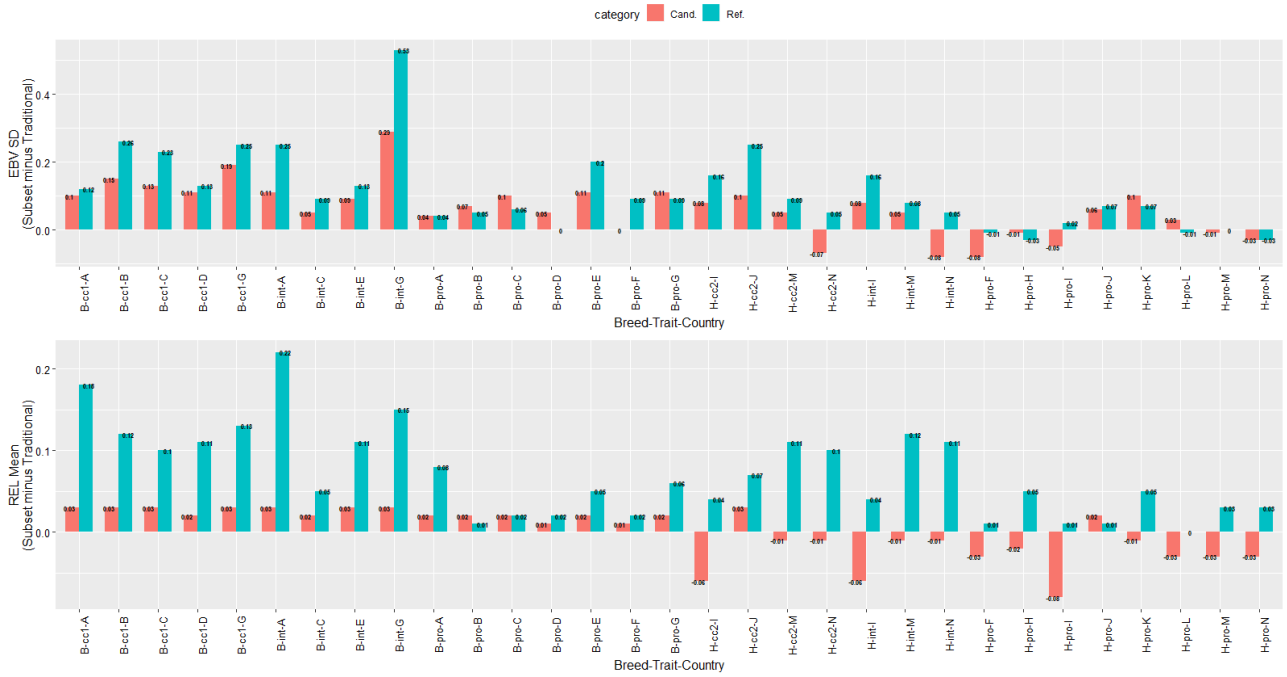


Figure 10 Subset-EBV and traditional-EBV standard deviation (top panel) and reliability average (bottom panel) differences after applying weighting rules for breeds-trait-country combination in MT approach

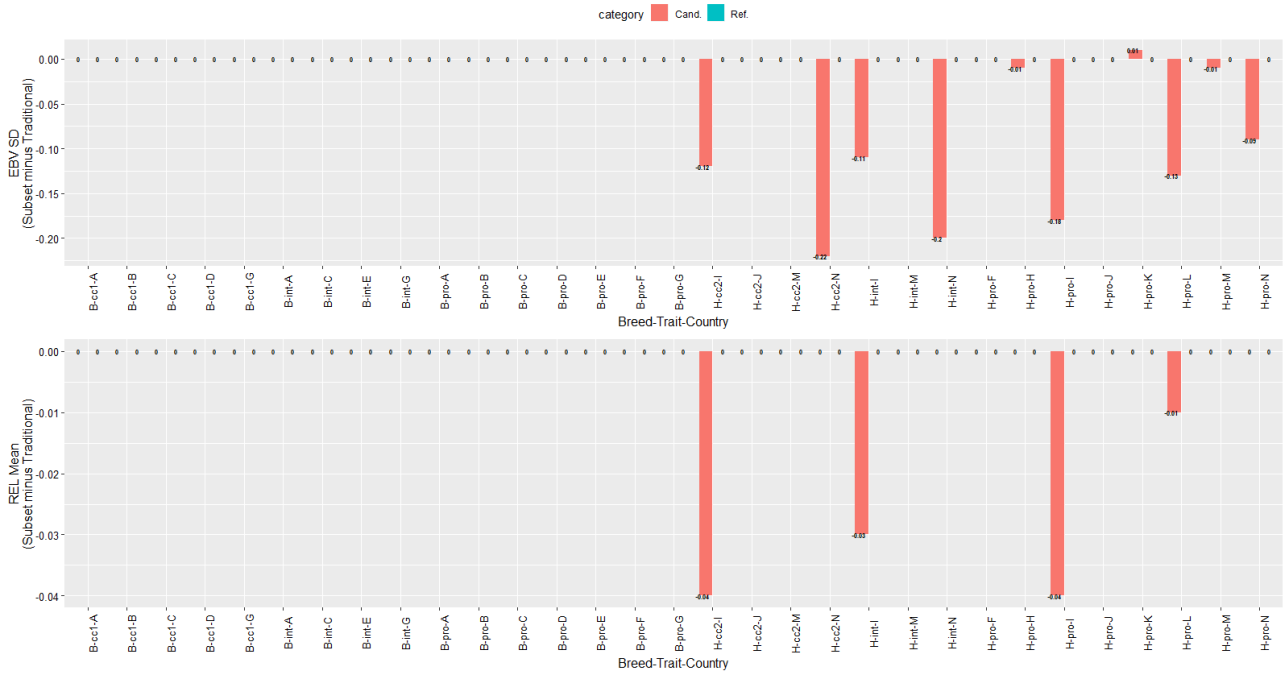


Table 6 Standard Deviation(SD) and average reliabilities(REL MEAN) of observation data (y, Input), DGV and GEBV for common reference bulls in MT and ST in addition to their national and MACE proofs in BSW

Trait		SD					REL MEAN				
country	Approach	Input	DGV	GEBV	NATIONAL	MACE	Input	GEBV	NATIONAL	MACE	*n*
Pro											
A	ST	22.236	23.573	24.542	20.801	22.236	90.867	93.553	84.886	90.875	210
	MT	20.801	18.945	21.659	20.801	22.236	83.99	90.027	84.886	90.875	210
	MT-ST	-1.435	-4.628	-2.883	0	0	-6.877	-3.526	0	0	0
B	ST	21.899	21.589	23.164	21.851	21.899	92.505	94.428	91.857	92.557	2375
	MT	21.851	19.758	22.69	21.851	21.899	91.267	93.157	91.857	92.557	2375
	MT-ST	-0.048	-1.831	-0.474	0	0	-1.238	-1.271	0	0	0
C	ST	18.029	17.499	19.068	17.997	18.029	91.49	93.848	89.611	91.518	3121
	MT	17.998	16.424	18.686	17.997	18.029	89.884	92.498	89.611	91.518	3121
	MT-ST	-0.031	-1.075	-0.382	0	0	-1.606	-1.35	0	0	0
D	ST	19.677	21.247	21.62	19.33	19.676	92.32	94.253	92.151	92.335	338
	MT	19.33	17.718	19.838	19.33	19.676	90.947	92.146	92.151	92.335	338
	MT-ST	-0.347	-3.529	-1.782	0	0	-1.373	-2.107	0	0	0
E	ST	27.609	29.16	31.537	27.356	27.609	87.24	91.445	90.463	87.25	1835
	MT	27.356	25.444	29.46	27.356	27.609	82.357	88.06	90.463	87.25	1835
	MT-ST	-0.253	-3.716	-2.077	0	0	-4.883	-3.385	0	0	0
F	ST	9.694	10.918	10.999	9.535	9.694	92.651	94.558	93.476	92.658	338
	MT	9.535	9.112	10.004	9.535	9.694	90.602	92.345	93.476	92.658	338
	MT-ST	-0.159	-1.806	-0.995	0	0	-2.049	-2.213	0	0	0
G	ST	19.135	20.134	21.385	18.874	19.136	85.163	90.499	87.584	85.179	896
	MT	18.875	17.918	20.54	18.874	19.136	79.545	84.978	87.584	85.179	896
	MT-ST	-0.26	-2.216	-0.845	0	0	-5.618	-5.521	0	0	0
cc1											
A	ST	5.746	7.043	7.48	5.243	5.746	73.473	83.581	58.437	73.467	167
	MT	5.243	5.347	5.801	5.243	5.746	55.369	69.457	58.437	73.467	167
	MT-ST	-0.503	-1.696	-1.679	0	0	-18.104	-14.124	0	0	0
B	ST	8.853	9.884	10.56	8.608	8.852	64.263	80.403	70.737	64.267	2324
	MT	8.608	9.945	10.685	8.608	8.852	51.619	68.696	70.737	64.267	2324
	MT-ST	-0.245	0.061	0.125	0	0	-12.644	-11.707	0	0	0
C	ST	8.951	9.372	10.11	8.89	8.951	66.709	81.153	63.882	66.701	2977
	MT	8.89	9.944	10.69	8.89	8.951	55.806	72.59	63.882	66.701	2977
	MT-ST	-0.061	0.572	0.58	0	0	-10.903	-8.563	0	0	0
D	ST	0.737	0.877	0.94	0.72	0.737	72.325	82.407	65.97	72.31	338
	MT	0.72	0.741	0.802	0.72	0.737	60.546	69.557	65.97	72.31	338
	MT-ST	-0.017	-0.136	-0.138	0	0	-11.779	-12.85	0	0	0
G	ST	2.145	2.4	2.596	2.09	2.145	64.183	78.416	67.604	64.188	639
	MT	2.09	2.319	2.549	2.09	2.145	50.137	62.099	67.604	64.188	639
	MT-ST	-0.055	-0.081	-0.047	0	0	-14.046	-16.317	0	0	0
int											
A	ST	5.508	6.101	6.526	5.275	5.508	78.369	86.358	66.933	78.35	149
	MT	5.275	5.604	6.07	5.275	5.508	55.572	74.122	66.933	78.35	149
	MT-ST	-0.233	-0.497	-0.456	0	0	-22.797	-12.236	0	0	0
C	ST	11.364	11.006	12.061	11.251	11.364	75.924	84.777	75.689	75.93	2949
	MT	11.251	11.193	12.221	11.251	11.364	70.155	80.219	75.689	75.93	2949
	MT-ST	-0.113	0.187	0.16	0	0	-5.769	-4.558	0	0	0
E	ST	14.694	14.756	16.062	14.237	14.693	74.062	83.924	63.957	74.067	1747
	MT	14.237	14.737	16.065	14.237	14.693	62.75	75.888	63.957	74.067	1747
	MT-ST	-0.457	-0.019	0.003	0	0	-11.312	-8.036	0	0	0
G	ST	1.939	2.138	2.33	1.998	1.939	64.945	80.287	64.706	64.952	884
	MT	1.998	2.255	2.466	1.998	1.939	48.368	63.23	64.706	64.952	884
	MT-ST	0.059	0.117	0.136	0	0	-16.577	-17.057	0	0	0

Table 7 Standard Deviation(SD) and average reliabilities(REL MEAN) of observation data (y, Input), DGV and GEBV for Common reference bulls in MT and ST in addition to their national and mace proofs in HOL

Trait		SD					REL MEAN				
country	Approach	Input	DGV	GEBV	NATIONAL	MACE	Input	GEBV	NATIONAL	MACE	*n*
pro											
H	ST	9.135	9.289	9.896	9.304	9.136	92.412	93.423	91.686	92.42	119
	MT	9.304	8.002	9.308	9.304	9.136	86.234	89.891	91.686	92.42	119
	MT-ST	0.169	-1.287	-0.588	0	0	-6.178	-3.532	0	0	0
I	ST	5.924	5.631	6.185	5.823	5.924	95.54	95.983	95.279	95.638	420
	MT	5.823	5.014	5.878	5.823	5.924	94.017	94.66	95.279	95.638	420
	MT-ST	-0.101	-0.617	-0.307	0	0	-1.523	-1.323	0	0	0
J	ST	14.951	14.169	15.679	14.901	14.951	93.546	94.312	92.83	93.618	1237
	MT	14.901	13.416	15.469	14.901	14.951	92.699	93.482	92.83	93.618	1237
	MT-ST	-0.05	-0.753	-0.21	0	0	-0.847	-0.83	0	0	0
K	ST	11.902	11.812	12.877	11.98	11.901	84.943	88.848	81.031	84.957	454
	MT	11.98	10.66	12.398	11.98	11.901	77.964	82.124	81.031	84.957	454
	MT-ST	0.078	-1.152	-0.479	0	0	-6.979	-6.724	0	0	0
L	ST	20.823	19.094	21.082	20.885	20.823	97.624	97.749	97.403	97.761	633
	MT	20.885	17.831	20.793	20.885	20.823	97.418	97.564	97.403	97.761	633
	MT-ST	0.062	-1.263	-0.289	0	0	-0.206	-0.185	0	0	0
F	ST	10.655	10.43	10.961	10.5	10.655	95.488	96.03	96.237	95.554	289
	MT	10.5	9.199	10.451	10.5	10.655	94.212	95.011	96.237	95.554	289
	MT-ST	-0.155	-1.231	-0.51	0	0	-1.276	-1.019	0	0	0
M	ST	5.001	4.846	5.26	5.102	5.001	92.653	93.577	89.833	92.645	222
	MT	5.102	4.396	5.167	5.102	5.001	88.484	91.013	89.833	92.645	222
	MT-ST	0.101	-0.45	-0.093	0	0	-4.169	-2.564	0	0	0
N	ST	13.56	12.873	14.151	13.783	13.56	92.846	93.852	89.109	92.834	221
	MT	13.783	11.556	13.731	13.783	13.56	89.55	91.483	89.109	92.834	221
	MT-ST	0.223	-1.317	-0.42	0	0	-3.296	-2.369	0	0	0
I	ST	4.332	4.35	4.704	4.24	4.332	86.747	88.707	73.451	86.73	415
	MT	4.24	4.575	4.997	4.24	4.332	73.165	76.844	73.451	86.73	415
	MT-ST	-0.092	0.225	0.293	0	0	-13.582	-11.863	0	0	0
cc2											
J	ST	2.722	2.889	3.158	2.626	2.722	64.583	75.044	83.885	64.598	1195
	MT	2.626	2.95	3.264	2.626	2.722	55.315	65.312	83.885	64.598	1195
	MT-ST	-0.096	0.061	0.106	0	0	-9.268	-9.732	0	0	0
M	ST	1.171	1.096	1.209	0.981	1.171	84.321	86.789	60.287	84.32	237
	MT	0.981	0.908	1.011	0.981	1.171	53.299	62.731	60.287	84.32	237
	MT-ST	-0.19	-0.188	-0.198	0	0	-31.022	-24.058	0	0	0
N	ST	14.07	13.62	15.093	11.352	14.07	84.375	87.382	61.466	84.39	208
	MT	11.352	11.27	12.544	11.352	14.07	63.014	71.148	61.466	84.39	208
	MT-ST	-2.718	-2.35	-2.549	0	0	-21.361	-16.234	0	0	0
int											
I	ST	4.363	4.35	4.721	4.24	4.363	86.737	88.391	73.451	86.747	415
	MT	4.24	4.621	4.981	4.24	4.363	73.165	76.761	73.451	86.747	415
	MT-ST	-0.123	0.271	0.26	0	0	-13.572	-11.63	0	0	0
M	ST	1.266	1.19	1.303	0.981	1.266	86.882	88.521	60.287	86.908	237
	MT	0.981	0.913	1.012	0.981	1.266	53.299	63.374	60.287	86.908	237
	MT-ST	-0.285	-0.277	-0.291	0	0	-33.583	-25.147	0	0	0
N	ST	13.281	12.434	13.769	11.352	13.281	85.135	87.609	61.466	85.145	208
	MT	11.352	11.263	12.451	11.352	13.281	63.014	71.43	61.466	85.145	208
	MT-ST	-1.929	-1.171	-1.318	0	0	-22.121	-16.179	0	0	0

5 Discussion

The genomically enhanced estimated breeding value (GEBV) in the current study is a result of combining 3 estimated breeding values for each bull: genomic value (DGV) and the other two traditional non-genomic values (subset-EBV and traditional-EBV). The discussion will begin with the genomic value (DGV), then the non-genomic values (subset-EBV and traditional-EBV) through discussing the combining process.

Direct genomic value (DGV) and associated reliability.

The direct genomic value in the current study is the sum of marker effects plus the associated polygenic effect. Estimation of marker effects in the current study based on the Bayesian framework using "Bayes A" prior, then the obtained DGV variance is mainly a function of the prior variance and the input data (y) variance. As the prior used in both ST and MT is the same, the DGV SD differences are supposed to be due to the SD differences in input data (y), which are in almost all breed-trait-country combination in favour of ST (Table 6-7). ST input data (y) comes from MACE process based on data of about 30 countries analyzed simultaneously by a multi-trait framework, whereas the MT input data (y) comes from national evaluations based on only single-country data. Therefore, less information is available in input data (y) of the current MT and consequently input SD differences are in favour of ST.

Even though the current MT includes information in a similar way as in MACE process, still the number of countries participating within the current MT (range 3 to 8) is much smaller than those in MACE process (~30). If the number of countries participating in MACE and the current MT were the same, the DGV SD differences between MT and ST would be expected to be close to zero.

Another reason for DGV SD being higher for ST approach is the size of the reference population, which is larger in ST than that in MT (Tables 1-2 in "Data" Section). Larger reference population could be viewed as a source of more input variances at the level of genomic (SNP) information and/or response variable (y) information.

In a few cases, even though both input data (y) SD differences and reference population size differences were in favor of ST, the DGV SD differences were in favor of MT as in the following breed-trait-country combinations: BSW-cc1-C (all, Ref., Cand. bulls), BSW-int-C (Ref. bulls only) and HOL-int-I,M,N (Ref. bulls only) as shown in Figures 3 and 5. Those findings emphasize the role of trait architecture, as both "cc1" and "int" are low heritability traits. In high heritable traits like "pro", more weight is given to own trait information with no more gain expected from using MT, especially if the genetic correlations are high i.e. information of input data (y) contributed by each trait within MT machine is more alike (less variance) then such information is less valuble. This explains why DGV SD differences between ST and MT are high in "pro" trait in comparison to low heritability traits (cc1, cc2 and int). On the other hand, in low heritable traits like "cc1", "cc2" and "int", more weight is given to the use of genetic correlations via MT than own trait information, even if some input data (y) is lacking, or less accurate. This could explain why DGV SD differences between ST and MT are small in "cc1", "cc2" and "int" in general, and in favor of MT in breed-trait-country combinations mentioned above (Figures 3 and 5). Our current conclusion is that MT approach may be a better choice than ST approach to get a slight increase in DGV variance (then that increase in DGV variance should be translated into increase in DGV reliability) for some breed-trait-country combinations of low heritability, but simultaneously other factors need to be considered as well : 1) genetic correlations between countries, and 2) the variability and reliability of the input data (y) contributed by each country, within MT approach.

In the current study, checking all trait-country combinations simultaneously (Figures 3 and 5) reveals that differences between MT and ST for DGV SD are high in high heritability trait (pro) and low in low heritability traits (int,cc1,cc2). This demonstrates that DGV SD differences follow a general pattern sensitive to data structure and trait architecture. However, the coressponding DGV REL average differences do not have the same pattern in the current study (Figures 3 and 5). In addition, checking each trait-country combinations separately (Figures 3 and 5) shows whenever the DGV SD difference in favour of ST, the DGV REL average difference in favour of ST as well for the same breed-trait-country combination except in few cases (2 cases in BSW and 3 cases in HOL) , for instance in BSW-cc1-

C, where the DGV REL average differences were in favor of ST even though the corresponding DGV SD differences were in favor of MT (Figure 3),this may not agree with the basic equation that describe reliability and variance of EBV; "variance(EBV)=REL* variance(TBV)", where the higher variance(EBV) should be associated with higher reliability average. This might indicate double counting of information that is susupected in ST approach but not in MT approach. Actually, ST relies on MACE proofs as pseudo-phenotypes for the reference bulls, and in the current process, all bulls that had a calculated MACE proof even if it were based only on pedigree information, were considered as a reference bulls (personal communication with Interbull Centre geneticists). Including bulls with no daughter information in any country in the reference population would lead into double counting of information as the phenotype of a cow from any country should contribute to only one bull's, i.e. her sire, (pseudo)phenotype (deregressed bull MACE EBV). If an old bull without own daughters received MACE EBV via pedigree, his EBV was contributed by his possible grand-daughters or great-granddaughters, etc. If this old bull has also a genotyped son, we would double count the phenotype contribution of his granddaughters, if we include this old bull in genomic reference population together with his son, because his grand-daughters contributed to his (ancestral) EBV and his son's MACE EBV simultaneously.
This issue does not occur in MT approach where reference bulls are defined based on direct domestic daughters information. Additionally, in ST, the MACE values were used as pseudo-phenotypes weighted by MACE REL, the latter do include a parental contribution besides the actual daughter contribution and might lead to a double counting of information in ST. A better approach would be to calculate an equivalent EDC derived from all national EDC using genetic correlations between countries (Liu, 2011).

Sufficient contribution (sufficiency in terms of trait architecture and contribution in terms of genomic & input data (y) information) of each country to the reference population could determine the extent of DGV SD gain for each country by MT approach over ST approach. For example in BSW breed, the country C contributes 2977 and 2947 bulls (Table 6) to the reference population for "cc1" and "int" trait, respectively, but the MT DGV SD is exceeding ST DGV SD for *all*, reference and candidate bulls in "cc1" trait, and for reference bulls only in "int" trait (Figure 3). Moreover, in some cases MT DGV SD exceeding ST DGV SD is restricted to the domestic reference bulls only as in cases of BSW-cc1-B (Table 6) and HOL-cc2-I,J (Table7).

Combining process

In ST combining process, subset-REL should be the lowest because the subset-EBV variance is expected be the lowest. The subset evaluation is based on non-genomic information of only genotyped ancestors (either being domestic or/and foreign), whereas traditional evaluation based on non-genomic information of *all* ancestors (genotyped and non-genotyped either being domestic or/and foreign; foreign here refers to countries participate in MACE process).

For reference bulls in ST, in all breed-trait-country combinations, both subset-EBV SD and subset-EBV REL average were higher than traditional-EBV SD and traditional-EBV REL average, respectively, before applying of weighting rules (Figure 7), and therefore equal to each other after applying weighting rules (Figure 8). Being average of subset-EBV REL higher than average of traditional-EBV REL before applying weighting rules is unreasonable, and indicate some double counting in subset evaluation reliability. That resulted a case of inconsistency between subset and traditional RELs, and by applying of weighting rules, they both had given a zeros index weights. Consequently, the GEBV SD of those reference bulls is the function of only the corresponding DGV SD (see Appendix C)

For candidate bulls in ST, in all breed-trait-country combinations, the subset-EBV REL was lower than the traditional-EBV REL even though the subsetEBV SD was higer than the traditionalEBV SD before (Figure 7) and after (Figure 8) applying the weighting rules. This inconsistency between the variance and the reliability can be explained by a potential double counting of information in the traditional part where we suspect the reliabilities being overestimated. As the rule "subsetREL > traditionalREL" is the condition used in the program to detect inconsistenty between subset and traditional evaluations and as in this case it is not verified, this leads to inappropriate combining of the three terms that will also lead to a double counting of information in the final reliabilities making them higher than what they should be.

When it comes to MT approach, both the subset EBV SD and REL averages were higher than the traditional ones (Figure 9) which is expected because of all the information that comes through genetic correlations when running the subset evaluation. As this is very well reflected in the associated reliability, the combining process works as expected in order to avoid double counting of information and the final reliabilities are expected to be more accurate than those coming out of the ST approach. This might explain why the gain in reliability from implementing the MT approach in certain traits was much lower than expected or even not achieved at all. Recent investigations carried out by Interbull center have shown that the current

reliabilities calculated following an ST approach were confirmed to be overestimated in HOL breed (personal communication). These findings confirm our assumptions in the current study and suggest that the MT approach might have more benefit than the one showed in this study once reliabilities from ST are adjusted.

6 Conclusions

Single-trait approach resulted in higher direct genomic values' variance and accuracy than multi-trait approach except in few cases limited to low heritability traits where the multi-trait direct genomic values' standard deviation (but not direct genomic values' reliability average) exceeds single-trait direct genomic values' standard deviation. In general, this indicates the importance of the MACE information coming from other countries than InterGenomis countries that we loose once we decide to use national information recorded only in the InterGenomics participating countries and that is even more obvious in HOL evaluation where all the big and exporting countries that are present in MACE are not participating in InterGenomics. Those cases where the multi-trait has led to an increase of the genetic variance but not necessarily followed by an increase in the reliability might indicate a double counting of information in the single-trait approach resulting probably from using bulls with no daughter information in any country as reference bulls. The use of MACE REL as input to the genomic evaluation might also lead to some double counting as MACE REL do not contain only daughter contribution but also a parental part. Removing old bulls with no daughter information from the single-trait and using EDC representing only daughter contribution could be recommended to improve the current single-trait process.

As initially expected and despite the loss of information due to the use of national proofs, this study confirmed that multi-trait approach provides a slight increase in direct genomic value' variances than the single-trait approach for some traits of low heritability. The current results might underestimate the benefit from implementing a multi-trait approach as reliabilities from the single-trait have been confirmed to be overestimated by Interbull Centre recently. A new analysis after adjusting the single-trait reliabilities is recommended.

7 Referenslista/References

Banos, G., Calus, M., Ducrocq, V., Dürr, J., Jorjani, H., Liu, Z., Mäntysaari, E., Sullivan, P., VanRaden, P., 2009. Preliminary report from Interbull Task Force on the role of genomic information in genetic evaluations. Interbull Bulletin 39(2009), 61.

Calus, M.P., Veerkamp, R.F., 2011. Accuracy of multi-trait genomic selection using different methods. Genet Sel Evol 43, 1–14. https://doi.org/10.1186/1297-9686-43-26

Garrick, D.J., Taylor, J.F., Fernando, R.L., 2009. Deregressing estimated breeding values and weighting information for genomic regression analyses. Genetics Selection Evolution 41, 55. https://doi.org/10.1186/1297-9686-41-55

Goddard, M.E., Hayes, B.J., 2009. Mapping genes for complex traits in domestic animals and their use in breeding programmes. Nature Reviews Genetics 10, 381–391. https://doi.org/10.1038/nrg2575

Guo, G., Zhao, F., Wang, Y., Zhang, Y., Du, L., Su, G., 2014. Comparison of single-trait and multiple-trait genomic prediction models. BMC Genet 15, 30. https://doi.org/10.1186/1471-2156-15-30

Jia, Y., Jannink, J.-L., 2012. Multiple-Trait Genomic Selection Methods Increase Genetic Value Prediction Accuracy. Genetics 192, 1513–1522. https://doi.org/10.1534/genetics.112.144246

Legarra, A., Christensen, O.F., Aguilar, I., Misztal, I., 2014. Single Step, a general approach for genomic selection. Livestock Science, Genomics Applied to Livestock Production 166, 54–65. https://doi.org/10.1016/j.livsci.2014.04.029

Liu, Z., 2011. Use of MACE results as input for genomic models. Interbull Bulletin 43 (2011).

Liu, Z., Seefried, F.R., Reinhardt, F., Rensing, S., Thaller, G., Reents, R., 2011. Impacts of both reference population size and inclusion of a residual polygenic effect on the accuracy of genomic prediction. Genet Sel Evol 43, 19. https://doi.org/10.1186/1297-9686-43-19

Misztal, I., Wiggans, G.R., 1988. Approximation of Prediction Error Variance in Large-Scale Animal Models. Journal of Dairy Science 71, 27–32. https://doi.org/10.1016/S0022-0302(88)79976-2

Schaeffer, L.R., 1994. Multiple-Country Comparison of Dairy Sires. Journal of Dairy Science 77, 2671–2678. https://doi.org/10.3168/jds.S0022-0302(94)77209-X

VanRaden, P.M., 2008. Efficient methods to compute genomic predictions. J. Dairy Sci. 91, 4414–4423. https://doi.org/10.3168/jds.2007-0980

VanRaden, P.M., Sullivan, P.G., 2010. International genomic evaluation methods for dairy cattle. Genet Sel Evol 42, 7. https://doi.org/10.1186/1297-9686-42-7

VanRaden, P.M., Van Tassell, C.P., Wiggans, G.R., Sonstegard, T.S., Schnabel, R.D., Taylor, J.F., Schenkel, F.S., 2009. Invited review: reliability of genomic predictions for North American Holstein bulls. J. Dairy Sci. 92, 16–24. https://doi.org/10.3168/jds.2008-1514

VanRaden, P.M., Wiggans, G.R., 1991. Derivation, calculation, and use of national animal model information. J. Dairy Sci. 74, 2737–2746. https://doi.org/10.3168/jds.S0022-0302(91)78453-1

8 Tack/Acknowledgements

Thanks to my supervisor **Erling Strandberg** for his guidance, valuable comments and continuous support along my thesis project. Unlimited thanks to my supervisor **Haifa Benhajali**; she accepted the challenge to supervise me starting from developing ideas and planing for my project along daily following up my progress until the end of my project. Also, thank you **Haifa Benhajali** for your great efforts to teach me Fortran programming. At many stages in my project, I got stuck with several issues. The most important thing I should thank **Haifa Benhajali** for, is that Haifa always gives me the feeling that I have my own wings and I can fly. For rest of my life, I can't forget Haifa sentence whenever I got stuck, Haifa was telling me: "You will solve it by yourself , just try again", that is why my thanks for you Haifa are unlimited. Many thanks to Interbull Center Team either geneticist, IT-specialists and the director **Antonius Roozen**, for their strong support during my project. Thanks to **Simone Savoia** for interesting discussions about interbull InterGenomic service, and **Alexis Michenet** for his tips in programming issues. Thanks to the quality manager at The Interbull Center **Valentina Palucci** for her recommendations regarding data resources handling. Finally, I thank **Sreten Andonov** for his kind discussion about population genetics.

And ..

Thanks for my examiner **Dirk-Jan De Koning,** your comments and suggestions to improve this manuscript are very appreciated, your questions opened my eyes into a very interesting issues, thank you.

9 Bilaga /Appendix

Appendix A1 Genetic correlation between countries for pro trait in HOL population

Breed	Trait		H	I	J	K	L	F	M	N
HOL	**pro**	H	1.00							
		I	0.69	1.00						
		J	0.83	0.62	1.00					
		K	0.82	0.69	0.83	1.00				
		L	0.80	0.68	0.83	0.80	1.00			
		F	0.81	0.70	0.84	0.82	0.81	1.00		
		M	0.81	0.69	0.84	0.80	0.80	0.82	1.00	
		N	0.81	0.70	0.88	0.81	0.80	0.82	0.80	1.00

Appendix A2 Genetic correlation between countries for cc2 trait in HOL population

Breed	Trait		I	J	M	N
HOL	**cc1**	I	1.00			
		J	-0.60	1.00		
		M	-0.84	0.49	1.00	
		N	0.87	-0.60	-0.78	1.00

Appendix A3 Genetic correlation between countries for int trait in HOL population

Breed	Trait		I	M	N
HOL	**int**	I	1.00		
		M	-0.87	1.00	
		N	0.87	-0.86	1.00

Appendix A4 Genetic correlation between countries for pro trait in BSW population

Breed	Trait		A	B	C	D	E	F	G
BSW	**pro**	A	1.00						
		B	0.86	1.00					
		C	0.86	0.92	1.00				
		D	0.84	0.84	0.81	1.00			
		E	0.85	0.85	0.89	0.82	1.00		
		F	0.82	0.81	0.81	0.81	0.81	1.00	
		G	0.89	0.83	0.82	0.86	0.83	0.82	1.00

Appendix A5 Genetic correlation between countries for cc1 trait in BSW population

Breed	Trait		A	B	C	D	G
BSW	**cc1**	A	1.00				
		B	0.79	1.00			
		C	0.79	0.95	1.00		
		D	0.71	0.69	0.67	1.00	
		G	0.74	0.67	0.67	0.92	1.00

Appendix A6 Genetic correlation between countries for int trait in BSW population

Breed	Trait		A	C	E	G
BSW	**int**	A	1.00			
		C	0.88	1.00		
		E	0.88	0.93	1.00	
		G	0.90	0.87	0.89	1.00

Appendix B1 DGV SD, correlations between DGV and REL averages from MT and ST, for all traits in BSW population for all, reference and candidates individuals, and number of bulls (n)

	Trait		DGV SD			**DGV**	REL Mean			
Breed	**country**	**Status**	**MT**	**ST**	**MT-ST**	**Corr**	**MT**	**ST**	**MT-ST**	**n**
	pro									
BSW	A	All	23.651	37.898	-14.247	0.962	0.32	0.837	-0.517	34093
		Ref	24.647	35.335	-10.688	0.985	0.711	0.883	-0.172	7128
		Cand	19.507	32.666	-13.159	0.962	0.216	0.824	-0.608	26603
BSW	B	All	22.999	26.368	-3.369	0.979	0.715	0.856	-0.141	34093
		Ref	23.525	25.622	-2.097	0.984	0.865	0.913	-0.048	7128
		Cand	18.835	21.835	-3	0.979	0.675	0.84	-0.165	26603
BSW	C	All	18.075	21.984	-3.909	0.974	0.761	0.859	-0.098	34093
		Ref	18.833	21.518	-2.685	0.985	0.885	0.918	-0.033	7128
		Cand	14.616	18.222	-3.606	0.974	0.728	0.843	-0.115	26603
BSW	D	All	21.635	33.522	-11.887	0.952	0.389	0.831	-0.442	34093
		Ref	22.252	31.085	-8.833	0.978	0.707	0.876	-0.169	7128
		Cand	18.217	29.295	-11.078	0.949	0.305	0.819	-0.514	26603
BSW	E	All	25.724	35.022	-9.298	0.964	0.648	0.847	-0.199	34093
		Ref	27.146	33.213	-6.067	0.983	0.828	0.897	-0.069	7128
		Cand	20.997	29.836	-8.839	0.965	0.6	0.833	-0.233	26603
BSW	F	All	10.499	14.751	-4.252	0.954	0.363	0.831	-0.468	34093
		Ref	10.851	13.678	-2.827	0.962	0.674	0.876	-0.202	7128
		Cand	8.978	12.891	-3.913	0.953	0.28	0.819	-0.539	26603
BSW	G	All	21.547	31.503	-9.956	0.958	0.493	0.834	-0.341	34093
		Ref	22.191	29	-6.809	0.98	0.742	0.879	-0.137	7128
		Cand	17.877	27.318	-9.441	0.957	0.427	0.821	-0.394	26603
	cc1									

BSW	A	All	4.567	7.217	-2.65	0.949	0.18	0.727	-0.547	34093
		Ref	5.384	7.774	-2.39	0.969	0.41	0.785	-0.375	5450
		Cand	4.367	6.941	-2.574	0.949	0.136	0.715	-0.579	28260
BSW	B	All	8.483	9.236	-0.753	0.979	0.574	0.773	-0.199	34093
		Ref	9.935	10.252	-0.317	0.989	0.708	0.837	-0.129	5450
		Cand	8.11	8.812	-0.702	0.981	0.548	0.761	-0.213	28260
BSW	C	All	8.939	8.883	0.056	0.982	0.643	0.775	-0.132	34093
		Ref	10.579	10.034	0.545	0.992	0.747	0.84	-0.093	5450
		Cand	8.539	8.47	0.069	0.984	0.623	0.762	-0.139	28260
BSW	D	All	0.599	0.943	-0.344	0.907	0.27	0.714	-0.444	34093
		Ref	0.681	0.98	-0.299	0.938	0.448	0.773	-0.325	5450
		Cand	0.577	0.908	-0.331	0.906	0.236	0.702	-0.466	28260
BSW	G	All	1.921	2.892	-0.971	0.897	0.303	0.713	-0.41	34093
		Ref	2.192	2.969	-0.777	0.934	0.466	0.773	-0.307	5450
		Cand	1.852	2.791	-0.939	0.894	0.271	0.701	-0.43	28260
	int									
BSW	A	All	5.272	9.183	-3.911	0.882	0.183	0.752	-0.569	34093
		Ref	5.786	6.648	-0.862	0.968	0.532	0.826	-0.294	4897
		Cand	5.088	9.297	-4.209	0.879	0.124	0.74	-0.616	28916
BSW	C	All	10.48	14.576	-4.096	0.902	0.688	0.778	-0.09	34093
		Ref	12.087	12.004	0.083	0.985	0.805	0.86	-0.055	4897
		Cand	9.869	14.442	-4.573	0.894	0.668	0.764	-0.096	28916
BSW	E	All	13.768	19.283	-5.515	0.903	0.558	0.771	-0.213	34093
		Ref	15.638	15.881	-0.243	0.982	0.743	0.85	-0.107	4897
		Cand	12.877	19.009	-6.132	0.894	0.526	0.758	-0.232	28916
BSW	G	All	1.907	3.548	-1.641	0.876	0.364	0.755	-0.391	34093
		Ref	2.023	2.322	-0.299	0.963	0.626	0.829	-0.203	4897
		Cand	1.867	3.636	-1.769	0.878	0.32	0.743	-0.423	28916

[1] MT, [2] ST, SD = standard deviation, Ref = Reference individuals, Cand = Candidate individuals

Appendix B2 DGV SD, correlations between DGV and REL averages from MT and ST, for all traits in HOL population for all, reference and candidates individuals, and number of bulls (n)

	Trait		DGV SD			**DGV**	REL Mean			
Breed	**country**	**Status**	**MT**	**ST**	**MT-ST**	**Corr**	**MT**	**ST**	**MT-ST**	**n**
	pro									
HOL	H	All	10.912	17.084	-6.172	0.926	0.333	0.742	-0.409	7173
		Ref	12.223	17.633	-5.41	0.946	0.658	0.83	-0.172	2603
		Cand	9.211	14.06	-4.849	0.925	0.144	0.675	-0.531	4031
HOL	I	All	4.803	9.742	-4.939	0.85	0.446	0.713	-0.267	7173
		Ref	5.257	10.436	-5.179	0.83	0.612	0.794	-0.182	2603
		Cand	4.039	7.338	-3.299	0.856	0.349	0.65	-0.301	4031
HOL	J	All	11.76	14.031	-2.271	0.935	0.634	0.783	-0.149	7173
		Ref	13.231	13.908	-0.677	0.961	0.836	0.896	-0.06	2603
		Cand	9.809	12.193	-2.384	0.945	0.517	0.703	-0.186	4031
HOL	K	All	13.153	18.516	-5.363	0.929	0.444	0.749	-0.305	7173
		Ref	14.578	19.077	-4.499	0.948	0.71	0.84	-0.13	2603
		Cand	11.347	15.533	-4.186	0.93	0.286	0.681	-0.395	4031
HOL	L	All	16.572	23.042	-6.47	0.933	0.538	0.758	-0.22	7173
		Ref	18.789	24.404	-5.615	0.944	0.765	0.858	-0.093	2603
		Cand	13.837	18.552	-4.715	0.941	0.403	0.685	-0.282	4031
HOL	F	All	9.111	12.441	-3.33	0.935	0.418	0.751	-0.333	7173
		Ref	10.363	13.255	-2.892	0.955	0.707	0.844	-0.137	2603

		Cand	7.663	10.374	-2.711	0.94	0.248	0.682	-0.434	4031
HOL	M	All	5.338	8.075	-2.737	0.927	0.381	0.745	-0.364	7173
		Ref	6.062	8.387	-2.325	0.954	0.686	0.835	-0.149	2603
		Cand	4.457	6.655	-2.198	0.921	0.201	0.678	-0.477	4031
HOL	N	All	12.936	19	-6.064	0.934	0.388	0.745	-0.357	7173
		Ref	14.535	19.597	-5.062	0.954	0.686	0.835	-0.149	2603
		Cand	10.948	15.886	-4.938	0.935	0.212	0.678	-0.466	4031
	cc2									
HOL	I	All	3.449	4.272	-0.823	0.877	0.347	0.662	-0.315	7173
		Ref	3.997	5.318	-1.321	0.891	0.488	0.752	-0.264	1783
		Cand	3.183	3.571	-0.388	0.901	0.298	0.602	-0.304	4521
HOL	J	All	2.36	2.871	-0.511	0.889	0.448	0.663	-0.215	7173
		Ref	3.184	3.409	-0.225	0.934	0.63	0.779	-0.149	1783
		Cand	1.935	2.47	-0.535	0.881	0.386	0.603	-0.217	4521
HOL	M	All	0.676	1.599	-0.923	0.747	0.204	0.642	-0.438	7173
		Ref	0.79	2.048	-1.258	0.777	0.355	0.722	-0.367	1783
		Cand	0.612	1.286	-0.674	0.791	0.147	0.583	-0.436	4521
HOL	N	All	10.225	22.461	-12.236	0.8	0.226	0.653	-0.427	7173
		Ref	11.924	27.965	-16.041	0.82	0.397	0.737	-0.34	1783
		Cand	9.348	18.213	-8.865	0.836	0.161	0.594	-0.433	4521
	int									
HOL	I	All	3.182	3.26	-0.078	0.89	0.33	0.606	-0.276	7173
		Ref	4.718	4.32	0.398	0.929	0.704	0.868	-0.164	651
		Cand	2.878	2.899	-0.021	0.903	0.288	0.545	-0.257	5621
HOL	M	All	0.663	0.787	-0.124	0.747	0.191	0.603	-0.412	7173
		Ref	1.017	0.927	0.09	0.829	0.61	0.857	-0.247	651
		Cand	0.591	0.718	-0.127	0.755	0.142	0.542	-0.4	5621
HOL	N	All	9.365	10.371	-1.006	0.845	0.205	0.601	-0.396	7173
		Ref	13.953	13.286	0.667	0.888	0.615	0.849	-0.234	651
		Cand	8.427	9.203	-0.776	0.859	0.155	0.54	-0.385	5621

SD = standard deviation, Ref = Reference individuals, Cand = Candidate individuals

Appendix B3 GEBV SD, correlations between GEBV and REL averages from MT and ST, for all traits in BSW population for all, reference and candidates individuals, and number of bulls (n)

	Trait		GEBV SD			GEBV	REL Mean			
Breed	country	Status	MT	ST	MT-ST	Corr	MT	ST	MT-ST	n
	pro									
BSW	A	All	23.651	36.196	-12.545	0.965	28.812	77.108	-48.296	34093
		Ref	24.647	35.334	-10.687	0.985	70.553	84.672	-14.119	7128
		Cand	19.508	30.147	-10.639	0.965	17.675	75.063	-57.388	26603
BSW	B	All	22.998	25.366	-2.368	0.979	63.134	79.68	-16.546	34093
		Ref	23.525	25.623	-2.098	0.984	84.57	88.871	-4.301	7128
		Cand	18.833	20.327	-1.494	0.979	57.423	77.203	-19.78	26603
BSW	C	All	18.074	21.187	-3.113	0.976	68.296	80.175	-11.879	34093
		Ref	18.833	21.519	-2.686	0.985	86.599	89.643	-3.044	7128
		Cand	14.615	16.954	-2.339	0.977	63.439	77.625	-14.186	26603
BSW	D	All	21.635	31.985	-10.35	0.955	34.394	76.336	-41.942	34093
		Ref	22.253	31.084	-8.831	0.978	69.665	83.647	-13.982	7128
		Cand	18.217	27.041	-8.824	0.953	25.022	74.359	-49.337	26603
BSW	E	All	25.724	33.542	-7.818	0.966	56.214	78.462	-22.248	34093
		Ref	27.146	33.212	-6.066	0.983	80.656	86.743	-6.087	7128

		Cand	20.996	27.583	-6.587	0.965	49.699	76.227	-26.528	26603
BSW	F	All	10.498	14.5	-4.002	0.964	31.472	75.77	-44.298	34093
		Ref	10.851	13.972	-3.121	0.98	66.18	83.051	-16.871	7128
		Cand	8.977	12.417	-3.44	0.965	22.238	73.802	-51.564	26603
BSW	G	All	21.546	30.076	-8.53	0.961	41.635	76.648	-35.013	34093
		Ref	22.19	29.001	-6.811	0.98	72.135	84.165	-12.03	7128
		Cand	17.876	25.209	-7.333	0.961	33.496	74.617	-41.121	26603
	cc1									
BSW	A	All	4.567	6.762	-2.195	0.954	15.78	63.575	-47.795	34093
		Ref	5.384	7.774	-2.39	0.969	39.693	71.913	-32.22	5450
		Cand	4.367	6.372	-2.005	0.954	11.167	61.932	-50.765	28260
BSW	B	All	8.483	8.691	-0.208	0.975	48.002	69.389	-21.387	34093
		Ref	9.935	10.252	-0.317	0.989	65.578	78.806	-13.228	5450
		Cand	8.11	8.117	-0.007	0.976	44.609	67.536	-22.927	28260
BSW	C	All	8.939	8.373	0.566	0.978	54.759	69.611	-14.852	34093
		Ref	10.579	10.035	0.544	0.992	69.085	79.109	-10.024	5450
		Cand	8.539	7.826	0.713	0.98	52.014	67.741	-15.727	28260
BSW	D	All	0.599	0.87	-0.271	0.916	22.984	62.183	-39.199	34093
		Ref	0.681	0.979	-0.298	0.938	42.307	70.303	-27.996	5450
		Cand	0.577	0.817	-0.24	0.92	19.293	60.587	-41.294	28260
BSW	G	All	1.921	2.652	-0.731	0.908	24.363	62.08	-37.717	34093
		Ref	2.192	2.969	-0.777	0.934	42.75	70.257	-27.507	5450
		Cand	1.852	2.493	-0.641	0.91	20.831	60.474	-39.643	28260
	int									
BSW	A	All	5.272	7.932	-2.66	0.905	16.285	67.021	-50.736	34093
		Ref	5.786	6.648	-0.862	0.968	52.433	77.639	-25.206	4897
		Cand	5.087	7.865	-2.778	0.901	10.142	65.193	-55.051	28916
BSW	C	All	10.48	12.897	-2.417	0.924	59.528	70.33	-10.802	34093
		Ref	12.086	12.005	0.081	0.985	76.341	82.225	-5.884	4897
		Cand	9.869	12.489	-2.62	0.917	56.686	68.285	-11.599	28916
BSW	E	All	13.768	17.075	-3.307	0.924	46.535	69.45	-22.915	34093
		Ref	15.639	15.881	-0.242	0.982	70.617	80.918	-10.301	4897
		Cand	12.877	16.443	-3.566	0.915	42.44	67.476	-25.036	28916
BSW	G	All	1.907	3.03	-1.123	0.897	29.6	67.45	-37.85	34093
		Ref	2.023	2.322	-0.299	0.963	59.598	78.153	-18.555	4897
		Cand	1.867	3.047	-1.18	0.896	24.496	65.608	-41.112	28916

[1] MT, [2]ST, SD = standard deviation, Ref = Reference individuals, Cand = Candidate individuals

Appendix B4 GEBV SD, correlations between GEBV and REL averages from MT and ST, for all traits in HOL population for all, reference and candidates individuals, and number of bulls (n)

	Trait		GEBV SD			GEBV	REL Mean			
Breed	country	Status	MT	ST	MT-ST	Corr	MT	ST	MT-ST	n
	pro									
HOL	H	All	10.916	16.65	-5.734	0.912	31.575	68.758	-37.183	7173
		Ref	12.222	17.633	-5.411	0.946	65.275	79.701	-14.426	2603
		Cand	9.21	12.866	-3.656	0.891	11.877	60.583	-48.706	4031
HOL	I	All	4.867	9.593	-4.726	0.841	41.85	65.937	-24.087	7173
		Ref	5.257	10.436	-5.179	0.83	58.682	74.695	-16.013	2603
		Cand	4.104	6.662	-2.558	0.842	32.443	59.164	-26.721	4031
HOL	J	All	11.761	13.672	-1.911	0.928	55.813	73.425	-17.612	7173
		Ref	13.231	13.907	-0.676	0.961	81.858	87.884	-6.026	2603
		Cand	9.809	11.331	-1.522	0.918	40.592	63.317	-22.725	4031
HOL	K	All	13.145	18.036	-4.891	0.915	39.831	69.603	-29.772	7173
		Ref	14.579	19.078	-4.499	0.948	69.666	81.022	-11.356	2603

		Cand	11.33	14.3	-2.97	0.897	22.115	61.159	-39.044	4031
HOL	L	All	16.59	22.511	-5.921	0.922	48.197	70.58	-22.383	7173
		Ref	18.789	24.404	-5.615	0.944	74.897	82.93	-8.033	2603
		Cand	13.828	17.092	-3.264	0.916	32.355	61.706	-29.351	4031
HOL	F	All	9.11	12.072	-2.962	0.924	38.067	69.81	-31.743	7173
		Ref	10.363	13.256	-2.893	0.955	69.75	81.478	-11.728	2603
		Cand	7.668	9.513	-1.845	0.911	19.422	61.251	-41.829	4031
HOL	M	All	5.338	7.878	-2.54	0.914	35.172	69.128	-33.956	7173
		Ref	6.062	8.387	-2.325	0.954	67.821	80.426	-12.605	2603
		Cand	4.451	6.13	-1.679	0.886	15.947	60.772	-44.825	4031
HOL	N	All	12.961	18.501	-5.54	0.921	36.02	69.171	-33.151	7173
		Ref	14.536	19.598	-5.062	0.954	67.841	80.309	-12.468	2603
		Cand	10.972	14.61	-3.638	0.903	17.134	60.888	-43.754	4031
	cc2									
HOL	I	All	3.505	4.008	-0.503	0.84	31.85	61.075	-29.225	7173
		Ref	3.997	5.318	-1.321	0.891	45.231	69.491	-24.26	1783
		Cand	3.267	3.047	0.22	0.865	27.513	54.932	-27.419	4521
HOL	J	All	2.36	2.734	-0.374	0.873	36.338	59.66	-23.322	7173
		Ref	3.184	3.409	-0.225	0.934	57.918	73.526	-15.608	1783
		Cand	1.935	2.207	-0.272	0.84	28.861	52.559	-23.698	4521
HOL	M	All	0.674	1.51	-0.836	0.713	17.563	58.52	-40.957	7173
		Ref	0.79	2.048	-1.258	0.777	33.131	65.849	-32.718	1783
		Cand	0.61	1.1	-0.49	0.751	11.588	52.567	-40.979	4521
HOL	N	All	10.327	21.096	-10.769	0.767	19.96	59.751	-39.791	7173
		Ref	11.924	27.963	-16.039	0.82	37.567	67.783	-30.216	1783
		Cand	9.438	15.233	-5.795	0.807	13.115	53.59	-40.475	4521
	int									
HOL	I	All	3.26	3.046	0.214	0.847	29.809	58.302	-28.493	7173
		Ref	4.719	4.321	0.398	0.929	68.437	85.462	-17.025	651
		Cand	2.969	2.591	0.378	0.842	25.76	52.118	-26.358	5621
HOL	M	All	0.662	0.718	-0.056	0.708	16.148	57.597	-41.449	7173
		Ref	1.017	0.927	0.09	0.829	59.059	84.153	-25.094	651
		Cand	0.59	0.633	-0.043	0.695	11.069	51.361	-40.292	5621
HOL	N	All	9.481	9.664	-0.183	0.801	17.634	57.344	-39.71	7173
		Ref	13.954	13.285	0.669	0.888	59.86	83.24	-23.38	651
		Cand	8.504	8.254	0.25	0.79	12.441	51.149	-38.708	5621

[1] MT, [2]ST, SD = standard deviation, Ref = Reference individuals, Cand = Candidate individuals

Appendix B5 Subset-EBV and traditional-EBV SD differences and REL mean differences before applying weighting rules for all breeds/all traits in ST

			EBV SD			EBV[1,2]	EBV REL MEAN			
Breed	Trait-country	Status	Subset[1]	Traditional[2]	Diff[1-2]	Corr	Subset[1]	Traditional[2]	Diff[1-2]	*n*
BSW	Pro-A	Ref	2.299	1.391	0.908	0.905	0.739	0.696	0.043	7490
		Cand	1.319	0.734	0.585	0.787	0.254	0.284	-0.03	26603
BSW	Pro-B	Ref	2.01	1.36	0.65	0.911	0.808	0.78	0.028	7490
		Cand	1.141	0.744	0.397	0.803	0.274	0.316	-0.042	26603
BSW	Pro-C	Ref	2.127	1.422	0.705	0.905	0.822	0.797	0.025	7490
		Cand	1.16	0.741	0.419	0.796	0.28	0.323	-0.043	26603
BSW	Pro-D	Ref	2.38	1.389	0.991	0.904	0.718	0.668	0.05	7490
		Cand	1.365	0.747	0.618	0.787	0.252	0.281	-0.029	26603
BSW	Pro-E	Ref	2.282	1.449	0.833	0.902	0.774	0.74	0.034	7490
		Cand	1.266	0.735	0.531	0.786	0.263	0.301	-0.038	26603

BSW	Pro-F	Ref	2.38	1.389	0.991	0.904	0.718	0.668	0.05	7490
		Cand	1.365	0.747	0.618	0.787	0.252	0.281	-0.029	26603
BSW	Pro-G	Ref	2.373	1.397	0.976	0.903	0.726	0.68	0.046	7490
		Cand	1.375	0.748	0.627	0.786	0.252	0.279	-0.027	26603
BSW	cc1-A	Ref	1.682	0.992	0.69	0.897	0.564	0.46	0.104	5833
		Cand	1.131	0.527	0.604	0.723	0.21	0.213	-0.003	28260
BSW	cc1-B	Ref	1.366	1.018	0.348	0.93	0.66	0.587	0.073	5833
		Cand	0.857	0.547	0.31	0.76	0.241	0.265	-0.024	28260
BSW	cc1-C	Ref	1.321	1	0.321	0.939	0.664	0.592	0.072	5833
		Cand	0.837	0.547	0.29	0.763	0.244	0.268	-0.024	28260
BSW	cc1-D	Ref	1.881	0.999	0.882	0.882	0.542	0.429	0.113	5833
		Cand	1.262	0.529	0.733	0.712	0.208	0.213	-0.005	28260
BSW	cc1-G	Ref	1.932	1.002	0.93	0.875	0.541	0.428	0.113	5833
		Cand	1.28	0.521	0.759	0.696	0.207	0.21	-0.003	28260
BSW	Int-A	Ref	1.441	1.018	0.423	0.909	0.661	0.592	0.069	5177
		Cand	1.057	0.435	0.622	0.549	0.215	0.25	-0.035	28916
BSW	Int-C	Ref	1.266	1.017	0.249	0.939	0.727	0.676	0.051	5177
		Cand	0.815	0.43	0.385	0.569	0.237	0.284	-0.047	28916
BSW	Int-E	Ref	1.255	1.001	0.254	0.94	0.709	0.654	0.055	5177
		Cand	0.816	0.438	0.378	0.585	0.228	0.273	-0.045	28916
BSW	Int-G	Ref	1.538	1.023	0.515	0.897	0.668	0.602	0.066	5177
		Cand	1.22	0.477	0.743	0.566	0.217	0.255	-0.038	28916
HOL	Pro-H	Ref	1.997	1.401	0.596	0.955	0.734	0.702	0.032	3142
		Cand	1.212	0.995	0.217	0.804	0.189	0.301	-0.112	4031
HOL	Pro-I	Ref	2.223	1.309	0.914	0.927	0.661	0.609	0.052	3142
		Cand	1.295	0.972	0.323	0.784	0.204	0.328	-0.124	4031
HOL	Pro-J	Ref	1.714	1.359	0.355	0.954	0.824	0.807	0.017	3142
		Cand	1.1	0.969	0.131	0.81	0.196	0.312	-0.116	4031
HOL	Pro-K	Ref	1.837	1.317	0.52	0.955	0.749	0.72	0.029	3142
		Cand	1.145	0.955	0.19	0.81	0.191	0.306	-0.115	4031
HOL	Pro-L	Ref	2.052	1.468	0.584	0.95	0.765	0.735	0.03	3142
		Cand	1.186	0.994	0.192	0.793	0.196	0.311	-0.115	4031
HOL	Pro-F	Ref	1.738	1.299	0.439	0.957	0.753	0.724	0.029	3142
		Cand	1.046	0.859	0.187	0.803	0.191	0.306	-0.115	4031
HOL	Pro-M	Ref	1.844	1.338	0.506	0.956	0.742	0.711	0.031	3142
		Cand	1.117	0.93	0.187	0.805	0.189	0.3	-0.111	4031
HOL	Pro-N	Ref	1.885	1.353	0.532	0.956	0.741	0.71	0.031	3142
		Cand	1.16	0.964	0.196	0.81	0.191	0.305	-0.114	4031
HOL	cc2-I	Ref	1.53	1.01	0.52	0.925	0.632	0.573	0.059	2652
		Cand	0.939	0.602	0.337	0.747	0.194	0.313	-0.119	4521
HOL	cc2-J	Ref	1.239	0.99	0.249	0.964	0.645	0.591	0.054	2652
		Cand	0.812	0.506	0.306	0.759	0.171	0.243	-0.072	4521
HOL	cc2-M	Ref	1.703	1.001	0.702	0.882	0.595	0.529	0.066	2652
		Cand	0.992	0.569	0.423	0.672	0.182	0.287	-0.105	4521
HOL	cc2-N	Ref	1.726	1.001	0.725	0.913	0.618	0.556	0.062	2652
		Cand	1.017	0.576	0.441	0.719	0.184	0.293	-0.109	4521
HOL	Int-I	Ref	1.124	1.011	0.113	0.987	0.783	0.762	0.021	1552
		Cand	0.746	0.589	0.157	0.728	0.171	0.331	-0.16	5621
HOL	Int-M	Ref	1.135	0.989	0.146	0.979	0.776	0.754	0.022	1552
		Cand	0.79	0.593	0.197	0.728	0.166	0.319	-0.153	5621
HOL	Int-N	Ref	1.125	1.005	0.12	0.983	0.772	0.75	0.022	1552
		Cand	0.747	0.563	0.184	0.7	0.164	0.317	-0.153	5621

Appendix B6 Subset-EBV and traditional-EBV SD differences and REL mean differences before applying weighting rules for all breeds/all traits in MT

			EBV SD			EBV[1,2]	EBV REL MEAN			
Breed	Trait-country	Status	Subset[1]	Traditional[2]	Diff[1-2]	COR	Subset[1]	Traditional[2]	Diff[1-2]	*n*
BSW	Pro-A	Ref	1.195	1.158	0.037	0.94	0.915	0.84	0.075	210
		Cand	0.618	0.577	0.041	0.974	0.284	0.266	0.018	2620
BSW	Pro-B	Ref	1.263	1.211	0.052	0.994	0.927	0.913	0.014	2375
		Cand	0.61	0.54	0.07	0.961	0.319	0.296	0.023	9778
BSW	Pro-C	Ref	1.424	1.362	0.062	0.995	0.916	0.899	0.017	3121
		Cand	0.623	0.522	0.101	0.958	0.315	0.293	0.022	16488
BSW	Pro-D	Ref	1.101	1.105	-0.004	0.987	0.925	0.909	0.016	338
		Cand	0.625	0.576	0.049	0.979	0.309	0.295	0.014	3796
BSW	Pro-E	Ref	1.985	1.789	0.196	0.986	0.877	0.824	0.053	1835
		Cand	0.734	0.623	0.111	0.926	0.288	0.264	0.024	9796
BSW	Pro-F	Ref	1.189	1.099	0.09	0.969	0.928	0.906	0.022	338
		Cand	0.511	0.515	-0.004	0.936	0.273	0.259	0.014	2506
BSW	Pro-G	Ref	1.237	1.15	0.087	0.973	0.854	0.796	0.058	897
		Cand	0.76	0.651	0.109	0.967	0.306	0.282	0.024	3025
BSW	cc1-A	Ref	1.149	1.025	0.124	0.889	0.734	0.554	0.18	167
		Cand	0.579	0.482	0.097	0.931	0.204	0.173	0.031	2269
BSW	cc1-B	Ref	1.282	1.018	0.264	0.941	0.636	0.516	0.12	2326
		Cand	0.737	0.586	0.151	0.934	0.266	0.235	0.031	10005
BSW	cc1-C	Ref	1.227	1.002	0.225	0.954	0.661	0.558	0.103	2977
		Cand	0.783	0.653	0.13	0.935	0.276	0.247	0.029	14986
BSW	cc1-D	Ref	1.22	1.092	0.128	0.953	0.714	0.605	0.109	338
		Cand	0.697	0.591	0.106	0.958	0.248	0.226	0.022	3915
BSW	cc1-G	Ref	1.267	1.014	0.253	0.952	0.633	0.501	0.132	639
		Cand	0.825	0.64	0.185	0.951	0.247	0.214	0.033	2984
BSW	Int-A	Ref	1.25	1.004	0.246	0.865	0.779	0.556	0.223	149
		Cand	0.626	0.513	0.113	0.942	0.214	0.183	0.031	1929
BSW	Int-C	Ref	1.116	1.027	0.089	0.972	0.756	0.702	0.054	2949
		Cand	0.555	0.51	0.045	0.945	0.296	0.272	0.024	14833
BSW	Int-E	Ref	1.143	1.011	0.132	0.945	0.74	0.627	0.113	1748
		Cand	0.607	0.517	0.09	0.933	0.263	0.232	0.031	8880
BSW	Int-G	Ref	1.775	1.244	0.531	0.947	0.638	0.484	0.154	884
		Cand	0.896	0.607	0.289	0.898	0.257	0.225	0.032	3447
HOL	Pro-H	Ref	0.864	0.894	-0.03	0.91	0.911	0.862	0.049	119
		Cand	0.439	0.452	-0.013	0.931	0.264	0.282	-0.018	181
HOL	Pro-I	Ref	1.105	1.086	0.019	0.995	0.948	0.94	0.008	420
		Cand	0.548	0.6	-0.052	0.89	0.223	0.302	-0.079	2456
HOL	Pro-J	Ref	1.606	1.536	0.07	0.998	0.933	0.927	0.006	1238
		Cand	0.589	0.534	0.055	0.962	0.314	0.296	0.018	352
HOL	Pro-K	Ref	1.061	0.989	0.072	0.958	0.825	0.78	0.045	454
		Cand	0.923	0.82	0.103	0.937	0.262	0.268	-0.006	466
HOL	Pro-L	Ref	1.489	1.494	-0.005	0.999	0.976	0.974	0.002	633
		Cand	0.65	0.622	0.028	0.909	0.272	0.305	-0.033	907
HOL	Pro-F	Ref	1.192	1.2	-0.008	0.989	0.952	0.942	0.01	289
		Cand	0.54	0.618	-0.078	0.703	0.253	0.279	-0.026	323
HOL	Pro-M	Ref	0.96	0.963	-0.003	0.961	0.918	0.885	0.033	222
		Cand	0.503	0.514	-0.011	0.9	0.23	0.263	-0.033	349
HOL	Pro-N	Ref	1.111	1.137	-0.026	0.979	0.921	0.896	0.025	221
		Cand	0.596	0.624	-0.028	0.908	0.254	0.286	-0.032	536
HOL	cc2-I	Ref	1.341	1.18	0.161	0.977	0.771	0.732	0.039	415

		Cand	0.807	0.729	0.078	0.931	0.198	0.259	-0.061	2826
HOL	cc2-J	Ref	1.237	0.988	0.249	0.961	0.622	0.553	0.069	1195
		Cand	0.681	0.586	0.095	0.933	0.25	0.219	0.031	353
HOL	cc2-M	Ref	1.314	1.227	0.087	0.949	0.646	0.533	0.113	237
		Cand	0.695	0.645	0.05	0.883	0.167	0.175	-0.008	471
HOL	cc2-N	Ref	1.062	1.01	0.052	0.94	0.732	0.63	0.102	208
		Cand	0.624	0.696	-0.072	0.873	0.203	0.216	-0.013	810
HOL	Int-I	Ref	1.342	1.18	0.162	0.977	0.769	0.732	0.037	415
		Cand	0.808	0.731	0.077	0.931	0.199	0.259	-0.06	2875
HOL	Int-M	Ref	1.305	1.227	0.078	0.946	0.653	0.533	0.12	237
		Cand	0.7	0.649	0.051	0.884	0.167	0.176	-0.009	476
HOL	Int-N	Ref	1.061	1.01	0.051	0.933	0.735	0.63	0.105	208
		Cand	0.631	0.706	-0.075	0.875	0.203	0.217	-0.014	840

Appendix C1 Statistics of selection index terms and coefficients in MT & ST for all traits in BSW evaluation

				EVB SD			M,S	REL MEAN				Sel index coefficients			
Breed	**Trait**	**Status**	**Terms**	**M**	**S**	**M-S**	**Corr**	**M**	**S**	**M-S**	***n***	**M**	**S**	**M-S**	***n***
BSW	**pro/A**	**all**	Final	23.651	36.227	-12.576	0.965	0.288	0.771	-0.483	34093				
			Genomic	23.651	37.898	-14.247	0.962	0.32	0.837	-0.517	34093	1	0.993	0.007	34093
			Subset	14.205	28.128	-13.923	0.532	0.234	0.349	-0.115	34093	-0.63	-0.129	-0.501	34093
			Traditional	14.205	22.602	-8.397	0.560	0.234	0.375	-0.141	34093	0.63	0.136	0.494	34093
			Sub. - Trad.	0	5.526			0	-0.026						
		old	Final	24.647	35.335	-10.688	0.985	0.706	0.847	-0.141	7128				
			Genomic	24.647	35.335	-10.688	0.985	0.711	0.883	-0.172	7128	1	1	0	7128
			Subset	17.891	26.431	-8.54	0.769	0.695	0.714	-0.019	7128	-0.286	0	-0.286	7128
			Traditional	17.891	26.431	-8.54	0.769	0.695	0.714	-0.019	7128	0.286	0	0.286	7128
			Sub. - Trad.	0	0			0	0						
		yng	Final	20.746	33.875	-13.129	0.958	0.178	0.751	-0.573	26965				
			Genomic	20.746	36.103	-15.357	0.959	0.217	0.825	-0.608	26965	1	0.991	0.009	26965
			Subset	12.383	25.604	-13.221	0.379	0.112	0.253	-0.141	26965	-0.721	-0.163	-0.558	26965
			Traditional	12.383	17.515	-5.132	0.368	0.112	0.285	-0.173	26965	0.721	0.172	0.549	26965
			Sub. - Trad.	0	8.089			0	-0.032						
BSW	**pro/B**	**all**	Final	22.998	25.383	-2.385	0.979	0.631	0.797	-0.166	34093				
			Genomic	22.999	26.368	-3.369	0.979	0.715	0.856	-0.141	34093	1	0.99	0.01	34093
			Subset	17.752	22.6	-4.848	0.818	0.325	0.384	-0.059	34093	-0.193	-0.145	-0.048	34093
			Traditional	17.751	19.142	-1.391	0.807	0.325	0.418	-0.093	34093	0.193	0.155	0.038	34093
			Sub. - Trad.	0.001	3.458			0	-0.034						
		old	Final	23.525	25.622	-2.097	0.984	0.846	0.889	-0.043	7128				
			Genomic	23.525	25.622	-2.097	0.984	0.865	0.913	-0.048	7128	1	1	0	7128
			Subset	21.902	21.731	0.171	0.906	0.799	0.799	0	7128	-0.114	0	-0.114	7128
			Traditional	21.902	21.731	0.171	0.906	0.799	0.799	0	7128	0.114	0	0.114	7128
			Sub. - Trad.	0	0			0	0						
		yng	Final	20.005	22.735	-2.730	0.973	0.575	0.773	-0.198	26965				
			Genomic	20.006	24.08	-4.074	0.975	0.676	0.841	-0.165	26965	1	0.988	0.012	26965
			Subset	14.415	19.814	-5.399	0.737	0.2	0.275	-0.075	26965	-0.214	-0.184	-0.03	26965
			Traditional	14.412	14.783	-0.371	0.681	0.2	0.317	-0.117	26965	0.214	0.195	0.019	26965
			Sub. - Trad.	0.003	5.031			0	-0.042						
BSW	**pro/C**	**all**	Final	18.074	21.202	-3.128	0.976	0.683	0.802	-0.119	34093				
			Genomic	18.075	21.984	-3.909	0.974	0.761	0.859	-0.098	34093	1	0.99	0.01	34093
			Subset	16.207	18.371	-2.164	0.868	0.357	0.393	-0.036	34093	-0.106	-0.145	0.039	34093
			Traditional	16.207	15.75	0.457	0.830	0.357	0.428	-0.071	34093	0.106	0.155	-0.049	34093
			Sub. - Trad.	0	2.621			0	-0.035						
		old	Final	18.833	21.518	-2.685	0.985	0.866	0.896	-0.03	7128				
			Genomic	18.833	21.518	-2.685	0.985	0.885	0.918	-0.033	7128	1	1	0	7128
			Subset	18.128	18.228	-0.1	0.939	0.816	0.817	-0.001	7128	-0.086	0	-0.086	7128
			Traditional	18.128	18.228	-0.1	0.939	0.816	0.817	-0.001	7128	0.086	0	0.086	7128

			Sub. - Trad.	0	0			0	0					
		yng	Final	15.612	19.143	-3.531	0.969	0.635	0.777	-0.142	26965			
			Genomic	15.613	20.25	-4.637	0.971	0.729	0.844	-0.115	26965	1	0.987	0.013	26965
			Subset	13.312	16.096	-2.784	0.799	0.236	0.281	-0.045	26965	-0.111	-0.184	0.073	26965
			Traditional	13.309	11.958	1.351	0.695	0.236	0.325	-0.089	26965	0.111	0.196	-0.085	26965
			Sub. - Trad.	0.003	4.138			0	-0.044					
BSW	pro/D	all	Final	21.635	32.016	-10.381	0.955	0.344	0.763	-0.419	34093			
			Genomic	21.635	33.522	-11.887	0.952	0.389	0.831	-0.442	34093	1	0.993	0.007	34093
			Subset	14.178	24.256	-10.078	0.640	0.262	0.341	-0.079	34093	-0.545	-0.131	-0.414	34093
			Traditional	14.178	19.306	-5.128	0.645	0.262	0.366	-0.104	34093	0.545	0.138	0.407	34093
			Sub. - Trad.	0	4.95			0	-0.025					
		old	Final	22.252	31.085	-8.833	0.978	0.697	0.836	-0.139	7128			
			Genomic	22.252	31.085	-8.833	0.978	0.707	0.876	-0.169	7128	1	1	0	7128
			Subset	17.043	22.528	-5.485	0.784	0.68	0.685	-0.005	7128	-0.29	0	-0.29	7128
			Traditional	17.043	22.528	-5.485	0.784	0.68	0.685	-0.005	7128	0.29	0	0.29	7128
			Sub. - Trad.	0	0			0	0					
		yng	Final	19.264	30.276	-11.012	0.946	0.251	0.744	-0.493	26965			0	
			Genomic	19.264	32.274	-13.010	0.946	0.305	0.819	-0.514	26965	1	0.991	0.009	26965
			Subset	12.337	22.439	-10.102	0.530	0.151	0.251	-0.1	26965	-0.612	-0.165	-0.447	26965
			Traditional	12.337	15.26	-2.923	0.492	0.151	0.282	-0.131	26965	0.612	0.174	0.438	26965
			Sub. - Trad.	0	7.179			0	-0.031					
BSW	pro/E	all	Final	25.724	33.568	-7.844	0.965	0.562	0.785	-0.223	34093			
			Genomic	25.724	35.022	-9.298	0.964	0.648	0.847	-0.199	34093	1	0.991	0.009	34093
			Subset	21.726	27.037	-5.311	0.842	0.301	0.367	-0.066	34093	-0.239	-0.145	-0.094	34093
			Traditional	21.726	22.251	-0.525	0.809	0.301	0.397	-0.096	34093	0.239	0.153	0.086	34093
			Sub. - Trad.	0	4.786			0	-0.03					
		old	Final	27.146	33.213	-6.067	0.983	0.807	0.867	-0.06	7128			
			Genomic	27.146	33.213	-6.067	0.983	0.828	0.897	-0.069	7128	1	1	0	7128
			Subset	25.542	26.32	-0.778	0.943	0.757	0.759	-0.002	7128	-0.146	0	-0.146	7128
			Traditional	25.542	26.32	-0.778	0.943	0.757	0.759	-0.002	7128	0.146	0	0.146	7128
			Sub. - Trad.	0	0			0	0					
		yng	Final	22.46	31.152	-8.692	0.958	0.498	0.763	-0.265	26965			
			Genomic	22.461	33.128	-10.667	0.961	0.6	0.833	-0.233	26965	1	0.989	0.011	26965
			Subset	18.08	24.1	-6.020	0.764	0.18	0.264	-0.084	26965	-0.264	-0.183	-0.081	26965
			Traditional	18.079	16.788	1.291	0.664	0.18	0.302	-0.122	26965	0.264	0.194	0.07	26965
			Sub. - Trad.	0.001	7.312			0	-0.038					
BSW	pro/F	all	Final	10.499	14.088	-3.589	0.954	0.315	0.763	-0.448	34093			
			Genomic	10.499	14.751	-4.252	0.954	0.363	0.831	-0.468	34093	1	0.993	0.007	34093
			Subset	7.209	10.673	-3.464	0.654	0.226	0.341	-0.115	34093	-0.591	-0.131	-0.46	34093
			Traditional	7.209	8.495	-1.286	0.564	0.226	0.366	-0.14	34093	0.591	0.138	0.453	34093
			Sub. - Trad.	0	2.178			0	-0.025					
		old	Final	10.851	13.678	-2.827	0.962	0.662	0.836	-0.174	7128			
			Genomic	10.851	13.678	-2.827	0.962	0.674	0.876	-0.202	7128	1	1	0	7128
			Subset	8.92	9.913	-0.993	0.745	0.641	0.685	-0.044	7128	-0.323	0	-0.323	7128
			Traditional	8.92	9.913	-0.993	0.745	0.641	0.685	-0.044	7128	0.323	0	0.323	7128
			Sub. - Trad.	0	0			0	0					
		yng	Final	9.5	13.322	-3.822	0.947	0.223	0.744	-0.521	26965			
			Genomic	9.5	14.202	-4.702	0.951	0.281	0.819	-0.538	26965	1	0.991	0.009	26965
			Subset	6.615	9.874	-3.259	0.642	0.116	0.251	-0.135	26965	-0.662	-0.165	-0.497	26965
			Traditional	6.615	6.715	-0.100	0.494	0.116	0.282	-0.166	26965	0.662	0.174	0.488	26965
			Sub. - Trad.	0	3.159			0	-0.031					
BSW	pro/G	all	Final	21.546	30.104	-8.558	0.961	0.416	0.766	-0.35	34093			
			Genomic	21.547	31.503	-9.956	0.958	0.493	0.834	-0.341	34093	1	0.993	0.007	34093
			Subset	14.305	22.753	-8.448	0.627	0.242	0.344	-0.102	34093	-0.46	-0.119	-0.341	34093
			Traditional	14.305	18.207	-3.902	0.674	0.242	0.367	-0.125	34093	0.46	0.125	0.335	34093
			Sub. - Trad.	0	4.546			0	-0.023					
		old	Final	22.191	29	-6.809	0.98	0.721	0.842	-0.121	7128			
			Genomic	22.191	29	-6.809	0.98	0.742	0.879	-0.137	7128	1	1	0	7128
			Subset	17.57	21.095	-3.525	0.855	0.682	0.697	-0.015	7128	-0.242	0	-0.242	7128
			Traditional	17.57	21.095	-3.525	0.855	0.682	0.697	-0.015	7128	0.242	0	0.242	7128
			Sub. - Trad.	0	0			0	0					
		yng	Final	18.983	28.279	-9.296	0.954	0.336	0.747	-0.411	26965			
			Genomic	18.983	30.145	-11.162	0.954	0.427	0.821	-0.394	26965	1	0.991	0.009	26965

			Subset	12.242	20.858	-8.616	0.475	0.125	0.25	-0.125	26965	-0.518	-0.15	-0.368	26965
			Traditional	12.242	14.196	-1.954	0.495	0.125	0.28	-0.155	26965	0.518	0.159	0.359	26965
			Sub. - Trad.	0	6.662			0	-0.03						
BSW	**cc1/A**	**all**	Final	4.567	6.77	-2.203	0.953	0.158	0.636	-0.478	34093				
			Genomic	4.567	7.217	-2.650	0.949	0.18	0.727	-0.547	34093	1	0.995	0.005	34093
			Subset	2.318	4.436	-2.118	0.611	0.121	0.242	-0.121	34093	-0.768	-0.091	-0.677	34093
			Traditional	2.318	3.28	-0.962	0.642	0.121	0.255	-0.134	34093	0.768	0.096	0.672	34093
			Sub. - Trad.	0	1.156			0	-0.013						
		old	Final	5.384	7.774	-2.39	0.969	0.397	0.719	-0.322	5450				
			Genomic	5.384	7.774	-2.39	0.969	0.41	0.785	-0.375	5450	1	1	0	5450
			Subset	3.828	5.078	-1.25	0.846	0.375	0.474	-0.099	5450	-0.582	0	-0.582	5450
			Traditional	3.828	5.078	-1.25	0.846	0.375	0.474	-0.099	5450	0.582	0	0.582	5450
			Sub. - Trad.	0	0			0	0						
		yng	Final	4.392	6.554	-2.162	0.949	0.112	0.62	-0.508	28643				
			Genomic	4.392	7.094	-2.702	0.946	0.137	0.715	-0.578	28643	1	0.994	0.006	28643
			Subset	1.898	4.295	-2.397	0.531	0.073	0.198	-0.125	28643	-0.804	-0.108	-0.696	28643
			Traditional	1.898	2.81	-0.912	0.502	0.073	0.213	-0.14	28643	0.804	0.114	0.69	28643
			Sub. - Trad.	0	1.485			0	-0.015						
BSW	**cc1/B**	**all**	Final	8.483	8.699	-0.216	0.975	0.48	0.694	-0.214	34093				
			Genomic	8.483	9.236	-0.753	0.979	0.574	0.773	-0.199	34093	1	0.992	0.008	34093
			Subset	6.432	6.96	-0.528	0.829	0.218	0.298	-0.08	34093	-0.284	-0.169	-0.115	34093
			Traditional	6.432	5.596	0.836	0.721	0.218	0.32	-0.102	34093	0.284	0.177	0.107	34093
			Sub. - Trad.	0	1.364			0	-0.022						
		old	Final	9.935	10.252	-0.317	0.989	0.656	0.788	-0.132	5450				
			Genomic	9.935	10.252	-0.317	0.989	0.708	0.837	-0.129	5450	1	1	0	5450
			Subset	8.353	8.625	-0.272	0.91	0.518	0.604	-0.086	5450	-0.182	0	-0.182	5450
			Traditional	8.353	8.625	-0.272	0.91	0.518	0.604	-0.086	5450	0.182	0	0.182	5450
			Sub. - Trad.	0	0			0	0						
		yng	Final	8.178	8.371	-0.193	0.971	0.447	0.676	-0.229	28643				
			Genomic	8.178	9.028	-0.850	0.977	0.549	0.761	-0.212	28643	1	0.99	0.01	28643
			Subset	5.986	6.596	-0.610	0.804	0.161	0.24	-0.079	28643	-0.304	-0.201	-0.103	28643
			Traditional	5.986	4.791	1.195	0.637	0.161	0.266	-0.105	28643	0.304	0.211	0.093	28643
			Sub. - Trad.	0	1.805			0	-0.026						
BSW	**cc1/C**	**all**	Final	8.939	8.378	0.561	0.978	0.548	0.696	-0.148	34093				
			Genomic	8.939	8.883	0.056	0.982	0.643	0.775	-0.132	34093	1	0.992	0.008	34093
			Subset	6.414	6.743	-0.329	0.865	0.243	0.301	-0.058	34093	-0.18	-0.167	-0.013	34093
			Traditional	6.413	5.458	0.955	0.776	0.243	0.323	-0.08	34093	0.18	0.175	0.005	34093
			Sub. - Trad.	0.001	1.285			0	-0.022						
		old	Final	10.579	10.034	0.545	0.992	0.691	0.791	-0.1	5450				
			Genomic	10.579	10.034	0.545	0.992	0.747	0.84	-0.093	5450	1	1	0	5450
			Subset	8.927	8.416	0.511	0.943	0.528	0.609	-0.081	5450	-0.133	0	-0.133	5450
			Traditional	8.927	8.416	0.511	0.943	0.528	0.609	-0.081	5450	0.133	0	0.133	5450
			Sub. - Trad.	0	0			0	0						
		yng	Final	8.579	8.012	0.567	0.974	0.52	0.678	-0.158	28643				
			Genomic	8.579	8.626	-0.047	0.980	0.623	0.763	-0.14	28643	1	0.99	0.01	28643
			Subset	5.751	6.358	-0.607	0.837	0.189	0.242	-0.053	28643	-0.189	-0.199	0.01	28643
			Traditional	5.749	4.688	1.061	0.698	0.189	0.269	-0.08	28643	0.189	0.209	-0.02	28643
			Sub. - Trad.	0.002	1.67			0	-0.027						
BSW	**cc1/D**	**all**	Final	0.599	0.871	-0.272	0.916	0.23	0.622	-0.392	34093				
			Genomic	0.599	0.943	-0.344	0.907	0.27	0.714	-0.444	34093	1	0.994	0.006	34093
			Subset	0.391	0.573	-0.182	0.663	0.16	0.236	-0.076	34093	-0.651	-0.107	-0.544	34093
			Traditional	0.391	0.389	0.002	0.697	0.16	0.25	-0.09	34093	0.651	0.113	0.538	34093
			Sub. - Trad.	0	0.184			0	-0.014						
		old	Final	0.681	0.98	-0.299	0.938	0.423	0.703	-0.28	5450				
			Genomic	0.681	0.98	-0.299	0.938	0.448	0.773	-0.325	5450	1	1	0	5450
			Subset	0.539	0.594	-0.055	0.894	0.38	0.443	-0.063	5450	-0.536	0	-0.536	5450
			Traditional	0.539	0.594	-0.055	0.894	0.38	0.443	-0.063	5450	0.536	0	0.536	5450
			Sub. - Trad.	0	0			0	0						
		yng	Final	0.579	0.846	-0.267	0.910	0.193	0.606	-0.413	28643				
			Genomic	0.579	0.933	-0.354	0.900	0.236	0.702	-0.466	28643	1	0.993	0.007	28643
			Subset	0.347	0.565	-0.218	0.598	0.118	0.197	-0.079	28643	-0.673	-0.127	-0.546	28643
			Traditional	0.347	0.336	0.011	0.601	0.118	0.213	-0.095	28643	0.673	0.134	0.539	28643
			Sub. - Trad.	0	0.229			0	-0.016						

BSW	**cc1/G**	**all**	Final	1.921	2.657	-0.736	0.908	0.244	0.621	-0.377	34093			
			Genomic	1.921	2.892	-0.971	0.897	0.303	0.713	-0.41	34093	1	0.994	0.006	34093
			Subset	1.216	1.743	-0.527	0.651	0.133	0.234	-0.101	34093	-0.636	-0.104	-0.532	34093
			Traditional	1.216	1.152	0.064	0.694	0.133	0.248	-0.115	34093	0.636	0.11	0.526	34093
			Sub. - Trad.	0	0.591			0	-0.014						
		old	Final	2.192	2.969	-0.777	0.934	0.428	0.703	-0.275	5450				
			Genomic	2.192	2.969	-0.777	0.934	0.466	0.773	-0.307	5450	1	1	0	5450
			Subset	1.659	1.769	-0.11	0.896	0.356	0.442	-0.086	5450	-0.496	0	-0.496	5450
			Traditional	1.659	1.769	-0.11	0.896	0.356	0.442	-0.086	5450	0.496	0	0.496	5450
			Sub. - Trad.	0	0			0	0						
		yng	Final	1.859	2.588	-0.729	0.901	0.209	0.605	-0.396	28643				
			Genomic	1.859	2.87	-1.011	0.890	0.272	0.702	-0.43	28643	1	0.993	0.007	28643
			Subset	1.109	1.729	-0.620	0.588	0.091	0.195	-0.104	28643	-0.663	-0.124	-0.539	28643
			Traditional	1.109	0.991	0.118	0.595	0.091	0.211	-0.12	28643	0.663	0.13	0.533	28643
			Sub. - Trad.	0	0.738			0	-0.016						
BSW	**int/A**	**all**	Final	5.272	7.937	-2.665	0.905	0.163	0.67	-0.507	34093				
			Genomic	5.272	9.183	-3.911	0.882	0.183	0.752	-0.569	34093	1	0.988	0.012	34093
			Subset	2.421	5.396	-2.975	0.600	0.13	0.27	-0.14	34093	-0.774	-0.165	-0.609	34093
			Traditional	2.421	3.07	-0.649	0.582	0.13	0.302	-0.172	34093	0.774	0.177	0.597	34093
			Sub. - Trad.	0	2.326			0	-0.032						
		old	Final	5.786	6.648	-0.862	0.968	0.524	0.776	-0.252	4897				
			Genomic	5.786	6.648	-0.862	0.968	0.532	0.826	-0.294	4897	1	1	0	4897
			Subset	4.2	5.365	-1.165	0.838	0.508	0.608	-0.1	4897	-0.461	0	-0.461	4897
			Traditional	4.2	5.365	-1.165	0.838	0.508	0.608	-0.1	4897	0.461	0	0.461	4897
			Sub. - Trad.	0	0			0	0						
		yng	Final	5.098	8.002	-2.904	0.898	0.102	0.652	-0.55	29196				
			Genomic	5.098	9.396	-4.298	0.879	0.125	0.74	-0.615	29196	1	0.986	0.014	29196
			Subset	1.96	5.288	-3.328	0.555	0.066	0.213	-0.147	29196	-0.826	-0.193	-0.633	29196
			Traditional	1.96	2.427	-0.467	0.372	0.066	0.25	-0.184	29196	0.826	0.207	0.619	29196
			Sub. - Trad.	0	2.861			0	-0.037						
BSW	**int/C**	**all**	Final	10.48	12.901	-2.421	0.924	0.595	0.703	-0.108	34093				
			Genomic	10.48	14.576	-4.096	0.902	0.688	0.778	-0.09	34093	1	0.985	0.015	34093
			Subset	6.86	9.17	-2.310	0.851	0.266	0.302	-0.036	34093	-0.16	-0.212	0.052	34093
			Traditional	6.86	6.252	0.608	0.814	0.266	0.343	-0.077	34093	0.16	0.227	-0.067	34093
			Sub. - Trad.	0	2.918			0	-0.041						
		old	Final	12.087	12.004	0.083	0.985	0.763	0.822	-0.059	4897				
			Genomic	12.087	12.004	0.083	0.985	0.805	0.86	-0.055	4897	1	1	0	4897
			Subset	10.886	10.84	0.046	0.962	0.646	0.694	-0.048	4897	-0.097	0	-0.097	4897
			Traditional	10.886	10.84	0.046	0.962	0.646	0.694	-0.048	4897	0.097	0	0.097	4897
			Sub. - Trad.	0	0			0	0						
		yng	Final	9.88	12.679	-2.799	0.912	0.567	0.683	-0.116	29196				
			Genomic	9.88	14.584	-4.704	0.892	0.668	0.765	-0.097	29196	1	0.982	0.018	29196
			Subset	5.527	8.443	-2.916	0.810	0.203	0.237	-0.034	29196	-0.171	-0.248	0.077	29196
			Traditional	5.528	4.729	0.799	0.677	0.203	0.284	-0.081	29196	0.171	0.266	-0.095	29196
			Sub. - Trad.	-0.001	3.714			0	-0.047						
BSW	**int/E**	**all**	Final	13.768	17.079	-3.311	0.924	0.465	0.694	-0.229	34093				
			Genomic	13.768	19.283	-5.515	0.903	0.558	0.771	-0.213	34093	1	0.985	0.015	34093
			Subset	8.883	12.108	-3.225	0.776	0.217	0.291	-0.074	34093	-0.318	-0.21	-0.108	34093
			Traditional	8.883	8.325	0.558	0.763	0.217	0.331	-0.114	34093	0.318	0.225	0.093	34093
			Sub. - Trad.	0	3.783			0	-0.04						
		old	Final	15.638	15.881	-0.243	0.982	0.706	0.809	-0.103	4897				
			Genomic	15.638	15.881	-0.243	0.982	0.743	0.85	-0.107	4897	1	1	0	4897
			Subset	13.628	14.059	-0.431	0.922	0.61	0.671	-0.061	4897	-0.185	0	-0.185	4897
			Traditional	13.628	14.059	-0.431	0.922	0.61	0.671	-0.061	4897	0.185	0	0.185	4897
			Sub. - Trad.	0	0			0	0						
		yng	Final	12.895	16.678	-3.783	0.911	0.425	0.675	-0.25	29196				
			Genomic	12.895	19.185	-6.290	0.893	0.526	0.758	-0.232	29196	1	0.983	0.017	29196
			Subset	6.93	11.077	-4.147	0.700	0.151	0.228	-0.077	29196	-0.34	-0.246	-0.094	29196
			Traditional	6.931	6.309	0.622	0.598	0.151	0.274	-0.123	29196	0.34	0.263	0.077	29196
			Sub. - Trad.	-0.001	4.768			0	-0.046						
BSW	**int/G**	**all**	Final	1.907	3.032	-1.125	0.896	0.296	0.675	-0.379	34093				
			Genomic	1.907	3.548	-1.641	0.876	0.364	0.755	-0.391	34093	1	0.987	0.013	34093
			Subset	1.857	2.114	-0.257	0.730	0.16	0.273	-0.113	34093	-0.569	-0.179	-0.39	34093

	Traditional	1.857	1.115	0.742	0.593	0.16	0.308	-0.148	34093	0.569	0.192	0.377	34093
	Sub. - Trad.	0	0.999			0	-0.035						
old	Final	2.023	2.322	-0.299	0.963	0.596	0.782	-0.186	4897				
	Genomic	2.023	2.322	-0.299	0.963	0.626	0.829	-0.203	4897	1	1	0	4897
	Subset	2.208	1.848	0.36	0.782	0.534	0.618	-0.084	4897	-0.318	0	-0.318	4897
	Traditional	2.208	1.848	0.36	0.782	0.534	0.618	-0.084	4897	0.318	0	0.318	4897
	Sub. - Trad.	0	0			0	0						
yng	Final	1.874	3.108	-1.234	0.893	0.246	0.657	-0.411	29196				
	Genomic	1.874	3.68	-1.806	0.878	0.32	0.743	-0.423	29196	1	0.985	0.015	29196
	Subset	1.791	2.13	-0.339	0.738	0.097	0.216	-0.119	29196	-0.611	-0.209	-0.402	29196
	Traditional	1.791	0.932	0.859	0.538	0.097	0.256	-0.159	29196	0.611	0.224	0.387	29196
	Sub. - Trad.	0	1.198			0	-0.04						

M= Multi-trait model, S= single-trait model, M-S = multi-trait minus single- trait, SD = standard deviation,
old = Reference individuals, yng. = Candidate individuals

Appendix C2 Statistics of selection index terms and coefficients in MT & ST for all traits in HOL evaluation

				EVB SD			M,S	REL MEAN				Sel index coefficients			
Breed	**Trait**	**Status**	**Terms**	**M**	**S**	**M-S**	**Corr**	**M**	**S**	**M-S**	***n***	**M**	**S**	**M-S**	***n***
HOL	**pro/H**	**all**	Final	10.916	16.649	-5.733	0.912	0.316	0.688	-0.372	7173				
			Genomic	10.912	17.084	-6.172	0.926	0.333	0.742	-0.409	7173	0.999	0.968	-0.031	7173
			Subset	6.794	13.479	-6.685	0.497	0.286	0.414	-0.128	7173	-0.655	-0.21	0.445	7173
			Traditional	6.8	12.727	-5.927	0.491	0.286	0.477	-0.191	7173	0.656	0.242	-0.414	7173
			Sub. - Trad.	-0.006	0.752			0	-0.063						
		old	Final	12.223	17.633	-5.41	0.946	0.653	0.797	-0.144	2603				
			Genomic	12.223	17.633	-5.41	0.946	0.658	0.83	-0.172	2603	1	1	0	2603
			Subset	9.857	13.518	-3.661	0.577	0.644	0.713	-0.069	2603	-0.338	0	0.338	2603
			Traditional	9.857	13.518	-3.661	0.577	0.644	0.713	-0.069	2603	0.338	0	-0.338	2603
			Sub. - Trad.	0	0			0	0						
		yng	Final	9.912	15.773	-5.861	0.884	0.124	0.625	-0.501	4570				
			Genomic	9.906	16.616	-6.710	0.914	0.149	0.691	-0.542	4570	0.999	0.949	-0.05	4570
			Subset	4.041	13.311	-9.270	0.480	0.081	0.243	-0.162	4570	-0.836	-0.329	0.507	4570
			Traditional	4.055	11.712	-7.657	0.413	0.082	0.342	-0.26	4570	0.837	0.38	-0.457	4570
			Sub. - Trad.	-0.014	1.599			-0.001	-0.099						
HOL	**pro/I**	**all**	Final	4.867	9.594	-4.727	0.841	0.418	0.659	-0.241	7173				
			Genomic	4.803	9.742	-4.939	0.850	0.446	0.713	-0.267	7173	0.973	0.96	-0.013	7173
			Subset	3.867	6.847	-2.980	0.672	0.305	0.381	-0.076	7173	-0.502	-0.226	0.276	7173
			Traditional	3.99	6.384	-2.394	0.694	0.333	0.451	-0.118	7173	0.528	0.267	-0.261	7173
			Sub. - Trad.	-0.123	0.463			-0.028	-0.07						
		old	Final	5.257	10.436	-5.179	0.83	0.587	0.747	-0.16	2603				
			Genomic	5.257	10.436	-5.179	0.83	0.612	0.794	-0.182	2603	1	1	0	2603
			Subset	4.742	6.335	-1.593	0.697	0.542	0.608	-0.066	2603	-0.38	0	0.38	2603
			Traditional	4.742	6.335	-1.593	0.697	0.542	0.608	-0.066	2603	0.38	0	-0.38	2603
			Sub. - Trad.	0	0			0	0						
		yng	Final	4.45	8.371	-3.921	0.837	0.323	0.609	-0.286	4570				
			Genomic	4.38	8.828	-4.448	0.855	0.351	0.667	-0.316	4570	0.958	0.936	-0.022	4570
			Subset	3.064	6.962	-3.898	0.671	0.17	0.252	-0.082	4570	-0.571	-0.355	0.216	4570
			Traditional	3.247	5.912	-2.665	0.659	0.214	0.361	-0.147	4570	0.613	0.418	-0.195	4570
			Sub. - Trad.	-0.183	1.05			-0.044	-0.109						
HOL	**pro/J**	**all**	Final	11.76	13.67	-1.910	0.928	0.558	0.734	-0.176	7173				
			Genomic	11.76	14.031	-2.271	0.935	0.634	0.783	-0.149	7173	1	0.968	-0.032	7173
			Subset	10.823	11.857	-1.034	0.798	0.348	0.463	-0.115	7173	-0.335	-0.194	0.141	7173
			Traditional	10.823	11.491	-0.668	0.782	0.348	0.529	-0.181	7173	0.335	0.226	-0.109	7173
			Sub. - Trad.	0	0.366			0	-0.066						
		old	Final	13.231	13.908	-0.677	0.961	0.819	0.879	-0.06	2603				
			Genomic	13.231	13.908	-0.677	0.961	0.836	0.896	-0.06	2603	1	1	0	2603
			Subset	13.696	12.393	1.303	0.831	0.78	0.835	-0.055	2603	-0.134	0	0.134	2603

			Traditional	13.696	12.393	1.303	0.831	0.78	0.835	-0.055	2603	0.134	0	-0.134	2603
			Sub. - Trad.	0	0			0	0						
		yng	Final	10.595	13.45	-2.855	0.913	0.41	0.652	-0.242	4570				
			Genomic	10.595	14.078	-3.483	0.936	0.519	0.718	-0.199	4570	1	0.95	-0.05	4570
			Subset	8.595	11.438	-2.843	0.789	0.102	0.252	-0.15	4570	-0.449	-0.305	0.144	4570
			Traditional	8.595	10.524	-1.929	0.741	0.102	0.355	-0.253	4570	0.449	0.355	-0.094	4570
			Sub. - Trad.	0	0.914			0	-0.103						
HOL	pro/K	all	Final	13.145	18.035	-4.890	0.915	0.398	0.696	-0.298	7173				
			Genomic	13.153	18.516	-5.363	0.929	0.444	0.749	-0.305	7173	0.999	0.967	-0.032	7173
			Subset	9.066	14.806	-5.740	0.623	0.309	0.422	-0.113	7173	-0.519	-0.207	0.312	7173
			Traditional	9.063	13.988	-4.925	0.611	0.31	0.487	-0.177	7173	0.52	0.24	-0.28	7173
			Sub. - Trad.	0.003	0.818			-0.001	-0.065						
		old	Final	14.578	19.077	-4.499	0.948	0.697	0.81	-0.113	2603				
			Genomic	14.578	19.077	-4.499	0.948	0.71	0.84	-0.13	2603	1	1	0	2603
			Subset	11.803	14.894	-3.091	0.685	0.672	0.733	-0.061	2603	-0.262	0	0.262	2603
			Traditional	11.803	14.894	-3.091	0.685	0.672	0.733	-0.061	2603	0.262	0	-0.262	2603
			Sub. - Trad.	0	0			0	0						
		yng	Final	12.062	17.156	-5.094	0.888	0.228	0.631	-0.403	4570				
			Genomic	12.077	18.05	-5.973	0.917	0.292	0.697	-0.405	4570	0.998	0.948	-0.05	4570
			Subset	6.884	14.584	-7.700	0.590	0.102	0.245	-0.143	4570	-0.666	-0.325	0.341	4570
			Traditional	6.876	12.933	-6.057	0.533	0.104	0.347	-0.243	4570	0.668	0.377	-0.291	4570
			Sub. - Trad.	0.008	1.651			-0.002	-0.102						
HOL	pro/L	all	Final	16.59	22.51	-5.920	0.922	0.482	0.706	-0.224	7173				
			Genomic	16.572	23.042	-6.470	0.933	0.538	0.758	-0.22	7173	0.995	0.967	-0.028	7173
			Subset	12.876	18.401	-5.525	0.757	0.352	0.432	-0.08	7173	-0.427	-0.205	0.222	7173
			Traditional	12.964	17.558	-4.594	0.758	0.358	0.497	-0.139	7173	0.432	0.239	-0.193	7173
			Sub. - Trad.	-0.088	0.843			-0.006	-0.065						
		old	Final	18.789	24.404	-5.615	0.944	0.749	0.829	-0.08	2603				
			Genomic	18.789	24.404	-5.615	0.944	0.765	0.858	-0.093	2603	1	1	0	2603
			Subset	16.532	19.278	-2.746	0.83	0.72	0.753	-0.033	2603	-0.229	0	0.229	2603
			Traditional	16.532	19.278	-2.746	0.83	0.72	0.753	-0.033	2603	0.229	0	-0.229	2603
			Sub. - Trad.	0	0			0	0						
		yng	Final	14.994	21.036	-6.042	0.903	0.33	0.635	-0.305	4570				
			Genomic	14.989	22.048	-7.059	0.926	0.408	0.701	-0.293	4570	0.993	0.948	-0.045	4570
			Subset	9.95	17.649	-7.699	0.707	0.143	0.249	-0.106	4570	-0.54	-0.322	0.218	4570
			Traditional	10.075	15.869	-5.794	0.679	0.151	0.351	-0.2	4570	0.547	0.375	-0.172	4570
			Sub. - Trad.	-0.125	1.78			-0.008	-0.102						
HOL	pro/F	all	Final	9.11	12.07	-2.960	0.924	0.381	0.698	-0.317	7173				
			Genomic	9.11	12.441	-3.331	0.935	0.418	0.751	-0.333	7173	0.998	0.967	-0.031	7173
			Subset	7.11	10.186	-3.076	0.558	0.31	0.424	-0.114	7173	-0.561	-0.206	0.355	7173
			Traditional	7.107	9.517	-2.410	0.583	0.312	0.489	-0.177	7173	0.563	0.239	-0.324	7173
			Sub. - Trad.	0.003	0.669			-0.002	-0.065						
		old	Final	10.363	13.255	-2.892	0.955	0.698	0.815	-0.117	2603				
			Genomic	10.363	13.255	-2.892	0.955	0.707	0.844	-0.137	2603	1	1	0	2603
			Subset	9.774	10.819	-1.045	0.636	0.681	0.738	-0.057	2603	-0.288	0	0.288	2603
			Traditional	9.774	10.819	-1.045	0.636	0.681	0.738	-0.057	2603	0.288	0	-0.288	2603
			Sub. - Trad.	0	0			0	0						
		yng	Final	8.188	11.284	-3.096	0.901	0.2	0.632	-0.432	4570				
			Genomic	8.183	11.92	-3.737	0.927	0.253	0.697	-0.444	4570	0.998	0.948	-0.05	4570
			Subset	4.764	9.729	-4.965	0.502	0.099	0.245	-0.146	4570	-0.717	-0.324	0.393	4570
			Traditional	4.766	8.541	-3.775	0.523	0.101	0.347	-0.246	4570	0.719	0.375	-0.344	4570
			Sub. - Trad.	-0.002	1.188			-0.002	-0.102						
HOL	pro/M	all	Final	5.337	7.877	-2.540	0.914	0.352	0.691	-0.339	7173				
			Genomic	5.338	8.075	-2.737	0.927	0.381	0.745	-0.364	7173	0.998	0.968	-0.03	7173
			Subset	3.477	6.467	-2.990	0.536	0.297	0.417	-0.12	7173	-0.6	-0.208	0.392	7173
			Traditional	3.484	6.123	-2.639	0.546	0.299	0.48	-0.181	7173	0.602	0.24	-0.362	7173
			Sub. - Trad.	-0.007	0.344			-0.002	-0.063						
		old	Final	6.062	8.387	-2.325	0.954	0.678	0.804	-0.126	2603				
			Genomic	6.062	8.387	-2.325	0.954	0.686	0.835	-0.149	2603	1	1	0	2603
			Subset	5.031	6.641	-1.61	0.649	0.664	0.724	-0.06	2603	-0.307	0	0.307	2603
			Traditional	5.031	6.641	-1.61	0.649	0.664	0.724	-0.06	2603	0.307	0	-0.307	2603
			Sub. - Trad.	0	0			0	0						
		yng	Final	4.772	7.445	-2.673	0.882	0.166	0.627	-0.461	4570				

			Genomic	4.776	7.817	-3.041	0.911	0.207	0.694	-0.487	4570	0.997	0.95	-0.047	4570
			Subset	2.059	6.283	-4.224	0.462	0.087	0.243	-0.156	4570	-0.767	-0.327	0.44	4570
			Traditional	2.072	5.58	-3.508	0.431	0.09	0.341	-0.251	4570	0.771	0.377	-0.394	4570
			Sub. - Trad.	-0.013	0.703			-0.003	-0.098						
HOL	**pro/N**	**all**	Final	12.96	18.5	-5.540	0.921	0.36	0.692	-0.332	7173				
			Genomic	12.936	19	-6.064	0.934	0.388	0.745	-0.357	7173	0.997	0.967	-0.03	7173
			Subset	8.381	15.112	-6.731	0.580	0.305	0.418	-0.113	7173	-0.586	-0.209	0.377	7173
			Traditional	8.422	14.268	-5.846	0.574	0.308	0.482	-0.174	7173	0.589	0.242	-0.347	7173
			Sub. - Trad.	-0.041	0.844			-0.003	-0.064						
		old	Final	14.535	19.597	-5.062	0.954	0.678	0.803	-0.125	2603				
			Genomic	14.535	19.597	-5.062	0.954	0.686	0.835	-0.149	2603	1	1	0	2603
			Subset	11.795	15.3	-3.505	0.662	0.665	0.722	-0.057	2603	-0.307	0	0.307	2603
			Traditional	11.795	15.3	-3.505	0.662	0.665	0.722	-0.057	2603	0.307	0	-0.307	2603
			Sub. - Trad.	0	0			0	0						
		yng	Final	11.812	17.616	-5.804	0.894	0.179	0.628	-0.449	4570				
			Genomic	11.775	18.537	-6.762	0.923	0.218	0.694	-0.476	4570	0.995	0.948	-0.047	4570
			Subset	5.474	14.853	-9.379	0.554	0.101	0.245	-0.144	4570	-0.744	-0.328	0.416	4570
			Traditional	5.566	13.155	-7.589	0.496	0.105	0.346	-0.241	4570	0.749	0.379	-0.37	4570
			Sub. - Trad.	-0.092	1.698			-0.004	-0.101						
HOL	**cc2/I**	**all**	Final	3.505	4.009	-0.504	0.840	0.318	0.611	-0.293	7173				
			Genomic	3.449	4.272	-0.823	0.877	0.347	0.662	-0.315	7173	0.975	0.952	-0.023	7173
			Subset	2.577	3.295	-0.718	0.790	0.206	0.334	-0.128	7173	-0.567	-0.285	0.282	7173
			Traditional	2.672	2.697	-0.025	0.783	0.232	0.409	-0.177	7173	0.592	0.333	-0.259	7173
			Sub. - Trad.	-0.095	0.598			-0.026	-0.075						
		old	Final	3.997	5.318	-1.321	0.891	0.452	0.695	-0.243	1783				
			Genomic	3.997	5.318	-1.321	0.891	0.488	0.752	-0.264	1783	1	1	0	1783
			Subset	2.982	3.406	-0.424	0.884	0.388	0.526	-0.138	1783	-0.463	0	0.463	1783
			Traditional	2.982	3.406	-0.424	0.884	0.388	0.526	-0.138	1783	0.463	0	-0.463	1783
			Sub. - Trad.	0	0			0	0						
		yng	Final	3.326	3.366	-0.040	0.847	0.274	0.583	-0.309	5390				
			Genomic	3.247	3.78	-0.533	0.885	0.301	0.633	-0.332	5390	0.966	0.936	-0.03	5390
			Subset	2.418	3.258	-0.840	0.755	0.146	0.27	-0.124	5390	-0.601	-0.379	0.222	5390
			Traditional	2.534	2.417	0.117	0.745	0.181	0.37	-0.189	5390	0.635	0.443	-0.192	5390
			Sub. - Trad.	-0.116	0.841			-0.035	-0.1						
HOL	**cc2/J**	**all**	Final	2.36	2.735	-0.375	0.873	0.363	0.597	-0.234	7173				
			Genomic	2.36	2.871	-0.511	0.889	0.448	0.663	-0.215	7173	1	0.974	-0.026	7173
			Subset	1.809	2.381	-0.572	0.709	0.171	0.326	-0.155	7173	-0.475	-0.253	0.222	7173
			Traditional	1.809	2.008	-0.199	0.705	0.171	0.372	-0.201	7173	0.475	0.279	-0.196	7173
			Sub. - Trad.	0	0.373			0	-0.046						
		old	Final	3.184	3.409	-0.225	0.934	0.579	0.735	-0.156	1783				
			Genomic	3.184	3.409	-0.225	0.934	0.63	0.779	-0.149	1783	1	1	0	1783
			Subset	2.597	2.778	-0.181	0.89	0.467	0.622	-0.155	1783	-0.167	0	0.167	1783
			Traditional	2.597	2.778	-0.181	0.89	0.467	0.622	-0.155	1783	0.167	0	-0.167	1783
			Sub. - Trad.	0	0			0	0						
		yng	Final	2.009	2.472	-0.463	0.833	0.292	0.551	-0.259	5390				
			Genomic	2.009	2.669	-0.660	0.868	0.388	0.625	-0.237	5390	1	0.965	-0.035	5390
			Subset	1.441	2.233	-0.792	0.600	0.073	0.228	-0.155	5390	-0.577	-0.337	0.24	5390
			Traditional	1.441	1.678	-0.237	0.532	0.073	0.289	-0.216	5390	0.577	0.372	-0.205	5390
			Sub. - Trad.	0	0.555			0	-0.061						
HOL	**cc2/M**	**all**	Final	0.675	1.511	-0.836	0.713	0.176	0.585	-0.409	7173				
			Genomic	0.676	1.599	-0.923	0.747	0.204	0.642	-0.438	7173	0.998	0.957	-0.041	7173
			Subset	0.452	1.158	-0.706	0.403	0.124	0.31	-0.186	7173	-0.757	-0.295	0.462	7173
			Traditional	0.455	0.904	-0.449	0.416	0.125	0.377	-0.252	7173	0.759	0.337	-0.422	7173
			Sub. - Trad.	-0.003	0.254			-0.001	-0.067						
		old	Final	0.79	2.048	-1.258	0.777	0.331	0.658	-0.327	1783				
			Genomic	0.79	2.048	-1.258	0.777	0.355	0.722	-0.367	1783	1	1	0	1783
			Subset	0.583	1.129	-0.546	0.576	0.288	0.469	-0.181	1783	-0.6	0	0.6	1783
			Traditional	0.583	1.129	-0.546	0.576	0.288	0.469	-0.181	1783	0.6	0	-0.6	1783
			Sub. - Trad.	0	0			0	0						
		yng	Final	0.631	1.22	-0.589	0.734	0.124	0.561	-0.437	5390				
			Genomic	0.633	1.369	-0.736	0.772	0.154	0.615	-0.461	5390	0.998	0.943	-0.055	5390
			Subset	0.395	1.168	-0.773	0.333	0.07	0.257	-0.187	5390	-0.809	-0.392	0.417	5390
			Traditional	0.399	0.816	-0.417	0.319	0.072	0.346	-0.274	5390	0.811	0.449	-0.362	5390

			Sub. - Trad.	-0.004	0.352			-0.002	-0.089					
HOL	cc2/N	all	Final	10.327	21.101	-10.774	0.767	0.2	0.598	-0.398	7173			
			Genomic	10.225	22.461	-12.236	0.800	0.226	0.653	-0.427	7173	0.997	0.957	-0.04	7173
			Subset	5.515	15.989	-10.474	0.525	0.148	0.322	-0.174	7173	-0.717	-0.288	0.429	7173
			Traditional	5.656	12.271	-6.615	0.558	0.151	0.39	-0.239	7173	0.72	0.331	-0.389	7173
			Sub. - Trad.	-0.141	3.718			-0.003	-0.068					
		old	Final	11.924	27.965	-16.041	0.82	0.376	0.678	-0.302	1783			
			Genomic	11.924	27.965	-16.041	0.82	0.397	0.737	-0.34	1783	1	1	0	1783
			Subset	7.314	15.313	-7.999	0.657	0.337	0.503	-0.166	1783	-0.573	0	0.573	1783
			Traditional	7.314	15.313	-7.999	0.657	0.337	0.503	-0.166	1783	0.573	0	-0.573	1783
			Sub. - Trad.	0	0			0	0					
		yng	Final	9.74	16.894	-7.154	0.793	0.141	0.571	-0.43	5390			
			Genomic	9.597	19.34	-9.743	0.824	0.17	0.625	-0.455	5390	0.996	0.943	-0.053	5390
			Subset	4.758	16.204	-11.446	0.485	0.085	0.261	-0.176	5390	-0.765	-0.384	0.381	5390
			Traditional	4.974	10.945	-5.971	0.513	0.089	0.353	-0.264	5390	0.769	0.441	-0.328	5390
			Sub. - Trad.	-0.216	5.259			-0.004	-0.092					
HOL	int/I	all	Final	3.26	3.046	0.214	0.847	0.298	0.583	-0.285	7173			
			Genomic	3.182	3.26	-0.078	0.890	0.33	0.606	-0.276	7173	0.974	0.913	-0.061	7173
			Subset	2.523	2.954	-0.431	0.816	0.18	0.298	-0.118	7173	-0.582	-0.385	0.197	7173
			Traditional	2.62	2.577	0.043	0.778	0.206	0.424	-0.218	7173	0.608	0.472	-0.136	7173
			Sub. - Trad.	-0.097	0.377			-0.026	-0.126					
		old	Final	4.718	4.32	0.398	0.929	0.684	0.855	-0.171	651			
			Genomic	4.718	4.32	0.398	0.929	0.704	0.868	-0.164	651	1	1	0	651
			Subset	3.985	3.98	0.005	0.92	0.647	0.828	-0.181	651	-0.159	0	0.159	651
			Traditional	3.985	3.98	0.005	0.92	0.647	0.828	-0.181	651	0.159	0	-0.159	651
			Sub. - Trad.	0	0			0	0					
		yng	Final	3.038	2.857	0.181	0.825	0.26	0.556	-0.296	6522			
			Genomic	2.955	3.105	-0.150	0.881	0.292	0.58	-0.288	6522	0.972	0.904	-0.068	6522
			Subset	2.311	2.819	-0.508	0.792	0.133	0.246	-0.113	6522	-0.624	-0.423	0.201	6522
			Traditional	2.417	2.375	0.042	0.735	0.162	0.384	-0.222	6522	0.652	0.519	-0.133	6522
			Sub. - Trad.	-0.106	0.444			-0.029	-0.138					
HOL	int/M	all	Final	0.662	0.718	-0.056	0.708	0.161	0.576	-0.415	7173			
			Genomic	0.663	0.787	-0.124	0.747	0.191	0.603	-0.412	7173	0.998	0.917	-0.081	7173
			Subset	0.444	0.684	-0.240	0.357	0.108	0.293	-0.185	7173	-0.77	-0.388	0.382	7173
			Traditional	0.447	0.567	-0.120	0.327	0.109	0.413	-0.304	7173	0.772	0.471	-0.301	7173
			Sub. - Trad.	-0.003	0.117			-0.001	-0.12					
		old	Final	1.017	0.927	0.09	0.829	0.591	0.842	-0.251	651			
			Genomic	1.017	0.927	0.09	0.829	0.61	0.857	-0.247	651	1	1	0	651
			Subset	0.825	0.819	0.006	0.626	0.545	0.809	-0.264	651	-0.271	0	0.271	651
			Traditional	0.825	0.819	0.006	0.626	0.545	0.809	-0.264	651	0.271	0	-0.271	651
			Sub. - Trad.	0	0			0	0					
		yng	Final	0.61	0.691	-0.081	0.680	0.119	0.549	-0.43	6522			
			Genomic	0.611	0.766	-0.155	0.733	0.149	0.577	-0.428	6522	0.998	0.909	-0.089	6522
			Subset	0.386	0.666	-0.280	0.299	0.064	0.241	-0.177	6522	-0.82	-0.427	0.393	6522
			Traditional	0.39	0.534	-0.144	0.235	0.066	0.374	-0.308	6522	0.822	0.518	-0.304	6522
			Sub. - Trad.	-0.004	0.132			-0.002	-0.133					
HOL	int/N	all	Final	9.481	9.665	-0.184	0.801	0.176	0.573	-0.397	7173			
			Genomic	9.365	10.371	-1.006	0.845	0.205	0.601	-0.396	7173	0.997	0.918	-0.079	7173
			Subset	5.271	9.258	-3.987	0.590	0.121	0.291	-0.17	7173	-0.738	-0.388	0.35	7173
			Traditional	5.431	7.841	-2.410	0.580	0.124	0.41	-0.286	7173	0.741	0.471	-0.27	7173
			Sub. - Trad.	-0.16	1.417			-0.003	-0.119					
		old	Final	13.953	13.286	0.667	0.888	0.599	0.832	-0.233	651			
			Genomic	13.953	13.286	0.667	0.888	0.615	0.849	-0.234	651	1	1	0	651
			Subset	9.703	11.872	-2.169	0.753	0.561	0.799	-0.238	651	-0.303	0	0.303	651
			Traditional	9.703	11.872	-2.169	0.753	0.561	0.799	-0.238	651	0.303	0	-0.303	651
			Sub. - Trad.	0	0			0	0					
		yng	Final	8.841	9.139	-0.298	0.778	0.134	0.548	-0.414	6522			
			Genomic	8.702	9.935	-1.233	0.835	0.164	0.576	-0.412	6522	0.997	0.91	-0.087	6522
			Subset	4.601	8.913	-4.312	0.561	0.078	0.24	-0.162	6522	-0.781	-0.427	0.354	6522
			Traditional	4.801	7.277	-2.476	0.529	0.081	0.372	-0.291	6522	0.785	0.517	-0.268	6522
			Sub. - Trad.	-0.2	1.636			-0.003	-0.132					

M= Multi-trait model, S= single-trait model, M-S = multi-trait minus single- trait, SD = standard deviation,
old = Reference individuals, yng. = Candidate individuals