# Trait specific computation of shared reference population

J. H. Jakobsen<sup>1</sup> and P. G. Sullivan<sup>2</sup>

<sup>1</sup>Interbull Centre, Box 7023, SE-750 07 Uppsala, Sweden

<sup>2</sup>Canadian Dairy Network, Guelph, ON, Canada

#### Introduction

The GenoList file (Interbull 733 file format), containing different genotype status codes of genotyped animals (e.g. "T"=used for training for protein yield) has so far served the purpose of computing the amount of shared genomic data among national reference populations. Both males and females holding a status code "T" in the GenoList have been used in the computations. Due to the lower reliability of female EBVs five females were assumed equivalent to one male, in terms of the effective information contributed for genomic predictions. The amount of sharing is used to prevent double counting of shared information at the national level, when combining the information in GMACE (VanRaden & Sullivan, 2010).

Until the August 2013 GMACE implementation run it has been assumed that countries have the same proportion of sharing across traits, even though the size of reference populations may differ for different traits. The amount of sharing  $(T_{ij})$  between countries i and j was computed as:

$$T_{ij} = \frac{shared \ reference \ bulls_{ij}}{\sqrt{reference \ bulls_i * reference \ bulls_i}}$$

Where five cows in a reference population contributed an equivalent of one reference bull.

Starting with the September 2013 GMACE test run it was decided to compute the amount of sharing based on the GenoList plus the

national EBVs submitted to Interbull for each individual trait for the corresponding classical

MACE run. Countries using females in their genomic reference population can only do so for traits evaluated with an animal model, and the EBVs of females are not submitted for classical MACE. Accounting for females by trait would be very difficult, and the GMACE WG therefore decided that females should no longer be used in the computation of reference sharing, when the sharing should be computed for each trait individually. The aim of this note was describe implementation of the trait-specific reference sharing.

## **Material and Methods**

#### Material

Twelve countries participated with young bull GEBV data for as many as 37 different traits for the September 2013 GMACE test run. These countries were Australia (AUS), Canada (CAN), Switzerland RHOL (CHR), Germany (DEU), Denmark-Finland-Sweden (DFS), France (FRA), Great Britain (GBR), Italy (ITA), The Netherlands (NLD), Poland (POL), Spain (ESP), and The United States of America (USA). Each country also provided a GenoList file with the reference population codes for protein.

# Methods

Firstly, one joint reference list was formed by selecting all animals used in training for protein by any country, in the country-provided GenoLists. Secondly, an Interbull

cross-reference file was applied to the animals in the joint reference list to prevent any double counting of aliases of the same animal. Trait-specific reference lists were then derived for each country, by assuming if a bull was used in the reference population for protein, and he is submitted for MACE for a second trait, that he was also included in the reference population for the second trait. T<sub>ij</sub> was still computed as:

$$T_{ij} = \frac{shared\ reference\ bulls_{ij}}{\sqrt{reference\ bulls_i * reference\ bulls_j}}$$

but now ignoring contributions from any reference females.

## **Results and discussion**

Number of reference bulls in trait-specific reference lists can be seen in the diagonals of Tables 1 through 6 for protein, stature,

somatic cell score, direct stillbirth, female fertility CC1, and milking speed. The numbers of reference bulls in common with other countries are shown below the diagonal and the proportion of shared reference bulls  $(T_{ij})$  are above the diagonal.

Numbers of bulls in reference populations were generally very similar for the different traits, with milking speed as an exception for countries in the "Intercontinental" consortium. Reference populations were much smaller for that trait because USA did not participate in classical MACE for milking speed and thus did not contribute any reference bulls with MACE proofs.

#### References

VanRaden, P.M. and Sullivan, P.G. 2010. International genomic evaluation methods for dairy cattle. Gen. Sel. Evol. 42: 7

Tabel 1. In diagonal: number of bulls in reference population for **protein**; below diagonal: number of reference bulls in common with other countries; above diagonal: proportion of shared reference bulls  $(T_{ij})$ 

CAN         DEU         DFS         FRA         ITA         NLD         USA         CHR         POL         GBR         ESP         A           CAN         22853         0.047         0.044         0.056         0.944         0.048         0.982         0.060         0.018         0.950         0.038         0.0           DEU         1139         25875         0.941         0.881         0.042         0.883         0.048         0.055         0.026         0.043         0.903         0.0           DFS         1025         23429         23956         0.902         0.039         0.900         0.044         0.052         0.026         0.040         0.919         0.0
DEU 1139 <b>25875</b> 0.941 0.881 0.042 0.883 0.048 0.055 0.026 0.043 0.903 0.000 DFS 1025 23429 <b>23956</b> 0.902 0.039 0.900 0.044 0.052 0.026 0.040 0.919 0.000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.000
DFS 1025 23429 <b>23956</b> 0.902 0.039 0.900 0.044 0.052 0.026 0.040 0.919 0.0
FRA 1284 21607 21275 <b>23241</b> 0.048 0.921 0.057 0.057 0.031 0.051 0.902 0.0
ITA 20664 981 865 1058 <b>20964</b> 0.047 0.942 0.052 0.019 0.945 0.037 0.0
NLD 1064 21009 20590 20772 1007 <b>21871</b> 0.050 0.060 0.028 0.045 0.932 0.0
USA 22454 1171 1036 1307 20622 1110 <b>22867</b> 0.060 0.018 0.939 0.040 0.0
CHR 539 522 474 518 449 528 540 <b>3503</b> 0.195 0.050 0.052 0.05
POL 142 215 211 250 143 220 140 604 <b>2731</b> 0.018 0.025 0.0
GBR 20839 1010 893 1138 19851 973 20596 429 135 <b>21041</b> 0.037 0.0
ESP 850 21365 20923 20231 796 20283 883 454 189 779 <b>21641</b> 0.0
AUS 474 400 385 405 321 462 469 225 110 435 372 <b>35</b>

Tabel 2. In diagonal: number of bulls in reference population for **stature**; below diagonal: number of reference bulls in common with other countries; above diagonal: proportion of shared reference bulls  $(T_{ij})$ 

	CAN	DEU	DFS	FRA	ITA	NLD	USA	CHR	POL	GBR	ESP
CAN	21629	0.048	0.045	0.057	0.954	0.049	0.984	0.061	0.018	0.951	0.039
DEU	1135	25809	0.941	0.882	0.043	0.883	0.049	0.055	0.026	0.044	0.903
DFS	1023	23374	23898	0.902	0.039	0.900	0.046	0.052	0.026	0.041	0.919
FRA	1276	21552	21221	23148	0.049	0.922	0.058	0.058	0.031	0.053	0.903
ITA	19868	977	863	1051	20064	0.048	0.953	0.054	0.019	0.954	0.038
NLD	1064	20955	20536	20720	1006	21807	0.051	0.060	0.029	0.047	0.933
USA	21247	1167	1034	1299	19818	1108	21566	0.062	0.018	0.941	0.041
CHR	534	522	474	518	449	528	535	3498	0.195	0.051	0.052
POL	142	215	211	250	143	220	140	602	2729	0.018	0.025
GBR	19708	1006	891	1131	19058	973	19474	429	135	19876	0.038
ESP	850	21315	20872	20183	796	20235	883	454	189	779	21592

Tabel 3. In diagonal: number of bulls in reference population for **somatic cell score**; below diagonal: number of reference bulls in common with other countries; above diagonal: proportion of shared reference bulls  $(T_{ij})$ 

	CAN	DEU	DFS	FRA	ITA	NLD	USA	CHR	POL	GBR
CAN	22796	0.047	0.044	0.056	0.945	0.048	0.984	0.060	0.018	0.951
DEU	1139	25874	0.941	0.881	0.042	0.883	0.048	0.055	0.025	0.043
DFS	1025	23428	23957	0.901	0.039	0.899	0.044	0.051	0.026	0.040
FRA	1283	21607	21275	23251	0.048	0.921	0.057	0.057	0.031	0.052
ITA	20634	981	865	1058	20934	0.047	0.943	0.052	0.019	0.946
NLD	1064	21009	20590	20778	1007	21882	0.050	0.060	0.028	0.045
USA	22422	1171	1036	1306	20591	1110	22755	0.060	0.018	0.942
CHR	539	522	474	518	449	528	540	3539	0.193	0.050
POL	142	215	211	250	143	220	140	604	2764	0.018
GBR	20785	1010	893	1137	19820	973	20565	429	135	20959

Tabel 4. In diagonal: number of bulls in reference population for **direct stillbirth**; below diagonal: number of reference bulls in common with other countries; above diagonal: proportion of shared reference bulls  $(T_{ii})$ 

	CAN	DEU	DFS	NLD
CAN	20077	0.053	0.049	0.054
DEU	1136	23131	0.939	0.877
DFS	1022	20822	21274	0.897
NLD	1046	18396	18044	19027

Tabel 5. In diagonal: number of bulls in reference population for **female fertility (CC1)**; below diagonal: number of reference bulls in common with other countries; above diagonal: proportion of shared reference bulls  $(T_{ij})$ 

	CAN	DEU	DFS	FRA	NLD	USA	CHR	GBR
CAN	20777	0.050	0.047	0.060	0.051	0.987	0.064	0.953
DEU	1134	24536	0.940	0.877	0.881	0.052	0.057	0.046
DFS	1020	22148	22609	0.900	0.899	0.048	0.054	0.043
FRA	1279	20328	20015	21895	0.921	0.061	0.060	0.055
NLD	1057	19729	19329	19486	20430	0.054	0.063	0.049
USA	20410	1165	1031	1298	1098	20564	0.065	0.945
CHR	539	522	474	518	525	540	3400	0.053
GBR	19038	1005	888	1133	967	18795	429	19222

Tabel 6. In diagonal: number of bulls in reference population for **milking speed**; below diagonal: number of reference bulls in common with other countries; above diagonal: proportion of shared reference bulls  $(T_{ij})$ 

	CAN	DEU	DFS	NLD	GBR
CAN	9588	0.069	0.066	0.069	0.905
DEU	1028	23279	0.944	0.891	0.066
DFS	945	21172	21591	0.906	0.061
NLD	947	18927	18530	19373	0.068
GBR	8000	903	815	859	8147