Breeding programs compared across countries, continents, and breeds

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Abstract

Breeding programs differ in generation intervals, pedigree completeness, genomic merit, and relationships to recent US animals as measured by expected future inbreeding (EFI) using pedigree or by genomic future inbreeding (GFI). Properties were examined using December 2023 files for proven bulls born 2016-2017 with milk-recorded daughters in ≥10 herds from Interbull, and genotyped females born 2018-2023 from the Council on Dairy Cattle Breeding (CDCB). Those genotypes included 3,709,707 females from USA and Canada, 498,480 from 13 countries in Asia, 378,650 from 17 countries in western Europe, 125,849 from 17 countries in eastern Europe, 153,362 from 12 countries in Latin America, 53,235 from 3 countries in Oceania, and 4,082 from 5 countries in Africa. Percentages of bulls with a foreign sire averaged 43% in Holsteins (HOL) and Brown Swiss, 12% in Red Dairy Cattle, and 9% in Jersey. The sire's age at son's birth averaged 2.2 to 2.9 years in 11 of the 20 countries for HOL, indicating rapid use of young sires, whereas other countries and breeds chose older sires of sons. Numbers of first crop daughters per selected young bull averaged 771 in HOL and 201-676 daughters in other breeds. Percentages of proven HOL bulls with genotypes used in the USA reference population differed widely by country from 0-100% and averaged 66%. Average pedigree completeness for HOL females ranged from 64.2% for Latin America to 86.1% for western Europe but was much higher and averaged 98% for proven bulls due to the Interbull exchange. Pedigree inbreeding, EFI, and GFI showed that proven bulls and genotyped females in many countries and continents are almost as related to US animals as US animals are to each other, but relationships are lower in other breeds and with wider ranges due to less genetic exchange. Other populations have higher genetic merit bulls for some breeds, but North American HOL had higher merit than all other regions.

Key words: genomic prediction, inbreeding, global breeding

Introduction

Breeding programs changed quickly after genomic selection began more than a decade ago (Garcia-Ruiz et al., 2016). Over a million foreign animals now have US genomic predictions. Their genotypes and pedigrees allow comparing breeding programs and relatedness within breeds around the world, including many countries that do not participate directly in Interbull services. Bull evaluations, pedigrees, and genotypes from countries that participate in multi-trait across-country evaluation (MACE) also allow directly comparisons. The 69 countries providing genotypes were grouped into 7 continental comparing the sires and selection methods used in each country. Goals were to examine relationships and use of foreign sires across countries, inbreeding, pedigree completeness, generation intervals, and genetic merit across countries and continents for several breeds.

Materials and Methods

The National Cooperator Database used for December 2023 official evaluations of CDCB included 3.3 million domestic and 1.4 million foreign genotyped females born 2018-2023 to provide recent

regions, with numbers for breeds Holstein (HOL) and Jersey (JER) shown in Tables 1 and

2. Individual countries providing the most foreign genotypes were 320,350 from Canada, 186,499 from Saudi Arabia, 160,558 from China, 135,971 from Japan, 114,501 from Italy, and 102,000 from Brazil.

Proven bulls born 2016-2017 with milk-recorded daughters in ≥10 herds from Interbull were examined using December 2023 official data from MACE on USA scale. Counts for breeds HOL, JER, Brown Swiss (BSW), and Red Dairy Cattle (RDC) are shown in Tables 3-6 for countries that had at least 10 domestic

Results & Discussion

For the recent genotyped HOL females, average Net Merit (NM$) was $480 in North America, $335 in Latin America, $381 in Western Europe, $370 in Eastern Europe, $317 in Africa, $366 in Asia, and $211 in Oceania (Table 1). Corresponding properties for 19,566 JER are in Table 2.

The average pedigree completeness for recent genotyped HOL females ranged from 64.2% for Latin America to 86.1% for western Europe. The average pedigree inbreeding for HOL females ranged from 8.7% for Africa and Oceania to 9.6% for North America. Oceania also had the lowest EFI of 9.0% and GFI of 9.4% compared to the highest EFI of 9.5% and GFI of 10.4% in North America. For JER females, pedigree completeness ranged from 57.3% in Latin America to 87.9% in North America. Western Europe had the lowest averages of 7.6% for pedigree inbreeding, 7.4% for EFI, and 5.7% for GFI compared to highest averages of 8.9% pedigree inbreeding, 9.0% GFI, and 7.7% EFI in North America.

For proven bulls, pedigree completeness was much higher and averaged 98% due to the Interbull exchange. HOL bulls had > 90% foreign sires in 7 of the 20 countries having at least 10 domestic proven bulls (counting DFS as 1 country), whereas NZL had 1% and USA had 11% foreign sires. The average was 43%

proven bulls during those 2 years, with Denmark-Finland-Sweden (DFS) treated as 1 country. German Simmental bulls (DEA) and French Montbeliard bulls (FRM) are reported on the HOL base because those breeds do not have a separate base in USA. Their evaluations include the expected 100% heterosis boost when mated to HOL females. Statistics for bulls included pedigree completeness (Ped%), percent of genotypes in USA reference (Gen%), percentage with foreign sires (ForSire%), and sire generation interval in years (SireGI).

foreign sires in HOL and BSW, 12% in RDC, and 9% in JER. The sire's age at son's birth averaged 2.2 to 2.9 years in 11 of the 20 countries for HOL, indicating rapid use of young sires, whereas other countries and breeds chose older sires of sons. Several populations average > 1,000 first crop daughters per young bull selected.

Percentages of proven bulls with genotypes used in the USA reference population differed widely by country from 0-100% and averaged 66% in HOL. For proven bulls, 11 of 20 countries had GFI of 10.0 to 11.3%; EFI patterns were similar. All other countries had GFI above 8.1% except ISR (3.2%) and NZL (2.4%). Compared to 19 years ago (VanRaden, 2005), pedigree completeness has improved a little but inbreeding levels for MACE bulls have more than doubled.

Tooker et al. (2015) summarized the first 200,000 foreign genotypes in Table 7. For recently genotyped HOL females, pedigree completeness decreased slightly compared to those born before 2015 on all continents except a small increase in Asia. Inbreeding levels have increased quickly, but foreign females are still almost as related to US animals as US animals are to each other (EFI and GFI). North American average NM$ remains higher than for all other continents but NM$ averages are not directly comparable to means from 2015 due to a base change in 2020 and other index formula changes. Other than the consistent increases in

inbreeding, properties in Tables 1 compared to 7 show good progress on all continents after 9 years of rapid growth in genotyping.

Conclusions

Most foreign HOL bulls and genotyped females are highly related to the USA reference population. Sire generation intervals were < 3 years in many HOL breeding programs but longer in other breeds and smaller populations. Almost half of HOL and BSW bulls had foreign sires but fewer in other breeds. HOL genetic merit was higher in North America than in all other continental regions but varied more in other breeds. Breeders in many countries are choosing genomic predictions from USA. Predictions for foreign animals should be almost as accurate as for domestic animals, but genetic correlations are unknown in many new markets.

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Table 1. Average pedigree completeness, inbreeding, expected future inbreeding, and genomic future inbreeding by continental region for genotyped **Holstein** females born 2018-2023.

Continent	Genotypes (N)	Pedigree completeness (%)	Net Merit ($)	Pedigree Inbreeding (%)	Expected future inbreeding (%)	Genomic future inbreeding (%)
North America	3,082,090	84.2	480	9.6	9.5	10.4
Latin America	141,679	64.2	335	9.1	9.4	9.9
Western Europe	288,475	86.1	381	9.1	9.2	10.2
Eastern Europe	96,940	74.5	370	8.8	9.2	9.7
Africa	3,964	70.5	317	8.7	9.1	9.8
Asia	491,371	76.5	366	8.8	9.2	9.7
Oceania	23,764	75.2	211	8.7	9.0	9.4

Table 2. Average pedigree completeness, inbreeding, expected future inbreeding, and genomic future inbreeding by continental region for genotyped **Jersey** females born 2018-2023.

Continent	Genotypes (N)	Pedigree completeness (%)	Net Merit ($)	Pedigree Inbreeding (%)	Expected future inbreeding (%)	Genomic future inbreeding (%)
North America	441,024	87.9	304	8.9	9.0	7.7
Latin America	8,902	57.3	75	8.5	8.7	7.0
Western Europe	4,948	75.8	118	7.6	7.4	5.7
Eastern Europe	519	79.4	284	7.8	8.0	6.2
Africa	107	85.0	90	8.0	8.4	7.8
Asia	1,430	74.6	41	8.1	8.6	7.1
Oceania	3,497	63.9	1	8.1	8.1	7.1

Table 3. Properties by country of ID for **Holstein** bulls and Simmental breed group bulls (DEA and FRM) expressed on HOL base.

Country	Bulls	Daughters	Ped%	Gen%	NM$	EFI	GFI	ForSire%	SireGI
USA	1754	1085	100	99	543	10.0	11.1	11	2.3
DEA	*1005*	*348*	*97*	*0*	*202*	*1.1*	*.*	*38*	*4.1*
DEU	590	871	100	88	378	8.6	10.1	79	2.4
NLD	444	1012	99	66	326	7.8	9.8	58	3.0
NZL	444	811	99	1	-61	2.8	2.4	1	5.9
CAN	332	1125	100	100	479	10.0	11.3	65	2.2
JPN	309	61	97	22	276	9.0	10.5	81	3.7
FRA	282	1289	94	52	257	8.0	10.1	79	2.6
FRM	*194*	*591*	*92*	*0*	*233*	*1.3*	*.*	*1*	*3.6*
ITA	186	329	99	75	315	7.6	10.7	90	2.8
DFS	162	1593	99	41	353	7.5	8.8	47	2.3
CHE	145	245	100	10	-23	5.0	9.3	50	4.0
POL	96	307	93	22	274	8.2	10.2	100	2.9
SVN	82	107	91	1	31	4.6	9.4	98	5.2
ISR	79	266	85	5	269	5.5	3.2	29	4.9
KOR	71	36	94	0	31	8.9	.	100	8.0
AUS	64	234	92	39	125	8.3	9.9	70	3.5
ESP	60	185	97	42	247	9.4	10.5	98	2.6
GBR	42	642	98	93	267	7.3	8.1	74	4.4
CZE	23	473	100	78	430	9.7	11.2	100	2.5
LUX	14	343	100	86	442	9.0	10.6	100	2.6
BEL	13	476	99	85	306	7.7	9.4	85	2.6

Globe	6412	771	98	54	324	7.0	10.7	43	3.2

Table 4. Properties by country of ID for **Jersey** bulls.

Country	Bulls	Daughters	Ped%	Gen%	NM$	EFI	GFI	ForSire%	SireGI
USA	359	594	95	100	279	9.1	7.4	4	3.1
NZL	207	455	98	4	-7	2.8	2.6	6	5.9
DFS	56	941	99	63	326	4.9	3.1	7	2.4
AUS	21	229	89	24	-6	8.1	7.7	57	6.2
CAN	19	176	100	100	69	8.4	8.1	47	2.5
Globe	673	551	96	65	177	6.7	7.0	9	4.0

Table 5. Properties by country of ID for **Brown Swiss** bulls.

Country	Bulls	Daughters	Ped%	Gen%	NM$	EFI	GFI	ForSire%	SireGI
DEA	157	213	96	93	436	5.4	6.3	37	4.4
CHE	100	287	99	39	123	5.2	0.3	32	3.7
ITA	57	116	99	93	289	6.2	6.8	63	3.8
USA	49	130	99	100	223	7.8	7.5	39	4.3
FRA	13	228	98	100	359	6.4	7.2	77	4.5
SVN	12	54	98	50	226	5.6	6.1	92	4.9
Globe	394	201	96	93	297	5.8	5.9	43	4.1

Table 6. Properties by country of ID for **Red Dairy Cattle** bulls.

Country	Bulls	Daughters	Ped%	Gen%	NM$	EFI	GFI	ForSire	SireGI
DFS	149	708	98	20	786	3.2	2.0	1	2.4
NOR	92	1177	97	0	652	2.2	.	4	4.4
NZL	27	56	95	0	438	2.1	.	33	8.3
CAN	18	99	100	94	412	7.3	5.8	33	5.3
AUS	15	90	76	0	432	3.2	.	60	6.5
GBR	11	147	83	64	57	6.1	4.2	27	9.4
USA	7	94	97	100	129	7.6	5.6	43	6.6
Globe	329	676	96	19	638	3.2	3.7	12	4.1

Table 7. Averages from Tooker et al. (2015) for pedigree completeness, inbreeding, expected future inbreeding, and genomic future inbreeding by continental region.

Continent	Pedigree completeness (%)	Net Merit ($)	Pedigree Inbreeding (%)	Expected future inbreeding (%)	Genomic future inbreeding (%)
North America	86.1	191	6.5	6.4	6.9
Latin America	67.7	9	5.9	6.0	6.0
Western Europe	97.6	146	6.1	6.1	6.7
Eastern Europe	88.0	111	5.5	5.8	6.2
Africa	87.4	64	6.3	6.6	7.3
Asia	71.9	48	5.8	6.0	6.3
Oceania	93.6	44	6.0	5.8	6.2