Genetic Variability Analysis of Canadian Sheep Breeds Using Pedigree Information

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Executive Summary

Genetic variability is critical in animal populations, as it is a major component of genetic progress. The loss of within-breed genetic diversity can lead to an increase in inbreeding, which is often the cause of genetic defects, and can also affect productivity and fitness on a longer term due to inbreeding depression. A pedigree analysis of registered Canadian sheep breeds was carried out in order to provide a retrospective portrait of genetic variability, based on inbreeding trends and probabilities of gene origin. Pedigree files provided by the Canadian Livestock Registration Corporation (CLRC) and the GenOvis program were merged and analyzed for the study. The initial file contained 1,085,583 purebred animals born from 1950 to 2012 in 50 different breeds. A total of 33 breeds with animals registered in the recent years were included in a detailed pedigree analysis, using females born between 2009 and 2011 as the reference population for each breed. Reference populations varied considerably in size, from 25 to 17,514 animals. Generation intervals were computed within and across breeds and ranged from 29 to 58 months (43 months on average). Pedigree completeness was moderately good and very variable, with 1.32 to 10.09 complete generation equivalents known depending on the breed (5.27 generations on average). Inbreeding levels and trends were analyzed for each breed, with average inbreeding coefficients ranging from 0.07% to 11.17% in most recent cohorts, and inbreeding trends ranging from -0.45 to +0.98% per year between 2000 and 2010. Eight breeds showed an inbreeding trend greater than 1% per generation in the recent years. The number of effective ancestors ranged between 5 and 180 (average=31) and the number of remaining founder genomes ranged from 2 to 66 (average=16) in the 33 breeds under study. The study found that some of the current large breeds actually have a small genetic size. From the trends on effective number of ancestors and founder genomes over the past 15 years, it appears that more attention should be paid very quickly to preserving genetic variability in all breeds. Some breeds are in a more critical situation as they deal with both high inbreeding trends and genetic size issues such as Berrichon du Cher, British Milk Sheep, Ile de France, Lincoln, Outaouais Arcott, Romanov, Rouge de l'Ouest. These issues should be addressed in priority. New recent tools now available on the CLRC website and as part of the GenOvis program will help monitoring and controlling inbreeding levels at the farm level. For all breeds, some collective approaches will also be required to manage genetic diversity in an optimized way. Depending on the population size, its history, implemented selection practices, number of herds involved, and the potential access to foreign genes, potential solutions will need to be tailored to each breed. Specific recommendations were provided for each breed in factsheets giving detailed information about past trends and current status regarding the main genetic variability indicators.

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Final Report

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1. Introduction

In Canada, 51 sheep breeds are officially recognized by the Canadian Sheep Breeders Association. All breeds experienced different events since their creation, with some breeds becoming more popular with Canadian sheep producers in different Canadian provinces. In the most common breeds, genetic improvement tools have been used over the past decades, especially since the creation of the GenOvis program for sheep genetic evaluations.

Genetic selection consists of choosing the best animals for breeding and maximizing the diffusion of their genes so that the whole population benefits from genetic progress on a specific trait or set of traits. Selection usually decreases the number of animals used to produce the next generations, and often leads to unbalanced use of the various families within each breed. Consequently, selection leads to a decrease in genetic variability. At the same time, genetic variability is necessary to achieve genetic progress. The most common way to describe genetic variability and its evolution across generations is through pedigree analysis. Inbreeding is frequently used to quantify trends in genetic diversity, but there are other approaches, also based on historical pedigree data, that can help to describe genetic variability within breeds. Inbreeding can lead to recessive genetic defects and negative effects on several traits such as reproductive performance and fitness. Genetic variability is important to guarantee future genetic progress, as well as opportunities for re-evaluating breeding goals. It is critical to avoid inbreeding in animal populations, but it is even more important to preserve genetic variability in the long term. Genetic variability has been studied in many different animal species, especially livestock species which were submitted to intense selection over the past decades. Short-term genetic gains are often the first priority, at the expense of long-term sustainability.

This study was carried out in order to provide an exhaustive portrait of current genetic variability and its recent trend in Canadian purebred sheep populations, in order to identify needs and opportunities for a better management of genetic variability in the future.

2. Material and Methods

2.1. Pedigree files

Pedigree files were obtained from two sources:

- The Canadian Livestock Records Corporation, which manages herd-books for registered species (www.clrc.ca).
- The GenOvis database, managed at University of Guelph, which includes all breeds on the Canadian genetic evaluation program (www.genovis.ca).

Following testing and validation, analyses were carried out using versions of pedigree files extracted in October 2012. Both files were merged to build a pedigree file as complete as possible for purebred sheep. A large proportion of animals in the GenOvis pedigree file were also in the CLRC file. In total, the final version of the merged pedigree file contained 1,085,583 purebred animals, born between 1950 and 2012. Older data exists for sheep breeds on paper, dating back to the creation of the Canadian Sheep Breeders Association (in June 1900), but herd-books were computerized in the 1960s, and only a few generations of ancestors were entered at that time. As it is often the case for this kind of study, analyses were carried out on computerized pedigree data, which traces back to a maximum of 60 years in this study and even less for breeds created more recently such as the Arcott populations. Because of that, we know that the genetic variability is actually overestimated, since all 'informatic' founders (ancestors without parents) are assumed to be unrelated, which is not true.

2.2. Analyses

The pedigree file constituted for the analysis was formatted to be processed using a set of programs available in the *Pedig* package (Boichard, 2002). These programs were developed to process large pedigree files and compute a list of useful indicators describing demography and genetic variability. The programs were slightly modified for this study, to read sheep IDs and to carry out within breed as well as across breed analyses.

Main criteria estimated by processing the sheep pedigree file were the following:

- **Pedigree completeness**: this phase is necessary to check the deepness of pedigree data available for each breed studied. Sub-criteria include:
    - Proportion of ancestors known at each generation
    - Maximum number of generations traced back
    - Average number of ancestors known
    - Number of complete generation equivalents: this number is computed in order to describe the average pedigree completeness of a population. It is defined as the sum over all generations of the proportion of known ancestors at each generation. For instance, if the parents, grand-parents and great-grand-parents are all known for an animal, the number of generation equivalents is equal to 3. If only the parents and 2 grand-parents are known, the number of complete generation equivalents will be equal to 1.5.

- **Generation intervals**: this criterion is the average age of parents when their progeny is born, and can be computed on four different paths (sire-son, sire-daughter, dam-son, dam-daughter).

- **Inbreeding:** based on all pedigree information available, individual inbreeding coefficients were computed for each animal in the pedigree file. Inbreeding is defined as the probability that at a given locus, both alleles are identical by descent, which means transmitted by a common ancestor. In other words, an inbred animal is born from two related parents, and its inbreeding coefficient depends on the degree of relationship between its sire and dam.
  - The effective population size (N_e) can be computed for each breed using the annual inbreeding trend (ΔF) and the average generation interval (L) for the breed, using the following formula: $N_e = \frac{1}{2 * \Delta F * L}$

- **Probabilities of gene origin**: approaches based on ancestors' contributions are usually more accurate because they are much less dependent on pedigree completeness and mating strategies. Various criteria can be computed for a given reference population. In this study, analyses were focused on:
  - **Effective number of founders (F_e)**: Virtual number of founders that would produce the same genetic variability than in the population under study. For example, a herd of 100 ewes can be born from 10 initial founders, which contribute alleles unequally. If each founder contributes to 10% of the population, the effective number of founders (F_e) is equal to 10. If a founder contributes to 91 % of the current population and the nine others 1% each, Fe is equal to 1.2.
  - **Effective number of ancestors (F_a)**: Number of virtual ancestors, founders or not, that would produce the same genetic variability as that observed in the population under study. For example, a herd of 100 ewes born of 10 initial founders but originating from 2 over-used rams and ewes at a given time and that are found in the pedigree of all current animals. The effective number of ancestors (F_a) would in that case be equal to 4. This approach takes into account bottlenecks in the population's history.
  - **Number of founder genome equivalents (N_g)**: By assuming that all initial founders in a population were not related and not inbred, the transmission of all alleles present initially in founders to the current population can be simulated, and the number of founder genomes that could be reconstituted is calculated. This approach takes into account the imbalanced founder contributions, bottlenecks in pedigrees and genetic drift (random loss of alleles over time).

3. Results

3.1. Number of animals

Table 1 – Population statistics for the 50 sheep breeds available for the genetic variability study

		Animals in the pedigree file				Birth year			Females born in		
breed code	**Breed(*)**	**Total**	**Females**	**Males**	**Other**	**Min**	**Max**	**1994-1996**	**1999-2001**	**2004-2006**	**2009-2011**
DC	**BERRICHON DU CHER**	247	147	100		1996	2009		6	40	25
FB	**BLACKFACE(1)**	407	268	139		1981	2012	4	4	23	66
BF	**BLUEFACED LEICESTER**	156	98	58		1977	2012	2		3	4
BC	**BORDER CHEVIOT(2)**	6164	3955	2209		1968	2012	244	129	172	210
BL	**BORDER LEICESTER(3)**	17764	11010	6747	7	1968	2012	896	611	439	288
BM	**BRITISH MILK SHEEP**	561	424	137		1990	2012		22	56	216
CD	**CANADIAN ARCOTT**	16537	9804	6733		1983	2012	837	1538	1359	1304
CO	**CHAROLLAIS**	6276	3399	2869	8	1982	2012	136	558	663	478
CF	**CLUN FOREST**	5083	3454	1223	406	1967	2012	400	331	220	356
CL	**COLUMBIA**	10784	7066	3635	83	1967	2010	513	466	110	13
CP	**COOPWORTH**	672	387	283	2	1980	2008				
CR	**CORRIEDALE(1)**	8816	5937	2689	190	1969	2012	204	70	28	69
CW	**COTSWOLD(2)**	1487	1039	446	2	1972	2012	113	105	81	80
DP	**DORSET**	211044	131055	78552	1437	1961	2012	11423	10537	10574	7397
DL	**DORSET LEICESTER SUFFOLK**	2755	1660	1095		1980	2008	470	127	20	
DO	**DORPER**	9028	6094	2926	8	1988	2012	34	381	1203	1799
EF	**EAST FRIESIAN DAIRY**	4122	2501	1619	2	1987	2012	236	543	457	126
LE	**ENGLISH LEICESTER**	144	72	72		1978	1998	7			
FN	**FINNSHEEP**	7078	4808	2268	2	1973	2012	493	295	291	501
HS	**HAMPSHIRE(4)**	40510	25144	15361	5	1950	2012	1870	1408	1214	1286
IL	**ICELANDIC**	20710	14045	6665		1984	2012	337	1849	3119	2638
IF	**ILE DE FRANCE**	2180	1151	1029		1993	2012	17	65	176	362
JA	**JACOB(1)**	597	381	216		1987	2012	17	55	45	26
KK	**KARAKUL(1)**	380	275	105		1975	2011	24	4	2	10
KA	**KATAHDIN**	5624	3335	2281	8	1976	2012	328	489	499	476
CU	**LACAUNE**	66	29	37		1995	2011	1	11	4	1
LI	**LINCOLN(1)**	6547	4010	2537		1972	2012	502	261	120	66
MM	**MERINO**	445	264	181		1974	2002	29	5		
MT	**MONTADALE**	880	670	210		1971	1998	28			
NC	**NORTH COUNTRY CHEVIOT**	33118	22558	10500	60	1967	2012	1410	1434	1065	1517
OU	**OUTAOUAIS ARCOTT**	11234	7544	3594	96	1969	2012	714	1250	959	360
OX	**OXFORD(2)**	14585	8740	5823	22	1963	2012	890	641	324	238
PE	**PERENDALE**	111	58	53		1977	1984				
PO	**POLYPAY**	56903	33576	23324	3	1967	2012	3179	4529	4906	3528
RG	**RAMBOUILLET(3)**	13060	10128	2917	15	1961	2010	643	438	194	17
RI	**RIDEAU ARCOTT**	160059	85188	71645	3226	1980	2012	4947	12822	15173	17514
RV	**ROMANOV**	49751	29768	19974	9	1971	2012	3922	2324	1633	5891
RM	**ROMNELET**	214	161	53		1971	1984				
RY	**ROMNEY(2)**	6161	4256	1905		1970	2012	651	334	211	121
RO	**ROUGE DE L'OUEST**	447	235	212		1997	2011		4	50	72
SL	**SHETLAND**	1194	774	420		1976	2012	113	104	123	37
SR	**SHROPSHIRE(1)**	5506	3338	2160	8	1969	2012	311	178	97	130
SY	**SOAY(1)**	60	35	25		1995	2008	1	8	7	
SA	**SOUTH AFRICAN MEAT MERINO**	452	261	191		1996	2004	7	60	22	
ST	**SOUTHDOWN(3)**	15763	10251	5499	13	1968	2012	918	711	389	360
SX	**ST. CROIX(1)**	92	49	43		1986	1996	32			
SU	**SUFFOLK**	282467	182216	97935	2316	1950	2012	9809	8593	6313	5306
TA	**TARGHEE**	1203	847	356		1965	2005	16		7	
TX	**TEXEL**	8826	5262	3564		1982	2012	305	455	1053	904
TU	**TUNIS(1)**	239	139	100		1982	2012	41	9	5	19

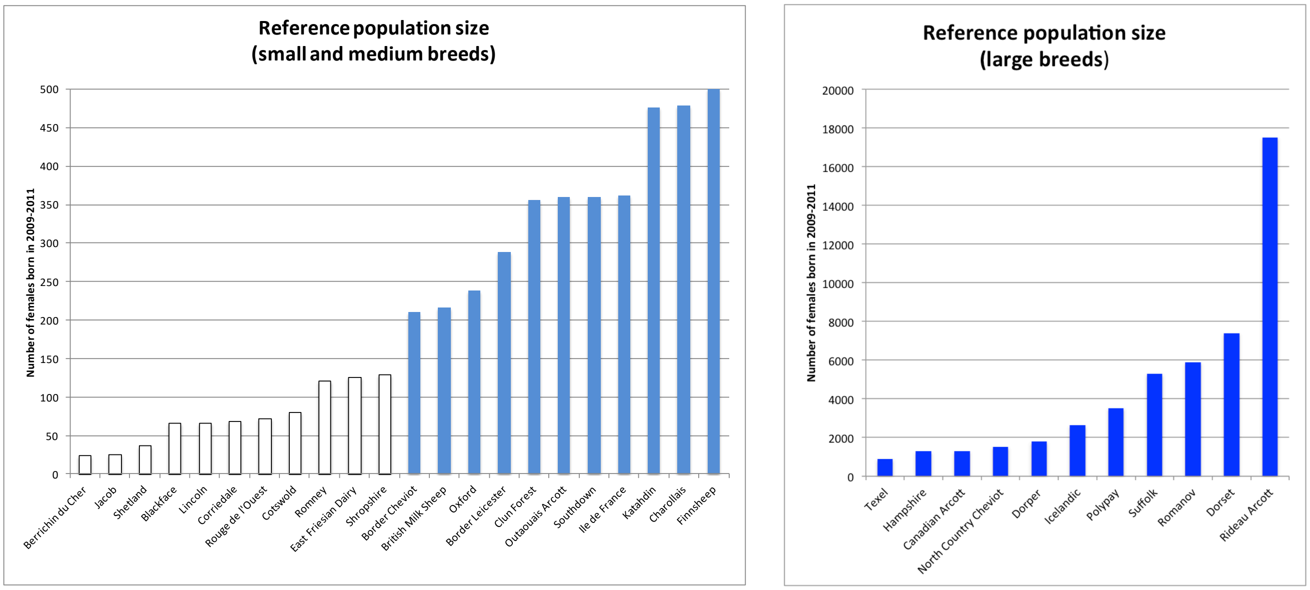
(*) Breeds with a superscript are listed with Rare Breeds Canada (1=critical; 2=endangered; 3=vulnerable; 4=at risk)

As shown in Table 1, the 50 sheep populations (and their pedigree files) available for the study vary considerably in size, from 66 to 282,467 animals in the total pedigree file. In 2012, sheep from 34 different breeds were registered at CLRC, with 11 breeds representing 87% of all registrations (Suffolk, Dorset, Rideau Arcott, Romanov, Icelandic, Dorper, North Country Cheviot, Hampshire, Polypay, Canadian Arcott, Texel) with 381 to 2243 registered animals in 2012. The remaining 23 breeds registered a total of 1746 individuals, ranging from 1 animal (Berrichon du Cher) to 224 animals (Charollais) registered in Canada in 2012 (CLRC, 2012).

For this study, four different cohorts were considered to describe the trend in genetic variability over time for each population. Females born from known parents in 1994-1996, 1999-2001, 2004-2006 and 2009-2011 were used in each breed. The most recent cohort (females born between 2009 and 2011) was chosen as the reference population for most of the results presented in the following sections. Some breeds included in the initial pedigree file don't have any recent registrations (Coopworth, Dorset Leicester Suffolk, English Leicester, Merino, Montadale, Perendale, Romnelet, South African Meat Merino, St Croix) whereas others have very small reference populations (Bluefaced Leicester, Columbia, Lacaune, Karakul, Rambouillet, Soay, Tunis) and were not included in the overall analyses based on recent animals.

A subgroup of 17 breeds (listed above) was excluded from analyses, based on their population size in recent years. Results presented in further sections were focused on 33 breeds. The most recent reference population (females born in 2009-2011) ranged from 25 to 17,514 animals, with an average of 1,629 per breed. This is a very variable data set in terms of reference population size. Eleven breeds could be classified as small populations (in white on Figure 1), with less than 200 animals in the reference population, eleven breeds could be classified as medium size with 200 to 500 animals in the reference population (light blue on Figure 1), and eleven breeds were considered as large breeds (dark blue on Figure 1), with more than 500 animals in the reference population. These eleven breeds represented 87% of CLRC's sheep registrations in 2012.

Figure 1 – Distribution of the reference population size (females born in 2009-2011) for the 33 breeds included in the analysis.



3.2. Generation Intervals

Using historical pedigree information, it is possible to compute interesting demographical criteria such as generation intervals. They tend usually to decrease in selected populations, due to the faster turnover of breeding animals. Shorter generation intervals allow for higher genetic gains and a faster increase in inbreeding. Longer generation intervals might also lead to lower genetic diversity because its means that breeding animals are used for a longer time, therefore increasing their contribution to subsequent generations at the expense of other younger animals and increases the probability that they may be bred to some of their progeny. Generation intervals depend on the reproductive performance of the population (age at puberty, number of lambing per year, longevity, etc) and are also influenced by breeding and culling decisions. Generation intervals are also part of the strategy for managing genetic variability in animal populations, with an optimum to be found based on population size, selection practices and targeted inbreeding trends.

Figure 2 – Trends in generation intervals (4 paths) in Canadian sheep breeds

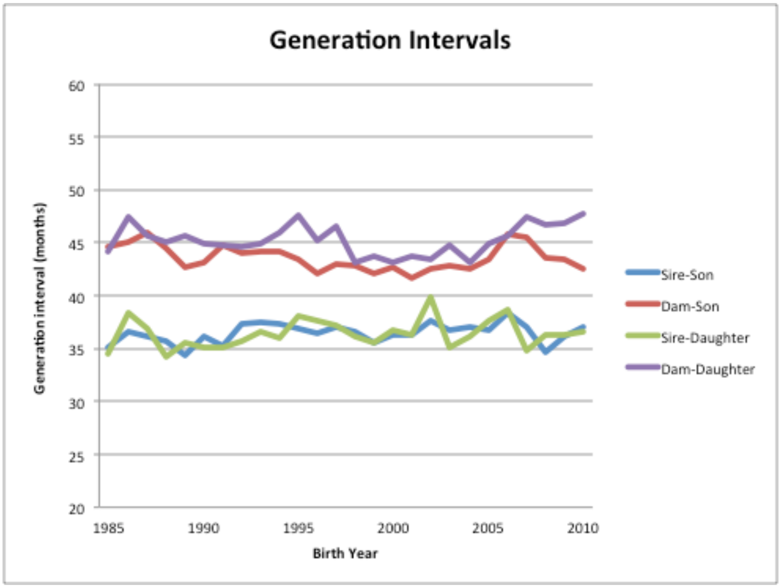


Figure 2 shows the trends in generation intervals across breeds, computed as the average age of parents for each birth year. The calculation was done only for progeny that ultimately became breeding animals themselves. The trend has been quite stable over the past 20 years, with a clear difference between sire-progeny and dam-progeny paths. For example, sires of lambs born in 2010 were on average 37 months old, whereas dams were 46 months old. In the past 5 years, there seems to be an increase in the dam-daughter interval and a decrease on the dam-son interval across breeds. These values vary across years and breeds. The average generation interval for the 2000-2010 period was 43 months across breeds, ranging from 29 months (Blackface) to 58 months (Clun Forest). Average generation intervals are provided in appendix for each breed separately.

3.3. Pedigree Completeness

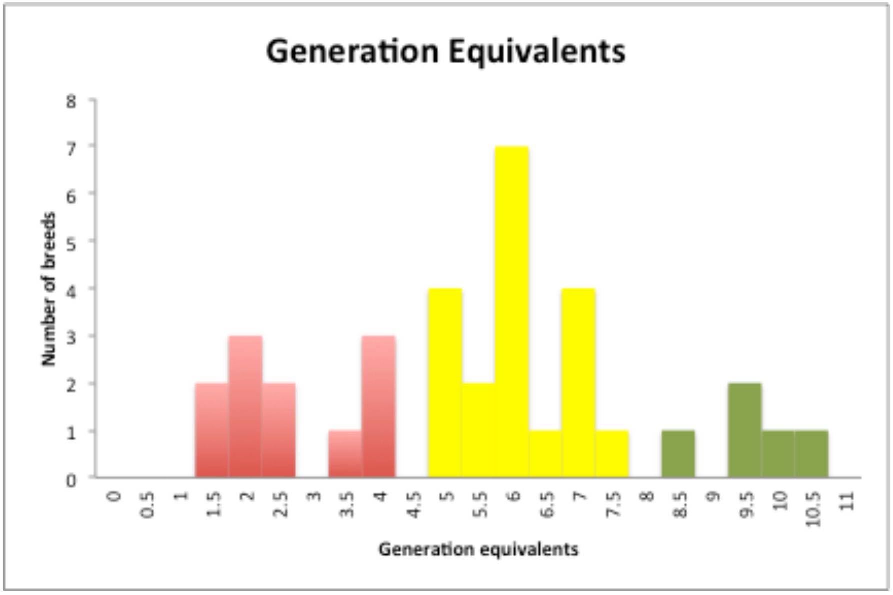
When only pedigrees are used to evaluate genetic variability in a population, it is critical to assess the amount of information available. Commonly used criteria such as inbreeding are very sensitive to pedigree completeness. In a population with on average 10 generations of known ancestors, the computed inbreeding coefficients would be more accurate than in a population with only 3 generations of known ancestors. Pedigree knowledge usually depends on the history of the breed and its access to foreign genes. Table 2 shows some statistics about pedigree completeness and is ranked based on the number of generation equivalents, which is a synthetic criteria commonly used to assess pedigree quality.

Table 2 – Pedigree completeness in breeds under study

	All animals in pedigree file			Females born in 2009-2011			
Breed	**total**	**founders**	**%founders**	**Number of females**	**maximum generations**	**average number of ancestors**	**generation equivalents**
BORDER LEICESTER	17764	1282	7.2	288	23	12541	10.09
ROMANOV	49751	1958	3.9	5891	24	9044	9.52
NORTH COUNTRY CHEVIOT	33118	1943	5.9	1517	26	13721	9.28
OUTAOUAIS ARCOTT	11234	1003	8.9	360	11	142	9.28
CLUN FOREST	5083	289	5.7	356	22	2756	8.15
ICELANDIC	20710	607	2.9	2638	20	1163	7.32
SHROPSHIRE	5506	604	11.0	130	22	3389	6.82
SUFFOLK	282467	28882	10.2	5306	29	4525	6.82
RIDEAU ARCOTT	160059	4699	2.9	17514	20	457	6.77
DORSET	211044	14638	6.9	7397	29	4104	6.73
ILE DE FRANCE	2180	190	8.7	362	14	519	6.47
HAMPSHIRE	40510	3009	7.4	1286	26	6194	5.97
CHAROLLAIS	6276	539	8.6	478	25	698	5.81
CANADIAN ARCOTT	16537	967	5.8	1304	12	194	5.78
BERRICHON DU CHER	247	35	14.2	25	14	146	5.77
ROMNEY	6161	1166	18.9	121	16	150	5.58
OXFORD	14585	1010	6.9	238	22	2005	5.56
DORPER	9028	1105	12.2	1799	13	287	5.39
POLYPAY	56903	4293	7.5	3528	19	641	5.24
EAST FRIESIAN DAIRY	4122	566	13.7	126	12	152	4.93
FINNSHEEP	7078	953	13.5	501	21	1016	4.91
LINCOLN	6547	412	6.3	66	24	3140	4.85
ROUGE DE L'OUEST	447	48	10.7	72	10	175	4.59
TEXEL	8826	1637	18.5	904	22	876	3.87
BORDER CHEVIOT	6164	839	13.6	210	25	1615	3.85
SOUTHDOWN	15763	1910	12.1	360	22	272	3.71
CORRIEDALE	8816	1574	17.9	69	20	751	3.18
BLACKFACE	407	132	32.4	66	11	31	2.27
BRITISH MILK SHEEP	561	141	25.1	216	7	16	2.01
KATAHDIN	5624	841	15.0	476	9	9	1.86
JACOB	597	173	29.0	26	10	29	1.62
SHETLAND	1194	496	41.5	37	7	4	1.47
COTSWOLD	1487	359	24.1	80	19	1389	1.32

The number of generation equivalents for females born in 2009-2011 ranges from 1.32 (Cotswold) to 10.09 (Border Leicester) with an average of 5.27, showing that the amount of information available is on average moderately good, but very variable across breeds. This means that various criteria computed using pedigree information, especially inbreeding, will have different accuracies depending on the breed. Figure 3 shows the distribution of the number of generation equivalents for the 33 breeds studied. Five breeds (Border Leicester, Romanov, North Country Cheviot, Outaouais Arcott, Clun Forest) have excellent pedigree completeness with more than 8 generation-equivalents known for the reference population. Ten breeds have less than 4 generation-equivalents known, which is considered low. Eighteen breeds have between 4 and 8 generation-equivalents known. The maximum number of generations traced back varies from 7 to 29. It depends on many factors, such as the generation interval in the breed, or the official date the breed was created. For instance, the three 'Arcott' breeds (Canadian Arcott, Rideau Arcott and Outaouais Arcott) were created in the early 1980s, which explains their relatively lower pedigree completeness compared to other breeds.

Figure 3 – Pedigree completeness for females born in 2009-2011



Overall, pedigree completeness is relatively good for Canadian sheep breeds (average=5.27 generation equivalents) but the amount of information available for analyses varies quite a bit from one breed to another, from less than 1.5 to more than 10 generations traced back on average. This factor has to be taken into account before interpreting genetic variability indicators presented in this report. Ideally, only breeds with similar pedigree quality should be compared. For each breed, a graph included in appendix illustrates the exact proportion of known ancestors per generation for the reference population.

3.4. Inbreeding

Individual inbreeding coefficients were computed for all animals in the pedigree file. Table 3 shows the total number of inbred animals in the whole pedigree file for each breed and their average inbreeding, as well as average inbreeding coefficients for the four reference populations defined previously. The 1970-2011 inbreeding trend is provided for each breed in appendix. The last 2 columns in Table 3 show the average annual inbreeding trend (2000-2010) and the computed effective population size (N_e). The table is sorted based on the average inbreeding trend.

Table 3 – Inbreeding statistics by breed

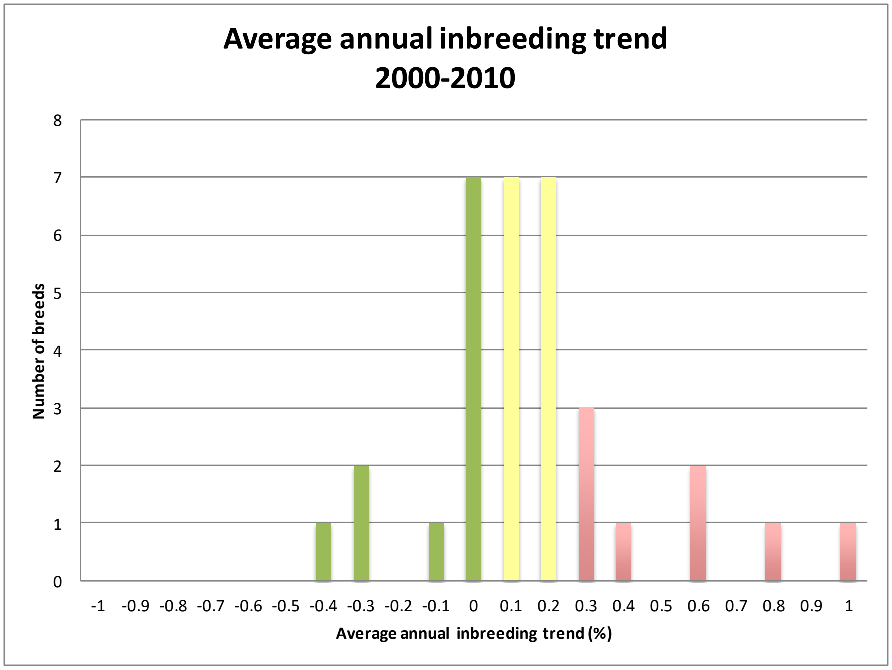
	All animals in pedigree file				Average inbreeding level (%) for different cohorts				Average annual inbreeding trend	
					Females born in				2000-2010	
breed	total	Inbred animals	%	average inbreeding for inbred animals	1994-1996	1999-2001	2004-2006	2009-2011	Trend (%/year)	N_e
COTSWOLD	1487	495	33.3	13.32	5.94	5.37	3.98	1.06	-0.45	
SHROPSHIRE	5506	2117	38.4	10.34	3.39	7.13	11.56	6.34	-0.35	
BLACKFACE	407	40	9.8	9.81			0.00	1.61	-0.32	
ICELANDIC	20710	16848	81.4	4.83	4.30	4.98	4.13	3.85	-0.11	
BORDER LEICESTER	17764	11998	67.5	7.84	6.82	7.32	8.60	7.43	-0.08	
JACOB	597	72	12.1	13.07	6.25	3.20	1.70	3.01	-0.08	
KATAHDIN	5624	960	17.1	8.47	1.86	0.99	0.95	1.03	-0.08	
ROMNEY	6161	1146	18.6	6.73	1.19	0.77	0.86	0.37	-0.07	
SHETLAND	1194	65	5.4	8.79	0.28	0.80	0.65	0.07	-0.07	
OXFORD	14585	9094	62.4	5.82	3.37	4.10	4.01	3.76	-0.06	
FINNSHEEP	7078	2456	34.7	9.81	2.26	8.86	8.45	5.81	-0.03	
BORDER CHEVIOT	6164	1642	26.6	7.02	0.77	1.47	3.21	3.78	+0.02	581
HAMPSHIRE	40510	19246	47.5	4.31	2.43	2.65	1.95	2.37	+0.04	313
DORSET	211044	118234	56.0	3.35	2.13	2.20	2.22	2.83	+0.07	166
SUFFOLK	282467	130945	46.4	3.56	2.39	2.31	2.76	3.25	+0.09	175
NORTH COUNTRY CHEVIOT	33118	21223	64.1	4.54	3.77	3.45	3.66	4.67	+0.09	142
CANADIAN ARCOTT	16537	9296	56.2	3.85	1.19	1.93	2.70	3.73	+0.10	114
CHAROLLAIS	6276	3123	49.8	3.80	0.22	1.94	2.16	2.80	+0.10	128
POLYPAY	56903	32917	57.8	3.53	1.46	2.40	2.18	3.63	+0.11	141
RIDEAU ARCOTT	160059	94222	58.9	4.23	2.18	2.07	2.36	3.30	+0.12	125
CLUN FOREST	5083	3629	71.4	7.13	4.55	6.68	7.52	7.80	+0.12	87
CORRIEDALE	8816	1924	21.8	9.18	5.01	2.81	4.95	3.13	+0.15	83
TEXEL	8826	2417	27.4	5.62	0.13	1.30	1.73	2.98	+0.15	97
SOUTHDOWN	15763	4287	27.2	6.57	1.57	1.20	1.76	2.72	+0.18	81
DORPER	9028	3834	42.5	5.51	0.55	0.87	2.24	3.82	+0.22	69
ROMANOV	49751	41727	83.9	5.48	3.66	3.91	6.00	5.66	+0.25	68
OUTAOUAIS ARCOTT	11234	4764	42.4	7.14	2.13	3.84	5.09	6.60	+0.28	47
LINCOLN	6547	4084	62.4	11.58	7.84	9.46	10.86	11.17	+0.29	45
EAST FRIESIAN DAIRY	4122	1685	40.9	5.27	0.24	2.09	4.16	4.45	+0.40	30
ROUGE DE L'OUEST	447	240	53.7	5.00				5.55	+0.51	36
ILE DE FRANCE	2180	1663	76.3	7.12	1.47	3.42	5.57	7.60	+0.54	23
BRITISH MILK SHEEP	561	348	62.0	13.33		6.25	10.18	7.85	+0.73	22
BERRICHON DU CHER	247	144	58.3	7.49				10.85	+0.98	14

N_e = Effective population size, based on inbreeding trend and generation interval

The average inbreeding coefficient for ewes born in 2009-2011 is 3.66% across breeds, and ranges from 0.07% (Shetland) to 11.17% (Lincoln). The inbreeding level is very dependent on pedigree completeness and mating strategies. Breeds with the highest inbreeding levels for the most recent cohort are: Shropshire (6.34%), Outaouais Arcott (6.60%), Border Leicester (7.43%), Ile de France (7.60%), Clun Forest (7.80%), British Milk Sheep (7.85%), Berrichon du Cher (10.85%) and Lincoln (11.17%). The lowest inbreeding levels are seen for Shetland (0.07%), Romney (0.37%), Katahdin (1.03%), Cotswold (1.06%) and Blackface (1.61%). However, for these 5 breeds except Romney, the pedigree completeness is very low suggesting that inbreeding levels are underestimated in these breeds.

More than the level, the inbreeding trend is a much better criterion to describe the trend in genetic variability and population genetic size. For most breeds, the average inbreeding level for the four cohorts shows a clear increase over time, which results from a combination of actual inbreeding accumulation and improving pedigree completeness over time. The annual inbreeding trend between 2000 and 2010 was +0.12% per year on average, ranging from -0.45% per year (Cotswold) to +0.98% per year (Berrichon du Cher). Figure 4 shows the distribution of average annual inbreeding trends.

Figure 4 – Distribution of average annual Inbreeding trends



Among the breeds studied, 11 showed a negative inbreeding trend between 2000 and 2010, which makes it impossible to compute an effective population size. Among them, 5 breeds have less than 4 generation-equivalents known, which might indicate that their inbreeding levels and trends are underestimated. Fourteen breeds have a positive, low to moderate inbreeding trend, between 0 and 0.24% per year. Finally, 8 breeds have an average annual inbreeding trend of 0.25% or higher, leading to more than 1% inbreeding increase per generation, which results in an effective population size lower than 50 (usually considered as a critical effective population size in animal populations). These breeds include two 'large' breeds (Romanov and Outaouais Arcott), one 'medium' breed (Ile de France) and five 'small' breeds (Lincoln, East Friesian Dairy, Rouge de l'Ouest, British Milk Sheep, Berrichon du Cher), based on the breed classification shown in Figure 1. The effective population size (N_e), computed only for breeds with a positive inbreeding trend, ranges from 14 to 581 for the population studied, with an average of 118.

Inbreeding levels and trends are strongly influenced by pedigree knowledge and mating strategies, which makes it difficult to compare breeds and assess genetic variability accurately, especially in small breeds where trends are usually irregular. Other approaches, based on probabilities of gene origin, can be used to corroborate results found with inbreeding. Some examples are shown in the next sections.

3.5. Probabilities of gene origin

Table 4 shows some statistics computed using the contributions of founders and ancestors of each breed to different cohorts of females. The number of effective founders (F_e) accounts for the imbalance in founder contributions and the number of effective ancestors (F_a) accounts, in addition, to bottlenecks in pedigrees related to over-used sires or dams. The number of founder genomes remaining in the population (N_g) accounts for unbalanced founder contributions, bottlenecks in pedigrees and genetic drift, which is the random loss of alleles. More detailed definitions are provided in section 2.2 of this report. Results on successive cohorts are presented to show how the genetic size of the various breeds evolved in the past years, and what would have been found if the same analysis had been performed 5 years ago, 10 years ago and 15 years ago. The analysis also helps identifying trend patterns and predicting how populations will evolve in the future years if they are still managed the same way. Table 4 is sorted based on ascending F_a for the most recent cohort.

Table 4 – Main criteria based on probabilities of gene origin for 4 different cohorts

	Effective Number of founders (F_e)				Effective Number of ancestors (F_a)				Number of founder genomes (N_g)			
	Cohort*				Cohort*				Cohort*			
Breed	**I**	**II**	**III**	**IV**	**I**	**II**	**III**	**IV**	**I**	**II**	**III**	**IV**
BERRICHON DU CHER			26	22			6	5			3	3
BLACKFACE			3	23			3	5			2	5
BRITISH MILK SHEEP		4	5	5		4	5	5		3	3	2
COTSWOLD	14	13	16	14	10	9	9	5	7	5	4	3
CORRIEDALE	80	46	17	9	43	19	5	6	25	11	4	5
JACOB	5	18	27	13	3	13	15	6	2	8	10	4
SHETLAND	53	129	80	6	50	64	32	6	28	35	19	4
OUTAOUAIS ARCOTT	44	33	16	15	40	20	9	7	32	15	6	4
FINNSHEEP	33	20	23	20	16	10	11	9	8	4	5	3
ROMNEY	84	97	92	33	51	36	36	10	39	21	22	7
ROUGE DE L'OUEST			38	37			8	10			6	5
LINCOLN				20				11	8	5	5	5
SHROPSHIRE	108	60	25	31	34	12	10	12	23	7	4	6
ILE DE FRANCE	33	49	58	50	6	8	15	15	5	6	9	9
CLUN FOREST	45	50	45	44	15	18	16	17	8	8	7	7
BORDER LEICESTER	62	59	58	61	30	24	15	18	13	10	7	7
EAST FRIESIAN DAIRY	68	75	56	38	43	46	33	24	33	28	17	11
KATAHDIN	22	57	42	28	16	50	32	25	10	41	26	21
BORDER CHEVIOT	55	69	123	38	41	21	38	26	33	16	21	18
CHAROLLAIS	71	94	89	70	40	51	40	28	29	36	26	16
DORPER	34	180	138	90	12	60	44	30	8	42	27	16
ROMANOV	72	67	57	64	35	37	33	30	18	16	11	9
OXFORD	72	80	54	59	45	42	26	32	27	24	16	17
CANADIAN ARCOTT	57	51	60	56	51	41	42	37	36	24	22	17
RIDEAU ARCOTT	56	53	46	43	51	48	40	37	42	35	25	20
NORTH COUNTRY CHEVIOT	100	114	114	118	50	54	41	38	24	25	19	17
POLYPAY	55	69	107	87	43	45	51	38	29	28	29	18
SOUTHDOWN	436	72	97	76	82	59	58	49	65	41	35	28
ICELANDIC	29	27	39	58	25	25	35	50	15	13	19	25
HAMPSHIRE	171	164	109	131	97	91	61	55	59	50	37	28
TEXEL	52	87	117	87	50	79	89	56	40	58	58	35
SUFFOLK	10	276	192	178	274	202	149	134	168	120	85	66
DORSET	455	457	375	384	253	218	171	180	151	115	88	83

Cohorts: I=females born in 1994-1996; II= females born in 1999-2001; III= females born in 2004-2006; IV= females born in 2009-2011

Sixteen breeds have less than 20 effective ancestors for their most recent cohort, including 10 'small' breeds and 6 'medium' breeds (British Milk Sheep, Outaouais Arcott, Finnsheep, Ile de France, Clun Forest and Border Leicester). Some medium breeds seem to perform better than others in terms of genetic variability based on Fa, such as the Oxford and Southdown breeds, which seem to have a larger genetic base than some of the other 'large' breeds. The 2 largest breeds based on Fa (Suffolk, Dorset) seem to be much more variable than other large breeds and are most likely the ones with broader access to foreign genes. There are no clear guidelines regarding the minimum number of effective ancestors and founder genomes. FAO has issued guidelines for the effective population size (Ne) based on inbreeding trends, which should be at least 50 (FAO, 2000). In several studies, thumb numbers of 20 and 10 are often used as recommended minima for Fa and Ng respectively.

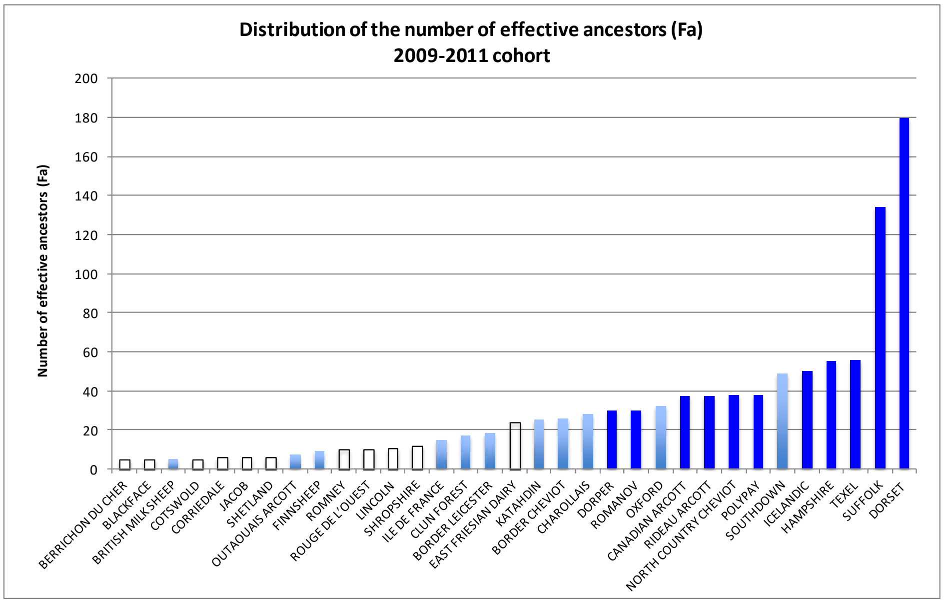


Figure 5 – Distribution of F_a for the most recent cohort (females born in 2009-2011).

The bar colour indicates the actual size of the reference population (white=small population (<200), light blue=medium size population (200 to 500), dark blue=large population (>500))

The number of founder genomes (N_g) was very consistent with F_a in most cases. For the 2009-2011 cohort, N_g ranges from 2 to 83, with an average of 16. The number of founder genomes is 1.5 to 2 times smaller than the number of effective ancestors for most breeds, but it is even smaller in Clun Forest, Finnsheep and Romanov breeds, showing that these breeds were affected by genetic drift over the past years, leading to the random loss of genetic diversity, most probably due to the loss of families or lines over this period. The trend pattern for F_a and N_g on the successive cohorts is similar for most breeds, showing a decrease over 15 years, except for the Icelandic, Ile de France, Jacob and Katahdin breeds. Some strong relative decreases have occurred even in breeds for which negative inbreeding trends were observed in the last 10 years (e.g. Shetland, Shropshire, Romney). The highest drop in F_a between the first and fourth cohorts were seen in Shetland (-89%), Corriedale (-86%), Outaouais Arcott (-83%) and Romney (-80%) breeds. Even in the two largest breeds based on F_a (Suffolk and Dorset), both F_a and N_g decreased by 40 to 60% in the last 15 years.

Table 5 shows the cumulative contributions of the most influential ancestors to reference populations by breed. It shows a summary of statistics for the cohort of females born in 2009-2011, as well as the contribution of the most influential ancestor to their gene pool, and the number of ancestors explaining 10, 25, 50, 90 and 99% of the current gene pool. The table is ranked based on the number of effective ancestors (F_a).

Table 5 – Cumulative contributions of the most influential ancestors to the reference population (females born in 2009-2011) in each breed

					Ancestors explaining x % of gene pool					
breed	**N**	**F**	**F_a**	**Contribution 1st ancestor**	**10%**	**25%**	**50%**	**75%**	**90%**	**99%**
BERRICHON DU CHER	25	79	5	27.4	1	1	3	4	6	9
BLACKFACE	66	40	5	41.8	1	1	2	7	13	22
BRITISH MILK SHEEP	216	9	5	32.5	1	1	2	4	6	8
COTSWOLD	80	41	5	33.3	1	1	2	4	7	10
CORRIEDALE	69	192	6	29.6	1	1	3	5	8	17
JACOB	26	31	6	35.4	1	1	3	6	10	12
OUTAOUAIS ARCOTT	360	65	7	26.2	1	1	3	6	10	32
SHETLAND	37	31	7	31.3	1	1	2	4	7	9
FINNSHEEP	501	106	9	22.0	1	2	3	7	14	29
ROMNEY	121	189	10	27.4	1	1	6	14	22	30
ROUGE DE OUEST	72	50	10	15.4	1	2	4	7	11	14
LINCOLN	66	411	11	20.2	1	2	4	11	22	41
SHROPSHIRE	130	158	12	17.5	1	2	5	11	23	38
ILE DE FRANCE	362	97	15	13.5	1	2	6	11	16	23
CLUN FOREST	356	124	17	12.6	1	3	7	13	20	37
BORDER LEICESTER	288	409	18	14.4	1	2	7	19	34	77
EAST FRIESIAN DAIRY	126	169	24	9.7	2	3	9	19	30	49
KATAHDIN	476	176	25	12.7	1	3	10	37	89	158
BORDER CHEVIOT	210	807	26	9.3	2	4	10	21	38	70
CHAROLLAIS	478	1238	28	7.6	2	4	10	22	40	72
OXFORD	238	336	32	10.9	1	4	13	29	54	99
DORPER	1799	619	30	9.9	2	3	11	39	97	282
ROMANOV	5891	599	30	7.8	2	4	11	24	44	144
CANADIAN ARCOTT	1304	282	37	8.3	2	5	14	38	76	168
RIDEAU ARCOTT	17514	1043	37	7.2	2	5	12	34	74	376
NORTH COUNTRY CHEVIOT	1517	1882	38	9.3	2	5	14	40	91	252
POLYPAY	3528	634	38	7.3	2	5	14	35	68	230
SOUTHDOWN	360	599	49	6.9	2	6	20	55	111	193
ICELANDIC	2638	544	50	6.7	2	6	21	50	94	190
HAMPSHIRE	1286	1943	55	7.2	2	7	20	58	125	298
TEXEL	904	807	56	6.7	2	7	21	57	115	238
SUFFOLK	5306	4238	134	3.2	5	15	49	142	323	>1000
DORSET	7397	4270	180	2.0	6	20	68	180	397	>1000

N=size of the reference population; F=number of founders; F_a=number of effective ancestors

The most influential ancestor explains more than 10% of the current gene pool for 18 breeds, and more than 20% for 11 breeds showing that many breeds in this study have major bottlenecks in their pedigrees. The number of ancestors explaining half of the gene pool ranges from 2 to 68, with an average of 12, while the number of ancestors explaining 99% of the gene pool ranges from 8 to over 1000. These findings show that few ancestors have a large contribution while many ancestors have a very small contribution, even in most of the large populations. In individual factsheets provided in appendix for each breed, the list of the 10 most influential ancestors is provided, and often accounts for a good part of the genetic diversity. One of the key challenges is to keep ancestor contributions as balanced as possible in order to avoid bottlenecks in pedigrees and potential accumulation of inbreeding in the longer term. This is especially challenging in selected populations, where elite animals are often overused and have many progeny kept for breeding.

4. Discussion

This study included many breeds, for which many criteria were analyzed. If we look only at the main criteria in each section to summarize the situation in terms of genetic variability, a good portrait can be drawn with pedigree completeness, inbreeding trends, effective numbers of ancestors and number of founder genomes. Table 6 provides an overview of these criteria for the 33 breeds analyzed. Numbers in red are outside of what could be potential guidelines for genetic variability indicators (less than 4 generation equivalents known, more than 0.25% inbreeding per year in the past 10 years, less than 20 effective ancestors or 10 founder genomes for the most recent female cohort (2009-2011)).

Table 6 – Summary table for pedigree completeness, inbreeding trends and probabilities of gene origin

Breed	Females born in 2009-2011	Generation equivalents	Average annual inbreeding trend 2000-2010 (%/year)	Effective number of ancestors (F_a)	Number of founder genomes (N_g)
BERRICHON DU CHER	25	5.77	+0.98	5	3
BLACKFACE	66	2.27	-0.32	5	5
BORDER CHEVIOT	210	3.85	+0.02	26	18
BORDER LEICESTER	288	10.09	-0.08	18	7
BRITISH MILK SHEEP	216	2.01	+0.73	5	2
CANADIAN ARCOTT	1304	5.78	+0.10	37	17
CHAROLLAIS	478	5.81	+0.10	28	16
CLUN FOREST	356	8.15	+0.12	17	7
CORRIEDALE	69	3.18	+0.15	6	5
COTSWOLD	80	1.32	-0.45	5	3
DORPER	1799	5.39	+0.22	30	16
DORSET	7397	6.73	+0.07	180	83
EAST FRIESIAN DAIRY	126	4.93	+0.40	24	11
FINNSHEEP	501	4.91	-0.03	9	3
HAMPSHIRE	1286	5.97	+0.04	55	28
ICELANDIC	2638	7.32	-0.11	50	25
ILE DE FRANCE	362	6.47	+0.54	15	9
JACOB	26	1.62	-0.08	6	4
KATAHDIN	476	1.86	-0.08	25	21
LINCOLN	66	4.85	+0.29	11	5
NORTH COUNTRY CHEVIOT	1517	9.28	+0.09	38	17
OUTAOUAIS ARCOTT	360	9.28	+0.28	7	4
OXFORD	238	5.56	-0.06	32	17
POLYPAY	3528	5.24	+0.11	38	18
RIDEAU ARCOTT	17514	6.77	+0.12	37	20
ROMANOV	5891	9.52	+0.25	30	9
ROMNEY	121	5.58	-0.07	10	7
ROUGE DE L'OUEST	72	4.59	+0.51	10	5
SHETLAND	37	1.47	-0.07	6	4
SHROPSHIRE	130	6.82	-0.35	12	6
SOUTHDOWN	360	3.71	+0.18	49	28
SUFFOLK	5306	6.82	+0.09	134	66
TEXEL	904	3.87	+0.15	56	35
Average	**1627**	**5.27**	**+0.12%/year**	**31**	**16**

From the summary results shown in Table 6, there are 8 breeds with high inbreeding trends and 17 with a low number of effective ancestors and/or founder genomes. Seven breeds have an issue for both criteria at the same time, including 3 small breeds (Berrichon du Cher, Lincoln, Rouge de l'Ouest), 3 medium breeds (British Milk Sheep, Ile de France, Outaouais Arcott) and one large breed (Romanov). Several small breeds with poor pedigree completeness did not show any inbreeding problem, but appear to have a very low genetic size based on ancestor contributions (Blackface, Corriedale, Cotswold, Jacob, Shetland). The Romanov breed has a special pattern, with a high inbreeding trend and low N_g, even though F_a is acceptable (30), which shows a larger impact of genetic drift in this population, most likely due to the drastic reduction in population size between 2002 and 2005.

Overall, the situation is very variable in terms of actual population size, pedigree completeness, inbreeding trends and probabilities of gene origin. On average, pedigree completeness is moderately good (5.24 complete generation equivalents) but it is quite poor for approximately one third of the breeds in this study, mainly small breeds but also larger ones using foreign genes (Texel, Border Cheviot, Katahdin, Southdown). In a recent, similar study carried out by the French *Institut de l'Elevage* on 35 sheep breeds (Danchin-Burge, 2010), the pedigree completeness was slightly higher, with 5.96 equivalent generations on average. They also reported an average number of effective ancestors of 66, which is more than twice as high as what was found in this study for Canadian sheep breeds. However, the French study included much larger populations, with 7,274 animals on average in the reference population, ranging from 96 to 33200.

Compared to other species, such as pigs and dairy cattle, in which selection has been very intense over the past decades and where artificial insemination has been widely used, genetic variability indicators look much better in Canadian sheep populations. For instance, the average number of effective ancestors has been reported to be between 20 and 30 in most French dairy cattle breeds (Boichard *et al.*, 1997). Recent results in Canadian dairy cattle breeds show inbreeding levels between 5.98 and 6.61% for heifers born in 2012, and annual inbreeding trends ranging from -0.09 to +0.22 % per year between 2000 and 2010 (CDN, 2013).

Even though the various breeds studied in this project are very different and each one requires a specific analysis, it is possible to group the different breeds studied into clusters based on some of the indicators presented previously. Table 7 shows the proposed clustering, based on pedigree completeness, recent inbreeding trends and effective population size based on probabilities of gene origin. Breeds in the same cluster seem to behave the same way, and share some potential recommendations for future management of genetic variability. Almost all possible scenarios for population structure were found in this study, reflecting the history of the breed, and the current strategy (if any) to preserve diversity. In some cases, there might be issues with the population size, which don't necessarily lead to an increase in inbreeding.

Based on results shown in Table 4 about trends in genetic population size (based on ancestor contributions), it is critical to realize that for most breeds, there is a clear trend showing an erosion of genetic diversity, more or less fast depending on the breed. Therefore, it is critical to implement some measures aiming at slowing down the process, even in breeds that don't seem to be in a critical situation today. The measures might differ depending on the population size, the number of farms involved and potential access to foreign genes. They might require some collective efforts in order to optimize the use of genetic resources available. They include for instance:

Within farm initiatives:

- Monitoring inbreeding and other genetic diversity indicators on a regular basis
- Using tools to manage inbreeding and long-term genetic variability, such as optimized mating plans
- Using more and younger breeding animals whenever possible
- Preserving as many families as possible
- Avoiding overuse of elite animals
- Using genes from other herds or provinces (or countries when possible), but always check the relationship with the herd
- Setting objectives, depending on herd size, such as a maximum annual increase for inbreeding, maximum number of litters produced / ram, maximum number of sons/daughters kept for breeding / ram

Within breed initiatives:

- Monitoring inbreeding and other genetic diversity indicators on a regular basis
- Defining the best strategies for preserving diversity: share genetics, develop A.I. programs, freeze semen/embryos
- Setting objectives, depending on breed size, such as a maximum annual increase for inbreeding

Table 7 – Clustering of Canadian sheep breeds based on the main genetic variability indicators

Pedigree completeness	Inbreeding trend	F_a and N_g	Breeds	Comments
Good	Low	Acceptable	Canadian Arcott, Charollais, Dorper, Dorset, Hamsphire, Icelandic, North Country Cheviot, Oxford, Polypay, Rideau Arcott, Suffolk	Breeds with a large base Good attention given to avoid inbreeding
	Low	Low	Border Leicester, Clun Forest, Finnsheep, Romney, Shropshire	Breeds with a smaller base Good attention given to avoid inbreeding Need for longer term management tools
	High	Acceptable	East Friesian Dairy	Breeds with a large base Need for tools to avoid inbreeding
	High	Low	Berrichon du Cher, Ile de France, Lincoln, Outaouais Arcott, Romanov, Rouge de l'Ouest	Breeds with a small genetic size and inbreeding issues Need for tools to avoid inbreeding and manage longer term variability
Poor	Low	Acceptable	Border Cheviot, Katahdin, Southdown, Texel	No problem identified but the pedigrees are too incomplete to known if results found are real
	Low	Low	Corriedale, Cotswold, Blackface, Jacob, Shetland	Inbreeding level and trend were most likely underestimated due to pedigree incompleteness
	High	Acceptable		
	High	Low	British Milk sheep	Breeds with a small genetic size and inbreeding issues Need for tools to avoid inbreeding and manage longer term variability The situation is probably even worse than described, due to pedigree incompleteness

5. Conclusions and Perspectives

Pedigree analysis of Canadian sheep breeds showed a broad range of situations in terms of population size and pedigree completeness. Thirty-three breeds with animals born in recent years were compared for common genetic variability indicators such as inbreeding rates, inbreeding trends and probabilities of gene origin. For some breeds, very limited pedigree information made it difficult to provide an accurate picture with regards to genetic variability. More attention should be paid to breeds such as Berrichon du Cher, Ile de France, Lincoln, Outaouais Arcott, Rouge de l'Ouest and Romanov, all of which are currently dealing with both inbreeding and genetic size issues. Observed trends in effective numbers of ancestors in the last 15 years showed a clear trend for erosion in genetic variability in most breeds especially in selected populations, which is not surprising as this is a typical trend when genetic improvement is the main goal pursued. Canadian sheep populations are also going through challenging times to maintain diversity due to scrapie eradication programs, which tend to create even more bottlenecks than in the past. Individual and collective measures are necessary to monitor and slow down the erosion of genetic diversity while maintaining with genetic progress.

This study aimed at giving a portrait of the current situation and recent trends, which is always useful to identify potential problems and predict what future trends would be if nothing was changed with regards to population management. There has actually been a growing interest in genetic variability in the past years, leading to the development of new tools for Canadian sheep breeders, such as the computation of inbreeding coefficients now displayed in GenOvis and on the CLRC website, as well as new tools to visualize repeated ancestors in pedigrees. More recently, mating plans using minimum co-ancestry mating and optimum founder contribution approaches have been implemented. These tools can be used by individual herds and have a relatively quick effect at the breed level. It is also important to look at collective approaches to optimize the preservation of genetic variability in the longer term.

This study was carried out on animals registered and/or existing in the GenOvis program. Actual purebred populations are most likely larger, but only a portion of them is registered. Increasing the size of registered populations, and/or the numbers of animals on the genetic evaluation program, would increase the size of the populations with a recognized pedigree record. This is usually a good way to find out about existing new lines and families. The access to foreign genes is often seen as the key solution to restore genetic variability, and it might be the only solution for some of the small breeds in this study, but it is important to first review the existing diversity within Canadian breeds. Foreign genetics, especially from new lines, has to be evaluated properly before being widespread, in order not to compromise many years of domestic selection.

This study should be repeated on a regular basis (at least every 3-4 years) to monitor trends and potential effects of new management practices. It would also be interesting to validate these results with different information sources, such as genomic information. With DNA SNP panels now available, which allow for genotyping of up to 700,000 individual markers across the sheep genome, it is now possible to determine 'true' genetic diversity. Pedigree analyses are based on probabilities that sometimes underestimate, sometimes overestimate the actual situation. Molecular approaches have the huge advantage to be completely independent from pedigree quality. They will provide new ways to assess and manage genetic variability.

The timing is perfect for Canadian sheep breeders to work together on managing genetic variability in their populations. Having many breeds is an asset but it is critical to also maintain within breed diversity, especially nowadays when selection and scrapie eradication programs tend to decrease variability at a very rapid pace. Yet, most breeds in this study still show adequate variability based on pedigree indicators, but recent trends show that actions need to be taken now to preserve it. In selected breeds, a compromise must be found between short-term genetic gains and long-term genetic variability.

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Appendices

Factsheets by breed