Irish sheep breeding
Current status and future plans

February 2014

Noirin McHugh[1], Donagh Berry[1], Sinead McParland[1], Eamon Wall[2] and Thierry Pabiou[2]

[1]Animal and Bioscience Research Department, Animal and Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork
[2]Sheep Ireland, Bandon, Co. Cork

Table of Contents

Executive summary ii
Section 1 Current State of Play 1
  1.1 Numbers recording 1
  1.2 Pedigree analysis and current inbreeding levels 17
  1.3 Genetic linkage 20
  1.4 Overview of current Sheep Value Index 22
  1.5 Current breeding programme 28
  1.6 DNA parentage summary to date 29
  1.7 Validation of index 30
  1.8 Genetic gain to date 31
Section 2 Future priorities 33
  2.1 Phenotypes 33
  2.2 Pedigree 38
  2.3 Linkage 41
  2.4 Genomic selection 42
Section 3 Breeding Programmes 47
  3.1 Improving accuracy 48
Section 4 Breeding objectives 50
  4.1 Bio-economic model 50
  4.2 New traits 51
Section 5 Genetic evaluations 52
  5.1 Developing superior statistical models 52
  5.2 Re-estimation of genetic parameters 53
  5.3 Across breed evaluations 54
  5.4 Validation experiments 55
Section 6 Knowledge exchange 57
  6.1 Current deficits in the system 57
  6.2 Reports 58
References 60

Executive summary

Sheep Ireland was established in 2008 to implement a dynamic genetic improvement breeding programme for the Irish sheep industry and increase flock productivity and profitability. Here we review progress to date and suggest short-medium and long term priorities.

The aim of this document is to review the current status of the breeding programme for sheep and highlight what components of the Irish breeding programme could be enhanced. This document summaries the progress to date, current gaps in knowledge, future plans, and recommendations for Sheep Ireland.

A summary of the main recommendations are outlined below:

- ***Data capture:***
  - Farmers must be encouraged to record **all** traits across **all** lambs **accurately**
- ***Pedigree information:***
  - Flockbooks should be encouraged to enter all back pedigree information to allow for the publication of accurate inbreeding coefficients
- ***Genetic linkage:***
  - The importance of genetic linkage for accuracy levels must be highlighted
  - Flocks with poor linkage should be encouraged to enter rams into the CPT
  - New linkage algorithms must be researched
- ***Breeding Objectives:***
  - Economically important traits will be added to the index once sufficient data is available
- ***Breeding Programme:***
  - Commercial data remains vitally important to the success of the genetic evaluations
  - More commercial farmers must be encourage to record data
- ***Parentage***
  - Further research into DNA options for parentage must be undertaken
- ***Index validation***

  - Validation of the index must be undertaken regularly to ensure genetic evaluations are reflective of performance on the ground
- ***Phenotypes***
  - Research must continue to focus on the identification of pertinent new traits that should be included in the genetic evaluations
  - A data quality index should be developed for sheep
- ***Genomic selection***
  - *A* DNA storage bank must be created for sheep
  - DNA should be collected from rams with large numbers of recorded progeny
  - Genotyping of animals will commence once the costs are reduced and/or a large training population has been established
- ***Breeding Programmes***
  - Research must be undertaken to ensure that the current breeding programme is yielding the greatest genetic gain achievable for the industry
- ***Genetic evaluations***
  - Re-estimation of genetic parameters must be undertaken
  - Superior statistical models will be developed for the national genetic evaluations as soon as possible
- ***Across breed evaluations***
  - To facilitate across breed evaluations accurate data must continue to be recorded on crossbred flocks
  - The CPT and MALP play a vital role in the generation of this data
- ***Knowledge exchange***
  - Clear, precise, easy to use online reports, combining genetic and phenotypic information, must be made available as soon as possible
  - Industry consultation meeting must be organised on a regular basis to inform all stakeholders on the latest research finding and changes to the genetic evaluations

Section 1 Current State of Play

1.1 Numbers recording

Since the formation of Sheep Ireland in 2008 the focus has remained on the collation of high quality data for use in the national genetic evaluations and management decisions for farmers. Data collected comes from two main sources: pedigree and commercial flocks, and covers a range of traits including growth, lambing and reproduction traits.

1.1.1 Weight recordings

Live-weights recorded on lambs fall into four main categories: birth, 40 day weights, weaning weight and scanning weight.

For birth weights, the average weight recorded in 2013 for the pedigree and commercial flocks was 4.54 kg and 4.36 kg, respectively, with a range of 1 to 8 kg recorded across both data sources (Table 1). The number of flocks recording birth weight has increasing dramatically (especially for the pedigree flocks) since the formation of Sheep Ireland. In 2013 a total of 266 (average flock size 74) and 27 (average flock size 359) pedigree and commercial flocks, respectively, recorded birth weights. The number of sires with progeny birth weight measurements has also increased. In 2013, the average number of progeny per sire was 19 (884 sires) and 43 (179 sires) for the pedigree and commercial flocks, respectively. In 2013, the total number of useable records in the genetic evaluations (i.e. where sire of lamb is known and at least four other lambs are measured on farm) was 16,778 for the pedigree flocks and 7,657 for the commercial flocks.

Across all years, the average 40 day weight recorded for the pedigree and commercial flocks was 19.64 kg and 18.17 kg, respectively (Table 1). The average age of lambs at recording was 46 and 48 days for the pedigree and commercial, respectively. In 2013 approximately 58% of pedigree and commercial lambs had both a birth weight and 40 day weight recorded.

Table 1 Total number of records (n), average live-weight in kg (µ), mean age at weighing, number of flocks, number of records with sire known and number of records used in genetic evaluations for birth and 40 day weight across years and within pedigree (ped) and commercial (com) flocks.

Weight Trait	Year	Data source	n	µ	Age	No. of flocks	Sire known	Used in Genetic
Birth	1980 to 2008	Ped	100,297	4.58	0	398	99,129	98,884
	2009	Ped	5,418	4.46	0	95	5,296	5,291
	2010	Ped	5,495	4.40	0	108	5,367	5,358
	2011	Ped	7,605	4.31	0	104	6,756	6,731
	2012	Ped	9,564	4.50	0	160	9,319	9,272
	2013	Ped	19,589	4.54	0	266	16,853	16,778
	2009	Com	1,643	4.21	0	3	1,643	0
	2010	Com	4,710	4.61	0	9	2,592	2,590
	2011	Com	4,741	4.66	0	11	3,005	3,003
	2012	Com	7,327	4.57	0	15	6,839	6,838
	2013	Com	9,701	4.36	0	27	7,658	7,657
40 day	1980 to 2008	Ped	6,644	19.00	51	47	6,665	6,615
	2009	Ped	2,249	19.96	47	63	2,247	2,231
	2010	Ped	2,387	19.02	46	57	2,277	2,255
	2011	Ped	3,320	19.10	47	69	3,162	3,106
	2012	Ped	3,796	19.89	48	88	3,710	3,668
	2013	Ped	11,372	18.86	46	212	9,346	9,245
	2009	Com	7,308	19.98	48	25	5,243	5,227
	2010	Com	12,233	16.75	45	30	7,978	7,978
	2011	Com	8,003	17.75	46	27	5,627	5,627
	2012	Com	8,600	18.60	49	26	7,350	7,350
	2013	Com	6,217	17.79	48	22	5,009	5,009

In 2013 the average weaning weight was 33 kg and 29 kg for the pedigree and commercial flocks, respectively. The proportion of recorded weaning weight records that were used in the genetic evaluations in 2013 was 79% and 86% for the pedigree and commercial flocks, respectively. The proportion of pedigree lambs with both a birth weight and weaning weights in 2013 was 52%; for commercial lambs 59% had a recorded birth and weaning weight. The average age at recorded weaning weight was 98 days for pedigree and 96 days for commercial flocks (Table 1).

The average weight at scanning was 48 kg and 38 kg for the pedigree and commercial flocks, respectively. The average age at scanning was similar for both the pedigree (145 d) and commercial (139 d) flocks. The proportion of lambs with scanning weights recorded was 22% and 16% for the pedigree and commercial flocks, respectively (Table 1). The number of pedigree flocks recording scanning weight in 2013 was 155 (up from 86 in 2012) with an average flock size of 28 lambs; 7 commercial flocks were recording scanning weight in 2013 with an average flock size of 226 lambs.

Table 2 Total number of records (n), average live-weight in kg (μ), mean age at weighing, number of flocks, number of records with sire known and number of records used in genetic evaluations (GE) for weaning and scan weight across years and within pedigree (ped) and commercial (com) flocks.

Weight Trait	**Year**	**Data source**	**n**	**μ**	**Age**	**No. of flocks**	**Sire known**	**Used in GE**
Weaning	1980 to 2008	Ped	1,824	26.5	81	38	1,826	1,754
	2009	Ped	1,184	34.47	92	43	1,181	1,159
	2010	Ped	1,658	32.39	94	58	1,585	1,545
	2011	Ped	2,835	33.01	96	65	2,618	2,586
	2012	Ped	3,070	33.89	95	79	3,016	2,984
	2013	Ped	10,276	32.78	98	206	8,188	8,130
	2009	Com	9,120	30.14	103	24	6,740	6,738
	2010	Com	9,609	29.83	102	30	5,860	5,860
	2011	Com	6,362	29.89	100	26	3,892	3,892
	2012	Com	8,073	28.63	104	25	7,162	7,162
	2013	Com	5,727	29.04	96	17	4,935	4,933
Scan	1980 to 2008	Ped	54,012	42.4	115	312	53,948	53,886
	2009	Ped	3,120	45.3	131	73	3,048	3,033
	2010	Ped	2,333	45.11	125	60	2,272	2,247
	2011	Ped	1,809	48.75	136	46	1,773	1,750
	2012	Ped	2,919	50.02	150	86	2,906	2,887
	2013	Ped	4,345	47.96	145	155	4,332	4,300
	2009	Com	596	33.98	144	1	441	441
	2010	Com	2,418	32.77	110	6	2,023	2,023
	2011	Com	2,237	32.69	103	7	2,178	2,176
	2012	Com	1,340	37.55	139	7	1,263	1,260
	2013	Com	1,584	37.71	139	7	1,528	1,528

1.1.2 Scanning data

Along with scan weight, two traits: ultrasonic muscle and fat depth are recorded at scanning. Across both data sources (i.e. pedigree and commercial), the majority of lambs were recorded for both ultrasonic muscle and fat depth. The average age of scanning was 146 days for the pedigree lambs and 139 days for commercial lambs (Table 2). The average muscle depth recorded at scanning was 32 mm and 28 mm for the pedigree and commercial flocks, respectively. On average, larger fat depths were recorded in the pedigree lambs (0.72 mm) compared to the commercial lambs (0.50 mm). The average number of pedigree flocks recording scan data has increased from 73 flocks in 2009 to 157 flocks in 2013. In 2013 the average pedigree flock size was 29 lambs. For the commercial flocks, 7 flocks were recording scanning data in 2013; the average flock size was 198 animals. The proportion of recorded scanning records used in the genetic evaluations in 2013 was 99% and 96% for the pedigree and commercial flocks, respectively.

Table 3 Total number of records (n), average scan depth in mm (μ), mean age at scanning, number of flocks, number of records with sire known and number of records used in genetic evaluations for ultrasonic muscle and fat depth across years and within pedigree (ped) and commercial (com) flocks.

Scanning trait	**Year**	**Data source**	**n**	**μ**	**Age**	**No. of flocks**	**Sire known**	**Used in GE**
Muscle	1980 to 2008	Ped	53,989	30.6	115	311	53,925	53,846
	2009	Ped	3,144	30.5	131	73	3,071	3,056
	2010	Ped	2,373	30.43	125	62	2,311	2,285
	2011	Ped	1,885	31.68	136	46	1,849	1,823
	2012	Ped	3,216	31.49	151	87	3,202	3,185
	2013	Ped	4,610	31.95	146	157	4,596	4,569
	2009	Com	577	23.89	144	1	426	426
	2010	Com	2,456	25.56	110	6	2,054	2,054
	2011	Com	2,260	26.18	103	6	2,195	2,193
	2012	Com	1,350	25.69	139	7	1,272	1,269
	2013	Com	1,582	28.36	139	7	1,525	1,525
Fat	1980 to 2008	Ped	53,874	0.98	115	312	53,814	53,735
	2009	Ped	3,173	0.74	131	73	3,100	3,085
	2010	Ped	2,373	0.86	125	60	2,312	2,286
	2011	Ped	1,903	1.06	137	46	1,867	1,838
	2012	Ped	3,367	0.63	152	87	3,353	3,336
	2013	Ped	4,771	0.72	147	157	4,757	4,725
	2009	Com	606	0.52	144	1	450	450
	2010	Com	2,524	0.46	110	6	2,110	2,110
	2011	Com	2,293	0.45	102	7	2,225	2,223
	2012	Com	1,331	0.41	139	7	1,255	1,252
	2013	Com	1,585	0.50	139	7	1,528	1,528

1.1.3 Lambing data

Traits recorded at lambing include: birth weight (described previously), lambing ease scores and lamb survival. Lambing ease is scored on a scale of 1 to 4 (1 = no assistance/unobserved; 2 = slight assistance; 3 = severe assistance; 4 = veterinary assistance) by the farmer. Lamb survival is defined as: whether a lamb survived from birth to 40 day weights in commercial flocks or whether a lamb was dead or alive at birth in pedigree flocks.

In 2013, a higher proportion of pedigree lambs had a lambing ease score assigned at birth compared to pedigree lambs that had a recorded birth weight; in the commercial flocks 99% of lambs had a recorded lambing ease score and a birth weight. Across all years, the average lambing ease score for the pedigree flock was 1.46 (i.e. no or slight assistance) and 1.58 (i.e. slight assistance) for the commercial flock (Table 3). In 2013, a total 296 pedigree flocks and 21 commercial flocks were assigning lambing ease scores to lambs. The average lamb survival rate recorded across years was 91% and 95% for the pedigree and commercial flocks, respectively. In 2013, lamb survival data was available from 303 pedigree flocks and 22 commercial flocks (Table 4).

For a record to be retained for the genetic evaluation a further edit was added to the lambing data to ensure that some variation existed within the two traits (i.e. to ensure all lambs were not assigned the same score within one farm). This edit led to a reduction in the proportion of data available for use in the genetic evaluations. In 2013, data on 62% of pedigree lambs and 34% of commercial lambs scored for lambing ease were in used in the genetic evaluations. For lamb survival the proportion of data included in the 2013 national genetic evaluations was 58% and 56% for the pedigree and commercial flocks, respectively.

Table 4 Total number of records (n), average value recorded for trait (µ), number of flocks, number of records with sire known and number of records used in genetic evaluations for lambing ease scores (1 to 4) and lamb survival across years and within pedigree (ped) and commercial (com) flocks.

Lambing Trait	Year	Data source	n	µ	No. of flocks	Sire known	Genetic evaluation
Ease	2009	Ped	3,199	1.67	69	2,855	2,723
	2010	Ped	4,306	1.47	115	3,782	3,235
	2011	Ped	6,443	1.37	126	4,952	3,851
	2012	Ped	7,615	1.45	193	6,624	5,607
	2013	Ped	20,324	1.35	296	12,587	12,576
	2009	Com	84	2.44	7	1	0
	2010	Com	3,683	1.53	24	2,587	2,586
	2011	Com	3,322	1.43	16	2,833	2,809
	2012	Com	7,608	1.28	22	6,851	3,924
	2013	Com	9,656	1.21	21	7,644	3,257
Survival	1980 to 2008	Ped	85,848	94%	361	84,892	60,976
	2009	Ped	4,629	92%	91	4,533	2,802
	2010	Ped	5,105	91%	114	4,864	3,266
	2011	Ped	6,110	89%	115	5,725	4,204
	2012	Ped	7,832	91%	170	7,679	5,371
	2013	Ped	18,871	0.92	303	10,947	10,943
	2009	Com	12,123	100%	26	7,789	0
	2010	Com	14,129	97%	32	8,798	2,710
	2011	Com	11,211	90%	28	6,631	3,699
	2012	Com	11,751	95%	26	10,072	6,492
	2013	Com	8,783	0.95	22	6,887	4,914

1.1.4 Number of lambs born (NLB)

The average NLB per ewe, across all years, was 1.53 and 1.59 for the pedigree and commercial ewes, respectively. The number of ewes with NLB data has increased slightly since the formation of Sheep Ireland in 2008, across both the commercial and pedigree flocks (Table 5). In 2013, 456 and 23 pedigree and commercial flocks, respectively had NLB data. The increase in the number of pedigree flocks recording NLB compared to other traits is due to the availability of the back pedigree on the entire flockbook for the Texel, Belclare and Galway breeds (i.e. information available on Lamb Plus and non recording flocks). The total proportion of available records that were used in the 2013 genetic evaluations was 61% for the pedigree data. For the commercial data, only 34% of the recorded NLB data was available for use in the 2013 genetic evaluations due mainly to ewes having unknown sires; however when compared to the same figure in 2009 (19%) the number of commercial ewes with recorded sires is increasing steadily.

Table 5 Total number of records (n), average NLB (number of lambs born; μ), number of flocks, number of records with sire known and number of records used in genetic evaluations for NLB across years and within pedigree (ped) and commercial (com) flocks.

Trait	**Year**	**Data source**	**n**	**μ**	**No. of flocks**	**Sire known**	**Genetic evaluation**
NLB	1980 to 2008	Ped	105,458	1.48	1,301	56,376	51,411
	2009	Ped	5,969	1.47	378	5,081	4,666
	2010	Ped	6,339	1.47	404	5,259	4,919
	2011	Ped	7,273	1.53	380	6,054	5,731
	2012	Ped	8,374	1.63	358	7,182	6,971
	2013	Ped	11,228	1.54	456	7,052	6,833
	2009	Com	4,455	1.64	25	882	874
	2010	Com	6,587	1.61	31	931	921
	2011	Com	5,032	1.53	27	2,195	2,188
	2012	Com	7,147	1.61	27	2,676	2,671
	2013	Com	6,336	1.55	23	2,139	2,138

1.1.5 Pedigree information by breed

Across all traits and breeds a substantial increase in the number of records was recorded mainly due to greater awareness among commercial farmers of the €uro-star genetic evaluations due to the STAP (Sheep Technology Adoption Programme).

Weight data. Across all five major breeds (Belclare, Charollais, Texel, Suffolk and Vendeen) the numbers of animals with birth weight recorded has increased from 2009 to 2013; proportionally the Charollais breed has seen the largest increase (253 lambs with birth weights in 2010 to 2,316 lambs in 2012; Figure 1a). In 2013, the average birth weight recorded across breed varied from 4.15 kg (Belclare) to 5.34 kg (Suffolk). In 2013, the Texel breed had the highest number of flocks (114) recording birth weight. Similarly, for 40 day weights, the Charollais breed has seen a dramatic increase in the number of lambs with records (45 in 2009 versus 1,394 in 2013; Figure 1b). The proportion of animals with both a birth and 40 day weight recorded varies from 46% for the Texel breed to 73% for the Belclare breed. Across all breeds an increase in the number of weaning records was observed across all breeds in 2013; the Suffolk breeds has seen the greatest increase in weaning records recorded in 2013 relative to 2009. For the Vendeen breed, the number of lambs with weaning weight recorded has increased from 57 in 2012 to 280 in 2013, however the overall number is small relative to the other pedigree breeds (Figure 1c). The proportion of lambs with a recorded birth and weaning weight ranges from 37% for the Suffolk breed to 67% for the Belclare breed. The average scanning weight varied from 41 kg for the Vendeen to 55 kg for the Suffolk lambs, however the average age at weighing differed across the breeds. The number of sires with recorded scanning weights varied from 467 for the Texel to 18 for the Belclare breed.

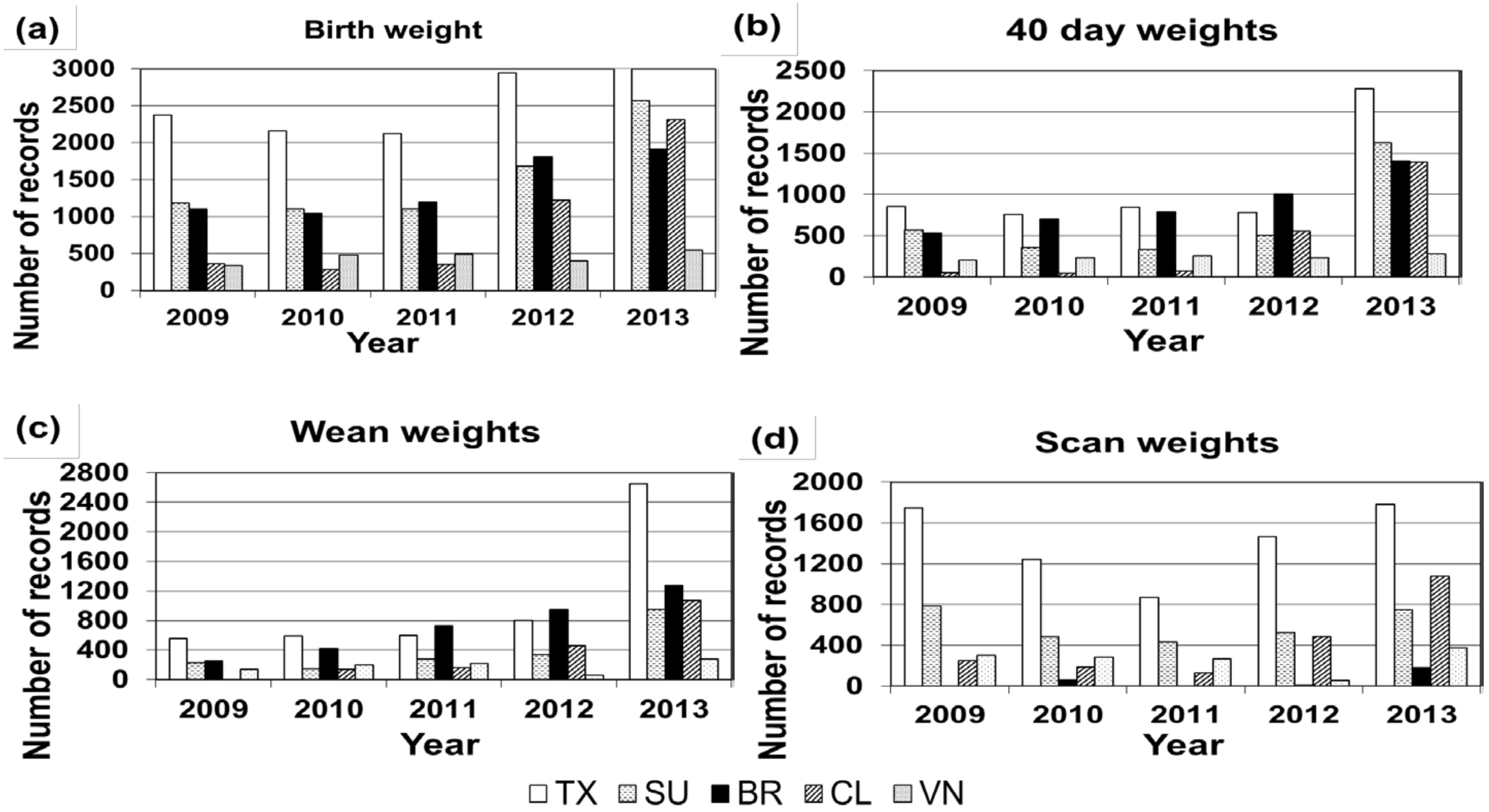


Figure 1 Number of records for (a) birth weight, (b) 40 day weight, (c) weaning weight, and (d) scan weight across the years 2009 to 2012 for TX (Texel), SU (Suffolk), BR (Belclare), CL (Charollais), and VN (Vendeen).

Scanning information. The number of lambs with scanning information recorded (i.e. ultrasonic muscle and fat depth) has increased substantially from 2012 to 2013 (Figure 2a & b). The average muscle depth varied from 29 mm for the Vendeen lambs (measured at 131 d) to 34 mm for the Suffolk lambs (measured at 157 d), however all breeds were not scored at the same age. The Belclare breed had the highest proportion of lambs (66%) with scanning information, while the Vendeen had the lowest proportion of lambs (20%) with scanning information.

Lambing information. Across all breeds there has been a substantial increase in the number of lambs with lambing ease and survival information from the years 2009 to 2013 (Figure 3a & b). In 2013 the lowest lambing ease scores were recorded for pedigree Belclare, while pedigree Suffolk lambs had the highest lambing ease scores. In 2013, the lowest levels of lamb survival (i.e., greatest levels of lamb mortality) were recorded the pedigree Texel and Vendeen lambs, with the highest levels of lamb survival recorded for the pedigree Belclare and Charollais lambs (92%).

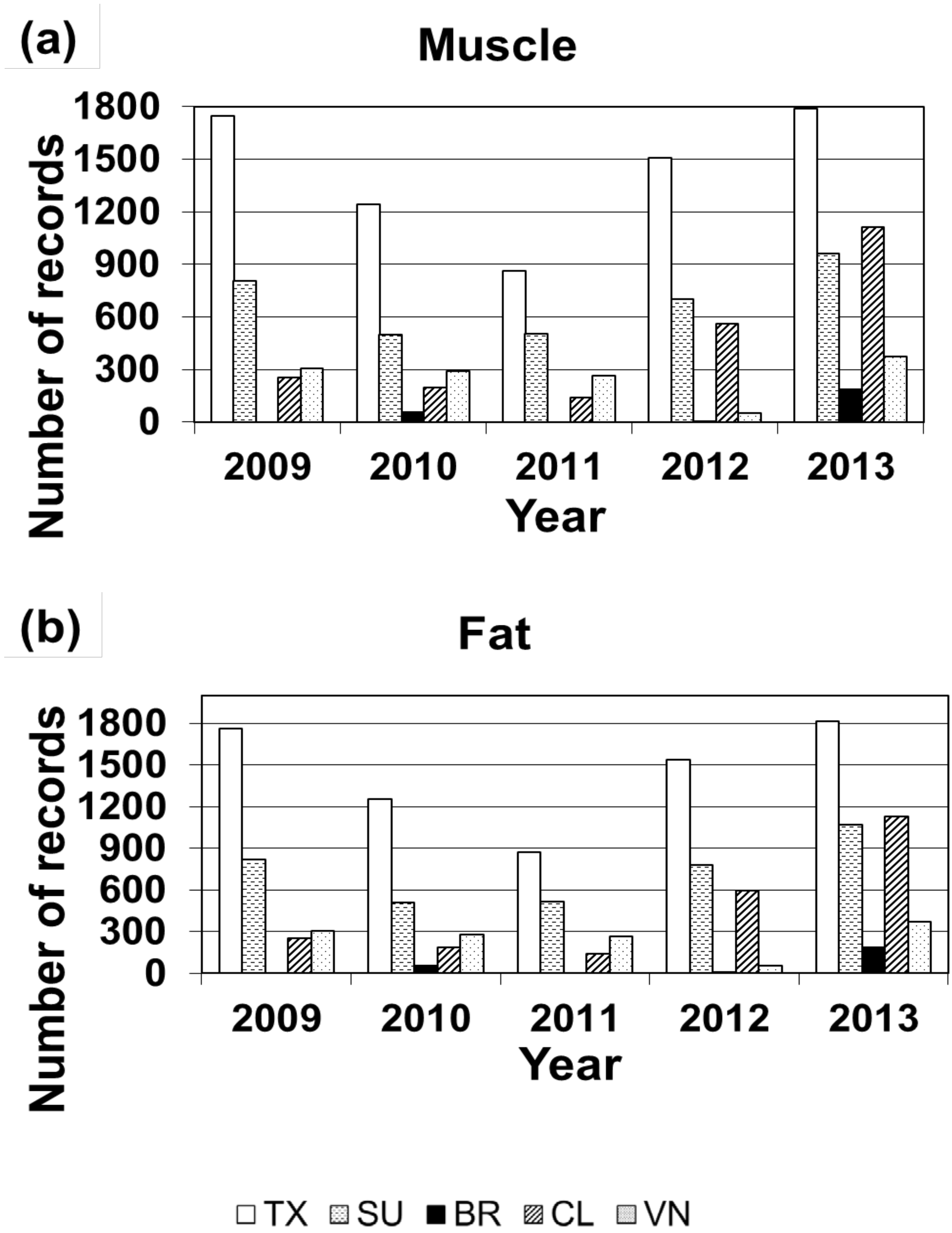


Figure 2 Number of records for ultrasonic (a) muscle, and (b) fat depth across the years 2009 to 2012 for TX, SU, BR, CL and VN.

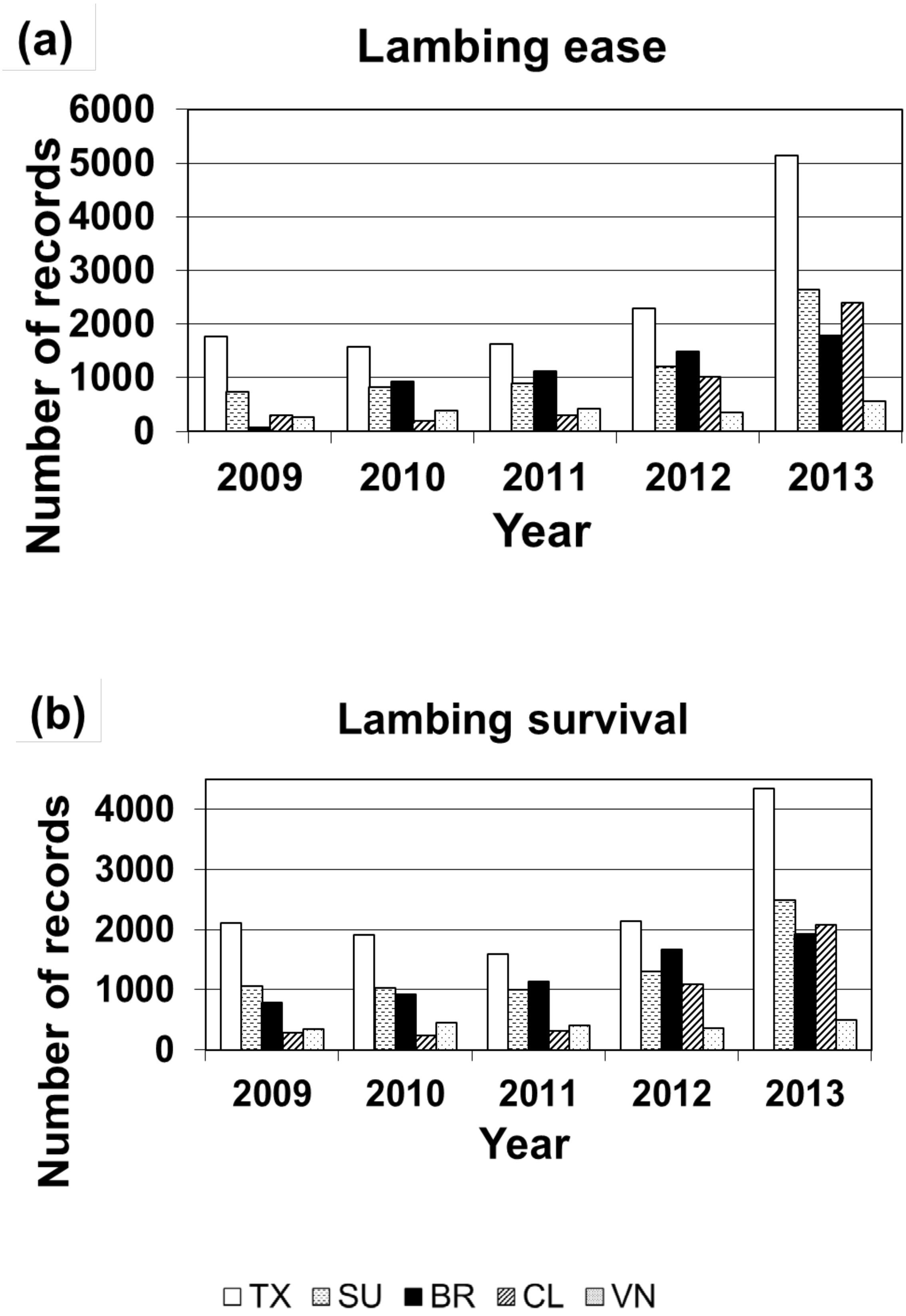


Figure 3 Number of records for (a) lambing ease score, and (b) lamb survival across the years 2009 to 2012 for TX, SU, BR, CL and VN.

NLB. The number of records for NLB data has increased across all breeds from 2009 to 2013. The Texel breed has a larger amount of available data due to the availability of the complete back pedigree for the entire flockbook (i.e. information on Lamb Plus flocks and non recording flocks are available). In 2013, the average NLB varied from 1.53 (Suffolk) to 1.79 (Belclare). The number of flocks with NLB data varied from 10 (Vendeen) to 223 (Texel).

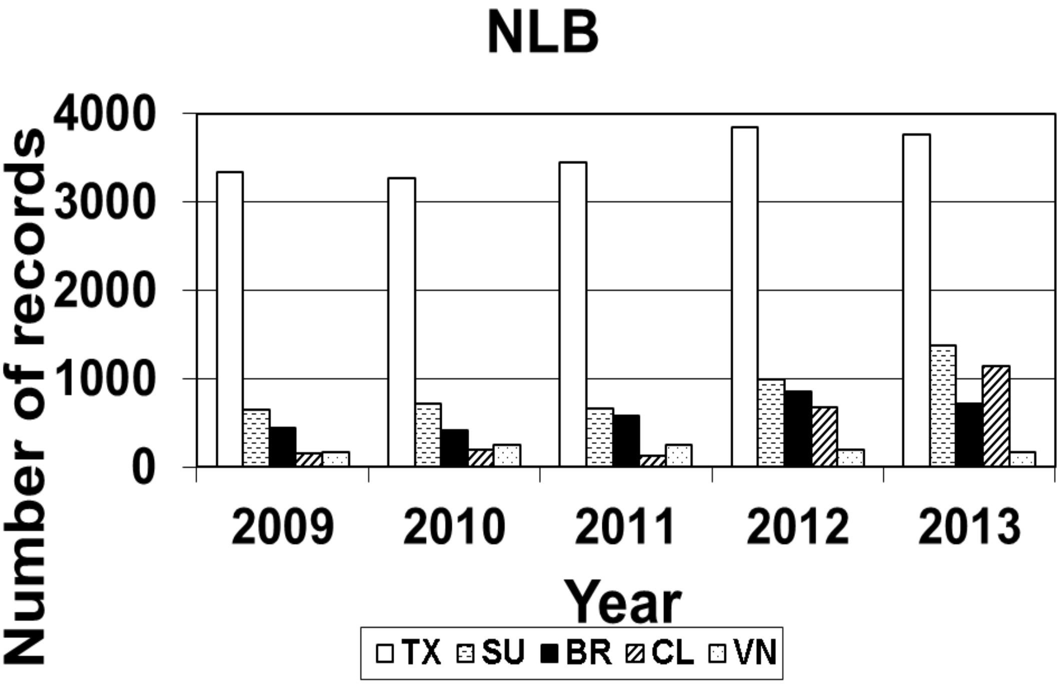


Figure 4 Number of records for NLB across the years 2009 to 2012 for Texel (white bars) Suffolk (black broken line bars), Belclare (black bars), Charollais (horizontal black line), and Vendeen (black bar white dots).

Recommendations

- Encourage more farmers to record 40 day and weaning weight
- Farmers who are not currently scanning lambs for fat and muscle depth should record weights at approximately 130 days of age
- Farmers that are participating in fat and muscle scanning should record all lambs or at the very least all lambs should be weighed to ensure the genetic evaluations are not bias
- Commercial farmers should be encouraged to enter lamb survival data at birth; this will allow lamb survival to be defined as whether a lamb was born alive or dead at birth. This may increase the heritability of the trait since less random error will be associated with the trait.
- Encourage farmers to record survival and lambing ease data accurately as a large amount of data is currently not usable in the genetic evaluations due to little or no variation in the scores recorded by some farmers.
- Pregnancy scan results should be recorded on the database. This will allow for more accurate evaluations for lamb survival and NLB. This data is also useful in detecting embryo mortality which could be due to inbreeding or lethal recessive genes.

1.2 Pedigree analysis and current inbreeding levels

Pedigree analysis is undertaken as a means of describing the genetic variability of a population and its evolution across generations. Pedigree completeness describes the depth of ancestry recorded in a population and reflects the quality of pedigree records used in all further analyses. In particular, all results in terms of inbreeding and relationship are dependent upon the pedigree completeness level of the population as the more complete the pedigree, the better the chance to detect true inbreeding. Pedigree completeness can be assessed in terms of complete generation equivalents (CGEs). For example one CGE is equivalent to one complete generation of ancestry recorded on the Sheep Ireland database (i.e. both sire and dam are known), while two CGE is equivalent to all four grandparents recorded on the database. A minimum of 1.5 CGE is required to detect traditional inbreeding in an animal.

The average CGE recorded for sheep born in 2012 is detailed in Figure 5b and varied according to the sheep population under study ranging from 1.16 (Easy Care) to 5.38 (Texel). The proportion of 2012 lambs with >= 2 CGE recorded on the Sheep Ireland database ranged from 6.8% (Easy Care) to 98% (Texel).

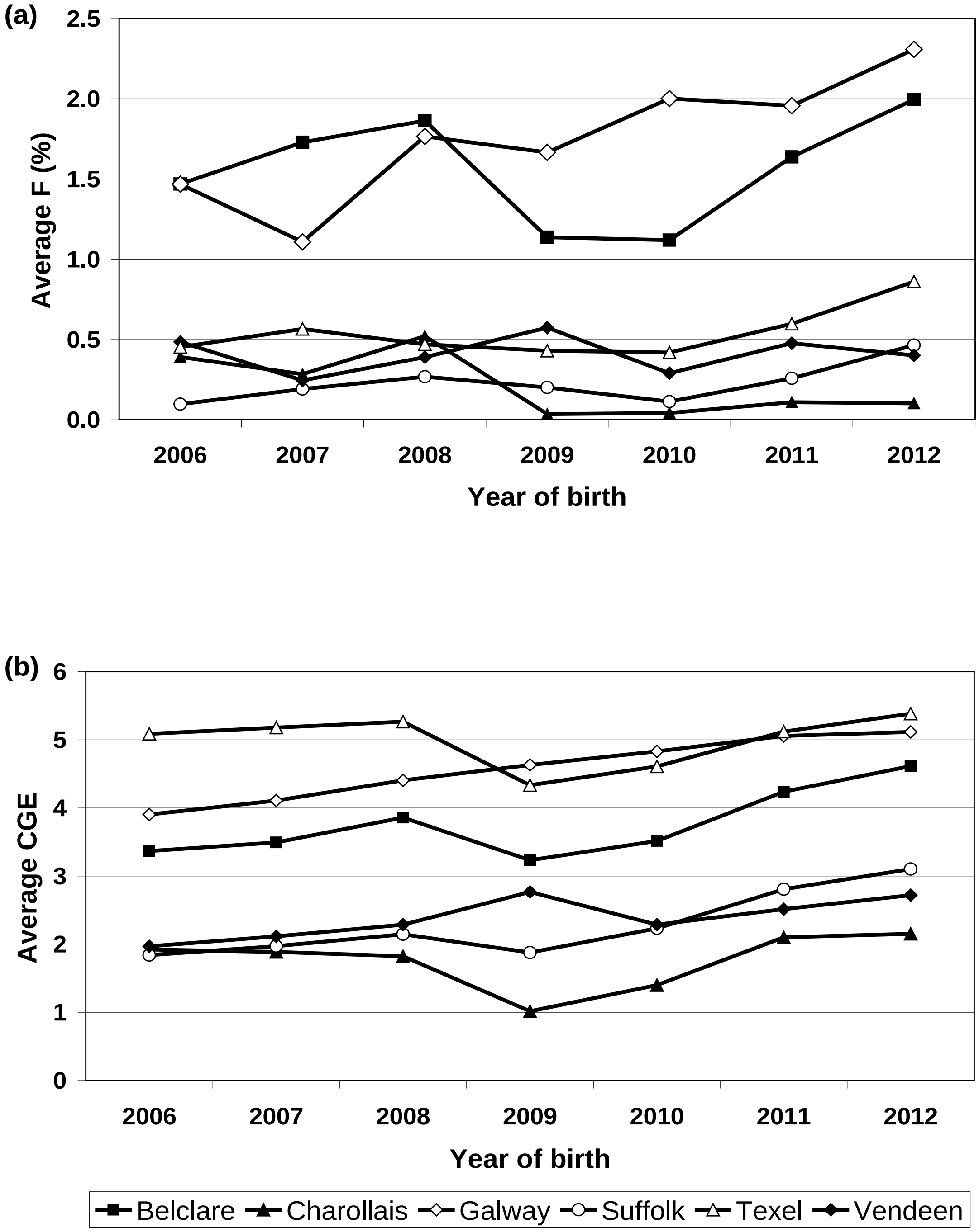


Figure 5 Population average (a) inbreeding percent (F) and, (b) number of complete generation equivalents (CGE) from lambs born from 2006 to 2012 for the Belclare (-■-), Charollais (-▲-), Galway (-◊-), Suffolk (-○-), Vendeen (-♦-) and, Texel (-Δ-) breeds.

Inbreeding has known deleterious effects on traits such as production, health and fertility (Mc Parland et al., 2007). The average level of inbreeding, within breed for sheep born in 2012 is provided in Table 6. Current levels of inbreeding remain low across the sheep populations, with a maximum average level of inbreeding observed in the Galway breed (F=2.31%). However, the calculation of inbreeding in highly dependent on ancestry information. With the exception of the Belclare, Galway and Texel breeds the level of ancestry recording remains low and therefore true levels of inbreeding remain unknown. The low levels of ancestry recorded for the Easy Care, Llyen, Mayo Connemara Mountain, Blackface Mountain, Charollais and Vendeen indicates that the inbreeding percentage may not be reflective of the true inbreeding within the breeds.

Table 6 Number of records (n), mean inbreeding percent (F; SD in parenthesis) and mean number of complete generation equivalents (CGE; SD in parenthesis) for lambs born in 2012.

Breed	**N**	**F**	**CGE**
Blackface Mountain	138	0.40 (1.53)	2.49 (0.86)
Belclare	3258	2.00 (3.60)	4.61 (1.52)
Easy Care	3050	0.01 (0.13)	1.16 (0.50)
Charollais	2265	0.11 (1.51)	2.15 (0.89)
Galway	1242	2.31 (3.69)	5.11 (0.98)
Llyen	601	0.17 (2.03)	1.53 (0.57)
Mayo Connemara Mountain	793	0.00	1.17 (0.77)
Suffolk	3273	0.46 (2.50)	3.10 (0.95)
Texel	7555	0.86 (2.79)	5.38 (1.27)
Vendeen	1182	0.40 (1.71)	2.72 (0.95)

Recommendations

- Encourage flockbooks to enter all back pedigree into the Sheep Ireland database
- Show farmers the benefits of recording parentage information for all lambs
- Publish inbreeding figures for all animals to prevent high levels of inbreeding; this is especially important for the smaller breeds
- Once genotypes are available calculate the underestimation of the F by the available pedigree

1.3 Genetic linkage

The fundamental mechanism of genetic evaluation is the genetic comparison of animals based on their phenotypic records and ancestry. Genetic linkage across flocks and years is critical to breeding programmes to provide an accurate measure of genetic merit. Linkage through the use of common rams allows for accurate statistical adjustment of environmental differences between farms (or years) in performance of progeny. This adjustment of environmental effects means that all animals in a well linked analysis can be directly compared. Without good genetic linkage the relativity of breeding values produced between years or flocks cannot be established and year-to-year or flock-to-flock data cannot be directly compared.

Table 7 Number of flocks unlinked, linked to central or other hubs (2 to 13).

			Other hubs											
	Unlinked flocks	Central hub	2	3	4	5	6	7	8	9	10	11	12	13	Total
No flocks	43	83	2	2	2	2	3	2	2	2	2	2	2	2	151

Currently genetic linkage is assessed using production traits (i.e., animals with production records in the last 3 years prior to the evaluation date) and a two-step method based on progeny of rams. The first step is based on progeny of sires across flocks, genetic distances between flocks are calculated. The second step involves a cluster analysis which allows flocks to be grouped into individual hubs based on their linkage. A central hub contains the most linked flocks and isolated flocks are identified as “other hubs” which are completely independent flocks that are not linked to any other hub. Table 7 highlights the number of flocks in each hub, while Table 8 breaks the hubs down by breed.

1.3.1 Importance of genetic linkage

Genetic linkage is of critical importance to allow for an accurate comparison of animals in the genetic evaluations. Genetic and environmental (farm, year, sex, level of feeding) effects can be disentangled, and accuracy can reflect this. Table 8 highlights the importance of genetic linkage on the published accuracy figures. Animals from flocks that are closed linked to the central hub can achieve accuracy levels 18% higher compared to unlinked flocks. All flocks entering the genetic evaluation should be linked to the central hub (1). Linkage is not static and must be kept up to date; currently we considered the last 3 year of data to assess linkage. Thus at the very least, flocks must review their linkage every 3 years through linkage reports provided by Sheep Ireland. The CPT flocks play a vital role in the genetic linkage between flocks and breeds in the genetic evaluations.

Table 8 Number of animals by breed* unlinked, linked to central hub or linked to other hubs (2 to 13).

			Other hubs												
Breed	**Unlinked flocks**	**Central hub**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**Grand Total**
BL	1,130	749													1,879
BM	237	51													288
BN		1													1
BR	1,917	12,021		386		15									14,339
BX	32	117												41	190
CA		71													71
CL	1,920	4,361		79	105	697		1,243	60						8,465
CV	48	1													49
DT		346													346
EC	282	339								2,398					3,019
GL	27														27
HN	34	9													43
IF		1,278													1,278
JO		3													3
LK	224	28													252
LY	609	307								62					978
MM	837	2,003													2,840
PR	49														49
RL	93	689													782
SW		92													92
SH	85														85
SU	997	13,257										200			14,454
TX	686	17,684	1480				760		37				760		21,407
UN	546	5,502								39					6,087
VN	396	4,267		20							304				4,987
WS		191								105					296
Total	10,149	63,367	1,480	485	105	712	760	1243	97	2,604	304	200	760	41	82,307

*Where BL= Bluefaced Leicester, BM= Blackface Mountain, BN= Bleu du Maine, BR= Belclare, BX= Beltex, CL= Charollais, CV= Cheviot, DT= Dorest Horn and Poll, EC= Easy Care, GL= Galway, HN= Hampshire Down, IF= Ile de France, JO= Jacob, LK= Lanark, LY= Llyen, MM= Mayo Connemara Mountain, PR= Primera, RL= Rouge de l'Ouest, SW= Swaledale, SH=Shropshire, SU= Suffolk, TX= Texel, UN= Unkown, VN= Vendeen and WS= Wilshirehorn.

Table 9 Number of animals (N), average (µ), and standard deviation (SD) for the level accuracy achieved for the production sub-index across different linkage clusters.

Linkage cluster*	N	µ	SD
0	16,339	**15%**	10%
1	198,035	**33%**	11%
2	263	**27%**	6%
3	25	**23%**	8%
4	13	**3%**	3%
5	93	**10%**	7%
6 to 11	5,960	**20%**	6%

* 0= unlinked, 1= most linked (i.e. central hub), 2 to 11= remaining linkage clusters.

Recommendations

- Educate farmers of the importance of genetic linkage for genetic evaluations
- Farmers who are not part of the central hub should be recommended to join the central hub through:
  - the sharing of rams
  - the purchase of rams that have good genetic linkage
  - the use of their stock rams in the CPT flocks

1.4 Overview of current Sheep Value Index

1.4.1 The breeding Goal

The establishment of a breeding goal is the first step for the implementation of a successful breeding programme irrespective of animal species. The breeding goal involves defining formally the direction in which the industry want to go. In Ireland, irrespective of species: sheep, beef or dairy, the breeding goal is profit. The breeding goal may differ across different production systems but for the majority of sheep farmers within Ireland the breeding goal is to generate genetically superior animals that will increase overall farm profitability. The importance of profit is reflected in the Sheep Value which acts as an indicator of the profitability that can be obtained from the animal's progeny.

1.4.2 Breeding Objective

The establishment of a breeding objective involves two main steps:

1. A list of traits influencing the breeding goal must first be identified;
2. Relative weightings must be generated for each identified trait.

New Breeding Objective

A comprehensive review of the Sheep Value breeding objective was undertaken in 2013 and after consultation with industry the decision was taken to split the existing Sheep Value Index into two overall indexes:

1. ***Terminal index* -** ranks animals based on their ability to produce live, fast growing terminal progeny with little lambing difficulty. This takes into account the progeny's growth rate, carcass characteristics, days to slaughter and also lamb survival and lambing difficulty.

2. ***Replacement index* -** ranks animals on the expected maternal performance such as milk yield, lamb survival and the ease of lambing, however it also includes some terminal traits to account for the efficiency at which animal's progeny are finished.

Both the terminal and replacement indexes are a measure of the genetic ability of the animal's progeny to generate profit at farm level.

1.4.3 Genetic parameters

Once a list of traits influencing the breeding goal is identified the next step involves research to establish if the traits are under genetic control, and if so to what extent. The process involves the estimation of genetic parameters. A heritability is defined as the efficiency of transmission of genetic superiority (or in some cases inferiority) of a trait from parent to offspring and can be referred to as the resemblance between relatives.

Once heritability is estimated it can tell a number of things:

1. the proportion of the difference that exists between individuals that is due to genetics,
2. the proportion of superiority within individuals that can be passed onto the subsequent generation, and
3. how fast or slow genetic improvement can be made within certain traits.

The calculation of heritabilities for all traits of economic importance is critical for the establishment of genetic evaluations. The calculation allows for environmental (i.e., level of feeding, managements, disease, climate, etc) differences between flocks to be accounted for thereby leaving an estimate of the genetic value for each trait. It uses all pedigree information on the animals (i.e., information on: the animal, the animal's ancestors and on the animal's progeny). Genetic parameters or heritabilities for each of the traits included in the genetic evaluations have been calculated by Tim Byrne from AbacusBio using Irish data (Table 10).

Table 10 Heritability estimates for each goal trait included in the replacement or terminal index.

Objective trait	**Heritability**
Days to slaughter	0.20
Carcase conformation	0.25
Carcase fat	0.15
Maternal days to slaughter	0.10
Maternal carcase conformation	0.12
Maternal carcase fat	0.08
Ewe mature weight	0.30
Maternal Lamb survival	0.01
Maternal Single Lambing ease	0.03
Maternal Multiple Lambing ease	0.03
NLB	0.07
Single Lambing ease	0.05
Multiple Lambing ease	0.05
Lamb survival	0.02

However, some traits of importance are difficult or costly to measure on farm in large quantities (i.e. carcass fat and conformation). Hence predictor or correlated traits that are easily measurable can be used as a proxy for the difficult to measure traits. Although predictor traits are usually not perfect measures of the goal trait they can provide early and useful predictors of especially difficult to measure traits (e.g. carcass fat) or traits that require a long time to measure (e.g. survival). Table 11 outlines the correlations between the predictor traits measured on farm and the goal traits for the genetic evaluations.

Table 11 Genetic correlations between traits measured on farm (predictor and goal traits) and final index goal traits.

	DTS	**Carcass conf.**	**Carcass fat**	**Ewe mature wt**	**Mat. DTS#**	**Mat.* carcass conf.**	**Mat. carcass fat**	**Lamb surv¥**	**Single lamb ease**	**Multiple lamb ease**	**Mat. lamb surv**	**Mat. single lamb ease**	**Mat. multiple lamb ease**	**NLB**
Scan weight	-0.7	0.6	0.4	0.5	0	0	0	0	0	0	0	0	0	0
Weaning weight	-0.4	0.4	0.2	0.3	0	0	0	0	0	0	0	0	0	0
40 day weight	-0.2	0.2	0.1	0.1	0	0	0	0	0	0	0	0	0	0
Muscle depth	-0.4	0.5	0.2	0.20	-0.4	0.4	0.1	0	0	0	0	0	0	0
Fat depth	-0.2	0.2	0.5	0.10	-0.2	0.2	0.5	0	0	0	0	0	0	0
Mat. scan weight	0	0	0	0	-0.6	0.5	0.3	0	0	0	0	0	0	0
Mat Wean weight	0	0	0	0	-0.4	0.4	0.2	0	0	0	0	0	0	0
Mat 40 day weight	0	0	0	0	-0.2	0.2	0.1	0	0	0	0	0	0	0
Birth weight	0	0	0	0	0	0	0	0	-0.3	0.2	0	0	0	0
Lamb survival	0	0	0	0	0	0	0	1	0.4	0.4	0	0	0	0
Single lambing ease	0	0	0	0	0	0	0	0.4	1	0.2	0	0	0	0
Mutliple lambing ease	0	0	0	0	0	0	0	0.4	0.2	1	0	0	0	0
Mat. lamb surv	0	0	0	0	0	0	0	0	0	0	1	0.4	0.4	0
Mat single lamb ease	0	0	0	0	0	0	0	0	0	0	0.4	1	0.2	0
Mat multiple lamb ease	0	0	0	0	0	0	0	0	0	0	0.4	0.2	1	0
NLB	0	0	0	0	0	0	0	0	0	0	0	0	0	1

DTS= Days to slaughter, *Mat= maternal, ¥ Surv= survival.

1.4.4 Economic values

The second step in establishing the breeding objective involves the estimation of the relative weightings for each trait. In Ireland these weightings are determined based on the extent the trait is under genetic control and their economic importance at farm level. Economic values in genetic evaluations provide a measurement of the economic importance of the trait in farm profitability and guide the relative selection emphasis that is placed on each trait. The estimation of the current economic values is based on a model developed by AbacusBio (Byrne et al., 2010). The economic value for each of the goal traits is highlighted in Table 12, along with the relative emphasis that is placed on each trait within the overall Sheep Value Index.

Table 12 Unit of measurement, economic value, and relative emphasis (%) for each goal trait within the terminal and replacement index.

Goal Trait	**Unit**	**Economic value**	**Relative Emphasis (%)**	
			Terminal	**Replacement**
Days to slaughter	per day	-€0.12	40.30%	12.12%
Carcase conformation	per grade	€1.40	7.80%	2.35%
Carcase fat	per score	-€1.93	14.98%	4.55%
Maternal days to slaughter	per day	-€0.08	-	12.36%
Maternal carcase conformation	per grade	€1.16	-	2.86%
Maternal carcase fat	per score	-€1.60	-	5.49%
Ewe mature weight	kg	-€0.36	-	15.93%
Maternal Lamb survival	per lamb weaned	€30.74	-	16.34%
Maternal Single Lambing difficulty	per 1% decrease	-€0.10	-	0.22%
Maternal Multiple Lambing difficulty	per 1% decrease	-€0.05	-	0.13%
NLB	per lamb born	€8.94	-	14.95%
Single Lambing difficulty	per 1% decrease	-€0.11	1.12%	0.37%
Multiple Lambing difficulty	per 1% decrease	-€0.06	0.60%	0.21%
Lamb survival	per lamb weaned	€33.69	35.20%	12.12%

Recommendations

- Review the economic values as changes occur in the prices and costs of inputs and output at farm level
- Continue to research and add economically important traits to the Sheep Value index

1.5 Current breeding programme

Although sire reference schemes were established in the late nineties by a small number of Texel and Charollais breeders, the Irish sheep sector lacked a breeding scheme that evaluated all breeds together (Byrne et al., 2009). In the past the breeding scheme focused on pedigree flocks and on terminal traits and uptake was poor by commercial farmers. Since the establishment of Sheep Ireland in 2008 the focused has shifted towards all economically important traits at commercial level for both the terminal and maternal traits. Under the new breeding schemes two different initiatives were undertaken to ensure that large amount of connected data would be generated across a short period of time that would help to identify the genetically superior animals. These two initiatives were: the MALP (Maternal Lamb Producer Groups) and CPT (Central Progeny Test) flocks.

1.5.1 MALP flocks

The MALP flocks compromises of 15 flocks in total. In order to test the robustness of the genetic evaluations across different systems the farms are geographically spread across a range of different land types and production systems. They were set up not just to provide data but also to provide a demonstration of the range of genetic merit among a group of rams. This is reflected in the main objective of the MALP flocks which is to help farmers to gain an appreciation for the value of improving genetics (Amer et al., 2009). To ensure that connectedness exists between the flocks, rams are swapped between the farms during the mating season thus providing genetic linkage across the farms. The MALP flocks also focus on financial and management aspects of sheep farming. All animals are electronically tagged and single sire mated for parentage matching. The use of electronic tagging helps to increase efficiency on farms by identifying problem animals earlier such as ewes that are persistently lame.

1.5.2 CPT

The CPT flocks are modelled on a similar system that has been used in New Zealand; rams from different breeds and spread across a diverse population of performance recording flocks are mated to a central group of ewes and their progeny are recorded in detail. Information on the progeny managed in a commercial environment feeds back into the genetic evaluations and provides predictions of the genetic merit of the pedigree rams used and also his relatives (Amer et al., 2009).

Recommendations

- Commercial data remain vitally important for genetic evaluations, therefore the role of the MALP farms remains critical to the success of Sheep Ireland
- Flocks with poor linkage should be encourage to provide rams for use in the CPT flocks

1.6 DNA parentage summary to date

Genetic evaluations rely on the availability of accurate phenotypic information and on the collection of pedigree information on each animal. One of the main hindrances for the sheep genetic evaluations here in Ireland is the availability of pedigree information on animals especially on the commercial ewe population. An alternative method for the accumulation of parentage information involves the use of DNA information to identify parents. The process involves the genotyping of all offspring and potential parents with 14 microsatellites. One drawback to this technology, however, is that it can be difficult to unambiguously assign parentage in a population of closely related animals. DNA parentage has been used to assign parentage (i.e. sire and dam) to the MALP flocks since 2008 on approximately 35,000 animals. However the results to date have been poor. Using 2012 as an example, only 51% of lambs could be assigned with definitive sire and dam parentage information; this results in a large amount of animals being excluded from the genetic evaluations. With the cost of such technologies high ~€12 per sample and poor results obtained from the genotyping the decision was taken in 2012 to discontinue with DNA parentage of lambs on the MALP flocks until further research is undertaken into the technology.

Recommendations

- Research into the use of DNA technology for parentage assignment is required urgently
- Parentage should be assigned to the MALP flocks using single sire mating

National genetic evaluations provide information to aid in selection decisions to increase long-term performance of the national flock. The accuracy of the national genetic evaluations can be tested by comparing the genetic merit of a sire with his progeny's performance. A small study was undertaken to quantify the difference in animal performance in sires differing in genetic merit for the production sub-index (5 stars versus 1 star) in 2012. Genetic merit of all sires, for the production sub-index, from the genetic evaluations published in May 2011 was extracted from the Sheep Ireland database. Only weaning weight data from June 2011 onwards was used so that the results are a truer reflection of the accuracy of the genetic evaluations. Weaning weight was corrected for age at weaning (linear and quadratic effect), gender of lamb, ewe parity number, birth and rearing rank of lamb, production star rating of sire, contemporary group (i.e. flock specific management effects).

Results from the study show that across all rams the difference in weaning weight between 1 versus 5 star rams on average was 0.91 kg (P=0.0024). Rams with accuracy's of 60% or greater the difference in weaning weight between the 1 versus 5 star rams on average was 3.82 kg (P=0.0018). These results show that selecting rams with high star ratings for production sub-index will, on average, increase weaning weight. The results also highlight the importance of breeding value accuracy when selecting breeding rams.

Recommendations

- Validation of the Sheep Value index and all sub-indexes on a regular basis to ensure that genetic evaluations are reflective of on the ground performance

1.8 Genetic gain to date

To calculate the genetic gain achieved to date a selection index was developed. The formation of the selection index involved the use of the genetic and phenotypic parameters that are included in the current genetic evaluations (Table 9), the previously reported genetic and phenotypic correlations between all goal traits included in the terminal and replacement indexes (Table 10) and the economic value for each trait (Table 11). These three information sources are combined to form a series of matrices which allows for the calculation of the response to selection for each trait.

Figure 7 illustrates the annual response to selection across the breeding objective (Terminal and Replacement Index). The graph shows that although considerable genetic gain has been achieved in the terminal traits, by comparison, little genetic gain has been achieved to-date in the maternal traits represented in the replacement index. However, with the accumulation of large amounts of maternal data and continual improvement in the national genetic evaluations there is significant scope to accelerate genetic gain across both terminal and maternal traits.

With the continual improvement of the national genetic evaluations the level of genetic gain achievable within the Irish sheep population will constantly evolve and therefore the response to selection must be monitored and calculated on an annual basis.

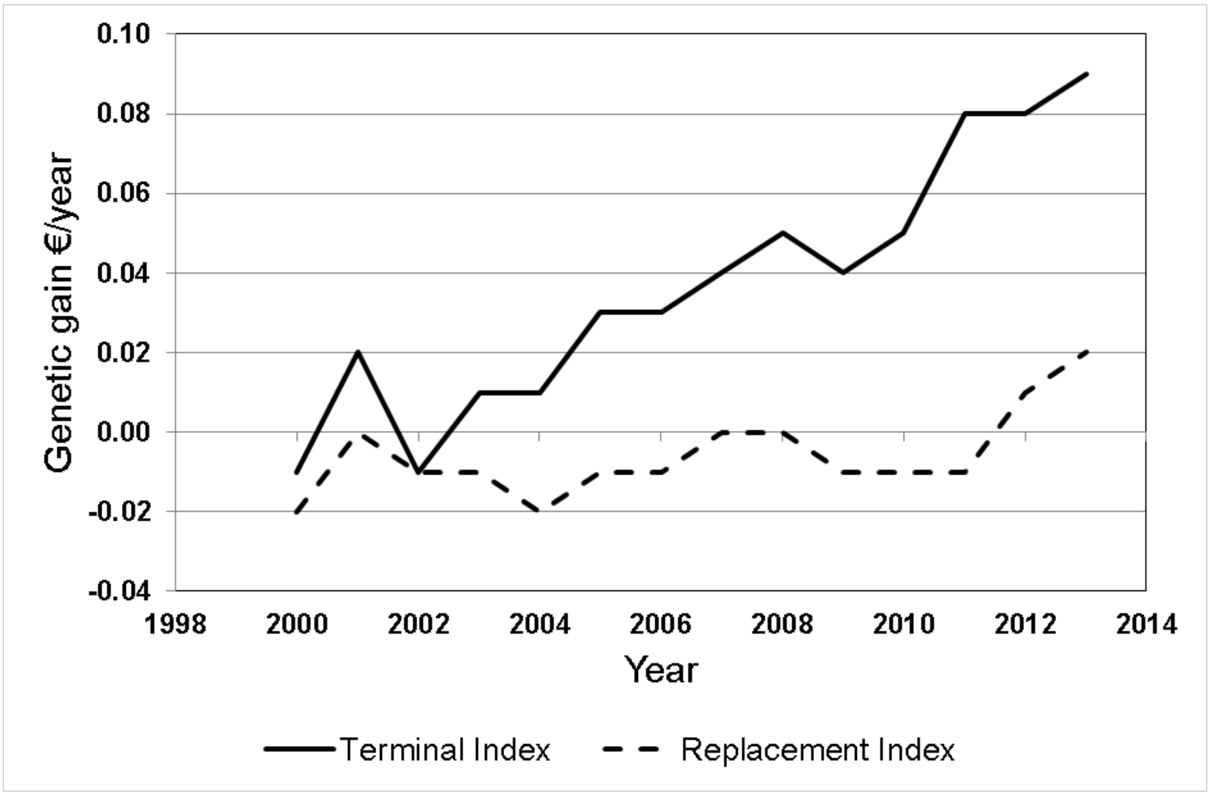


Figure 6 Annual rates of genetic gain (€ per year) achieved in the terminal (-) and replacement (--) index from 2000 to 2013.

Recommendations

- Levels of genetic gain should be calculated on an annual basis for the sheep population

Section 2 Future priorities

2.1 Phenotypes

Phenotypes for breeding can be broadly categorised into: 1) goal traits or 2) index traits. Goal traits are those which have an associated (economic) value and therefore are included in the Sheep Value. Examples of these traits are number of lambs born, carcass weight etc. Index traits are traits that underpin the goal traits and are measured in the field. So for example, ultrasound fat depth is an index trait as a predictor of carcass fat.

To be included in a breeding goal, goal traits: 1) must be important (economically, socially or environmentally), 2) must exhibit genetic variation, and 3) must be measurable or genetically correlated with a heritable trait that can be measured.

Goal traits can be further broken down into traits: of critical importance, that should be measured where possible and for research purposes, of short to medium and long term importance (Table 13).

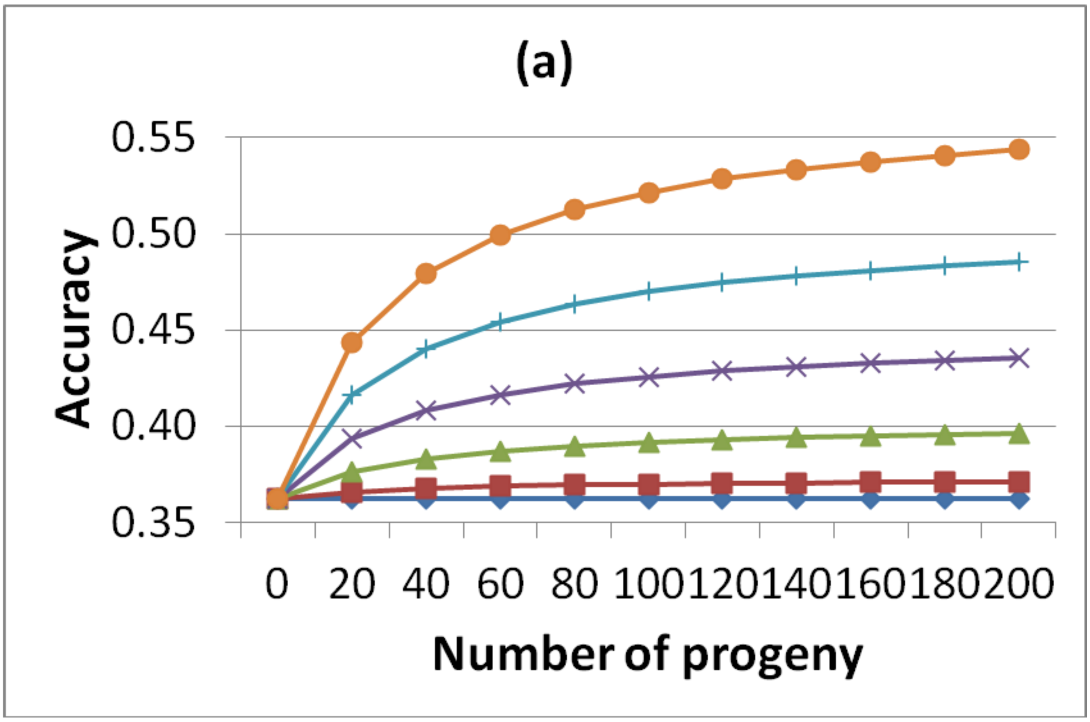
When a decision is made on priority goal traits then approaches have to be tested, as to how, best to include this goal trait in the Sheep Value index. First whether the trait is heritable must be established. The dataset size required to obtain precise estimates is dictated by: the heritability of the trait, the number of families represented and the dispersal of animals across flocks. Guessestimates of the heritability can be generated from international data as well as biological understanding of the trait. For a trait with a heritability of 0.03 (e.g., fertility or health) a study size of approximately 8,000 animals is required to generate precise estimates of genetic parameters for inclusion in a multi-trait genetic evaluation. If the heritability is expected to be approximately 0.10 then records on 3,000 animals is required while if the heritability is expected to be 0.35 then a study population size of approximately 1,500 animals at least is required. Ideally the study population should be undertaken across breeds with many sire families represented and across many herds/environments.

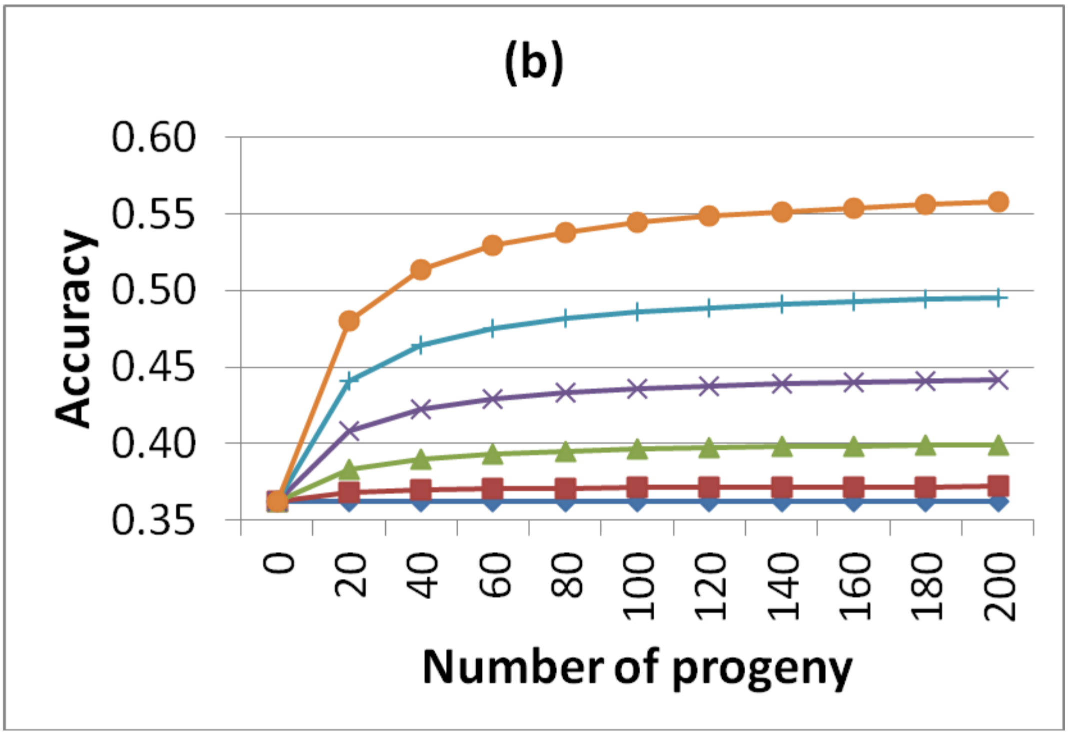
Table 13 List of traits of critical importance, traits which should be recorded, and research traits (short to medium term and long term).

Importance	Short to medium term	Long term
Critical Importance	Birth weight	Factory carcass data
	Lamb ease score	VIA data
	Lamb survival	Fertility traits
	40 day weight	Growth profiles for lambs and ewes
	Weaning weight	Ratio of ewe weight to lambs weaning weight
	140 day weight/ scan weight	
	Ewe mature weight	
	NLB	
	Ultrasonic muscle	
	Ultrasonic fat	
Should be recorded (where possible)	Ewe BCS	Ewe lamb bareness
	Dag score	Ewe bareness
	Lamb quality/ degree of finishing	Age at first lambing
	Prolapse	Lambing interval
	Other health traits	Average daily gain
	Pregnancy scan	Lean growth rate
	Genetic defects	Lamb viability
	Reason for culling	Mothering ability
	Reason for death	Ram functionality
	Lameness	
	Mastitis	
	Ewe survival	
	Faecal egg counts	
Research traits	Feed intake	Meat quality
	Ram functionality	Methane emissions
	Colostrum quality and quantity	NIR technology on faeces to predict digestibility
	Milk yield	Innate immune measures
		Docility or flightiness

2.1.1 Importance of predictor traits

Even if a trait is not a goal trait it can increase the accuracy of selection through a multi-trait genetic evaluation. For example, research from dairy cattle clearly show that body condition score (BCS) can be a useful predictor of fertility and that genetic gain in low heritability traits like fertility and health can be augmented by exploiting information on heritable correlated traits. Figure 7 shows the accuracy of selection achievable for a low heritability goal trait (0.03) by exploiting information on a correlated trait. When no information on the goal trait is available on an animal or its parents the estimate of genetic merit for that animal will come solely from the correlated trait; the maximum accuracy of selection achievable using this approach is the strength of the genetic correlation between the two traits. As progeny or self information on the goal trait becomes available the emphasis on the correlated trait will reduce. Such approaches of exploiting information on correlated traits to augment the accuracy of selection and thus genetic gain are used in the Irish dairy and beef genetic evaluations.





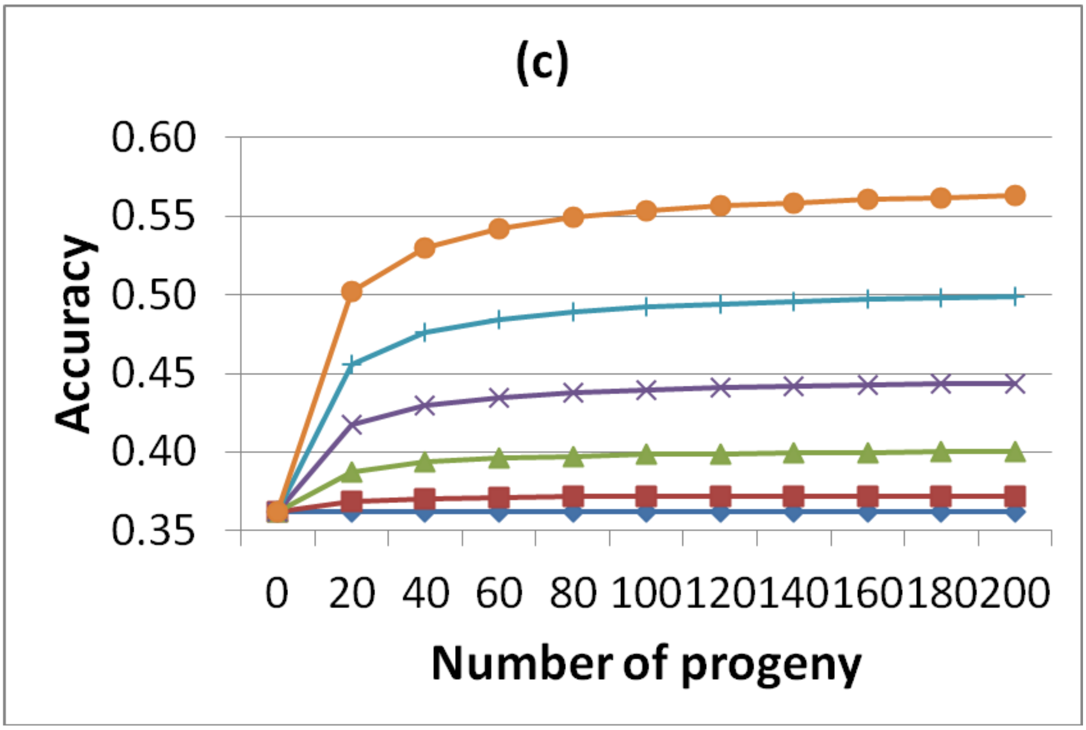


Figure 7 Accuracy of estimates of genetic merit when the goal trait has a heritability of 0.03 with records on 30 progeny and information is also available on an ancillary traits with a heritability of: (a) 0.10, (b) 0.20 and (c) 0.30 and a genetic correlation between the ancillary trait and goal trait of 0.0 (blue diamond), 0.10 (red square), 0.20 (green triangle), 0.30 (purple x), 0.40 (blue +) and 0.50 (orange circle).

2.1.2 Data quality

Data quality is key to accurate genetic evaluations. Data quality includes correct parentage assignment, correct recording of information (e.g., recording all stillbirths) and allocation to the correct individual, as well as, full and correct reporting of environmental effects (e.g., if preferential treatment is undertaken such as creep feeding of some animals). Within flock heritability (as opposed to population heritabilities used in the genetic evaluations) and comparison of variance components can be used as a measure of data quality although it can be confounded by other issues. Flock heritability estimates can be calculated for individual flocks across all goal traits; the magnitude of the heritability estimates across a range of traits will allow a quality measure to be inferred on each flock. In addition cognisance will also be taken of the phenotypic data, for example a higher score will be rewarded to farmers that enter birth data soon after lambing.

2.1.3 Fixed effects solutions

The key to any successful breeding strategy is to ensure that there is widespread understanding and uptake of the national evaluations by the end users. This can entail the condensing of information received by farmers into clear, concise recommendations or decision support tools. One such example of such decision support tool involves the utilization of live-weight data to provide flock-level animal growth profiles which can be used as a benchmarking tool that allows farmers to compare the growth performance of their flock with contemporaries, while simultaneously adjusting for the genetic merit of the flock.

Recommendations

- Research must be conducted into new easy to measure phenotypes before traits can be considered for inclusion in the genetic evaluations
- The importance of predictor traits must also be researched
- Within flock variance components should be estimated and incorporated into a flock specific Data Quality Index.
- The Data Quality Index is one potential approach to identify and discard (or place reduced emphasis) from genetic evaluations flocks deemed to have poor data quality
- Similar to beef evaluations a data quality index should be developed for sheep
- Research should be conducted into the development of decision support tools for sheep farmers

2.2 Pedigree

2.2.1 Overview effects of inbreeding on traits

Inbreeding depression refers to the loss in performance and vitality associated with inbreeding and predominantly affects fitness traits including: fertility, production and health, thus impacting on farm profitability. Inbreeding depression has been shown in all livestock populations, including sheep, however its effects on traits of importance to Irish sheep is unknown. Inbreeding depression is not consistent on its effects on animal performance. Factors such as: age, breed, production level and climate impact the degree of loss in performance associated with inbreeding. Therefore, although we can assume the impact of inbreeding on sheep traits of importance from the literature, the true inbreeding depression of Irish sheep should be calculated using Irish data

2.2.2 Deficits in pedigree recording

A recent pedigree analysis undertaken of Irish sheep populations (Section 1.5; Table 5) highlighted a lack of ancestry recorded in the Sheep Ireland database for the majority of sheep breeds. The Texel population was the only population studied with an acceptable level of pedigree completeness (CGE = 5.38 for sheep born in 2012). Lack of ancestry recorded will inhibit the computation of true inbreeding and bias the effect of inbreeding depression. In addition, lack of ancestry recorded will exclude large numbers of sheep from future breeding schemes such as contract matings, since if parentage of ewes is unknown, suitable rams cannot be identified as mates.

Deficits in pedigree recording can be overcome through DNA verification. However this is expensive, and would be cost beneficial only for animals that would be used widely in the national breeding programme.

2.2.3 Parentage: SNP versus microsatellite

Microsatellite markers have been successfully used for parentage identification in livestock over the last few decades. However, results to date for Sheep Ireland (see section 1.6) have been poor. Errors in pedigree recording can bias the genetic evaluations and breeding values, and therefore reduce the rate of genetic gains achievable for the industry. A new technology that uses SNP markers has been developed that allows for parentage verification. The advantages of using SNP genotyping rather than microsatellites include: lower error rates, standardization between laboratories, lower costs (McClure et al., 2012) and the data is also useful for the development genomic selection (see section 2.4). Initial results from the Research Demo Flock in Athenry shows that the LD SNP chip (i.e. 5k) was 100% accuracy at assigning parentage to all lambs; these results were presented at the Sheep Ireland industry meeting in autumn 2013. More research is underway between Teagasc and AgReserch NZ to evaluate the usefulness to lower density (and lower cost) SNP markers for parentage verification in the Irish sheep population.

2.2.4 Calculating inbreeding depression

To estimate inbreeding depression, the performance of an individual is regressed on the individuals own inbreeding coefficient. The inbreeding coefficient may be treated as linear, quadratic, or higher order polynomials or as a categorical variable. Mixed models which link to the pedigree of the animal either through the animal itself, its sire or its dam are more useful to calculate inbreeding depression than fixed models. To minimise bias in the results, animals with a minimum of three complete generations of ancestry should be included in the computation of inbreeding depression.

2.2.5 Genetic conservation

Genetic conservation is a tool used to preserve populations facing endangerment or extinction. Conservation of a population may take the form of specialised mating schemes to promote greater genetic diversity in the next generation. This method of conservation is preferred since the population can continue to develop and change to changing circumstances.

Alternatively, or in conjunction with the specialised mating schemes, conservation may involve the preservation of genetic material from current animals in the population for use in future generations. This method may be used to provide back-up to a population if its numbers reached threatening levels due to a disease outbreak, for example.

Currently in Ireland, only one sheep population, the Galway sheep is considered endangered. A document detailing considerations for breed societies wishing to use genetic conservation as a tool was recently completed and describes various methods of genetic conservation available, provides cost estimates of genetic conservation for populations and details information required by breed societies who wish to set up genetic conservation programme for their population.

Recommendations

- Results from research into SNP markers for parentage verification will be presented at industry meeting (2015)

2.3 Linkage

2.3.1 Research new algorithms

The current linkage analysis is based on phenotypes recorded for weight traits and on the direct genetic link between rams and their relevant progeny. The method is therefore not very robust but may be too restrictive (connections other than progeny are ignored, female connections are omitted). Tarres et al. (2010) used a method from Fouilloux et al. (2008) based on the evaluation of disconnectedness between random effects to determine linkage, thus considering all sources of linkage involved in the estimation of genetic random effects. Mathur et al. (1998) has also tested a similar approach based on pair-wise comparisons of EBVs in pig breeding. These approaches should be tested on the Irish sheep populations and results should be compared and presented to the industry.

2.3.2 Contract mating

Contract mating can be used to generate germplasm for the future breeding programme of any population. Once the breeding goal has been identified, females and males, elite for the breeding goal can be identified from the population and mated optimally to generate the most elite group of offspring for future breeding use. Contract mating may be undertaken to optimise genetic gain, for any trait or combination of traits in a population provided the traits required are recorded in the population. Alternatively contract mating may be designed to optimise genetic diversity in a population or to optimise gain and diversity simultaneously.

Recommendations

- Alternative approaches in the generation of linkage estimates between animals must be investigated and compared to the current approach

2.4 Genomic selection

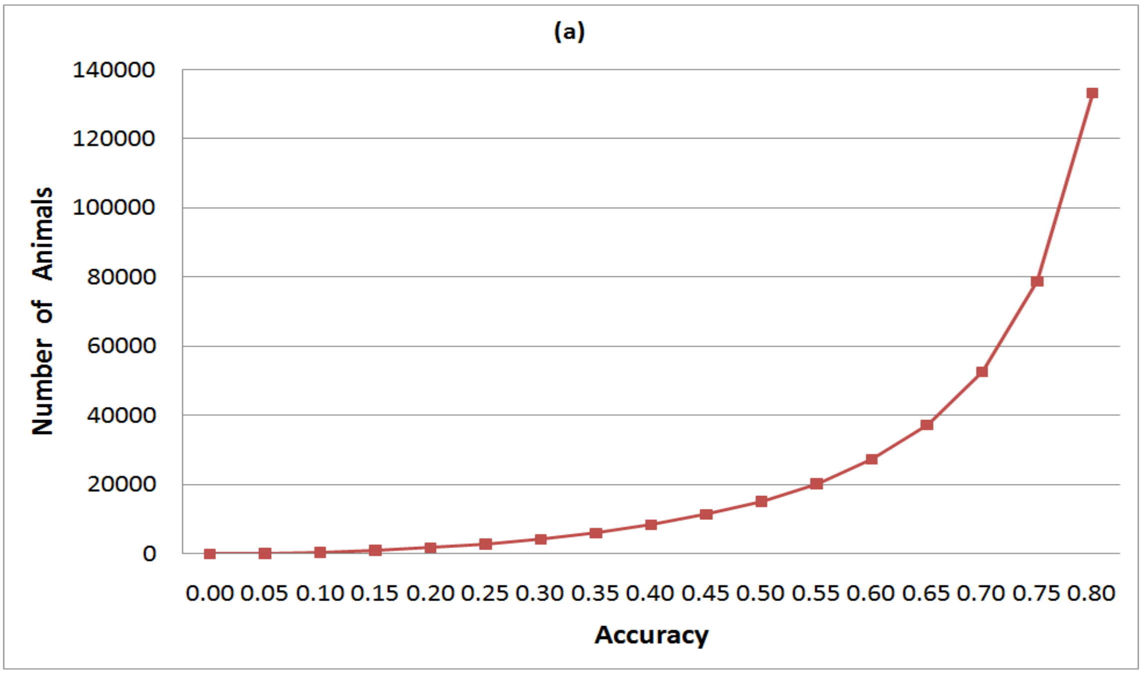
2.4.1 What is genomic selection

Genomic selection is the method of estimating the associations between tens of thousands of genetic markers along the DNA of a sheep and related performance traits, thereby facilitating more accurate estimates of the genetic merit of the sheep. The technology is currently available to measure over 54,000 genetic markers in sheep. Although little information is available internationally, this panel may be approximately half as powerful as its equivalent in cattle (i.e., linkage disequilibrium appears to be weaker in sheep). The difficult component to a successful genomic selection programme is the accurate estimation of each genetic marker. To do this a *training population* or a *reference population* is required which constitutes several thousand genotyped and phenotyped animals.

2.4.2 Accuracy of genomic selection

The benefit of genomic selection is increased accuracy of estimates of genetic merit and the increase in accuracy achievable with genomic selection is a function of a number of parameters, most notably the number of animals that are both genotyped and phenotyped and the heritability of the traits; other factors like inbreeding levels and the number of genetic markers on the available technology platform also influence the accuracy. The lower the number of animals phenotyped and genotyped, the lower will be the improvement in accuracy with genomic selection. Furthermore, assuming the same number of animals genotyped and phenotyped, a greater increase in accuracy will be achieved for high heritability traits (e.g., growth rate) compared to low heritability traits (e.g., number of lambs born).

Figure 8 shows the accuracy of genomic predictions for different numbers of genotyped and phenotyped animals per breed for three traits, a low heritability traits (h^2=0.03; Figure 1a), a moderately-low heritability traits (h^2=0.20; Figure 1b) and a moderate-high heritability trait (h^2=0.35; Figure 1b) which may be reflective of a population of rams with estimated breeding value accuracies of 0.60. To achieve an accuracy of genomic evaluations of 0.50 approximately 2,000 animals must be genotyped when the heritability is 0.20 to 0.35; when the heritability is 0.03 the number of genotyped and phenotyped animals required increases to 15,000. One approach to increase the effective heritability is to use rams of moderate to high accuracy. Using rams with a mean accuracy of 0.60 in the training population is equivalent to a heritability of 0.36. The Irish dairy cattle genomic selection programme was released with a training population size of just under 1,000 bulls because they were all high reliability bulls (i.e., accuracy >0.90).



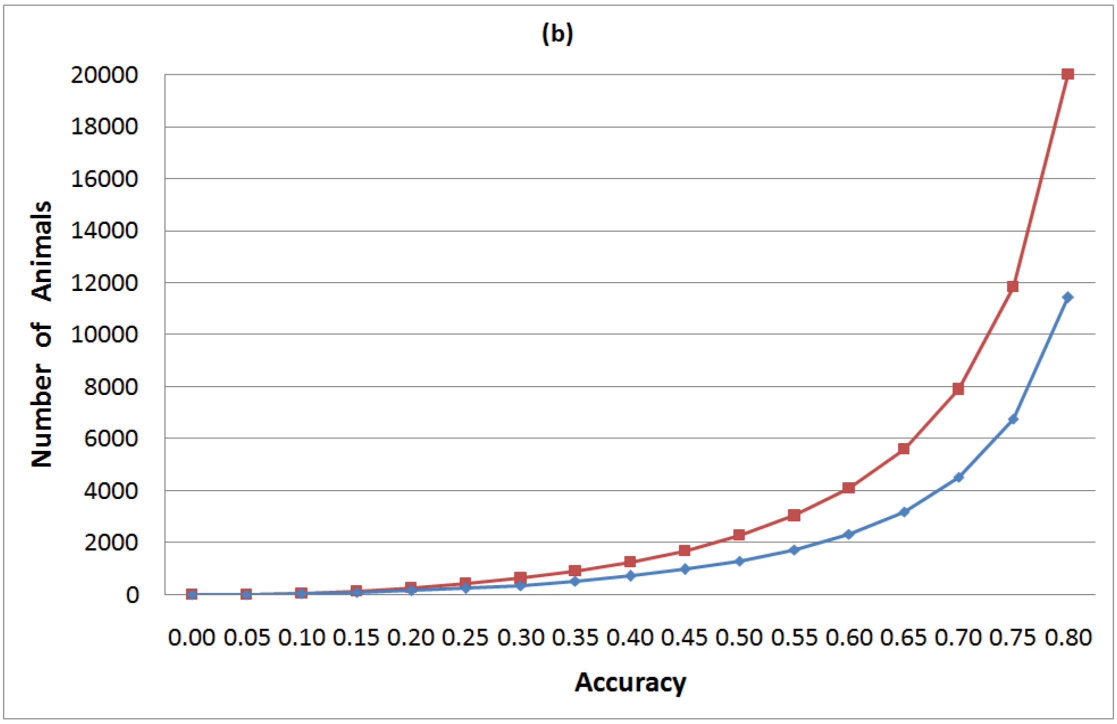


Figure 8 Number of animals required to achieve a given accuracy of genomic evaluations for a heritability of 0.03 (Figure a), 0.20 (Figure b; Red square) and 0.35 (Figure b; Blue diamond).

Therefore, to reduce the cost of genomic selection, rams with many progeny should be genotyped and included in the training population. In sheep however acquiring sufficient numbers of animals per breed will be extremely difficult or impossible. The current genotyping technology is probably only appropriate for within breed genomic predictions and therefore genomic selection across breed using the currently available technology is probably not possible. This statement will be reviewed once international research on this topic has been published and the results scrutinised.

2.4.3 Recommendations for the sheep industry

It is highly recommended that DNA of phenotyped animals is immediately collected, catalogued (i.e., the full animal ID) and stored appropriately. Rams with many progeny and therefore high accuracy of genetic evaluations should be particularly targeted. Animals should not be genotyped. This is because sufficient animals will not be available to successful implement a genomic selection programme probably for some years and by the time a sufficiently sized training population is available: 1) the cost of the genomic technology may have reduced or changed considerably and/or 2) genotyping for a greater number of genetic markers may be possible, thereby possibly facilitating across breed genomic evaluations. The number of phenotyped animals with DNA will be constantly monitored. The current cost of the 54K SNP chip is €85 to €90 per sample and €175 per sample for the HD (High density) SNP chip. Once a biological bank is generated the most informative animals based on phenotypic values and marginal contributions can be selectively genotyped to maximise the statistical power while constraining the costs.

2.4.4 Benefits of genomic selection

Simulation studies in cattle suggest that genetic gain can be increased by 50% with an appropriate genomic selection breeding programme. Expected response to selection from genomic selection may actually be greater in Irish sheep since the base accuracy of selection in the currently genetic evaluation system is low and therefore the potential scope for improvement is considerable. The accuracy of estimated genetic merit of newborn calves in Ireland is approximately 0.55 which compares to 0.18 in sheep.

2.4.5 Strategic genotyping

Although the cost of genotyping has reduced dramatically in recent years, generating a suitable reference population for genomic selection is still nonetheless expensive and therefore should be optimised. It has been shown that sampling phenotypically extreme animals yields higher accuracy than selecting animals at random or only selecting the best animals (Jiménez-Montero et al., 2012). Selecting the best animals, in fact, yielded the lowest accuracy. Many studies have shown that the degree of relationship between reference populations and selection candidates affects the prediction accuracy (Habier et al., 2007, Pszczola et al., 2012). These relationships are especially important for small reference populations (Wientjes et al., 2013). Additionally, it has been shown that strong relationships among animals in the reference population in fact have a negative effect on the average accuracy of genomic predictions in selection candidates (Pszczola et al., 2012). As a consequence, the optimal reference population design maximises the relationships between the reference population and the evaluated animals, while minimising the relationship among animals in the reference population.

Both from the perspective of relationship to the evaluated animals and from the perspective of sampling extreme phenotypes, it is likely that adding ‘unique’ animals to the reference population leads to higher increases in accuracy compared to adding animals at random. This implies that for traits where phenotypes are abundant, animals could be selected based on extreme phenotypes, i.e. selecting the best and the worst animals. For traits where phenotypes are difficult or expensive to obtain, or in future scenarios where the majority of animals in a population are genotyped, entire populations could be screened based on genotypes to select an optimal set of animals that needs to be phenotyped and subsequently included in the reference population, because they optimally contribute to the accuracy of genomic prediction in the whole population.

Implementing the aforementioned theoretical optimum design of a reference population may of course not be possible due to practical limitations. To achieve sufficiently high accuracy of genomic prediction, several alternative strategies exist. Phenotypic data may be available from past experiments but no DNA of these animals may be available. Those records can however be used in the analysis, using either relationship matrices that combine genomic and pedigree based relationship matrices (Aguilar et al., 2010, Veerkamp et al., 2011), or using sophisticated imputation algorithms to derive their genotypes (Hickey et al., 2012).

Recommendations

- A DNA storage bank must be created for sheep
- Samples should be taken on all phenotyped animals
- Genotyping of animals will commence once the costs are reduced and/or a large training population size has been established

Section 3 Breeding Programmes

To ensure that successful breeding strategies are implemented, breeding programmes must be developed to quantify its success. It also identifies genetically elite parents for subsequent generations and designs optimal matings for these animals appropriately to ensure sustainable long-term genetic gain with minimal accumulation of inbreeding. This is done through the modelling of the whole breeding programme and ensures that the breeding programme in operation is yielding the greatest benefit for the sector. All variables that are considered as a measurement of the overall effectiveness of the breeding programme are included.

Examples include: 1) the rate of genetic gain in the breeding goal achieved in the commercial population, 2) the economic benefit to the industry accounting for all factors affecting farm productivity, and 3) the profit for commercial sheep farmers.

A number of scenarios will be investigated using simulation data. These scenarios' include:

1. Nucleus recording flock within a flock
2. Large flocks recording small amounts of data versus small flocks recording large amount of data
3. Breeding programmes for hill flocks

Key predictors of the success of a breeding programme include: the rate of genetic gain, levels of inbreeding and recorded accuracy's.

The sheep industry must continuously review the breeding programmes to ensure that current and futures changes at the farm or industry level are accounted for. For example, Amer (2011) conducted a cost-benefit analysis of the potential gains of different genomic breeding programmes in the Irish dairy industry; similar research needs to be undertaken for sheep.

3.1 Improving accuracy

An improvement in the accuracy of the genetic evaluations will result in increased industry confidence in the published breeding values. Table 14 highlights the impact that sire's accuracy levels can have on economically important traits such as days to slaughter. Progeny from sires with low levels of accuracy (e.g. 10%) can finish approximately one month earlier or later than was indicated by the published breeding value. However, at high levels of accuracy (i.e. 80%) the expected range around the breeding value is reduced considerably to 18 days. At 99% accuracy the range around the published breeding value is 4 days. High accuracy levels will therefore reduce fluctuations in the published breeding values and therefore increase farmer's confidence in the genetic evaluations. Levels of accuracy can be improved through a variety of means including:

- Recording of high volumes of accurate data
- Use of predictor traits on difficult to measure traits
- Improving genetic linkage
- Use of rams in the CPT
- Development of genomic selection
-

Table 14 Range in EBV (estimated breeding values) for days to slaughter (+/-; in days) at a given level of accuracy.

Accuracy	Days to slaughter (+/-)
10%	29.56
20%	29.11
30%	28.34
40%	27.23
50%	25.73
60%	23.77
70%	21.22
80%	17.83
90%	12.95
95%	9.28
99%	4.19
100%	0.00

Recommendations

- Breeding programme research must be undertaken to ensure that the current breeding value is yielding the greatest gains achievable
- The importance and ways to improve accuracy must be highlighted continuously to farmers

Section 4 Breeding objectives

All traits included in the national breeding objectives are of economic importance to Irish production systems and are optimally weighted within the objectives. However, the breeding objective requires regular updates as changes occur: to the cost of inputs and outputs at farm level; new easily measurable important traits or predictor traits are identified.

4.1 Bio-economic model

Bio-economic models through the modelling of whole farm systems play an important role in identifying the pertinent inputs and outputs at farm level that have the largest impact on farm profitability. Bio-economic models have been developed for dairy and beef cattle in Ireland; however, to date no bio-economic model has been developed for the sheep sector. Cumulative discounted genetic expressions must be calculated for each trait using the algorithms already derived for cattle in Ireland (Berry et al., 2006). Economic values will be generated from the bio-economic model and will be implemented into the national sheep genetic evaluations. This bio-economic model will be developed by as part of a Walsh Fellow PhD (in conjunction with Dr. Laurence Shalloo; Alan Bohan commenced his PhD in October 2013.

Recommendations

- A bio-economic model must be developed urgently for the Sheep industry.

4.2 New traits

The feasibility of breeding for a given trait is dictated by the availability of data, either for the trait itself or a genetically related trait. Ideally the data should be measurable early in life, preferably also across genders, and be available at a low marginal cost. Research will continue to focus on evaluating state-of-the-art technologies and statistics to identify easy to implement tools to predict traits of economic importance in breeding goals. This will also include a review of the literature on possible predictor traits. It is likely in the future that the use of farmer scored traits will become even more important. This research will involve close collaboration with Sheep Ireland, Teagasc and the Teagasc BETTER farms. Examples of such predictor traits include meat quality traits, vigour scored at birth as a predictor of viability, weight bands used as predictors of birth weight and farmer scored traits as predictor of performance traits.

Recommendations

- Research will continue into the development of new traits for inclusion into genetic evaluations.

Section 5 Genetic evaluations

The current genetic evaluations are based on research conducted in 2008 to 2009. Table 15 provides an overview of the fixed and random effects (described in section 5.1) currently included in the genetic evaluations for each trait. However, since the initial research was conducted, a large amount of commercial and pedigree data has accumulated. Research will focus on estimating the genetic variation present among traits, as well as developing superior statistical model which reflects the underlying biology, and accounts for non-genetic effects. This research will be incorporated into the national genetic evaluations as soon as possible.

Table 15 List of fixed and random effects included in current genetic evaluations for all traits included in the two indexes.

Traits	Fixed effect	Random effects
40 day weight Weaning weights Weight at scanning Ultrasound scan	Sex Birth rank x Rear rank Flock x Birth year (FB) Contemporary Group Age at weighing x FB	Animal Dam (weight traits only)
Birth weight Lamb ease single birth Lamb ease multiple birth Lamb survival at birth	Age of dam Birth rank Contemporary Group	Animal Dam
NLB	Age of ewe Birth year Contemporary Group	Animal (ewe) Permanent Environment

5.1 Developing superior statistical models

5.1.1 Fixed effects

The inclusion of fixed effects in the model allow for difference in animal performance due to systematic differences to be identified (i.e. age of animal at weighing, breed of animal, feeding level on farm) and disentangled from the true genetic merit of the animal, or in other words if a farmer feeds all lambs creep feed this will not impact his genetic merit in the slightest. Since the formation of the original models used in the genetic evaluations there has been an accumulation of larger amounts of accurate on farm data. This will allow for research to be conducted into the development of a superior statistic model that better accounts for the fixed effects.

5.1.2 Random effects

For statistical models random effects are effects that are sampled from a probability distribution (i.e. not all animals are measured). For genetic models, these effects can be measured on the similarity between relatives as the effect of identical genes within one family. To date random effects included in the models were animal and sire; however, research must be conducted to investigate the potential benefit of including: maternal, permanent environmental effects and contemporary groups as random effects within the genetic evaluations.

Recommendations

- Research into superior statistical models should be conducted urgently
- Changes to the models used within the genetic evaluations will be implemented by the end of 2014

5.2 Re-estimation of genetic parameters

A large amount of data has been accumulated by Sheep Ireland since the initial research was carried out on the original genetic parameters for the Irish sheep population. A comprehensive review must now be taken which may result in the generation of new genetic parameters for the genetic evaluations. Research for the new genetic parameters will include the potential aforementioned changes to the statistical model (i.e. new fixed and random effects).

Recommendations

- Re-estimation of genetic parameters must be researched in 2014
- All changes to genetic parameters must be implemented in end 2014

5.3 Across breed evaluations

Across breed genetic evaluations facilitates comparisons of animals regardless of their breeds. To do so, the genetic evaluation model must correct for breed differences. The current genetic evaluations are conducted within breed, with a post-evaluation adjustment to a base of animals born in 2005 and to Texel EBV scale.

Research conducted to date has shown that the current data structure doesn't yet allow for an accurate across breed genetic evaluation. Annual tests will be run to re-assess the feasibility of producing accurate across breed breeding values. Research to date has shown that few breeds (TX, SU, CL, VN, BR, MM, and BL) have crossbred records, mainly through the collection of weight and lambing records from the MALP and CPT flocks. This research has also highlighted the importance of collection of cross bred phenotypes across all traits and all breeds to allow for accurate across breed evaluation in sheep.

Recommendations

- To allow for the development of across breed evaluations MALP and CPT flocks must continue to provide good quality crossbred data
- The recording of on farm phenotypes should be tighten, especially for lambing traits in the MALP flocks.
- MALP farmer should be encouraged to retain their own replacements where possible in order to improve the genetic evaluation for maternal traits.
- CPT flocks should provide good quality across breed data through chosen matings.
- Surplus ewe lambs not retained as replacements within the CPT flocks should be placed in commercial farm routinely recording phenotypes.
- Annual tests will be run to re-assess the feasibility of producing accurate across breed breeding values

5.4 Validation experiments

Genetic indexes, like all new technologies, will have to be demonstrated to deliver results on commercial farms before there will be large scale industry buy-in. Although validation of the production sub-index has been undertaken through data accumulated through Sheep Ireland (section 1.7), controlled experiments for animals divergent for genetic merit can also be undertaken. A new genetically elite flock is currently being established in Athenry to aid in evaluating the replacement index to ensure that animals deemed to be of high genetic merit for maternal traits are generating more profit at flock level. A further objective of this flock is to determine the suitability of New Zealand genetics for Irish grass based production systems. As part of this study a nucleus sheep flock, comprising of elite Suffolk and Texel females, representing the top genetic merit animals in the Irish and New Zealand genetic evaluations, respectively across a range of maternal traits will be evaluated. A third group of national average genetic merit Irish ewes will also be established to access the rates of genetic gain achievable under the current replacement index (Figure 9). This flock will access the biological and economic efficiency between the Irish and New Zealand genetically elite animals and monitor the relationship between the animal’s genetic merit and the phenotypic performance.

Recommendations

- The establishment of a validation experiment is underway but should be discussed in detail with the industry

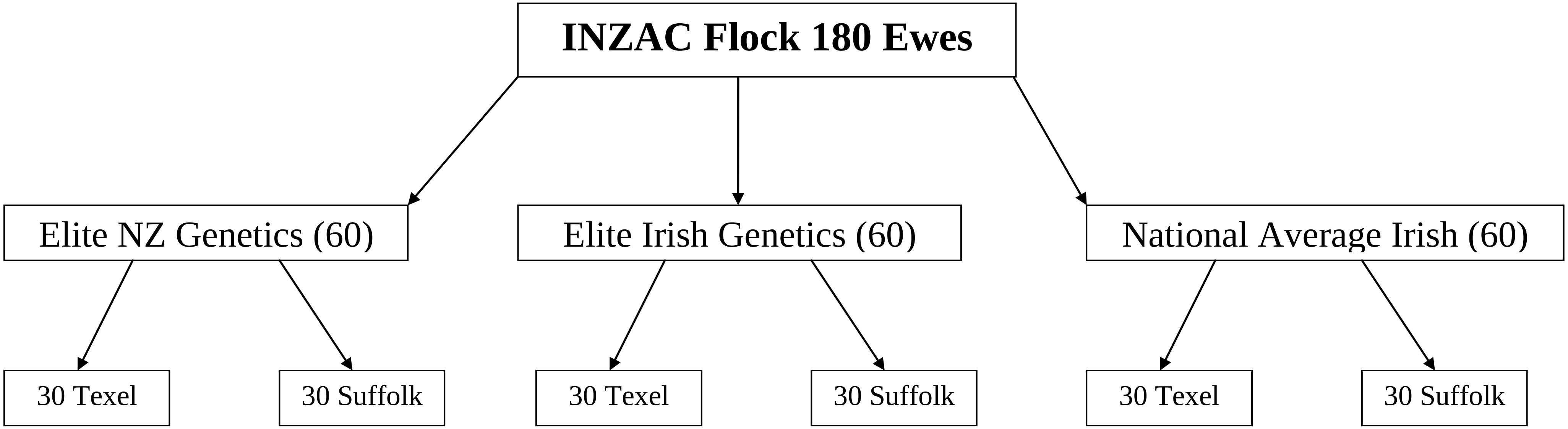


Figure 9 Summary of the study design for the INZAC flock (consisting of Elite New Zealand (60 ewes), Elite Irish (60 ewes) and National Average Irish (60 ewes) genetics.

Section 6 Knowledge exchange

Key to the success of any genetic evaluations is the uptake of the genetic information by producers. Sheep Ireland must strive to provide all relevant information to farmers in a timely manner in easy to interoperate reports.

6.1 Current deficits in the system

6.1.1 Inbreeding analysis

Inbreeding coefficients must be circulated to all breeders for their flocks in advance of the 2014 breeding season (depending on the levels of back pedigree recording; see section 1.2). This information will be of limited value to breeders without an easy to use facility, to allow breeders assess the risk of breeding specific ewes with specific rams. An online facility is being developed by Sheep Ireland to help breeders achieve this. It is hoped that this will be available before the main 2013 breeding season.

6.1.2 Annual report on CPT and MALP performance

Sheep Ireland are gathering a large volume of hugely valuable information for the industry, however this information is not being displayed to the wider industry. There is a need for a summary document to be prepared for both the CPT and MALP programmes and annual reports to be prepared from 2013.

6.1.3 Ram Sales Card

Breeders currently do not have access to an easy to use on-line facility to produce an individual ram sales card. Up to now breeders have been dependent on the circulation of €uro-Star information from Sheep Ireland – which is not a good model.

STAP has greatly increased the priority for this facility as farm sales of performance recorded rams will increase.

6.2 Reports

6.2.1 Flock reports

Although Sheep Ireland are focused on delivering benefit to the industry through the use of genetic evaluations, we acknowledge the desire from all performance recording flocks for simple performance reports, detailing various raw measurement data – weight gains, lambing difficulty etc. The reporting of this information has not been to the standard required up to now and this needs to be addressed in 2014 to deliver reports to all participating flocks once all weight measurements are recorded on the Sheep Ireland database.

6.2.2 Maternal Performance Report

Manually generated reports have been supplied to breeders on a sporadic basis, detailing the maternal performance of individual ewes. These reports are highly desired by commercial farmers. An automated report of this kind is required so that all recording breeders can generate a report at any time.

Ewes should be listed according to the numbers of lambs born, and then on average daily gain per lamb. Other important phenotypes can be included easily. An online version of this report is essential, which would allow participating farmers to sort ewes based a wide range of criteria. Paper reports are very limited in this regard. Approximately 25% of all flocks currently participating in Sheep Ireland are recording data via paper, although this number is decreasing slightly annually.

Although these physical performance reports are useful, the experience up to now has been that farmers will use these reports to select ewe replacements in place of genetic evaluation information. Trust needs to build in the €uro-Stars, which will only be achieved by regular demonstration of the benefits same.

6.2.3 Ram Report

Each participating recording flock needs to receive an annual report on the performance of their rams annually. Most flocks contain rams that are not performing as they should for many different reasons, but are never identified due to poor record keeping or poor use of recorded data.

Sheep Ireland needs to provide breeders with a greater level of data on their rams recorded data. These reports should detail a summary of:

- Total number of recorded progeny on the Sheep Ireland database
- The origin of these records – LambPlus/MALP/CPT/Other Commercial
- Number of lambs born
- Lamb survival % & difficulty %
- Growth performance of lambs – ADG (within Pedigree and commercial, if applicable)
- €uro-Star evaluation summary

Recommendations

- Inbreeding coefficients will be made available to farmers where sufficient back pedigree is available
- An online ram search tool will be launched as soon as possible
- Clear, precise, easy to use online reports combining genetic and phenotypic information must be made available to all Sheep Ireland users as soon as possible
- Industry consultations meetings will be organised at least twice per year where latest research results and changes to genetic evaluations will be presented

References

Aguilar, I., I. Misztal, D. Johnson, A. Legarra, S. Tsuruta, and T. Lawlor. 2010. Hot topic: a unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score. J. Dairy Sci. 93:743-752.

Byrne, T.J., Amer, P.R., Fennessy, P.F., Cromie, A., Keady, T.W.J., Hanrahan, J.P., McHugh, M.P. and Wickham, B.W. 2010. Breeding objectives for sheep in Ireland: A bio-economic approach. Livestock Science. 132: 135-144.

Fouilloux, M.N., Clement, V., and Laloe, D. 2008. Measuring connectedness among herds in mixed linear models: From theory to practice in large-size genetic evaluations. Genetics Selection Evolution. 40: 145-159.

Hickey, J., B. Kinghorn, B. Tier, J. van der Werf, and M. Cleveland. 2012. A phasing and imputation method for pedigreed populations that results in a single-stage genomic evaluation. Genetics Selection Evolution 44:9.

Jiménez-Montero, J. A., O. Gonzalez-Recio, and R. Alenda. 2012. Genotyping strategies for genomic selection in dairy cattle. Animal 6:1216-1224.

Habier, D., R. Fernando, and J. Dekkers. 2007. The impact of genetic relationship information on genome-assisted breeding values. Genetics 177:2389-2397.

McClure, M., Sonstegard, T., Wiggans, G., and Van Tassell, C.P. 2012. Imputation of microsatellite alleles from dense SNP genotypes for parental verification. Frontiers in Genetics, 3: 140 (1-9).

Mathur, P.K., Sullivan, B., and Chesnais, J. 1998. A New Method for Assessing Connectedness Between Herds. Proceedings from National Swine Improvement Federation Conference and Annual Meeting 1998. http://www.nsif.com/Conferences/1998/mathur.htm

Mc Parland, S., Kearney, J.F., Rath, M. and Berry, D.P. 2007. Inbreeding effects on milk production, calving performance, fertility, and conformation in Irish Holstein-Friesians. Journal of Dairy Science, 90: 4411- 4419.

Tarres, J., Fina, M., and Peidrafita, J. 2010. Connectedness among herds of beef cattle bred under natural service. Genetics Selection Evolution, 42: 6.

Pszczola, M., T. Strabel, H. A. Mulder, and M. P. L. Calus. 2012. Reliability of direct genomic values for animals with different relationships within and to the reference population. J. Dairy Sci. 95:389-400.

Veerkamp, R. F., H. A. Mulder, R. Thompson, and M. P. L. Calus. 2011. Genomic and pedigree-based genetic parameters for scarcely recorded traits when some animals are genotyped. J. Dairy Sci. 94:4189-4197.