Combined breed analysis for terminal sheep breeds

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Milestone 4: Provision of EBVs and index recommendations

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Introduction

This report is the fourth milestone of the combined breed analysis for terminal sheep breeds. Included are objectives 6 and 7.

Objective 6: Extensively test the resulting EBVs such that EGENES are confident and then you provide to industry for review

A series of test runs were undertaken and are reported in **Appendix A** (separate document). A summary of key test runs and the final set of EBVs ready for industry testing are reported in the main document.

Methods used by other countries

There is a crossbreed evaluation for sheep available in several countries like New Zealand, Australia or Ireland. There are different approaches for dealing with heterosis and recombination between different breeds/breed types. Ireland is using method 2 (described below), while New Zealand treats sheep alike, beside the breed/breed type (i.e. there are no heterosis and recombination effects included in the models). Section below describes the methods tested in order to choose the best approach for UK.

Impact of changing method of calculating heterosis/recombination

Three methods were evaluated and they are as described below.

Method 1: 3 breed types with 6 terms fitted in total. Assumes crosses within breed types have no hybrid vigour.

Method 2: consider each breed separately but sum to a total amount and fit 2 terms. Assumes the hybrid vigour is the same for each type of breed cross.

Method 3: Is the same as Method 2, but also the addition of several key crosses; in this case Texel*Suffolk & Texel*Charollais as the 2 most frequent crosses. The heterosis and recombination effects for the key crosses are subtracted so as not to be considered twice. In this case we terms are fitted in the model.

Batch id 20130061 showed the results for method 1 and batch 20130066 method 2 and batch 20130067 is method 3.

While the EBVs are not the final version, the only difference between these batches is the method of accounting for hybrid vigour, so can be used to assess and determine which method of hybrid vigour we should model.

Correlation between EBVs?

The different methods appear to have no impact on the EBVs produced. For all traits the correlations between the EBVs were 0.99+ and the distribution of EBVs were almost identical so are not reported. This suggests that on a population wide level the impact of the method for hybrid vigour has little to no impact.

Estimates of hybrid vigour?

The values quoted here are in the same units as the measured trait – showing the impact of 1% heterosis or recombination.

So for an F1 cross between two breeds the impact of heterosis is 100 x the solution presented.

For example – The influence of heterosis upon Scan Weight is a phenotypic difference of 1.8kg (based on Job 1 of the method 2 solutions in the tables below).

The recombination values can be ignored in an F1 cross as the recombination coefficient is 0, thus 0* the recombination solution = 0. However, for crosses other than F1 the hybrid vigour can be estimated as (heterosis coefficient * heterosis solution) + (recombination coefficient * recombination solution).

As maternal ability EBV is the maternal component of 8 week weight it does not receive a separate heterosis/recombination estimate as the 8 week weight is adjusted for hybrid vigour and then the direct (8 week weight EBV) and maternal (Maternal ability EBV) is partitioned out.

The raw solutions for heterosis and recombination from MiX99 are presented below for method 1 (batch 20130061). Note job 1 and job 2 refer to 2 phases with a subset of traits run in each phase.

	Job 1						**Job 2**					
	heterosis			**recombination**			**heterosis**			**recombination**		
types*	**1,2**	**1,3**	**2,3**	**1,2**	**1,3**	**2,3**	**1,2**	**1,3**	**2,3**	**1,2**	**1,3**	**2,3**
w8w	0.006	0.057	0.048	0.017	-0.086	-0.064	0.004	0.071	0.069	0.025	-0.116	-0.092
Swt	0.020	0.183	0.090	0.035	-0.230	-0.134	0.022	0.180	0.070	0.025	-0.267	-0.150
Md	0.009	0.116	0.058	0.011	-0.147	-0.077	0.010	0.132	0.073	0.008	-0.182	-0.117
Fd	0.001	0.018	-0.003	0.002	-0.018	0.003						
mat_sz							-0.050	0.490	0.364	0.294	-0.736	-0.591
Lsb							0.0003	0.004	0.005	0.002	-0.004	-0.005
Lsr							0.00004	-0.001	0.001	0.002	0.002	-0.001
ct_lean	0.007	0.016	-0.018	0.009	-0.039	0.040						
ct_fat	-0.001	-0.011	-0.106	0.008	0.014	0.115						
ct_musc							0.002	0.523	0.818	0.157	-0.818	-1.054
lfec_S							-0.0004	-2.244	-10.563	0.001	2.536	12.097
lfec_N							-0.0003	-0.335	-0.536	-0.002	0.318	0.629
Bwt	0.001	-0.004	0.006	0.008	0.002	-0.006						
LE	-0.014	0.000	-5.129	0.007	0.016	5.365						

***Breed types:**

1 European Terminal; 2 native terminal; 3 other (non-terminal breeds)

The raw solutions for heterosis and recombination from MiX99 are presented below for method 2 (batch 20130066). Note job 1 and job 2 refer to 2 phases with a subset of traits run in each phase.

	Job 1		**Job 2**	
	heterosis	**recombination**	**heterosis**	**recombination**
w8w	0.005	0.004	0.003	0.002
Swt	0.018	0.008	0.017	0.008
Md	0.009	0.001	0.009	-0.002
Fd	0.001	0.003		
mat_sz			-0.026	-0.011
Lsb			-0.00004	-0.0004
Lsr			0.0002	-0.0002
ct_lean	0.006	0.00003		
ct_fat	0.0003	0.002		
ct_musc			0.017	0.019
lfec_S			-0.0004	0.0002
lfec_N			-0.0002	-0.004
Bwt	0.001	0.001		
LE	-0.010	-0.002		

The raw solutions for heterosis and recombination from MiX99 are presented below for method 3 (batch 20130067). Note job 1 and job 2 refer to 2 phases with a subset of traits run in each phase.

	Job 1						**Job 2**					
	heterosis			**recombination**			**heterosis**			**recombination**		
types*	**all**	**T*S**	**T*C**	**all**	**T*S**	**T*C**	**all**	**T*S**	**T*C**	**all**	**T*S**	**T*C**
w8w	0.003	0.011	0.002	-0.004	0.016	0.018	0.001	0.008	-0.0002	-0.008	0.026	0.014
Swt	0.012	0.027	0.008	-0.004	0.037	0.009	0.017	0.022	0.030	-0.022	0.031	0.051
Md	0.010	0.011	-0.006	-0.006	0.011	-0.012	0.011	0.010	-0.0004	-0.015	0.010	0.0001
Fd	0.002	0.002	0.0004	-0.00009	0.003	0.007						
mat_sz							-0.034	-0.065	0.000	-0.055	0.407	0.000
Lsb							-0.0002	0.001	-0.0009	-0.0003	0.0003	-0.002
Lsr							0.0001	0.001	-0.0003	-0.0005	0.001	-0.001
ct_lean	0.007	0.008	0.000	-0.004	0.009	0.097						
ct_fat	0.003	0.001	0.000	-0.003	0.008	-0.206						
ct_musc							0.043	0.003	0.000	-0.095	0.161	1.414
lfec_S							-0.328	-0.0005	0.000	0.346	0.001	0.000
lfec_N							-0.174	-0.0003	0.000	0.173	-0.002	0.000
Bwt	0.001	0.002	-0.001	-0.0002	0.007	0.001						
LE	-0.815	-0.014	0.005	0.807	0.007	0.147						

Hybrid vigour of a first cross animal using the 3 methods

The table below looks at the hybrid vigour of first cross animals (het=100 and rec=0) for different crosses based on the solutions reported above (where I had solutions from 2 jobs I used the solutions from the 1st for these calculations).

First cross	w8w	Swt	Md	Fd	mat_sz	Lsb	Lsr	ct_lean	ct_fat	ct_musc	lfec_S	lfec_N	Bwt	LE
Method 1														
Tex*Suf	5.7	18.3	11.6	1.8	49	0.4	-0.1	1.6	-1.1	52.3	-224.4	-33.5	-0.4	0
Tex*Char	0.6	2	0.9	0.1	-5	0.03	0.004	0.7	-0.1	0.2	-0.04	-0.03	0.1	-1.4
Suf*Char	5.7	18.3	11.6	1.8	49	0.4	-0.1	1.6	-1.1	52.3	-224.4	-33.5	-0.4	0
Texel*ML	5.7	18.3	11.6	1.8	49	0.4	-0.1	1.6	-1.1	52.3	-224.4	-33.5	-0.4	0
Method 2														
Tex*Suf	0.5	1.8	0.9	0.1	-2.6	-0.004	0.02	0.6	0.03	1.7	-0.04	-0.02	0.1	-1
Tex*Char	0.5	1.8	0.9	0.1	-2.6	-0.004	0.02	0.6	0.03	1.7	-0.04	-0.02	0.1	-1
Suf*Char	0.5	1.8	0.9	0.1	-2.6	-0.004	0.02	0.6	0.03	1.7	-0.04	-0.02	0.1	-1
Texel*ML	0.5	1.8	0.9	0.1	-2.6	-0.004	0.02	0.6	0.03	1.7	-0.04	-0.02	0.1	-1
Method 3														
Tex*Suf	1.1	2.7	1.1	0.2	-6.5	0.1	0.1	0.8	0.1	0.3	-0.05	-0.03	0.2	-1.4
Tex*Char	0.2	0.8	-0.6	0.04	0	-0.09	-0.03	0	0	0	0	0	-0.1	0.5
Suf*Char	0.3	1.2	1	0.2	-3.4	-0.02	0.01	0.7	0.3	4.3	-32.8	-17.4	0.1	-81.5
Texel*ML	0.3	1.2	1	0.2	-3.4	-0.02	0.01	0.7	0.3	4.3	-32.8	-17.4	0.1	-81.5
EasyRams Spark award														
Tex*Suf	-1.8	1.6	1.8	0.4	0.0	-0.76	-	-4.2	3.3	3.1	-4.1	-1.5	-	-

From the results above it can be shown that as the number of categories increases we get some pretty unbelievable solutions for traits that are not well recorded; mature size, ct muscling, FEC and lambing ease to name the main traits affected. I suspect that this is because there is very little data for cross bred animals, so providing these EBVs to crossbred animals may not be appropriate regardless of the method for modelling hybrid vigour. Grouping breeds into broad breed types resulted in higher hybrid vigour estimates for the different first cross examples. For comparison I have also included the hybrid vigour from the initial Easyrams Spark award project. Even using method 2 with no subgroups we still see some solutions that are unexpected for traits like mature size. This is likely to be because the number of cross bred animals with these traits recorded is small, and of those that are recorded the crosses are smaller than the purebred. In these instances it may not be appropriate for cross bred EBVs to be supplied, or if they are then a health notice accompanies them.

What do the EBVs look like for first cross Texel and Suffolk animals?

To further assess the impact on the first cross Texel-Suffolk animals were extracted and their EBVs compared. For all traits the correlation between the EBVs from different methods were all 0.99+ showing that on a practical level the choice of method had little impact, given the current structure of the data.

XBREED (N=1410)

	METHOD 1				**METHOD 2**				**METHOD 3**			
	mean	**stdev**	**min**	**max**	**mean**	**stdev**	**min**	**max**	**mean**	**stdev**	**min**	**max**
w8w	-0.57	2.85	-5.66	6.12	-0.51	2.84	-5.61	6.09	-0.76	2.93	-5.81	6.08
Maternal	-0.20	0.85	-2.01	1.95	-0.18	0.85	-2.01	1.98	-0.21	0.85	-1.99	1.92
Swt	-2.02	6.39	-12.11	14.16	-1.89	6.38	-12.01	14.13	-2.34	6.53	-12.78	14.11
Md	-0.10	1.80	-2.95	4.57	-0.08	1.80	-2.94	4.52	-0.17	1.82	-3.09	4.55
Fd	0.19	0.26	-1.03	1.61	0.19	0.26	-1.03	1.61	0.17	0.27	-1.06	1.61
mat_sz	-0.70	1.24	-2.31	3.39	-0.68	1.24	-2.30	3.40	-0.69	1.24	-2.34	3.39
Lsb	-0.06	0.07	-0.29	0.23	-0.06	0.07	-0.28	0.25	-0.07	0.07	-0.30	0.23
Lsr	-0.04	0.05	-0.20	0.15	-0.04	0.05	-0.19	0.16	-0.04	0.05	-0.20	0.14
ct_lean	-0.68	1.77	-3.46	3.69	-0.64	1.77	-3.44	3.68	-0.76	1.81	-3.58	3.68
ct_fat	-0.17	0.86	-1.87	2.05	-0.14	0.86	-1.86	2.05	-0.22	0.88	-1.88	2.04
ct_musc	-0.68	2.52	-4.82	7.08	-0.63	2.55	-4.76	7.08	-0.68	2.53	-4.83	7.10
FEC	-0.03	0.20	-1.41	1.35	-0.03	0.20	-1.41	1.40	-0.04	0.20	-1.40	1.35
Bwt	-0.18	0.30	-0.87	0.57	-0.18	0.30	-0.86	0.59	-0.21	0.31	-0.89	0.56
LE	-0.01	0.30	-1.62	0.76	-0.01	0.30	-1.60	0.79	-0.02	0.30	-1.62	0.83

What do the EBVs look like for first cross Texel and Charollais animals?

To further assess the impact on the first cross Texel-Charollais animals were extracted and their EBVs compared. For all traits the correlation between the EBVs from different methods were all 0.98+ showing that on a practical level the choice of method had little impact, given the current structure of the data.

XBREED (N=1762)

	METHOD 1				**METHOD 2**				**METHOD 3**			
	mean	**stdev**	**min**	**max**	**mean**	**stdev**	**min**	**max**	**mean**	**stdev**	**min**	**max**

w8w	0.16	1.94	-5.08	5.30	0.21	1.96	-5.03	5.39	0.20	1.89	-5.06	5.17
Maternal	-0.12	0.52	-1.94	1.53	-0.13	0.51	-1.95	1.50	-0.16	0.51	-1.94	1.48
Swt	0.31	3.66	-10.87	8.83	0.36	3.73	-10.84	9.02	0.38	3.65	-10.87	8.83
Md	0.18	0.99	-2.29	3.28	0.21	1.04	-2.48	3.47	0.23	1.01	-2.22	3.42
Fd	0.06	0.43	-0.97	2.30	0.05	0.43	-0.95	2.26	0.03	0.39	-0.86	2.15
mat_sz	0.49	1.25	-2.14	3.95	0.49	1.26	-2.14	3.94	0.52	1.25	-2.13	3.95
Lsb	-0.01	0.07	-0.23	0.23	-0.01	0.07	-0.22	0.23	0.00	0.07	-0.19	0.23
Lsr	-0.02	0.05	-0.14	0.13	-0.02	0.05	-0.15	0.13	-0.01	0.04	-0.13	0.13
ct_lean	-0.15	1.14	-3.49	2.76	-0.14	1.15	-3.46	2.79	-0.12	1.14	-3.47	2.78
ct_fat	0.09	0.63	-1.55	2.16	0.08	0.63	-1.56	2.15	0.07	0.60	-1.56	2.07
ct_musc	-0.25	1.42	-4.94	3.93	-0.24	1.45	-4.99	3.99	-0.33	1.39	-4.93	3.90
FEC	-0.01	0.12	-0.59	0.52	-0.01	0.12	-0.59	0.52	-0.01	0.13	-0.59	0.53
Bwt	-0.04	0.30	-0.80	0.81	-0.04	0.31	-0.80	0.81	-0.04	0.30	-0.80	0.79
LE	-0.08	0.37	-1.61	0.80	-0.08	0.37	-1.60	0.79	-0.08	0.37	-1.61	0.79

Conclusions

All 3 methods of modelling hybrid vigour are possible. On a practical level based on the Texel-Suffolk and Texel-Charollais first cross animals – which should be most affected by hybrid vigour – we see that there is no real impact on the resulting EBVS. When we look at the hybrid vigour solutions we see – especially for traits not widely recorded – differences in the solutions. Although the hybrid vigour solutions are different for the 2 crosses fitted on a practical level we see no impact of the different methods on the EBVs – or the way the 2 crosses compared to each other.

To conclude while these results show that any method would be suitable for implementation I would suggest method 2 as the heterosis and recombination estimates were more sensible for the less well recorded traits. However, I can see the benefit of method 3 with respect to PR of the new system.

This was discussed with Signet and it was decided to implement method 2 with the option of re considering method 3 in the future when more cross bred data is available.

Revising the genetic parameters for use in the evaluation.

Milestone 2 looked at the different genetic parameters of the 12 participating breeds and set the combined breed parameters to be those of the Texel breed with a scaling factor to account for the different phenotypic variances across the 12 individual breeds. As part of the runs in Appendix A the scaling factors were all set to 1 (so no scaling) with the view of reconsidering when assessing the breed differences. With scaling switched off it is assuming that the phenotypic variances of each breeds are identical. If breed A has a higher phenotypic variance than breed B, then this will be seen in the EBVs with more breed A animals appearing in the top and bottom of the distribution.

The (Texel) parameters that are currently used in the evaluations are below;

Variances and heritability estimates

Trait	**Direct**	**Maternal**	**PE**	**Residual**	**Phenotypic**	**h^2_{direct}**	**$h^2_{maternal}$**	**h^2_{pe}**
8 WK	3.303	1.205	2.508	6.033	13.049	0.25	0.09	0.19
SWT	12.598	-	-	18.408	31.006	0.41	-	-
MD	2.053	-	-	5.063	7.116	0.29	-	-
FD	0.402	-	-	0.662	1.064	0.38	-	-
MS	4.536	-	-	8.424	12.96	0.35	-	-
LSB	0.042	0.021	-	0.355	0.418	0.10	0.05	-
LSR	0.02	0.01	-	0.34	0.37	0.05	0.06	-
CT_L	1.062	-	-	1.43	2.492	0.43	-	-
CT_F	0.606	-	-	1.31	1.916	0.32	-	-
CT_M	11.80	-	-	27.1	38.9	0.30	-	-
FECS	0.295	-	-	0.839	1.134	0.26	-	-
FECN	0.210	-	-	0.342	0.552	0.38	-	-
BWT	0.134	0.073	0.106	0.322	0.635	0.21	0.11	0.17
LE	0.071	0.015	0.322	0.095	0.503	0.14	0.03	0.64

* all co-variances between maternal effects and between pe effects are 0

Direct Covariances (below) and correlations (above)

	8 WK	**SWT**	**MD**	**FD**	**MAT**	**MS**	**LSB**	**LSR**	**CT_L**	**CT_F**	**CT_M**	**FECS**	**FECN**	**BWT**	**LE**
8 WK		0.90	0.49	0.36	0	0	0	0	0.82	0.67	0.56	-0.13	0.17	0.63	0.11
SWT	5.803		0.47	0.37	0	0	0	0	0.83	0.68	0.56	-0.13	0.17	0.46	0.06
MD	1.278	2.374		0.24	0	0	0	0	0.41	0.23	0.26	-0.05	0.21	0.10	0.21
FD	0.418	0.843	0.216		0	0	0	0	-0.06	0.55	0.41	-0.06	0	0.03	0.20
MAT	0	0	0	0		0.15	0	0	0	0	0	0	0	0	0
MS	0	0	0	0	0.351		0.20	0.06	0	0	0	0	0	0	0
LSB	0	0	0	0	0	0.087		0.04	0	0	0	0	0	0	0
LSR	0	0	0	0	0	0.018	0.017		0	0	0	0	0	0	0
CT_L	1.545	3.049	0.603	-0.039	0	0	0	0		0.38	0.38	-0.15	0.20	0.56	0.08
CT_F	0.948	1.871	0.257	0.269	0	0	0	0	0.306		0.26	-0.15	0.17	0.43	0.02
CT_M	3.470	6.779	1.28	0.90	0	0	0	0	1.354	0.703		0	0	0.36	0.26
FECS	-0.128	-0.251	-0.039	-0.021	0	0	0	0	-0.085	-0.064	0		0.60	0	0
FECN	0.140	0.276	0.138	0	0	0	0	0	0.095	0.061	0	0.149		0	0
BWT	0.419	0.603	0.054	0.006	0	0	0	0	0.21	0.121	0.45	0	0		0.24
LE	0.051	0.053	0.079	0.033	0	0	0	0	0.021	0.004	0.238	0	0	0.023	

Residual Covariances (below) and correlations (above)

	8 WK	**SWT**	**MD**	**FD**	**MS**	**LSB**	**LSR**	**CT_L**	**CT_F**	**CT_M**	**FECS**	**FECN**	**BWT**	**LE**
8 WK		0.84	0.47	0.37	0.10	0	0	0.75	0.63	0.25	-0.01	-0.10	0.39	0.22
SWT	8.882		0.61	0.49	0	0	0	0.86	0.74	0.25	0.004	-0.13	0.18	0.19
MD	2.603	5.907		0.38	0	0	0	0.61	0.44	0.40	-0.06	-0.12	0.09	0.02
FD	0.74	1.712	0.695		0	0	0	0.45	0.53	0.06	-0.12	-0.03	-0.02	-0.07
MS	0.712	0	0	0		0.10	0	0	0	0	0	0	0	0
LSB	0	0	0	0	0.173		0	0	0	0	0	0	0	0
LSR	0	0	0	0	0	0		0	0	0	0	0	0	0
CT_L	2.217	4.42	1.642	0.436	0	0	0		0.62	0.45	0.001	-0.15	0.29	-0.08
CT_F	1.772	3.655	1.136	0.495	0	0	0	0.852		0.17	0.10	-0.10	0.25	-0.01
CT_M	3.145	5.494	4.685	0.25	0	0	0	2.777	1.035		0	0	0.10	-0.12
FECS	-0.025	0.014	-0.131	-0.089	0	0	0	0.001	0.11	0		0.23	0	0
FECN	-0.143	-0.317	-0.158	-0.013	0	0	0	-0.106	-0.069	0	0.123		0	0
BWT	0.544	0.438	0.115	-0.005	0	0	0	0.20	0.16	0.284	0	0		0.34
LE	0.167	0.25	0.015	-0.018	0	0	0	-0.03	-0.002	-0.20	0	0	0.06	

The revised set of parameters to use in the evaluations is below; Values that have been modified are shown in red. For the 4 core traits; weights and ultrasound scans - the heritability and phenotypic variances were set as the average of all 12 breeds. Mature size was kept unchanged as most breeds were these estimates, and those that were not had higher variances and/or heritabilities but were poorly recorded for the trait. Litter size born heritability was unchanged as the average was 0.10 (direct) and 0.05 (maternal) which was the Texel value. The phenotypic variance was changed to being the average of all breeds. The Dorset values were used for litter size reared. For the 3 CT traits only the parameters of the 3 main breeds with data was used; Texel, Suffolk and Charollais. Due to the poor nature of recording for FEC – and all parameters being the same – the parameters were unchanged. For birth weight an average between Dorset and Texel was used as the only 2 breeds estimated for this trait, and for lambing ease the Texel parameters were used as the only breed recorded for this trait.

In all cases the direct, maternal and PE variance are simply mathematical functions of the heritabilities and phenotypic variances. Details of the individual breeds are shown below in Appendix A.

Variances and heritability estimates

Trait	Direct	Maternal	PE	Residual	Phenotypic	h^2_{direct}	$h^2_{maternal}$	h^2_{pe}
8 WK	2.350	1.768	1.806	5.654	11.579	0.20	0.15	0.16
SWT	9.832	-	-	22.940	32.772	0.30	-	-
MD	1.824	-	-	4.930	6.754	0.27	-	-
FD	0.400	-	-	0.978	1.378	0.29	-	-
MS	4.536	-	-	8.424	12.96	0.35	-	-
LSB	0.038	0.019	-	0.319	0.375	0.10	0.05	-
LSR	0.01	0.005	-	0.25	0.265	0.04	0.02	-
CT_L	0.972	-	-	1.188	2.16	0.45	-	-
CT_F	0.793	-	-	1.350	2.143	0.37	-	-
CT_M	11.538	-	-	21.429	32.967	0.35	-	-
FECS	0.295	-	-	0.839	1.134	0.26	-	-
FECN	0.210	-	-	0.342	0.552	0.38	-	-
BWT	0.111	0.103	0.099	0.234	0.548	0.20	0.19	0.18
LE	0.071	0.015	0.322	0.095	0.503	0.14	0.03	0.64

* all co-variances between maternal effects and between pe effects are 0

Reviewing the genetic and residual correlations and with Signets feedback the following changes to the parameters were made;

- FEC EBVs will be considered as uni-variates with all correlations set to 0 with other non-fec traits. This is due to the poor recording nature of these traits, and the relative unknown true correlations.
- Lambing ease remained as Texel as they were the only breed with this trait
- 8 and 21 week weight and ultrasound traits were generally similar with the average correlation of all the breeds, except Shropshire which seem unusual compared to the others.
- Birth weight was the average of Dorset and Texel the only 2 breeds with this trait, except for CT traits where Dorset are not recorded.
- CT traits were taken as the average of the 3 main breeds.
- Apart from the correlation between LSB & LSR (which comes from the Dorset parameter work), both litter traits will not be correlated with the other traits. This is to be risk adverse as we have not estimated these parameters yet in main terminal breeds.
- Mature size parameters have generally not been estimated so breeds tend to have them or not. However, given the relationship with the other growth traits it is appropriate for the correlations to be positive. The final correlations with the 4 core traits were an average of all the breeds where the correlation was not 0.
- Correlations with maternal traits are another difficult trait to come to a consensus. To err on the side of caution the parameters were kept to 0 as reliable estimates are not available for terminal breeds.

Due to the variance changes the co-variances all needed changing even if the correlation remained constant.

The following tables show the genetic and residual correlations to be used in the evaluations with those that have changed marked in red.

Direct Covariances (below) and correlations (above)

	8 WK	**SWT**	**MD**	**FD**	**MAT**	**MS**	**LSB**	**LSR**	**CT_L**	**CT_F**	**CT_M**	**FECS**	**FECN**	**BWT**	**LE**
8 WK		0.81	0.41	0.35	0	0.49	0	0	0.76	0.68	0.31	0	0	0.55	0.11
SWT	3.893		0.45	0.40	0	0.57	0	0	0.81	0.69	0.31	0	0	0.37	0.06
MD	0.849	1.906		0.28	0	0.27	0	0	0.48	0.32	0.29	0	0	0.18	0.21
FD	0.339	0.793	0.239		0	0.24	0	0	-0.02	0.53	0.10	0	0	0.06	0.20
MAT	0	0	0	0		0	0	0	0	0	0	0	0	0	0
MS	1.600	3.807	0.777	0.323	0		0	0	0	0	0	0	0	0.01	0
LSB	0	0	0	0	0	0		0.58	0	0	0	0	0	0	0
LSR	0	0	0	0	0	0	0.011		0	0	0	0	0	0	0
CT_L	1.149	2.504	0.639	-0.012	0	0	0	0		0.42	0.37	0	0	0.56	0.08
CT_F	0.928	1.927	0.385	0.298	0	0	0	0	0.369		0.09	0	0	0.43	0.02
CT_M	1.614	3.302	1.330	0.215	0	0	0	0	1.239	0.272		0	0	0.36	0.26
FECS	0	0	0	0	0	0	0	0	0	0	0		0.60	0	0
FECN	0	0	0	0	0	0	0	0	0	0	0	0.149		0	0
BWT	0.281	0.387	0.081	0.013	0	0.007	0	0	0.184	0.128	0.407	0	0		0.24
LE	0.045	0.050	0.076	0.034	0	0	0	0	0.021	0.005	0.235	0	0	0.021	

Residual Covariances (below) and correlations (above)

	8 WK	**SWT**	**MD**	**FD**	**MS**	**LSB**	**LSR**	**CT_L**	**CT_F**	**CT_M**	**FECS**	**FECN**	**BWT**	**LE**
8 WK		0.78	0.46	0.40	0.20	0	0	0.72	0.68	0.25	0	0	0.35	0.22
SWT	8.883		0.53	0.44	0.25	0	0	0.89	0.84	0.25	0	0	0.22	0.19
MD	2.429	5.636		0.36	0.23	0	0	0.51	0.42	0.32	0	0	0.11	0.02
FD	0.941	2.084	0.790		0.13	0	0	0.37	0.59	0.12	0	0	0.07	-0.07
MS	1.380	3.475	1.482	0.373		0	0	0	0	0	0	0	0.32	0
LSB	0	0	0	0	0		0.41	0	0	0	0	0	0	0
LSR	0	0	0	0	0	0.116		0	0	0	0	0	0	0
CT_L	1.866	4.646	1.234	0.399	0.000	0	0		0.67	0.25	0	0	0.29	-0.08
CT_F	1.879	4.675	1.084	0.678	0.000	0	0	0.848		0.20	0	0	0.25	-0.01
CT_M	2.752	5.543	3.289	0.549	0.000	0	0	1.261	1.076		0	0	0.10	-0.12
FECS	0.000	0.000	0.000	0.000	0.000	0	0	0.000	0.000	0.000		0.23	0	0
FECN	0.000	0.000	0.000	0.000	0.000	0	0	0.000	0.000	0.000	0.123		0	0
BWT	0.403	0.510	0.118	0.033	0.449	0	0	0.153	0.141	0.224	0.000	0.000		0.34
LE	0.161	0.280	0.014	-0.021	0.000	0	0	-0.027	-0.004	-0.171	0.000	0.000	0.051	

The genetic and residual matrixes were checked for being positive definite and bended to be positive definite which resulted in small changes. The final genetic and residual co-variances used for the evaluation are reported below.

Variances and heritability estimates

Trait	Direct	Maternal	PE	Residual	Phenotypic	h^2_{direct}	$h^2_{maternal}$	h^2_{pe}
8 WK	2.369	1.768	1.806	5.654	11.579	0.20	0.15	0.16
SWT	9.864	-	-	22.946	32.810	0.30	-	-
MD	1.827	-	-	4.930	6.757	0.27	-	-
FD	0.406	-	-	0.979	1.385	0.29	-	-
MS	4.573	-	-	8.426	12.999	0.35	-	-
LSB	0.038	0.019	-	0.319	0.376	0.10	0.05	-
LSR	0.01	0.005	-	0.25	0.265	0.04	0.02	-
CT_L	1.138	-	-	1.235	2.373	0.48	-	-
CT_F	0.882	-	-	1.377	2.259	0.39	-	-
CT_M	11.539	-	-	21.429	32.968	0.35	-	-
FECS	0.295	-	-	0.839	1.134	0.26	-	-
FECN	0.210	-	-	0.342	0.552	0.38	-	-
BWT	0.112	0.103	0.099	0.255	0.569	0.20	0.18	0.17
LE	0.071	0.015	0.322	0.141	0.549	0.13	0.03	0.59

* all co-variances between maternal effects and between pe effects are 0

Direct Covariances (below) and correlations (above), variances on the diagonal

	8 WK	**SWT**	**MD**	**FD**	**MAT**	**MS**	**LSB**	**LSR**	**CT_L**	**CT_F**	**CT_M**	**FECS**	**FECN**	**BWT**	**LE**
8 WK	**2.369**	0.81	0.41	0.34	0	0.48	0	0	0.67	0.61	0.31	0	0	0.56	0.11
SWT	3.918	**9.864**	0.45	0.39	0	0.56	0	0	0.73	0.64	0.31	0	0	0.37	0.06
MD	0.857	1.916	**1.827**	0.27	0	0.27	0	0	0.43	0.29	0.29	0	0	0.18	0.21
FD	0.329	0.780	0.235	**0.406**	0	0.25	0	0	0.03	0.53	0.10	0	0	0.05	0.20
MAT	0	0	0	0	**1.768**	0	0	0	0	0	0	0	0	0	0
MS	1.573	3.773	0.767	0.337	0.000	**4.573**	0	0	0.03	0.03	0	0	0	0	0
LSB	0	0	0	0	0	0	**0.038**	0.56	0	0	0	0	0	0	0
LSR	0	0	0	0	0	0	0.011	**0.010**	0	0	0	0	0	0	0
CT_L	1.092	2.431	0.617	0.019	0.000	0.078	0	0	**1.138**	0.49	0.34	0	0	0.48	0.08
CT_F	0.886	1.873	0.369	0.320	0.000	0.057	0	0	0.491	**0.882**	0.09	0	0	0.38	0.02
CT_M	1.610	3.297	1.329	0.217	0.000	0.005	0	0	1.249	0.280	**11.539**	0	0	0.36	0.26
FECS	0	0	0	0	0	0	0	0	0	0	0	**0.295**	0.60	0	0
FECN	0	0	0	0	0	0	0	0	0	0	0	0.149	**0.210**	0	0
BWT	0.286	0.393	0.083	0.010	0	0.001	0	0	0.170	0.118	0.406	0	0	**0.112**	0.24
LE	0.044	0.049	0.076	0.034	0	0.001	0	0	0.023	0.006	0.235	0	0	0.021	**0.071**

Residual Covariances (below) and correlations (above), variances on the diagonal

	8 WK	SWT	MD	FD	MS	LSB	LSR	CT_L	CT_F	CT_M	FECS	FECN	BWT	LE
8 WK	**5.654**	0.78	0.46	0.40	0.20	0.00	0.00	0.71	0.67	0.25	0.00	0.00	0.34	0.18
SWT	8.883	**22.946**	0.53	0.44	0.25	0.00	0.00	0.87	0.83	0.25	0.00	0.00	0.22	0.15
MD	2.429	5.637	**4.930**	0.36	0.23	0.00	0.00	0.50	0.42	0.32	0.00	0.00	0.11	0.01
FD	0.941	2.087	0.790	**0.979**	0.13	0.00	0.00	0.36	0.58	0.12	0.00	0.00	0.08	-0.08
MS	1.380	3.472	1.482	0.372	**8.426**	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.30	0.01
LSB	0.000	0.000	0.000	0.000	0.000	**0.319**	0.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00
LSR	0.000	0.000	0.000	0.000	0.000	0.116	**0.250**	0.00	0.00	0.00	0.00	0.00	0.00	0.00
CT_L	1.865	4.629	1.232	0.392	0.009	0.000	0.000	**1.235**	0.68	0.25	0.00	0.00	0.22	0.05
CT_F	1.878	4.662	1.083	0.672	0.007	0.000	0.000	0.884	**1.377**	0.20	0.00	0.00	0.20	0.07
CT_M	2.752	5.543	3.289	0.549	0.000	0.000	0.000	1.262	1.077	**21.429**	0.00	0.00	0.10	-0.10
FECS	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.839**	0.23	0.00	0.00
FECN	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.123	**0.342**	0.00	0.00
BWT	0.403	0.521	0.119	0.038	0.443	0.000	0.000	0.122	0.117	0.223	0.000	0.000	**0.255**	0.11
LE	0.160	0.263	0.012	-0.028	0.009	0.000	0.000	0.019	0.031	-0.170	0.000	0.000	0.020	**0.141**

The revised parameters were updated and new genetic evaluation was undertaken to assess the impact.

The following table summarises the EBVs before and after the new parameters were implemented and the correlation between the 2 sets of EBVs. For the 4 main traits there is minimal re-ranking with correlations all 0.99+, although the distribution of the EBVs did change with the outer ranges of the EBVs generally decreasing. Again minimal re-ranking was observed of the ewe with correlations ranging from 0.92 for mature size to 0.99 for LSB. The biggest distribution changes for these traits were for Maternal which saw an increase in the range of EBVs. The biggest impact on the CT traits was for CT_muscling with a correlation of 0.77 suggesting significant re-ranking, most likely due to the reduction of some of the very strong correlations with other traits. For the FEC traits it is a mixed bag with correlations of 0.46 (FEC_S) and 0.84 (FEC_N) – we switched off all correlations to these traits so re-ranking is expected. The 2 birth traits showed minimal re-ranking and similar distributions.

		Previous parameters				**New parameters**			
trait	**correlation**	**avg**	**std**	**min**	**max**	**avg**	**std**	**min**	**max**
decMatEBVW8W	0.99	-0.97	1.20	-9.96	8.03	-0.66	1.51	-8.74	6.16
decEBVSWT	0.99	-2.58	2.92	-24.92	18.96	-2.12	3.46	-18.35	14.15
decEBVMD	0.99	-0.67	1.14	-6.53	8.08	-0.64	1.17	-6.50	7.97
decEBVFD	0.99	0.02	0.29	-2.74	4.00	0.01	0.32	-2.36	3.36
decEBVMaternal	0.94	-0.28	0.78	-4.51	4.38	-0.18	0.90	-7.24	6.57
decMatEBVSZ	0.92	-0.58	1.78	-15.49	16.05	-0.98	1.36	-14.28	15.38
decEBVLitBorn	0.99	-0.04	0.08	-0.61	0.98	-0.04	0.09	-0.52	1.01
decEBVLitReared	0.98	-0.02	0.05	-1.11	2.01	-0.02	0.06	-0.95	1.90
decEBVCTLean	0.98	-0.83	1.16	-7.16	6.85	-0.79	1.19	-8.46	7.11
decEBVCTFat	0.96	-0.23	0.51	-3.42	6.31	-0.28	0.46	-4.52	6.92
decEBVCTMusc	0.77	-1.05	1.04	-12.20	9.75	-0.56	1.60	-11.46	9.14
decEBVLFecS	0.46	0.02	0.06	-0.99	0.95	-0.02	0.06	-1.49	1.34
decEBVLFecN	0.84	-0.07	0.11	-1.25	1.29	-0.04	0.12	-2.04	1.86
decEBVBWT	0.99	-0.17	0.22	-1.86	1.15	-0.15	0.25	-1.82	1.13
decEBVLE	0.96	-0.93	3.23	-73.74	6.98	-0.73	3.70	-73.42	6.98

Review the genetic group solutions.

Genetic group definitions were taken from the within breed evaluations and applied to the CBA. The below table reports the solutions from batch 20130069 with the revised genetic parameters. While it is outside the scope of this project to overhaul the group structures for breed subsets, we need to check that the adaptations (i.e. using dominant breed to determine which genetic groupings are applied) for CBA have not resulted in erroneous solutions. Only the traits in the first job (job 1 from the heterosis work) is run with genetic groups, the other traits do not have genetic groups and are not reported below.

Breed	Desc	grp	Count(mix)	8wk	swt	md	fd	ct_lean	ct_fat	bwt	le
Vendeen	M pre 1980	-2	20361	-0.29	-3.57	-1.65	0.13	-1.67	-0.99	-0.17	-0.13
Vendeen	F pre 1980	-4	140	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Vendeen	M 1980-84	-5	12967	-0.69	-3.40	-0.95	0.00	-0.75	-1.35	-0.17	2.29
Vendeen	F 1980-84	-7	234	-4.25	-5.05	-1.49	-0.23	-3.38	-1.19	-1.02	-1.11
Vendeen	M 1985 -89	-8	4978	-0.99	-2.88	-0.70	-0.07	0.60	1.92	-0.15	0.47
Vendeen	C 1985-89	-9	50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Vendeen	F 1985-89	-10	664	-1.28	-4.10	-0.74	0.06	-6.13	-3.05	-0.05	0.12
Vendeen	M 1990 - 94	-11	6872	-0.62	-1.25	-0.28	0.06	-1.43	-1.02	-0.13	-0.94
Vendeen	F 1990 - 94	-13	858	-1.57	-3.54	-0.43	0.14	-0.02	1.20	-0.21	0.51
Vendeen	M 1995 +	-14	12784	-0.17	1.25	0.43	-0.13	-0.25	-0.41	-0.30	-1.57
Vendeen	C 1995 +	-15	2	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Vendeen	F 1995 +	-16	376	-1.07	-0.97	0.16	0.03	7.18	6.51	-0.06	0.25
Texel	MCF pre 1980	-17	21858	-0.87	-2.32	0.53	0.09	0.39	-0.20	-0.09	0.35
Texel	MCF 1980 - 89	-18	7986	-1.09	-3.42	0.02	0.17	-1.11	-1.06	-0.09	-0.52
Texel	M 1990+	-19	704	-0.02	-0.56	-0.02	0.04	2.85	1.58	-0.09	-0.13
Texel	C 1990+	-20	12	0.35	0.58	0.13	0.05	0.16	0.13	0.04	0.01
Texel	F 1990 +	-21	49438	-2.54	-1.63	-0.13	-0.05	-0.29	-0.42	0.06	-1.54
Hampshire	MCF pre 1980	-22	4088	-0.88	-0.68	-0.18	-0.22	-1.41	0.53	0.04	-0.75
Hampshire	MCF 1980 - 89	-23	2830	-1.01	-1.03	-0.15	-0.73	-0.64	1.42	-0.12	-0.95
Hampshire	M 1990+	-24	264	-1.59	0.15	0.13	0.18	-0.40	2.29	0.09	0.13
Hampshire	C 1990+	-25	4	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Hampshire	F 1990 +	-26	1600	0.15	-1.33	0.22	-0.14	-1.36	-2.11	-0.27	-2.05
BleuDuMaine	MCF pre 1980	-27	142	-0.01	1.99	2.00	-0.24	0.65	-0.11	-0.24	-0.02
BleuDuMaine	MCF 1980 - 84	-28	400	-0.12	-5.08	-2.86	-0.74	-0.88	-0.66	0.34	-0.04
BleuDuMaine	MCF 1985 - 89	-29	2048	-0.87	-2.29	-2.01	-0.48	-0.93	-0.80	-0.70	-0.24
BleuDuMaine	MCF 1990 - 94	-30	992	-0.34	-1.95	-2.04	-0.55	-0.50	-0.52	-0.18	-0.14
BleuDuMaine	MCF 1995 - 99	-31	744	-1.50	-2.61	-1.57	-0.45	-0.58	-0.56	0.06	-0.03
BleuDuMaine	M 2000+	-32	44	0.40	-0.41	-0.73	-0.39	0.19	-0.07	0.25	0.00
BleuDuMaine	F 2000+	-34	154	1.41	-1.08	-1.41	-0.44	-0.14	-0.20	-0.12	-0.12
Charollais	MCF pre 1980	-35	2216	0.09	-1.79	0.28	-0.26	-0.40	-0.32	-0.34	-0.04
Charollais	MCF 1980 - 84	-36	2220	-1.62	-4.35	-1.10	-0.22	-2.12	-0.49	-0.31	-0.10
Charollais	MCF 1985 - 89	-37	8244	-1.01	-3.27	-0.77	-0.11	-1.96	-0.44	-0.45	-0.09
Charollais	MCF 1990 - 94; C 1995+	-38	10196	-0.50	-2.06	-0.56	0.03	-1.56	-0.04	-0.29	-0.07
Charollais	M 1995 +	-39	864	0.08	0.83	0.45	-0.15	-1.01	0.48	-0.26	-0.09
Charollais	F 1995 +	-40	8858	-0.29	0.31	0.28	-0.03	-0.89	0.34	-0.01	-0.02
Dorset	MCF pre 1980	-41	19118	-0.15	-1.30	0.85	0.08	-0.26	-0.16	-0.10	0.02
Dorset	MCF 1980 - 84	-42	9418	-0.46	-2.49	-0.17	-0.04	-0.77	-0.46	-0.36	-0.09
Dorset	MCF 1985 - 89	-43	7562	-0.48	-1.42	-0.07	0.12	-0.49	-0.19	-0.14	0.00
Dorset	MCF 1990 - 94; C 1995+	-44	6952	0.01	-0.38	0.25	0.20	-0.15	0.05	-0.09	0.09
Dorset	M 1995 +	-45	444	1.13	1.22	0.51	0.29	0.17	0.29	-0.15	-0.02
Dorset	F 1995 +	-46	5030	0.35	0.60	0.42	0.35	0.08	0.29	0.05	0.09
Suffolk	MCF pre 1980	-47	77614	-0.20	-3.08	-0.97	-0.03	-1.28	-0.26	-0.09	0.01
Suffolk	MCF 1980 - 84	-48	13670	-0.63	-2.72	-0.94	-0.07	-0.96	-0.08	-0.13	-0.65
Suffolk	MCF 1985 - 89	-49	8032	-0.93	-3.00	-1.14	-0.11	-0.49	-0.08	-0.09	0.55
Suffolk	MCF 1990 - 94	-50	5416	-0.98	-1.57	-0.95	0.04	-1.34	-0.45	-0.11	0.08
Suffolk	MCF 1995 - 99	-51	2832	-0.74	-0.07	-0.49	-0.04	-0.53	0.34	-0.55	0.36
Suffolk	MCF 2000+	-52	6620	0.99	2.00	0.60	0.26	0.56	0.75	-0.28	-0.28
Meatlinc	MCF 1900-2020	-53	1628	2.05	1.37	2.01	0.28	-0.65	0.84	0.02	-0.86
Southdown	MCF 1900-2020	-54	4038	-0.71	-3.11	-1.48	-0.16	-0.91	-0.50	-0.21	-0.07
Shropshire	MCF 1900-2020	-55	2492	-1.76	-1.21	0.91	0.78	-0.41	0.29	0.45	0.27

Beltex	MCF 1900-2020	-56	3666	-0.99	-0.60	2.32	0.50	0.46	0.34	-0.08	-0.33
Blue Texel	MCF 1900-2020	-57	348	3.87	1.38	-0.77	1.65	-0.09	1.63	0.49	0.20
other breeds	MCF 1900-2020	-58	13449	-0.44	-1.02	0.00	0.08	-1.16	-0.11	-0.09	-0.47

To help compare the different breeds, the genetic group solutions of the most recent groups per breed are extracted and sorted by scan weight and shown in the table below.

Breed	**Desc**	**grp**	**Count(mix)**	**8wk**	**swt**	**md**	**fd**	**ct_lean**	**ct_fat**	**bwt**	**le**
Suffolk	MCF 2000+	-52	6620	0.99	2.00	0.60	0.26	0.56	0.75	-0.28	-0.28
Blue Texel	MCF 1900-2020	-57	348	3.87	1.38	-0.77	1.65	-0.09	1.63	0.49	0.20
Meatlinc	MCF 1900-2020	-53	1628	2.05	1.37	2.01	0.28	-0.65	0.84	0.02	-0.86
Vendeen	M 1995 +	-14	12784	-0.17	1.25	0.43	-0.13	-0.25	-0.41	-0.30	-1.57
Dorset	M 1995 +	-45	444	1.13	1.22	0.51	0.29	0.17	0.29	-0.15	-0.02
Charollais	M 1995 +	-39	864	0.08	0.83	0.45	-0.15	-1.01	0.48	-0.26	-0.09
Dorset	F 1995 +	-46	5030	0.35	0.60	0.42	0.35	0.08	0.29	0.05	0.09
Charollais	F 1995 +	-40	8858	-0.29	0.31	0.28	-0.03	-0.89	0.34	-0.01	-0.02
Hampshire	M 1990+	-24	264	-1.59	0.15	0.13	0.18	-0.40	2.29	0.09	0.13
BleuDuMaine	M 2000+	-32	44	0.40	-0.41	-0.73	-0.39	0.19	-0.07	0.25	0.00
Texel	M 1990+	-19	704	-0.02	-0.56	-0.02	0.04	2.85	1.58	-0.09	-0.13
Beltex	MCF 1900-2020	-56	3666	-0.99	-0.60	2.32	0.50	0.46	0.34	-0.08	-0.33
Vendeen	F 1995 +	-16	376	-1.07	-0.97	0.16	0.03	7.18	6.51	-0.06	0.25
other breeds	MCF 1900-2020	-58	13449	-0.44	-1.02	0.00	0.08	-1.16	-0.11	-0.09	-0.47
BleuDuMaine	F 2000+	-34	154	1.41	-1.08	-1.41	-0.44	-0.14	-0.20	-0.12	-0.12
Shropshire	MCF 1900-2020	-55	2492	-1.76	-1.21	0.91	0.78	-0.41	0.29	0.45	0.27
Hampshire	F 1990 +	-26	1600	0.15	-1.33	0.22	-0.14	-1.36	-2.11	-0.27	-2.05
Texel	F 1990 +	-21	49438	-2.54	-1.63	-0.13	-0.05	-0.29	-0.42	0.06	-1.54
Southdown	MCF 1900-2020	-54	4038	-0.71	-3.11	-1.48	-0.16	-0.91	-0.50	-0.21	-0.07

This table show Suffolk to have the largest GG for SWT and this is supported by the breed having one of the largest SWT phenotypic averages in the last decade (AHDB report on genetic progress). The 2nd largest breed is the Blue Texel (also the highest for 8 week weight), this solution is based on approx. 174 individuals and we have no phenotype data to compare, but given the Texel origins it is perhaps more appropriate to concatenate the Blue Texel genetic groups with the Texel, using Texel definitions. At the other end is Southdown, and this is in line with the average scan weight reported for the breed.

The table below shows the average EBVS for 2014 born mostly purebred (PEB>70%) males with accuracy of 50%+ from each breed for comparison.

8wk weight	**BreedCode**	**number**	**average**	**stdev**	**min**	**max**
meatlinc	1055	578	3.49	0.83	-0.22	5.55
blue texel	1502	54	2.76	0.82	-0.27	4.26
Suffolk	3	5472	1.38	1.29	-2.82	6.12
Texel	2	15497	1.25	1.05	-5.00	5.50
dorset (centurion)	1047	2255	1.16	0.86	-1.93	3.79
bleu du maine	1084	103	0.59	0.74	-2.45	2.49
charollais	1077	3175	0.54	0.97	-3.82	4.31
Hampshire	1000	1203	-0.07	1.02	-3.22	3.03
vendeen	1087	182	-0.53	0.77	-2.29	1.79
southdown	1052	271	-1.21	0.95	-3.33	1.71
beltex	1090	312	-1.81	0.94	-5.20	1.84
shropshire	1051	499	-1.93	0.90	-4.16	0.59

Scan weight	**BreedCode**	**number**	**average**	**stdev**	**min**	**max**
meatlinc	1055	574	5.79	1.56	-0.42	9.26
Texel	2	11469	3.21	2.31	-9.97	13.89
Suffolk	3	4112	2.46	2.67	-6.62	12.27
dorset (centurion)	1047	2247	1.94	1.78	-4.72	8.60
charollais	1077	3119	1.33	2.03	-5.94	9.15
Hampshire	1000	934	0.41	1.96	-5.85	6.35
bleu du maine	1084	97	0.28	1.55	-3.63	3.71
vendeen	1087	182	-0.50	1.49	-4.30	3.37
blue texel	1502	51	-1.03	1.73	-5.16	2.42
shropshire	1051	497	-1.87	1.87	-7.29	2.57
beltex	1090	309	-2.26	1.87	-8.84	5.01
southdown	1052	263	-4.17	1.81	-8.74	0.45

Muscle depth	**BreedCode**	**number**	**average**	**stdev**	**min**	**max**
meatlinc	1055	570	4.87	0.83	1.19	7.46
beltex	1090	303	1.68	0.78	-0.29	4.09
dorset (centurion)	1047	2140	1.31	0.80	-1.62	4.16
vendeen	1087	182	1.31	0.65	-1.42	2.83
charollais	1077	2931	1.25	0.92	-1.70	4.22
Texel	2	10570	1.07	1.13	-2.76	5.95
shropshire	1051	480	0.85	0.80	-1.70	3.37
Hampshire	1000	764	0.77	0.87	-1.90	3.33
Suffolk	3	3843	0.65	1.51	-3.35	5.10
bleu du maine	1084	88	-0.24	0.63	-1.88	1.75
southdown	1052	220	-1.56	0.95	-3.59	1.89
blue texel	1502	27	-1.70	0.62	-2.69	-0.64

Fat depth	BreedCode	number	average	stdev	min	max
blue texel	1502	27	1.64	0.15	1.42	1.97
shropshire	1051	477	0.86	0.41	-0.20	2.11
beltex	1090	303	0.51	0.28	-0.17	1.37
meatlinc	1055	571	0.47	0.30	-0.30	2.45
Suffolk	3	3859	0.27	0.37	-1.07	1.63
dorset (centurion)	1047	2132	0.26	0.39	-0.85	1.86
vendeen	1087	182	0.02	0.30	-0.80	0.81
Texel	2	10654	-0.01	0.33	-1.49	1.47
charollais	1077	2941	-0.08	0.43	-1.53	1.72
Hampshire	1000	776	-0.15	0.46	-2.36	2.15
bleu du maine	1084	91	-0.17	0.23	-0.63	0.62
southdown	1052	222	-0.22	0.36	-1.25	0.78

QA on individual flock level

While the above het/rec, parameters and genetic groups may change as a result of QA, the CBA is now complete and all that remains is QA and sanity checking the results in detail. Which will then enable sensible decisions to be made regarding the publication of results. At a Signet/EGENEs meeting July 2016 it was discussed perhaps delaying roll out until 2018 to ensure we are not rushed and can communicate the changes effectively with industry.

Up until now all the work has been undertaken using the same BASCO extract (data source 3068; BASCO_LIVE_SHEEP_20150722). This is 12 months old so the evaluation system was re run (batch 20130070) with the data updated to data source 3433; BASCO_LIVE_SHEEP_20160729.

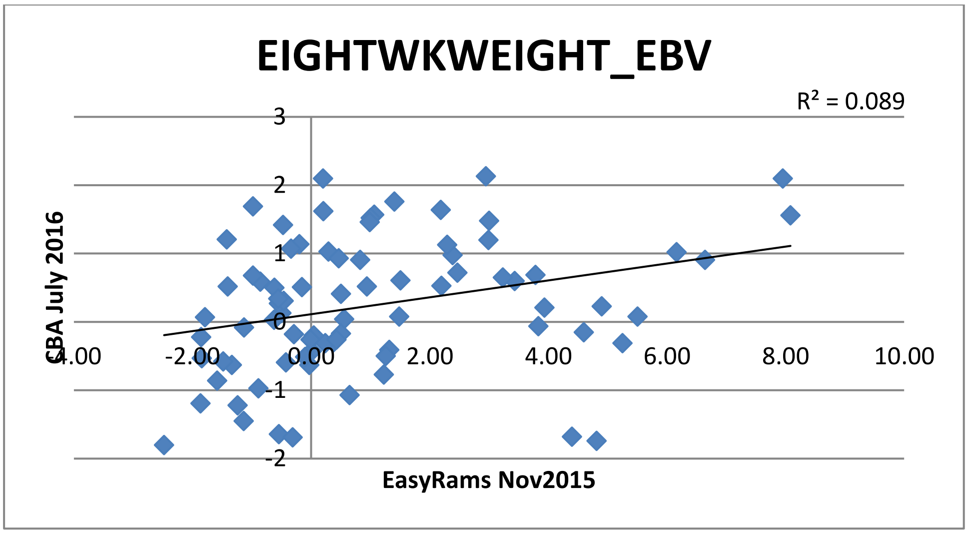
Robyn Hulme – EASYRams

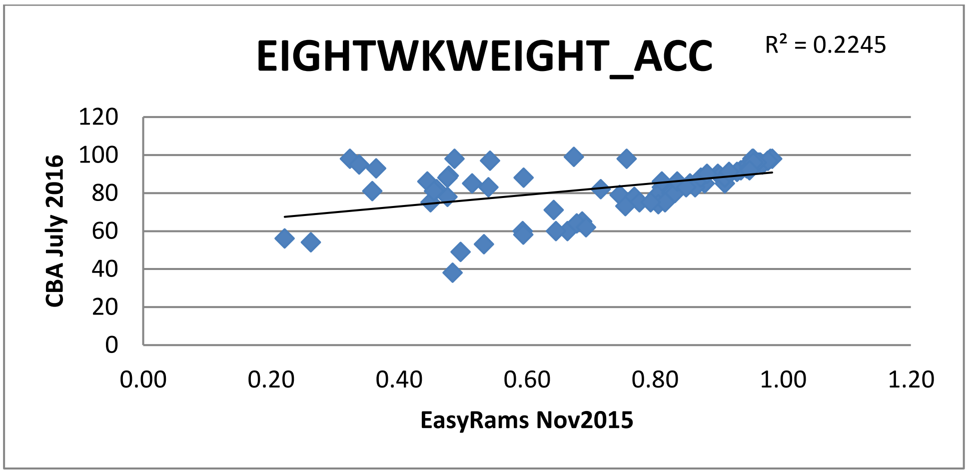
The table [Sheep_run_acrossbreeds].[dbo].[tblSystemSecondaryToPrimaryFlockId] records the following linked flocks for R Hulme. These 4 flocks will all be treated like they are infact the primary flock.

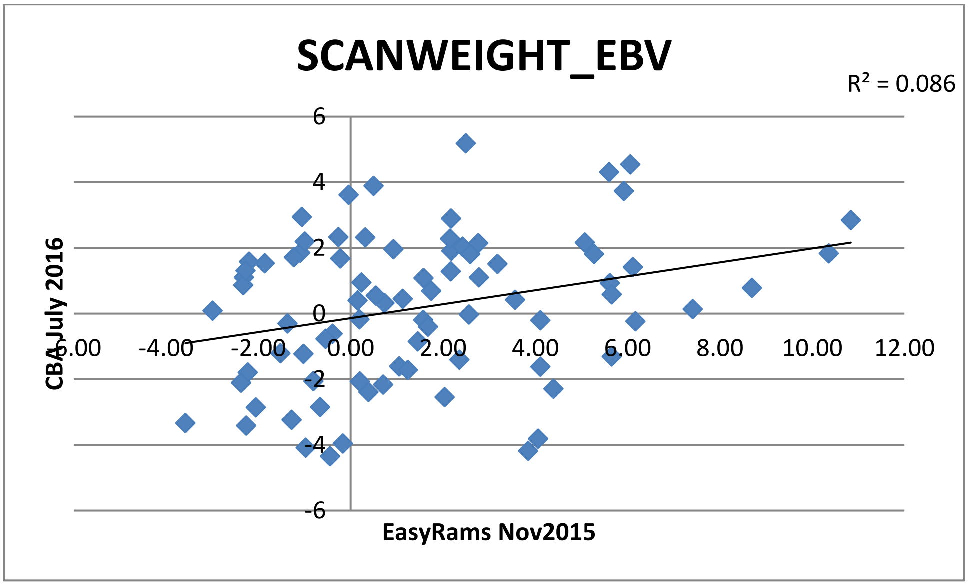
intPrimaryBreedId	intPrimaryFlockId	intSecondaryBreedId	intSecondaryFlockId	intStartDate	intEndDate	chrDescription	Datemodified
3	35333	3	46690	1900-01-01	2020-01-01	R Hulme	2016-02-05
3	35333	2	46691	1900-01-01	2020-01-01	R Hulme	2016-02-05
3	35333	2	49445	1900-01-01	2020-01-01	R Hulme	2016-02-05
3	35333	2	49528	1900-01-01	2020-01-01	R Hulme	2016-02-05

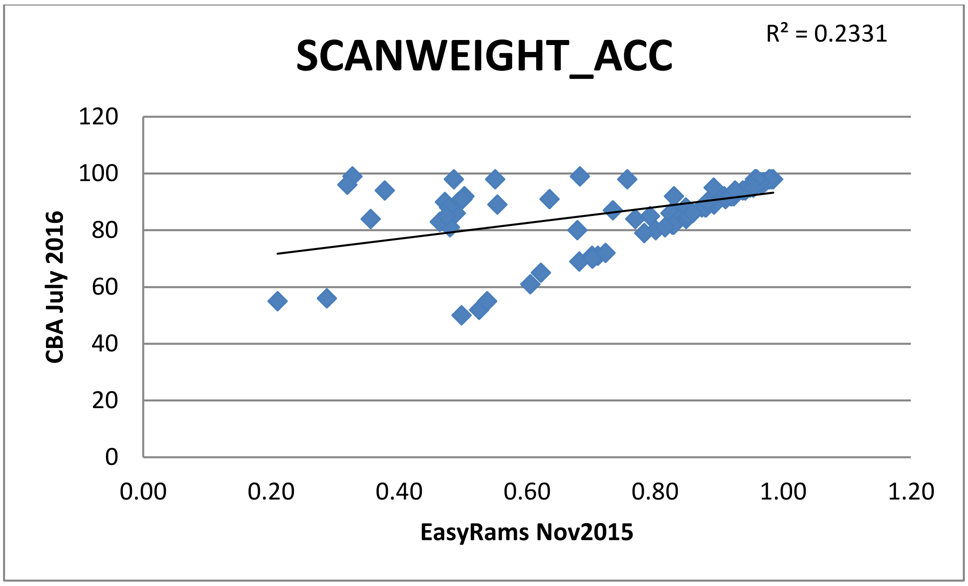
The last Easyrams evaluation was November 2015 (so keep in mind the data differences). In this analysis 83 sires were identified of EasyRams sheep. Of these 81 received EBVs from the latest CBA batch of EBVs. The following compares the EBVs, although note absolute values cannot be compared we are more interested in rankings.

For 8 week weight the 2 sets of EBVs had correlations of r=0.30. The correlation was higher (r=0.47) for accuracy with a significant number of sires having much higher accuracy compared with the EasyRams subset. Similar correlations were found for scan weight; EBV r=0.29 & acc r=0.48. Plots for these 2 traits are shown below.

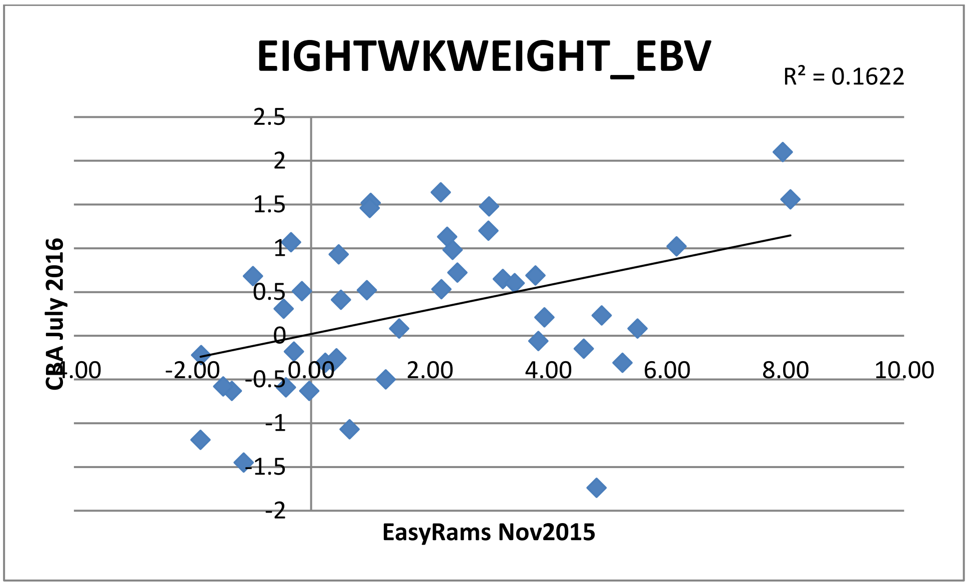

EIGHTWKWEIGHT_EBV
R² = 0.089
CBA July 2016
EasyRams Nov2015
3
2
1
0
-1
-2
-4.00
-2.00
0.00
2.00
4.00
6.00
8.00
10.00

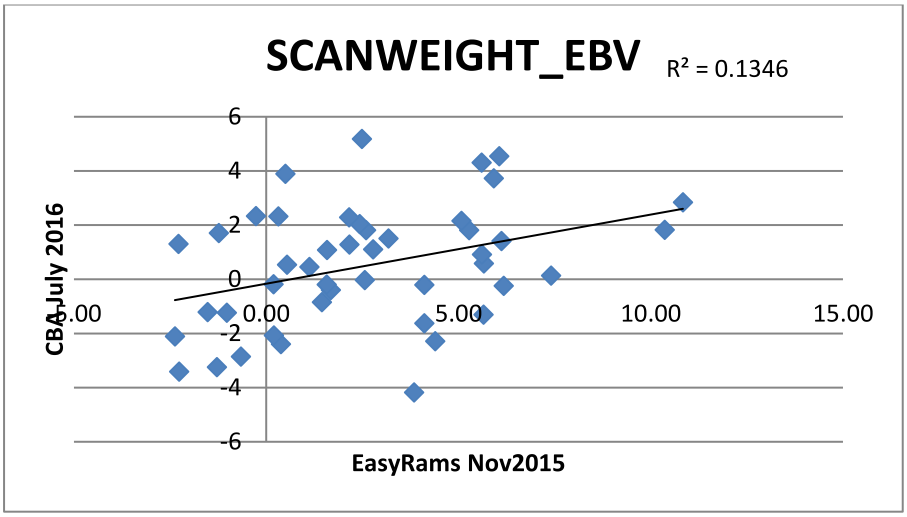

EIGHTWKWEIGHT_ACC
R² = 0.2245
CBA July 2016
EasyRams Nov2015
120
100
80
60
40
20
0
0.00
0.20
0.40
0.60
0.80
1.00
1.20


SCANWEIGHT_EBV
R² = 0.086
CBA July 2016
EasyRams Nov2015
6
4
2
0
-2
-4
-6
-6.00
-4.00
-2.00
0.00
2.00
4.00
6.00
8.00
10.00
12.00



Removing 23 sires where the accuracy was more than 10% different between the 2 sets of EBVS improved the 8 week correlation to 0.38 and scan weight to 0.36. If the accuracy levels were limited to those with 80%+ this kept ~ 44 sires and the correlations were 0.40 and 0.37, respectively for 8 week and scan weight. The graphs below show the relationships for those sires with little change in accuracy and accuracy of 0.8+.





Clearly there is a lot of data differences between the 2 runs, 1 has all possible data, and 8 months more of it, compared with the other which is a select cohort of flocks. These are quite significant changes so it perhaps not surprising the correlation between these sires is only ~0.4 for the 2 weight traits.

Taking Scan weight – the biggest changers from the above subset were investigated.

FINNTEX . – A76/99 (1717481) went from SWT of 10.4 (0.91) to 1.8 (0.92) with high accuracy levels. The ram is 100% Texel in both the analysis, and in BASCO has 36 progeny, most but not all are in Robyn's flocks. He has gone from being the 2nd highest sire for swt to being middle, maybe slightly above average.

In contrast, GOLDSTREAM NZ 192:2005 (7811055) has gone from SWT of 2.49 (0.96) to 5.18 (0.98) with high accuracy levels. The ram is 100% (NZ) Suffolk in both the analysis, and in BASCO has 402 progeny, in many different herds. He has gone from being middle of rams to being the 2nd highest sire for swt.

Both sires are themselves not performance recorded.

Finntex has swt progeny in 7 CG. His progeny were on average 0.81 kg higher than those of their contemporaries. If you compare the min/max values to CG means we see -6.2/5.7 kg differences in the extremes of the CG.

CG	N	Avg	Min	Max	Stdev	CG total N	CG AVG
116174	2	47.00	45	49	2.83	32	46.88
266726	5	43.40	28	54	9.63	176	45.26
294190	1	55.00	55	55	NULL	34	53.03
389561	7	42.57	33	48	5.56	165	40.91
510215	1	31.00	31	31	NULL	26	31.46
522834	7	42.00	28	50	7.62	35	42.46
59936	10	55.10	47	63	6.01	30	50.43

Goldstream has swt progeny in 21 CG, none of which also contained progeny from Finntex. The progeny by Goldstream were on average 2.72 kg higher than those of their contemporaries. If you compare the min/max values to CG means we see -5.1/11.6 kg differences in the extremes of the CG, showing that those progeny that perform well have performed a lot better than the CG average.

CG	N	Avg	Min	Max	Stdev	CG total N	CG AVG
111028	6	55.00	41	70	10.86	53	52.53
141228	3	46.27	40.8	53.1	6.26	12	44.55
156690	1	41.50	41.5	41.5	NULL	5	41.7
220904	7	52.36	38.5	66	9.16	23	50.11
284109	2	47.60	47.6	47.6	0.00	16	44.19
314532	5	47.72	40.4	59	7.29	30	43.46
318460	8	55.38	50	60	3.93	20	50.1
34899	9	51.33	42	56	4.39	42	49.21
352166	33	53.67	40	71	7.31	72	52.57
398392	2	68.75	64.5	73	6.01	63	64.07
415387	12	44.96	33.5	53.5	6.26	27	42.31
423188	4	58.38	56.5	61	2.06	37	53.82
437431	8	38.06	28	53.5	8.88	25	33.6
440370	2	58.75	58	59.5	1.06	6	53.75
462342	16	51.38	39.5	65.5	6.63	30	45.7
508131	12	47.81	42.2	64	7.26	26	48.96
52178	7	51.14	40	62	7.36	11	48.45
526290	26	41.31	32	53	6.57	71	41.54
544160	30	47.87	34	58	5.56	59	47.8
557050	21	45.10	38	53	4.27	43	44.49
77326	8	53.50	46	65	6.85	20	47.73

The genetic group information from this evaluation for SWT was 1.89 & -0.42, respectively for Suffolk and Texel.

Based on this information, it is very plausible that Goldstream would rank higher than Finntex. So why was this not seen in the EasyRams subset?

The same data from the EasyRams analysis is shown below. Although the 2 rams compare favourable on the surface, the genetic group solutions are very different which is why Finntex ranks higher in EasyRams. The other reason for the difference in ranks is that in the CBA analysis we do not scale the phenotypes by breed and we did in EasyRams, and this tended to increase the raw phenotypes of the progeny of Texels compared to Suffolk.

Finntex has swt progeny in 5 CG. His progeny were on average 2.44 kg higher than those of their contemporaries. If you compare the min/max values to CG means we see -7.9/9.4 kg differences in the extremes of the CG.

CG	N	Avg	Min	Max	Stdev	CG total N	CG AVG
1005	10	58.48	49.9	66.9	6.38	29	51.41
1141	7	47.83	37.1	53.9	6.23	98	44.22
1354	1	32.90	32.9	32.9	NULL	26	31.54
1357	7	44.59	29.7	53.1	8.09	35	42.97
1486	5	48.74	31.4	60.6	10.83	122	50.19

Goldstream has swt progeny in 11 CG, none of which also contained progeny from Finntex. The progeny by Goldstream were on average 2.77 kg higher than those of their contemporaries. If you compare the min/max values to CG means we see -5.7/12.9 kg differences in the extremes of the CG, showing that those progeny that perform well have performed a lot better than the CG average.

CG	N	Avg	Min	Max	Stdev	CG total N	CG AVG
1008	8	44.63	36	48	4.03	27	45.93
1054	7	51.14	40	62	7.36	11	48.45
1119	12	44.96	33.5	53.5	6.26	27	42.31
1136	7	52.36	38.5	66	9.16	23	50.11
1145	5	47.72	40.4	59	7.29	30	43.46
1240	8	38.06	28	53.5	8.88	25	33.6
1257	3	46.27	40.8	53.1	6.26	12	44.55
1295	8	53.50	46	65	6.85	20	47.73
1396	12	47.81	42.2	64	7.26	26	48.96
1438	16	51.38	39.5	65.5	6.63	30	45.7
1564	2	47.60	47.6	47.6	0.00	16	44.19

The genetic groups from easyram analysis for SWT were -0.68, -0.61, 6.02, 13.49 & -0.06, respectively for UK Suffolk, NZ Suffolk, UK Texel, NZ Texel & other.

The Meatlinc purebred and cross bred flocks were considered and all appeared sensible. These have been reported in other short reports to the Meatlinc project and provided to Signet separately.

The Ram Compare data has also been considered and the sire rankings appeared sensible and broadly similar – although there was significant re-ranking among the first cross progeny. These have been reported in other short reports to the Ram Compare project and provided to Signet separately.

Gilman – Suffolk x Texel flock

I think this is the Suffolk flock with the Rutland Rams prefix from Lincolnshire. I have no linked flocks recorded in the [Sheep_run_acrossbreeds].[dbo].[tblSystemSecondaryToPrimaryFlockId] table so this assumes all sheep are contained in the one Suffolk flock? Certainly there are no Texel or composite flocks in Lincolnshire with the surname Gilman. The internal flock id for this flock is 47800 and the DomesticBreederID is 113044.

To investigate this flock the CBA run with batch id 20130073 will be used, that is based on the Snapshot BASCO_LIVE_SHEEP_20160919 and only lets in animals that are at least 80% of the allowed breeds (in this case the 12 terminal breeds).

In the raw data on BASCO there are 450 animals listed under the flock id and these animals range from 2009 born to 2016 born, of which 133 was 2016 born and 105 2015 born under the Rutland Rams prefix. I think it therefore sensible to focus on the 2015 and 2016 born lambs and their sires for this QA.

There were 238 lambs of interest recorded in the [Sheep_run_acrossbreeds].[dbo].[tblAnimalDataArchive] table. Animals tended to be recorded for birth weight, weaning weight, scan weight, muscle and fat depth. Therefore, this QA will focus on these traits. These lambs were sired by 4 sires each with between 14 and 108 progeny. In 2 lamb's case the sire was unknown. With one exception all the data from the sires is within the cohort of lambs considered in this summary.

Sire	Breed	N prog	N prog 2015	N prog 2016	Other lambs on basco
9213304	Texel pb	108	58	50	97 2014 lambs in this flock
9450897	Texel pb	54	31	23	None
9475663	Suffolk pb	14	14		None
9629347	Suffolk pb	60		60	None

The following table looks at the EBVs produced in the CBA evaluation for each of the sires, as well as the EBVs from the purebred Suffolk and Texel evaluations. All rams are in the Suffolk evaluation as that is where the progeny have been recorded, but only the 2 Texel rams are in the Texel evaluation with EBVs based on own records and relatives – i.e. the progeny do not contribute.

We can see from these EBVs that the purebred Suffolk evaluation did not give accurate rankings for the Texel sires, as it was not accounting for the different breed or hybrid vigour as well as ignoring their own phenotypes which can be a significant contributor to the EBVs. The impact was greatest for the weight traits.

We can see the following;

- Birth weight
  - CBA has the 2 Suffolk tups with better (lower) EBVS compared with the Texel tups (which have the same EBVS but below average). However, only 1 Suffolk tup had EBVs above average.
  - The Texel evaluation has a difference between the 2 Texel tups, but do show them as being below average which is in agreement with CBA.
- Weaning weight
  - CBA shows all 4 sires are above average, and there are differences with 1 Suffolk tup being the best, and the other the worst – with the 2 Texel tups similar
  - The Texel evaluation also has the Texel tups being broadly similar in EBVs, with 1 only slightly better than the other.
  - The Suffolk evaluation has a different ranking than the CBA EBVS. In Suffolk the 2 Texel tups have the lowest EBVs, whereas the CBA evaluation has the Texel's almost as good as the better Suffolk ram.
- Scan weight
  - CBA shows the Texel tups to be higher, with the better Suffolk close behind and the other Suffolk much lower.
  - Again the Texel evaluation show the Texel rams to perform very well.
  - While the Suffolk evaluation did not rank the Texels as high
- Muscle Depth
  - CBA shows the Suffolk tups and one of the Texel Tups to be very similar, with the most used Texel being only about average.
  - The Texel evaluation show the different Texel rankings that are similar to that in CBA.
  - While the Suffolk evaluation still shows a bias against the Texel sires, this bias is not as great.
- Fat depth
  - CBA shows the tups are not as widely spread out with similar rankings, the better Suffolk has slightly higher FD EBVs.
  - The Texel evaluation show the Texel rams rank the same, but average.
  - While the Suffolk evaluation ranked the 2 Texel's the same, it was below average compared to the Suffolk rams.
- Lambing ease
  - All the evaluations show the EBVs to be similar.

Sire EBVs from CBA and purebred evaluations.

Sire	**Run**	**9213304**	**9450897**	**9475663**	**9629347**
BWT EBV (ACC,CALC)	CBA	0.48 (67,74)	0.46 (68,75)	-0.09 (59,112)	0.37 (66,81)
	SUFFOLK	-	-	-	-
	TEXEL	1.00 (66,58)	0.74 (65,77)	-	-
8WK EBV (ACC,CALC)	CBA	4.08 (96,135)	3.86 (84,133)	2.34 (74,117)	4.71 (83,142)
	SUFFOLK	3.63 (96,103)	3.03 (84,97)	4.87 (77,115)	6.36 (86,130)
	TEXEL	7.44 (71,141)	6.54 (71,132)	-	-
SWT EBV (ACC,CALC)	CBA	10.89 (97,146)	8.37 (90,134)	3.07 (82,107)	7.63 (89,130)
	SUFFOLK	8.21 (97,107)	5.84 (89,94)	8.34 (82,107)	10.86 (90,120)
	TEXEL	18.25 (77,151)	14.32 (76,132)	-	-
MUSCLE DEPTH EBV (ACC,CALC)	CBA	1.08 (97,106)	3.83 (89,132)	3.27 (80,127)	3.31 (88,127)
	SUFFOLK	0.83 (97,93)	3.80 (89,120)	5.29 (83,133)	4.66 (90,128)
	TEXEL	2.56 (71,113)	4.10 (71,133)	-	-
FAT DEPTH EBV (ACC,CALC)	CBA	0.13 (97,104)	0.14 (90,105)	0.26 (81,109)	0.52 (89,119)
	SUFFOLK	-0.11 (97,92)	-0.05 (90,94)	0.34 (84,110)	0.55 (91,118)
	TEXEL	0.17 (75,113)	0.17 (75,113)	-	-
LAMBING EASE EBV (ACC,CALC)	CBA	0.10 (43,100)	0.16 (64,95)	-0.02 (49,109)	0.07 (58,102)
	SUFFOLK	-	-	-	-
	TEXEL	-1.34 (64,110)	-1.52 (49,109)	-	-

In all cases the 238 lambs PEB values summed to 100% Texel/Suffolk.

The table on the next page shows the breed make up of the progeny for each sire, but we can see that the progeny of the Texel sires were 1st crosses (het=100; rec=0), while those of the Suffolk sires were mostly a Suffolk tup over a first cross (het=50; rec=25). In terms of hybrid vigour the progeny of the Texel rams will be showing the most hybrid vigour in the raw phenotypes.

The following table shows a summary of the progeny EBVs and phenotypic performance for each of the sires.

We can see the following;

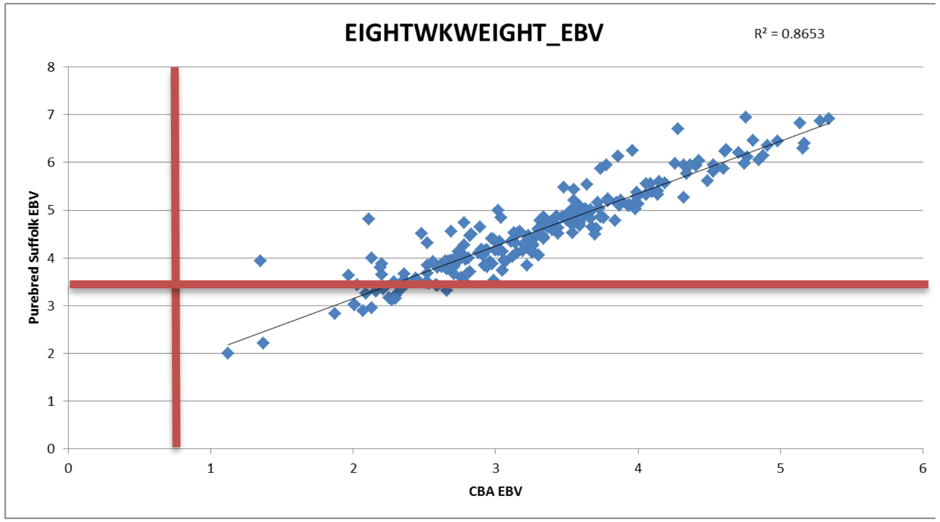
- Birth weight
    - The progeny from Suffolk rams did have lower average birth weights compared to the Texel tups, and the ranking of progeny groups is consistent with the sires EBVs
- Weaning weight
    - The raw phenotypes for the 2 texel rams were similar, as were the sire EBVs. There is some quirky results for the Suffolk with the Suffolk with the lightest lambs at lambing having the heaviest EBV! I don't this has to do with adjustment for hybrid vigour as both Suffolk's would be adjusted the same. Given that the Suffolk evaluations also rank the animals accordingly – it is likely to be the result of other related data outside of this flock contributing. Also the 2 Suffolk rams do not have progeny at the same time so are not directly compared, so this could easily be a year/season effect. Also the Suffolk ram with the poorest progeny performance, had a higher raw weaning weight which would increase the EBV.
- Scan weight
    - Again the Texels and one of the Suffolk rams were similar phenotypes, with the Texel ram EBVs being similar.. however there are quirky results for the Suffolks with the ram with the lighter lambs having the better EBV! I don't this has to do with adjustment for hybrid vigour as both Suffolk's would be adjusted the same. Given that the Suffolk evaluations also rank the animals accordingly – it is likely to be the result of other related data outside of this flock contributing. Also the 2 Suffolk rams do not have progeny at the same time so are not directly compared, so this could easily be a year/season effect.
- Muscle Depth
    - The 2 Texel rams ranked differently in EBV and this is supported by the phenotypes. Again we see quirks with the Suffolk rams, but as they are used across different years
- Fat depth
    - The Texel progeny performed the same, as did their EBVs. Again the 2 Suffolk rams were different than you might expect based only on progeny.
- Lambing ease
    - Only 3 rams had progeny recorded for LE, we did see a difference in the number of lambs with easy births and the EBVs were ranked accordingly.

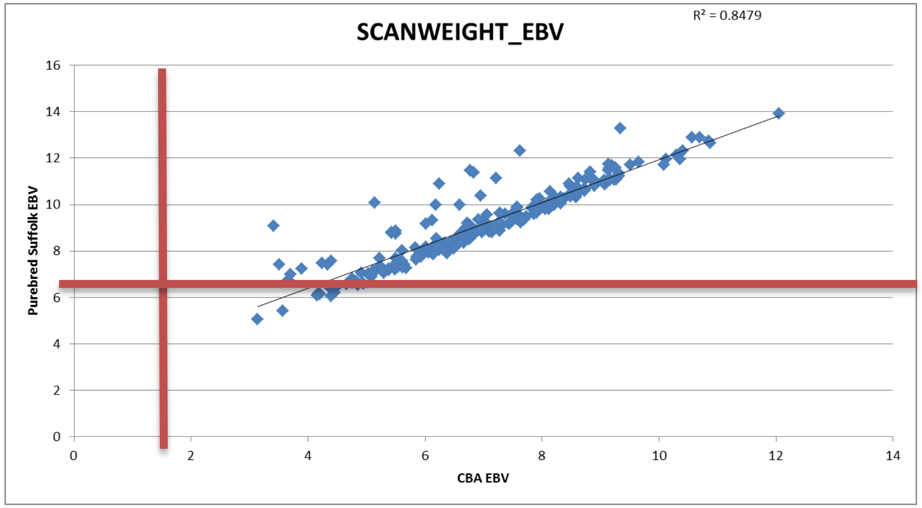
The following is a summary of the data per sire, and the sire's EBVs

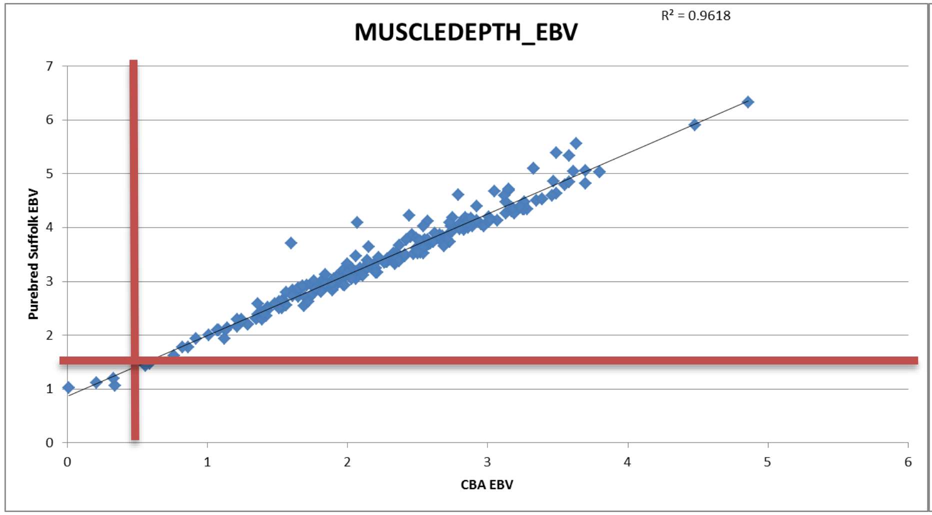
Sire	9213304	9450897	9475663	9629347
Progeny PEB	50 Suffolk : 50 Texel	50 Suffolk : 50 Texel	75 Suffolk : 25 Texel	75 Suffolk : 25 Texel (n=51) + 100% Suffolk (n=9)
BWT EBV (RANGE)	0.26 (0.03,0.51)	0.20 (0.08,0.32)	0.06 (-0.02,0.17)	0.31 (0.06,0.48)
BWT ACC (RANGE)	52 (49,59)	45 (40,49)	41 (39,43)	43 (39,47)
BWT CALC (RANGE)	89 (72,104)	93 (85,101)	102 (95,107)	86 (74,102)
N BWT RECORDED	102	51	14	41 + 8
AVG BWT (RANGE)	5.6 (3.6,8.0)	5.4 (3.6,8.1)	4.9 (3.4,6.2)	5.3 (3.5,7.2) + 5.1 (4.0,6.8)
8WK EBV (RANGE)	3.32 (1.12,5.16)	2.84 (1.87,3.74)	2.68 (1.97,3.55)	4.03 (2.52,5.34)
8WK ACC (RANGE)	66 (60,68)	62 (56,64)	59 (53,60)	60 (52,63)
8WK CALC (RANGE)	127 (103,147)	122 (112,132)	120 (113,130)	135 (119,149)
N 8WK RECORDED	93	41	11	33 + 4
AVG 8WK (RANGE)	22.7 (10.6,34.9)	21.8 (12.8,29.9)	21.4 (17.0,27.4)	20.3 (11.4,29.3) + 18.9 (15.4,22.4)
SWT EBV (RANGE)	7.8 (3.1,12.1)	5.5 (4.2,7.5)	5.1 (3.7,7.0)	7.7 (3.5,10.7)
SWT ACC (RANGE)	69 (58,72)	67 (57,70)	66 (55,68)	64 (56,70)
SWT CALC (RANGE)	131 (107,152)	119 (112,129)	117 (110,126)	130 (109,145)
N SWT RECORDED	90	40	12	31+4
AVG SWT (RANGE)	42.4 (26.8,60.0)	40.6 (26.8,56.2)	41.8 (35.4,48.2)	35.6 (26.6,50.0)+33.9 (26.2,44,6)
MD EBV (RANGE)	1.7 (0.0,3.1)	2.9 (1.8,4.9)	2.5 (1.6,3.2)	2.7 (1.1,3.7)
MD ACC (RANGE)	68 (56,70)	65 (55,68)	64 (54,66)	63 (54,68)
MD CALC (RANGE)	112 (95,125)	123 (113,142)	120 (110,126)	121 (106,131)
N MD RECORDED	90	40	12	31+4
AVG MD (RANGE)	25.5 (17.8,32.4)	27.1 (19.6,35.8)	28.4 (23.3,31.5)	23.3 (17.5,28.1)+24.0 (21.9,25.8)
FD EBV (RANGE)	0.3 (-0.4,0.9)	0.3 (-0.1,0.6)	0.3 (-0.2,0.7)	0.4 (0.1,0.8)
FD ACC (RANGE)	68 (56,71)	66 (55,70)	65 (54,67)	64 (54,69)
FD CALC (RANGE)	111 (85,133)	109 (97,120)	110 (93,124)	116 (104,131)
N FD RECORDED	90	40	12	31+4
AVG FD (RANGE)	2.4 (0.8,7.0)	2.4 (0.9,4.8)	3.8 (1.9,6.5)	1.4 (0.7,3.4)+1.5 (1.0,2.4)
LE EBV (RANGE)	0.06 (-0.05,0.14)	0.09 (0.02,0.18)	0.02 (-0.01,0.07)	0.06 (-0.06,0.13)
LE ACC (RANGE)	47 (44,54)	35 (32,40)	35 (33,36)	34 (30,39)
LE CALC (RANGE)	103 (96,111)	100 (93,106)	106 (102,108)	103 (98,112)
N LE RECORDED	49	19	0	38
% LE easy	67	47	-	82

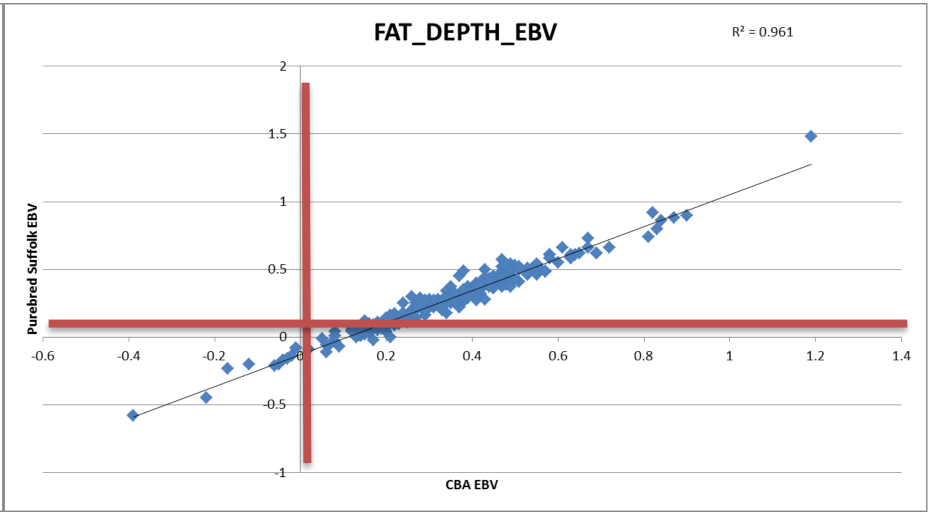
There were 227 animals that had both CBA EBVS and purebred Suffolk EBVs. The following page shows the 4 key EBVs for both sets of EBVs. We see in all cases, especially the ultrasound scans the relationship between the CBA and Suffolk EBVs is very strong. The red lines represent the 100 (average) standardised values. We see for 8 week weight in the CBA analysis the flocks animals are all very much above average compared to all terminal sire breeds included. Compared to the purebred Suffolk evaluation they were still above average but to a lesser degree. The same can be seen with Scan weight, but there is less difference in overall rankings for the 2 ultrasound traits.

Conclusion – that the CBA does a much better job of assessing the Texel rams compared to including them into the Suffolk run where the system we knew could not handle it. Although having said that the progeny rankings were broadly similar, although in the case of the 2 weight traits there is a section of animals who have significantly changed EBVs with CBA tending to decrease their EBVs. The data of the Suffolk rams was a little difficult to compare as they were used in different years, but also they had a lot more data (i.e. their own, and more accurate parent average starting points) than just progeny contributing to make it a clear head on head comparison.


EIGHTWKWEIGHT_EBV
R² = 0.8653
Purebred Suffolk EBV
CBA EBV
0
1
2
3
4
5
6
7
8
0
1
2
3
4
5
6


SCANWEIGHT_EBV
R² = 0.8479
Purebred Suffolk EBV
CBA EBV
0
2
4
6
8
10
12
14
16
0
2
4
6
8
10
12
14


MUSCLEDEPTH_EBV
R² = 0.9618
Purebred Suffolk EBV
CBA EBV
0
1
2
3
4
5
6
7
0
1
2
3
4
5
6


FAT_DEPTH_EBV
R² = 0.961
Purebred Suffolk EBV
CBA EBV
-1
-0.5
0
0.5
1
1.5
2
-0.6
-0.4
-0.2
0
0.2
0.4
0.6
0.8
1
1.2
1.4

Is it sensible and correct to directly compare EBVs from different breeds?

In the same logic that flocks need to be sufficiently connected in an across flock evaluation in order to directly compare animals from different flocks, there needs to be enough genetic links between the different breeds to directly compare animals from different breeds. If there is not sufficient links, then it won't impact on the comparisons within a breed, but may mean that the rankings across the breeds is less reliable. Short of a connectedness for breeds which is not possible given the data restrictions of the current software, it is difficult to quantify in statistical terms but rather will be assessed by looking at the EBVs of the different breeds.

Mostly purebred (PEB of 80% for a given breed) animals born September 2014 to August 2015 were extracted and the EBVs compared. These comparisons are shown in the following series of tables below for each trait. It is worth highlighting that Texel, Suffolk and Hampshire all use BASCO for their flock books and thus have all sheep, and not just performance recorded sheep, included. This is reflected in the average accuracy value but may also influence the rankings.

8 week weight

Breed	Breedcode	Num	Avg	Min	Max	STD	Avg Acc
blue texel	1502	639	3.18	0.60	5.12	0.83	52
meatlinc	1055	3492	2.90	-0.20	6.31	0.80	62
dorset (centurion)	1047	14094	1.18	-2.23	4.92	0.86	62
texel	2	193044	0.91	-4.24	5.91	0.97	43
suffolk	3	78306	0.67	-3.05	6.16	1.03	39
charollais	1077	21360	0.49	-3.81	4.00	0.94	62
bleu du maine	1084	540	0.10	-2.70	2.14	0.89	58
hampshire	1000	12378	0.07	-2.99	3.58	0.92	49
beltex	1090	1767	0.02	-2.53	2.26	0.87	60
vendeen	1087	972	-0.04	-1.91	1.68	0.62	63
southdown	1052	2169	-0.87	-3.55	1.60	0.86	60
shropshire	1051	3201	-1.74	-4.67	0.90	0.88	63

Scan weight

Breed	Breedcode	Num	Avg	Min	Max	STD	Avg Acc
meatlinc	1055	3492	5.89	-1.16	11.66	1.54	66
dorset (centurion)	1047	14094	2.36	-5.26	8.40	1.77	64
texel	2	193044	2.04	-9.20	14.00	2.07	45
charollais	1077	21360	1.37	-5.67	9.45	1.92	65
suffolk	3	78306	0.83	-6.43	11.95	2.15	40
vendeen	1087	972	0.69	-2.79	4.34	1.20	68
hampshire	1000	12378	0.67	-5.29	7.83	1.82	51
bleu du maine	1084	540	0.53	-3.96	4.05	1.55	61
beltex	1090	1767	-1.61	-6.25	3.02	1.76	56
shropshire	1051	3201	-2.08	-7.53	3.16	1.79	66
southdown	1052	2169	-3.51	-9.42	1.80	1.79	65
blue texel	1502	639	-4.09	-7.51	0.27	1.36	56

Muscle Depth

Breed	Breedcode	Num	Avg	Min	Max	STD	Avg Acc
meatlinc	1055	3492	4.84	1.13	7.58	0.92	63
beltex	1090	1767	2.27	-0.14	5.05	0.76	63
vendeen	1087	972	1.49	-0.87	3.92	0.65	65
dorset (centurion)	1047	14094	1.35	-1.50	5.43	0.83	59
charollais	1077	21360	0.68	-2.78	4.52	0.93	61
texel	2	193044	0.61	-2.68	6.47	0.88	44
hampshire	1000	12378	0.48	-1.78	4.36	0.85	47
shropshire	1051	3201	0.38	-1.80	3.32	0.83	61
bleu du maine	1084	540	0.16	-1.38	2.19	0.67	56
suffolk	3	78306	-0.33	-3.36	5.59	1.12	38
southdown	1052	2169	-1.47	-4.00	1.29	0.95	61
blue texel	1502	639	-1.61	-2.97	-0.21	0.47	52

Fat depth

Breed	Breedcode	Num	Avg	Min	Max	STD	Avg Acc
beltex	1090	1767	0.80	0.26	1.64	0.22	64
shropshire	1051	3201	0.57	-0.43	2.21	0.39	62
meatlinc	1055	3492	0.47	-0.39	1.99	0.31	64
dorset (centurion)	1047	14094	0.37	-0.89	2.22	0.42	60
vendeen	1087	972	0.18	-0.85	1.19	0.39	66
charollais	1077	21360	0.07	-1.80	2.26	0.40	62
hampshire	1000	12378	0.06	-1.69	2.36	0.36	48
suffolk	3	78306	0.04	-1.02	2.51	0.27	39
texel	2	193044	-0.06	-1.70	1.86	0.26	44
blue texel	1502	639	-0.09	-0.72	1.34	0.26	52
southdown	1052	2169	-0.22	-1.75	1.52	0.43	61
bleu du maine	1084	540	-0.22	-1.11	1.35	0.39	56

Maternal Ability

Breed	Breedcode	Num	Avg	Min	Max	STD	Avg Acc
meatlinc	1055	3492	1.57	-0.57	2.92	0.46	62
suffolk	3	78306	1.32	-1.58	4.35	0.48	39
dorset (centurion)	1047	14094	0.64	-1.01	2.99	0.52	62
hampshire	1000	12378	0.57	-1.00	2.51	0.44	49
bleu du maine	1084	540	0.55	-1.45	2.01	0.68	58
charollais	1077	21360	0.31	-2.96	3.60	0.70	62
vendeen	1087	972	0.25	-0.45	1.11	0.33	63
shropshire	1051	3201	-0.01	-1.23	1.42	0.47	63
southdown	1052	2169	-0.25	-1.37	0.93	0.36	60
blue texel	1502	639	-0.41	-1.52	0.82	0.36	52
texel	2	193044	-0.46	-2.47	2.19	0.39	43
beltex	1090	1767	-0.76	-1.77	0.50	0.40	60

Mature Weight

Breed	Breedcode	Num	Avg	Min	Max	STD	Avg Acc
texel	2	193044	2.22	-7.07	13.55	1.36	39
charollais	1077	21360	0.66	-5.10	7.93	1.36	55
meatlinc	1055	3492	0.64	-1.72	2.87	0.61	55
dorset (centurion)	1047	14094	-0.53	-6.96	6.26	1.20	54
bleu du maine	1084	540	-0.71	-3.67	0.78	0.72	42
hampshire	1000	12378	-0.77	-5.58	4.97	0.97	42
vendeen	1087	972	-0.84	-2.27	0.63	0.50	55
shropshire	1051	3201	-1.34	-4.65	3.31	0.88	53
southdown	1052	2169	-1.34	-6.41	2.95	1.14	52
beltex	1090	1767	-1.74	-5.82	0.29	0.80	53
suffolk	3	78306	-1.90	-9.69	8.01	1.31	34
blue texel	1502	639	-2.21	-3.93	-0.68	0.60	42

Litter Size Born

Breed	Breedcode	Num	Avg	Min	Max	STD	Avg Acc
texel	2	193044	0.07	-0.21	0.33	0.06	47
charollais	1077	21360	0.00	-0.25	0.28	0.07	47
suffolk	3	78306	-0.02	-0.31	0.20	0.06	47
hampshire	1000	12378	-0.03	-0.23	0.18	0.06	47
dorset (centurion)	1047	14094	-0.03	-0.23	0.19	0.07	48
vendeen	1087	972	-0.03	-0.17	0.14	0.06	42
beltex	1090	1767	-0.05	-0.21	0.17	0.06	41
blue texel	1502	639	-0.06	-0.16	0.04	0.04	40
bleu du maine	1084	540	-0.08	-0.20	0.02	0.05	43
southdown	1052	2169	-0.10	-0.33	0.07	0.06	45
shropshire	1051	3201	-0.10	-0.28	0.06	0.05	47
meatlinc	1055	3492	-0.22	-0.39	-0.05	0.06	46

Litter Size Reared

Breed	Breedcode	Num	Avg	Min	Max	STD	Avg Acc
texel	2	193044	0.03	-0.11	0.14	0.03	36
dorset (centurion)	1047	14094	-0.01	-0.11	0.10	0.03	38
suffolk	3	78306	-0.01	-0.11	0.10	0.02	35
charollais	1077	21360	-0.01	-0.12	0.10	0.03	38
vendeen	1087	972	-0.02	-0.07	0.05	0.02	33
hampshire	1000	12378	-0.02	-0.14	0.07	0.03	34
beltex	1090	1767	-0.03	-0.11	0.05	0.03	30
blue texel	1502	639	-0.04	-0.09	0.00	0.02	27
bleu du maine	1084	540	-0.04	-0.10	0.01	0.02	32
shropshire	1051	3201	-0.05	-0.15	0.05	0.03	36
southdown	1052	2169	-0.06	-0.15	0.03	0.03	34
meatlinc	1055	3492	-0.12	-0.22	-0.04	0.03	36

CT lean weight

Breed	Breedcode	Num	Avg	Min	Max	STD	Avg Acc
meatlinc	1055	3492	2.87	-0.14	5.02	0.57	62
vendeen	1087	972	1.11	-0.61	5.20	0.90	63
texel	2	193044	0.99	-2.12	4.57	0.63	43
dorset (centurion)	1047	14094	0.41	-1.66	2.22	0.53	59
charollais	1077	21360	0.06	-2.20	2.46	0.67	60
bleu du maine	1084	540	0.05	-1.46	1.33	0.49	56
hampshire	1000	12378	-0.14	-1.77	2.07	0.59	47
suffolk	3	78306	-0.32	-2.47	3.90	0.76	38
blue texel	1502	639	-0.67	-1.80	0.52	0.37	50
shropshire	1051	3201	-0.97	-2.58	0.47	0.55	60
southdown	1052	2169	-1.12	-2.98	0.93	0.61	58
beltex	1090	1767	-1.94	-3.38	0.96	0.57	61

CT fat weight

Breed	Breedcode	Num	Avg	Min	Max	STD	Avg Acc
meatlinc	1055	3492	1.45	-0.05	2.88	0.40	59
vendeen	1087	972	0.97	-0.36	4.27	0.77	60
hampshire	1000	12378	0.77	-0.88	2.56	0.44	45
dorset (centurion)	1047	14094	0.53	-1.00	2.11	0.41	57
charollais	1077	21360	0.36	-1.13	1.92	0.40	58
suffolk	3	78306	0.26	-1.23	3.03	0.43	36
texel	2	193044	0.16	-1.77	2.51	0.38	41
blue texel	1502	639	0.13	-0.86	1.03	0.32	58
bleu du maine	1084	540	-0.08	-1.35	0.75	0.38	53
shropshire	1051	3201	-0.08	-1.20	1.28	0.41	58
beltex	1090	1767	-0.33	-1.44	1.12	0.36	58
southdown	1052	2169	-0.54	-1.53	0.61	0.37	55

CT muscularity

Breed	Breedcode	Num	Avg	Min	Max	STD	Avg Acc
meatlinc	1055	3492	4.44	0.05	8.66	1.25	47
charollais	1077	21360	0.86	-3.89	7.86	1.33	47
vendeen	1087	972	0.65	-1.17	2.62	0.67	46
dorset (centurion)	1047	14094	0.49	-3.62	3.55	0.96	45
texel	2	193044	0.47	-3.64	8.15	0.96	35
suffolk	3	78306	0.23	-4.02	7.90	1.14	31
hampshire	1000	12378	0.22	-3.02	4.25	0.89	35
bleu du maine	1084	540	-0.17	-1.82	2.08	0.86	39
shropshire	1051	3201	-0.29	-3.01	2.26	0.80	43
southdown	1052	2169	-0.31	-4.02	2.93	0.91	39
beltex	1090	1767	-0.39	-3.14	2.98	0.92	44
blue texel	1502	639	-1.21	-3.40	0.21	0.51	32

FEC

Breed	Breedcode	Num	Avg	Min	Max	STD	Avg Acc
meatlinc	1055	3492	-0.15	-0.15	-0.15	0.00	3
vendeen	1087	972	-0.15	-0.15	-0.15	0.00	0
dorset (centurion)	1047	14094	-0.15	-0.15	-0.15	0.00	2
hampshire	1000	12378	-0.15	-0.15	-0.15	0.00	1
bleu du maine	1084	540	-0.15	-0.15	-0.15	0.00	1
shropshire	1051	3201	-0.15	-0.15	-0.15	0.00	0
southdown	1052	2169	-0.15	-0.15	-0.15	0.00	0
blue texel	1502	639	-0.15	-0.15	-0.15	0.00	0
beltex	1090	1767	-0.13	-0.15	-0.06	0.02	2
charollais	1077	21360	-0.09	-0.45	0.31	0.08	9
texel	2	193044	0.02	-1.96	1.35	0.09	7
suffolk	3	78306	0.15	-2.30	1.86	0.15	10

Birth Weight

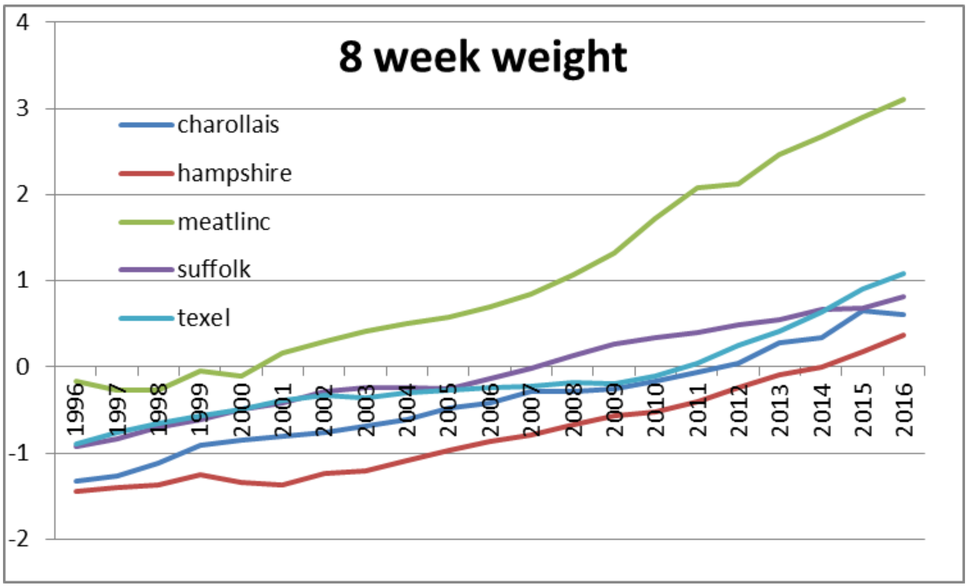
Breed	Breedcode	Num	Avg	Min	Max	STD	Avg Acc
southdown	1052	2169	-0.22	-0.61	0.12	0.12	43
beltex	1090	1767	-0.16	-0.48	0.24	0.12	44
bleu du maine	1084	540	-0.15	-0.75	0.26	0.21	32
vendeen	1087	972	-0.12	-0.39	0.16	0.08	49
charollais	1077	21360	-0.11	-0.58	0.37	0.13	48
shropshire	1051	3201	-0.09	-0.50	0.34	0.14	47
dorset (centurion)	1047	14094	-0.04	-0.56	0.45	0.12	47
hampshire	1000	12378	-0.04	-0.45	0.47	0.13	39
suffolk	3	78306	0.11	-0.81	0.70	0.13	33
meatlinc	1055	3492	0.13	-0.27	0.66	0.11	46
texel	2	193044	0.13	-0.61	0.77	0.13	36
blue texel	1502	639	0.51	0.10	0.75	0.12	32

Lambing Ease

Breed	Breedcode	Num	Avg	Min	Max	STD	Avg Acc
meatlinc	1055	3492	0.44	-0.71	0.64	0.15	36
texel	2	193044	0.18	-1.38	0.48	0.07	33
shropshire	1051	3201	0.12	-0.75	0.30	0.10	35
blue texel	1502	639	0.08	-0.38	0.20	0.12	24
dorset (centurion)	1047	14094	0.05	-1.16	0.27	0.13	38
charollais	1077	21360	-0.02	-0.81	0.17	0.07	41
suffolk	3	78306	-0.02	-0.96	0.24	0.06	28
bleu du maine	1084	540	-0.03	-0.83	0.10	0.11	32
southdown	1052	2169	-0.04	-0.59	0.14	0.07	32
beltex	1090	1767	-0.24	-0.94	-0.06	0.07	35
vendeen	1087	972	-0.37	-0.65	-0.12	0.08	38
hampshire	1000	12378	-0.62	-1.04	-0.29	0.09	30

To help answer the breed comparison question, the **5 ram compare breeds** will be used as we have year 1 data contributing as well as the Meatlinc cross breeding data also contributing to the genetic links. For each breed mostly purebred (PEB of 80% for a given breed) animals were extracted and the genetic trends produced.

The genetic trends for 8 week and scan weight traits show the same relationships. With 4 of the terminal breeds all grouped relatively together, but Meatlincs showing higher EBVs, especially for more recent animals. This is perhaps not what you would initially expect, but given that in the late 1990’s the Meatlinc breed was more similar to the other breeds and the divergence has happened in recent years – this suggests that the difference in recent born animals is truly due to genetic improvement. This is further supported when you look at the genetic trends between 2000 & 2015 for these breeds from their current conventional genetic evaluations; Meatlincs have made phenomenal progress compared to the other breeds. Considering scan weight for Meatlinc, Texel and Charollais breeds, the Meatlinc has seen a genetic improvement of 7.58kg, which the Texel and Charollais has only made 3.94 and 3.83kg, respectively. This is almost double the rate of their competitor breeds, and I don’t think the large number of unrecorded Texel’s is driving this difference as we have a comparable dataset with the Charollais. Also as they were much closer in genetic merit at the end of the 1990’s this is evidence that genetic groups and starting populations are not the reason for this rapid genetic improvement. Adding genetic groups for Meatlincs is also unlikely to impact the starting position as the level of pedigree recording is very high for the breed so the starting point of early founders will be very similar to the starting point of no breed specific genetic group which is the current situation – and even if you did force the early Meatlincs to perform badly, the rapid genetic gain observed will mean they will soon outperform every one again. The meatlinc is a very different type of ‘breed’ to be a Meatlinc breeder you have to follow the Meatlinc philosophy which means the breed as a whole moves in the same direction much quicker than a breed where individual breeders all have different breeding goals, and the level of performance recording is lower. If we believe the genetic trends that are currently published for the breeds based on their official evaluations then we have to believe that the Meatlincs are also seeing the same rapid genetic trends in CBA system, and as a result are outperforming the other terminal breeds on a genetic level. Within the larger breeds, there are likely to be pockets of breeders that can match the performance of the Meatlinc, but as an overall breed they can’t.


8 week weight
charollais
hampshire
meatlinc
suffolk
texel
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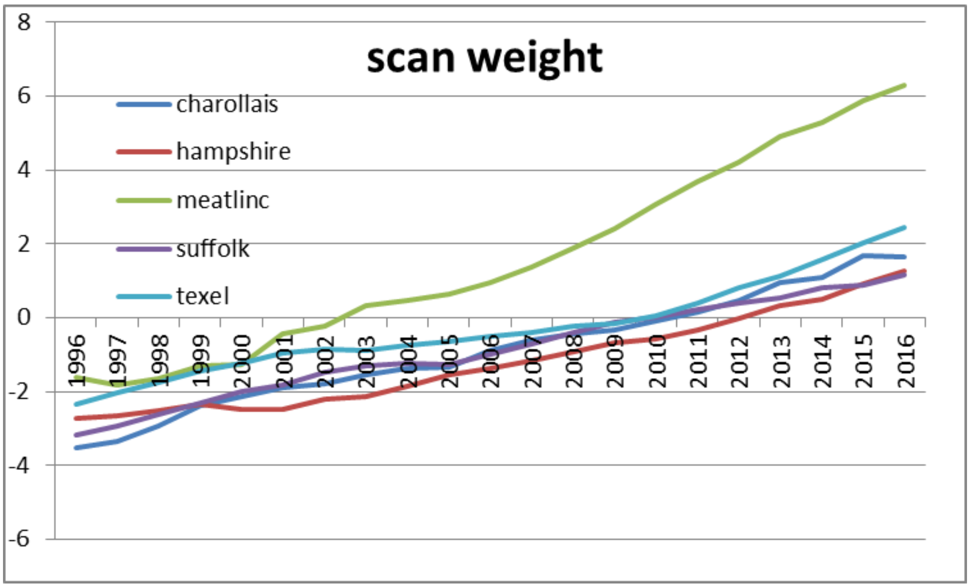
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charollais
hampshire
meatlinc
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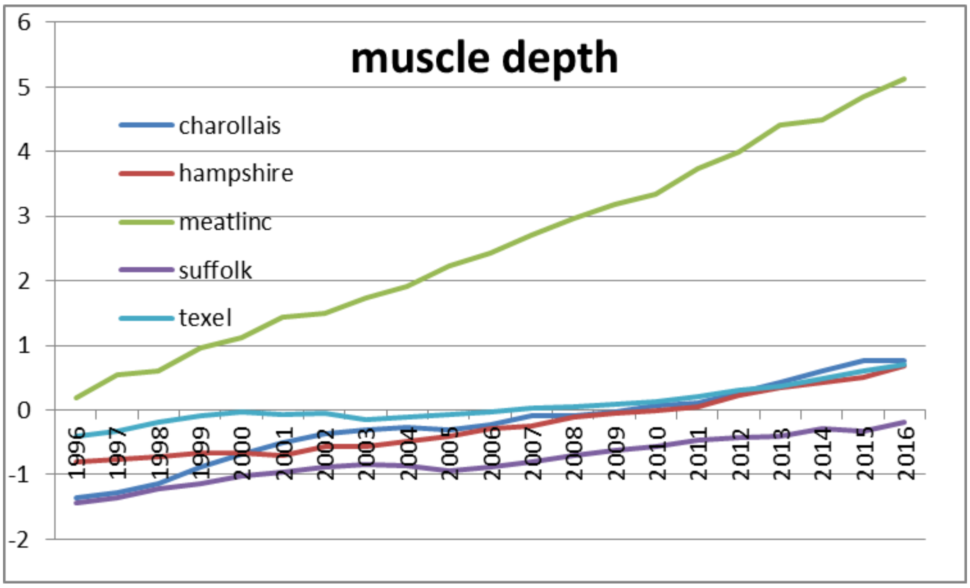
muscle depth
charollais
hampshire
meatlinc
suffolk
texel
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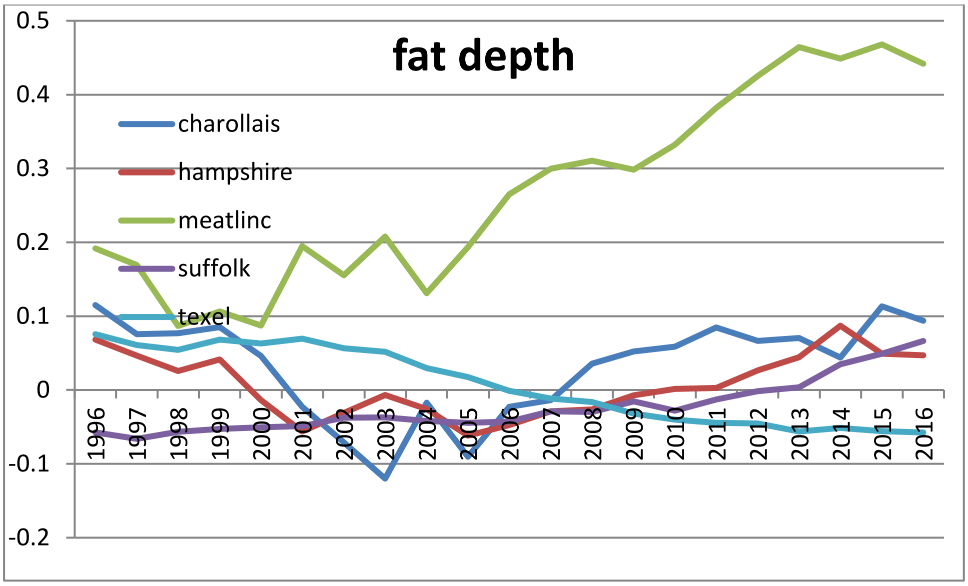

Conclusions

From the results above I have concluded that it is correct that the 5 ram compare breeds be compared together and that the differences in EBVs are down to true genetic differences.

The same cannot be said for the smaller terminal breeds i.e. Blue Texel, and it is difficult to conclusively investigate if the performance is as expected. In most cases the minor breeds sit amongst the middle of the breeds in ranking and this causes less concern about the industry getting an incorrect message about whether a small breed is better/worse for different traits.

There is clearly an issue with Blue Texel as it is ranked breed number 1 for weaning weight and breed number 12 for scan weight which is unlikely. The solution here is to combine the Blue Texel genetic group into the Texel genetic groups and see if that stabilises the small breed. This is outside the scope of this research project so will need to be done and funded as a separate development task.

Although not a small breed, Dorset is a breed that performs well compared to other breeds and looking at the genetic trends for scan weight from their current evaluations – they are achieving genetic gains comparable to Texel/Charollais.

Shropshire and Southdown appear to be the least performing breeds (at least for live weight), but looking at their current genetic trends they are showing slower progress than the other breeds so this is perhaps correct.

In all of these comparisons we also need to keep in mind that the standard deviations tend to be large enough that it is difficult for us to be able to say one breed is better than another.

To conclude, I think we can proceed to publish with all the breeds on one scale. In some cases with major breeds we can believe the better performance, but with the smaller terminal breeds we should advise caution when comparing until more data (in particular cross breeds to give the links) builds up. The exception is of course Blue Texel which should be addressed looking at the genetic groups.

Objective 7: A review of breeding indexes and initial recommendations for the industry.

Currently each breed has an individual (or in some cases two) indices tailored to the genetic parameters and breeding objectives of that breed. For the 12 breeds currently considered there are 15 indices. However, in most cases the indices are aimed at achieving the same end point and will broadly select the same animals. The tables below shows the current emphasis placed on the different traits for the different breeds.

Raw Index weights:

	w8w	swt	md	fd	maternal	lsb	ct_lean	ct_fat	ct_musc	ATAN1	ATAN2	ATAN3
Beltex	-0.058	0.128	0.057	-0.607			2.492	-0.795	0.022	3	-0.1	2.38
Bleu Du Maine		0.378	1.09	-1.916								
Blue Texel		0.378	1.09	-1.916								
Charollais	0.2	0.06	0.2	0.5			1.9	-0.25	0.104	3	0.65	4.76
Dorset (1)	0.273	0.681	1.962	-0.896						3	0.65	1.19
Dorset (2)	1.03			0.15	0.71	6.35				3	0.65	1.19
Hampshire	0.022	0.531	0.111	-0.951			1.057	-1.317	0.157	3	-0.1	1.19
Meatlinc	0.084	-0.007	0.026	0.153			2.587	-1.017	0.103	3	-0.1	4.76
Shropshire (1)		0.49	1.1	2.38	0.83					3	0.65	2.38
Shropshire (2)	-0.194	1.086	0.384	2.38						3	0.65	2.38
Southdown		0.378	1.09	-1.916						3	0.4	2.38
Suffolk (1)	-0.005	-0.005	0.042	0.023			1.225	-0.405	0.051	3	-0.1	2.38
Suffolk (2)	0.37				1.33	7.15						
Texel	-0.121	-0.086	0.36	0.24			1.593	-0.5	0.055	3	-0.1	1.19
Vendeen		0.292	0.802	2.38						3	0.65	2.38

Genetic variance (from milestone 2 report – = h^2*Vp)

	w8w	swt	md	fd	maternal	lsb	ct_lean	ct_fat	ct_musc
Beltex	5.1794	17.2431	5.0048	0.5293			1.3035	0.9	27.23
Bleu Du Maine		9.5256	1.2672	0.3312					
Blue Texel		9.5256	1.2672	0.3312					
Charollais	3.1614	11.5102	1.878	0.4692			0.8694	0.8208	10.872
Dorset (1)	1.1517	5.4837	1.943	0.5373					
Dorset (2)	1.1517			0.5373	1.58	0.0297			
Hampshire	2.9928	7.8606	1.8522	0.5112			0.9	0.8474	10.872
Meatlinc	2.9502	10.9922	2.628	0.2387			0.69	0.63	10.036
Shropshire (1)		2.3275	1.2	0.2835	0.995				
Shropshire (2)	0.7656	2.3275	1.2	0.2835					
Southdown		9.5256	1.2672	0.3312					
Suffolk (1)	3.6015	12.1055	2.272	0.5145			0.966	0.94	11.92
Suffolk (2)	3.6015				0.857	0.042			
Texel	3.2625	12.7141	2.0648	0.4028			1.0707	0.6144	11.67
Vendeen		13.8624	2.1142	0.4186					

Proportion emphasis in the index:

	w8w	swt	md	fd	maternal	lsb	ct_lean	ct_fat	ct_musc
Beltex	0.04	0.29	0.04	0.04			0.42	0.09	0.08
Bleu Du Maine		0.64	0.25	0.11					
Blue Texel		0.64	0.25	0.11					
Charollais	0.13	0.14	0.08	0.05			0.34	0.04	0.23
Dorset (1)	0.04	0.45	0.46	0.06					
Dorset (2)	0.46			0.03	0.44	0.07			
Hampshire	0.01	0.48	0.02	0.06			0.11	0.13	0.20
Meatlinc	0.06	0.02	0.02	0.01			0.46	0.16	0.27
Shropshire (1)		0.29	0.33	0.17	0.21				
Shropshire (2)	0.04	0.66	0.12	0.18					
Southdown		0.64	0.25	0.11					
Suffolk (1)	0.01	0.03	0.04	0.01			0.50	0.16	0.26
Suffolk (2)	0.48				0.41	0.11			
Texel	0.08	0.22	0.15	0.02			0.34	0.06	0.13
Vendeen		0.60	0.25	0.15					

With the CBA system all of the breed use the same genetic parameters, and thus it would be only different breeding objectives that would warrant a separate breed specific indices, especially since the previous section concluded that it was not necessary to re base individual breeds to avoid across breed comparisons.

There are a couple of points to consider in the index discussion;

- It is likely that each of the 12 breeds will want their own index for non – scientific reasons, like marketing of their breed. Looking at the 15 indices above it is clear there are enough differences to think that a single terminal index may not be desired across the breeds; there is those with and without the fat ATAN, with and without the CT traits as not all record CT without even looking at the different emphasis placed on growth verses muscle.
- As the system currently stands there is only space for 2 indexes for the CBA run. The obvious choice would then be to have a terminal carcass index and a separate maternal index, balancing them appropriately so as not to be totally extreme in the goal. However, this is unlikely to sufficient to service all the animals in the existing CBA evaluation.
- Any additional index would require a rethink of the current index system and require a coding solution to create more ‘holes’ to publish additional indices into.
- I think there are 2 options on how we handle the demand for extra indices;
- 1) create more holes on BASCO so breeds can have breed specific indices or
- 2) stick to the 2 index approach in basco (or discontinue it even) but invest in customised indices. In other work (dairy and fish) at EGENES we have developed customised indices webpages that take the EBVs and then apply a customised index to the data. This has the added advantage of each breed

having their own index (I'm sure we can have that as a default option) but then breeders can further tailor the index to their needs – perhaps with Signet breeding consultants advice – to have a breeder specific index.

- If further development in indices is required I think that going the customised index route will represent better value and allow more flexibility for the future and be better received by industry.

APPENDIX B: Individual breed parameters and the averages to produce the combined breed genetic parameters.

Variances and heritabilities

	8 week weight / maternal ability				Scan weight		Muscle depth		Fat depth		Birth weight	
	Vp	**h2**	**h2m**	**h2pe**	**Vp**	**h2**	**Vp**	**h2**	**Vp**	**h2**	**Vp**	**h2**
Beltex	11.020	0.26	0.09	0.18	27.37	0.37	7.36	0.32	0.79	0.33		
Shopsire	6.384	0.12	0.16	0.21	12.25	0.19	4	0.3	0.81	0.35		
Blue Texel	9.000	0.20	0.29	0.11	39.69	0.24	5.76	0.22	1.44	0.23		
Bleudumaine	9.000	0.20	0.29	0.11	39.69	0.24	5.76	0.22	1.44	0.23		
Vendeen	13.988	0.20	0.29	0.11	57.76	0.24	9.61	0.22	1.82	0.23		
Southdown	9.000	0.20	0.29	0.11	39.69	0.24	5.76	0.22	1.44	0.23		
Hampshire	12.468	0.24	0.06	0.11	23.82	0.33	6.86	0.27	2.13	0.24		
Dorset	10.470	0.11	0.15	0.23	20.31	0.27	6.7	0.29	1.99	0.27	0.460	0.20
Meatlinc	13.405	0.22	0.02	0.20	32.33	0.34	8.76	0.3	0.77	0.31		
Charollais	14.368	0.22	0.07	0.16	30.29	0.38	6.26	0.3	1.38	0.34		
Suffolk	17.146	0.21	0.06	0.13	39.05	0.31	7.1	0.32	1.47	0.35		
Texel	12.700	0.26	0.07	0.20	31.01	0.41	7.12	0.29	1.06	0.38	0.635	0.21
Average	**11.579**	**0.20**	**0.15**	**0.16**	**32.772**	**0.30**	**6.754**	**0.27**	**1.378**	**0.29**	**0.548**	**0.20**

	Mature size		Litter size born		Litter size reared		CT_lean		CT_fat		CT_muscle	
	Vp	**h2**	**Vp**	**h2**	**Vp**	**h2**	**Vp**	**h2**	**Vp**	**h2**	**Vp**	**h2**
Beltex	12.96	0.35	0.42	0.1								
Shopsire	27.03	0.46	0.18	0.12								
Blue Texel	12.96	0.35	0.42	0.1								
Bleudumaine	12.96	0.35	0.42	0.1								
Vendeen	12.96	0.35	0.42	0.1								
Southdown	12.96	0.35	0.42	0.1								
Hampshire	12.96	0.35	0.31	0.1								
Dorset	11.53	0.27	0.33	0.09	0.27	0.04						
Meatlinc	39.83	0.5	0.32	0.12								
Charollais	12.96	0.35	0.42	0.1			1.89	0.46	2.16	0.38	30.2	0.36
Suffolk	12.96	0.35	0.42	0.1			2.1	0.46	2.35	0.40	29.8	0.40
Texel	**12.96**	0.35	**0.42**	0.1			2.49	0.43	1.92	0.32	38.9	0.30
Average	**16.253**	**0.37**	**0.375**	**0.10**	**0.27**	**0.04**	**2.160**	**0.45**	**2.143**	**0.37**	**32.967**	**0.35**