Review and estimation of Beltex genetic parameters
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Introduction: The genetic parameters for the Beltex sheep breed were requested to be estimated. Given the available data only the growth traits could be considered with the maternal traits and components unlikely to be estimable. QMS and EBLEX funded work to estimate genetic parameters for traits where there was sufficient data available.

Current situation: The Beltex breed received within flock evaluations in 2007 and then commenced across breed evaluations in 2008. The existing genetic parameters that are used are those from the Texel evaluation and not specifically for Beltex. Although this is reasonable given that the Beltex breed is relatively new to the UK and were derived from a Texel population, albeit from Belgium. The following tables show the existing genetic parameters for Texel/Beltex.

Variances

Trait	V-additive	V-dam	V-litter	V-residual	V-phenotypic	H2add	H2mat	H2lit
8 WK	3.3	1.205	2.508	6.033	13.046	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	0.395	-	-	0.662	1.057	0.37		
MATERNAL	0.592	0.4569	2.508	7.857	11.4139	0.05	0.04	0.22
MATURE	4.536	-	-	8.424	12.96	0.35		
LSB	0.042	0.021	-	0.355	0.418	0.10	0.05	
CT_LEAN	1.059	-	-	1.31	2.369	0.45		
CT_FAT	0.606	-	-	0.896	1.502	0.40		
CT_MUSC	11.80	-	-	27.1	38.9	0.30		

Co-variances (below) and Correlations (above)

Maternal effects

	8 WK	MATERNAL	LSB
8 WK		0	0
MATERNAL	0		0
LSB	0	0	

Permanent environment effects

	8 WK	MATERNAL
8 WK		0
MATERNAL	0	

Additive effects

	8 WK	SWT	MD	FD	MATERNAL	MATURE	LSB	CT_LEAN	CT_FAT	CT_MUSC
8 WK		0.90	0.49	0.37	0	0	0	0.83	0.67	0.56
SWT	5.803		0.47	0.38	0	0	0	0.83	0.68	0.56
MD	1.279	2.374		0.24	0	0	0	0.41	0.23	0.26
FD	0.422	0.843	0.215		0	0	0	-0.07	0.55	0.42
MATERNAL	0	0	0	0		0.15	0	0	0	0
MATURE	0	0	0	0	0.246		0.20	0	0	0
LSB	0	0	0	0	0	0.087		0	0	0
CT_LEAN	1.548	3.049	0.602	-0.044	0	0	0		0.38	0.38
CT_FAT	0.947	1.871	0.257	0.27	0	0	0	0.307		0.26
CT_MUSC	3.470	6.779	1.28	0.90	0	0	0	1.354	0.703	

Residual effects

	8 WK	SWT	MD	FD	MATERNAL	MATURE	LSB	CT_LEAN	CT_FAT	CT_MUSC
8 WK		0.84	0.47	0.37	0	0	0	0.79	0.76	0.25
SWT	8.882		0.61	0.49	0	0	0	0.90	0.90	0.25
MD	2.603	5.907		0.38	0	0	0	0.64	0.53	0.40
FD	0.74	1.712	0.695		0	0	0	0.47	0.64	0.06
MATERNAL	0	0	0	0		0.10	0	0	0	0
MATURE	0	0	0	0	0.813		0.10	0	0	0
LSB	0	0	0	0	0	0.173		0	0	0
CT_LEAN	2.217	4.42	1.642	0.436	0	0	0		0.79	0.47
CT_FAT	1.772	3.655	1.136	0.495	0	0	0	0.852		0.21
CT_MUSC	3.145	5.494	4.685	0.25	0	0	0	2.777	1.035	

Estimation of Beltex genetic parameters:

The Dataset: This work was undertaken based on data available on the 28/04/2009. Internal batch ids are 20080487 and data source id was 799. In total there were ~2,600 Beltex animals recorded in the pedigree. All these animals were recoded to meet software requirements (i.e. numbering for ASReml) and used in the pedigree of the analysis. The table below shows that for each trait considered there were between 840 and 929 records available before edits and restrictions.

Trait	N	Mean	SD	Min	Max	N rec with 5+ in CG
8WK	929	18.8	3.8	6.5	30.4	917
SWT	909	37.7	6.8	16.0	67.0	877
MD	848	27.4	3.6	15.7	42.0	814
FD	840	2.8	1.3	0.5	8.0	806

The table below looks at the number of animals that have different combinations of traits available and then also with sufficient number of animals in the contemporary groups (CG's). CG definitions are outlined in the table detailing models. For example, the CG for 8 week weight was Flock, Season and Sex. In the total there were 795 animals that had all 4 traits recorded.

Trait	8 wk	+SWT	+SWT + MD	+SWT + MD + FD
8WK	929	850	803	795
N with 5+ in CG	917	825	779	771

For each trait, it was required that there were 5 or more animals in the relevant CG. Animals were retained in the dataset as long as they had one trait that met the criteria.

The Models: The models that were used were the same as those in the routine genetic evaluations

Trait	Fixed class effects	Fixed co-variate effects	Random effects
8 WK	Flock|season|sex LSR Dam_age		Animal Dam Litter
SWT	LSR Dam_age Flock|year|season|sex|management group	Scan_age* Flock|year|season|sex|management group	Animal
MD	LSR Dam_age Flock|year|season|sex|management group	Scan_age* Flock|year|season|sex|management group	Animal
FD	LSR Dam_age Flock|year|season|sex|management group	Scan_age* Flock|year|season|sex|management group	Animal

The genetic parameter estimation: A series of uni-variate and multi-variate ASreml analysis were undertaken. Consistently across all the analysis it was found that the additive effects were being overestimated, resulting in inflated heritabilities for the traits. The phenotypic variances estimated did appear to be reasonable. Estimates of the correlations were also sensible. With the number of records and very few data edits applied to retain records the inability to partition additive variances is understandable. To obtain useful genetic parameters the initial Beltex parameters were blended with estimates from Texel's. Given the challenges of partitioning maternal effects, maternal variances were calculated assuming similar heritabilities as were previously used in the parameters. The resulting genetic parameters are shown below. The traits that were not re-estimated are also included with altered co-variances to reflect changes to the growth traits.

Variances

Trait	V-additive	V-dam	V-litter	V-residual	V-phenotypic	H2add	H2mat	H2lit
8 WK	2.87	0.99	1.98	5.18	11.02	0.26	0.09	0.18
SWT	10.20	-	-	17.17	27.37	0.37		
MD	2.33	-	-	5.03	7.36	0.32		
FD	0.26	-	-	0.53	0.79	0.33		
MATERNAL	0.592	0.4569	2.508	7.857	11.4139	0.05	0.04	0.22
MATURE	4.536	-	-	8.424	12.96	0.35		
LSB	0.042	0.021	-	0.355	0.418	0.10	0.05	
CT_LEAN	1.059	-	-	1.31	2.369	0.45		
CT_FAT	0.606	-	-	0.896	1.502	0.40		
CT_MUSC	11.80	-	-	27.1	38.9	0.30		

Co-variances (below) and Correlations (above)

Maternal effects

	8 WK	MATERNAL	LSB
8 WK		0	0
MATERNAL	0		0
LSB	0	0	

Permanent environment effects

	8 WK	MATERNAL
8 WK		0
MATERNAL	0	

Additive effects

	8 WK	SWT	MD	FD	MATERNAL	MATURE	LSB	CT_LEAN	CT_FAT	CT_MUSC
8 WK		0.90	0.48	0.39	0	0	0	0.83	0.67	0.56
SWT	4.869		0.53	0.45	0	0	0	0.83	0.68	0.56
MD	1.241	2.584		0.32	0	0	0	0.41	0.23	0.26
FD	0.341	0.728	0.246		0	0	0	-0.06	0.48	0.37
MATERNAL	0	0	0	0		0.15	0	0	0	0
MATURE	0	0	0	0	0.246		0.20	0	0	0
LSB	0	0	0	0	0	0.087		0	0	0
CT_LEAN	1.447	2.728	0.644	-0.032	0	0	0		0.38	0.38
CT_FAT	0.884	1.691	0.273	0.191	0	0	0	0.307		0.26
CT_MUSC	3.259	6.144	1.363	0.645	0	0	0	1.354	0.703	

Residual effects

	8 WK	SWT	MD	FD	MATERNAL	MATURE	LSB	CT_LEAN	CT_FAT	CT_MUSC
8 WK		0.72	0.42	0.32	0	0	0	0.79	0.76	0.25
SWT	6.790		0.63	0.49	0	0	0	0.90	0.90	0.25
MD	2.144	5.855		0.40	0	0	0	0.64	0.53	0.40
FD	0.530	1.478	0.653		0	0	0	0.47	0.64	0.06
MATERNAL	0	0	0	0		0.10	0	0	0	0
MATURE	0	0	0	0	0.813		0.10	0	0	0
LSB	0	0	0	0	0	0.173		0	0	0
CT_LEAN	2.058	4.268	1.643	0.392	0	0	0		0.79	0.47
CT_FAT	1.637	3.530	1.125	0.441	0	0	0	0.852		0.21
CT_MUSC	2.962	5.393	4.670	0.227	0	0	0	2.777	1.035	

Comparison of new genetic parameters with existing parameters: The parameters are generally comparable. The biggest difference is that the variances estimated in the present study are generally smaller. This was generally across all the variance components with heritabilities comparable. Genetic correlations with 8 week weight were similar to previous estimates. Correlations between the 3 ultrasound traits were sensible but slightly higher than previous parameters. Residual correlations were similar to previous estimates with slightly smaller correlations between 8 week and scan weight. These parameters appear to be within the limits of previous published parameter estimates

Test Run: To look at the effects that the new parameters would have on evaluations a test run was performed. Using the same data as the live 0902 evaluation (batch id = 20080571 data from 14/9/09), the parameters were changed and the evaluation re-run (batch id = 20080606) and compared.

Summary of Data (from Mix99 program)

```
    TR TR-NAME       N-OBS      MEAN        SD      MINIMUM      MAXIMUM
    ------------------------------------------------------------------
     1  w8w           1438     18.795     3.9345      6.5000      33.500
     2  swt           1392     36.987     6.9163      14.000      68.500
     3  md            1331     27.513     3.6587      15.200      42.000
     4  fd            1323     2.5377     1.2778      0.17000     8.0000
     5  mat_w8w       1438     18.795     3.9345      6.5000      33.500
     6  maturesz         0
     7  lsb           1067     1.5876     0.62210     1.0000      5.0000
     8  ct_lean         84     17.168     2.1507      11.076      21.644
     9  ct_fat          82     3.0836     1.2105      1.0224      6.0157
    10  ct_musc         84     68.875     5.8553      56.100      81.300
```

Summary of EBV for 3310 animals

Trait		Prior to test run				After changing parameters				r
		Mean	Std	Min	Max	Mean	Std	Min	Max	
8wk	EBV	-0.05	0.8	-3.68	4.13	-0.06	0.81	-3.69	4.08	0.9976
8wk	ACC	48.27	24.33	0	96	48.11	24.35	0	96	
swt	EBV	-0.03	1.57	-7.82	8.02	-0.04	1.52	-7.4	7.55	0.9925
swt	ACC	50.48	25.25	0	97	49.03	24.63	0	99	
md	EBV	-0.02	0.69	-3.34	3.32	-0.02	0.74	-3.66	3.62	0.9988
md	ACC	43.49	22.81	0	95	44.79	23.35	0	95	
fd	EBV	0.01	0.29	-1.09	1.52	0.01	0.27	-1.06	1.48	0.9927
fd	ACC	46.92	24.73	0	96	45.61	23.99	0	95	
maternal	EBV	-0.03	0.19	-0.92	0.95	-0.03	0.19	-0.92	0.95	0.9999
maternal	ACC	21.56	11.3	0	59	21.56	11.31	0	59	
maturesize	EBV	-0.01	0.13	-0.58	0.65	-0.01	0.13	-0.58	0.65	0.9999
maturesize	ACC	7.16	4.6	0	61	7.16	4.6	0	61	
lsb	EBV	0	0.05	-0.19	0.34	0	0.05	-0.19	0.34	0.9999
lsb	ACC	26.67	13.38	0	68	26.67	13.38	0	68	
ct_lean	EBV	-0.02	0.43	-1.99	2.15	-0.03	0.47	-2.09	2.21	0.9938
ct_lean	ACC	49.02	24.63	0	96	48.43	24.4	0	96	
ct_fat	EBV	0	0.28	-1.24	1.33	-0.01	0.29	-1.28	1.44	0.9911
ct_fat	ACC	42.76	22.17	0	94	41.67	21.71	0	93	
ct_musc	EBV	-0.03	1.08	-4.83	5.97	-0.06	1.18	-5.26	7.01	0.9883
ct_musc	ACC	37.55	20.23	0	90	36.84	19.96	0	90	
index	index	96.01	34	-50.62	275.48	96.36	34.55	-46.44	261.5	
index	ACC	49.68	24.87	0	96	49.26	24.69	0	97	

Comparison of 2008 males (n=266)

Trait		Prior to test run				After changing parameters				r
		Mean	**Std**	**Min**	**Max**	**Mean**	**Std**	**Min**	**Max**	**r**
8wk	**EBV**	-0.2	1	-3.68	2.67	-0.22	1	-3.69	2.77	0.9979
8wk	**ACC**	64.52	9.76	21	91	64.47	9.81	21	91	
swt	**EBV**	-0.29	1.99	-7.82	5.5	-0.31	1.91	-7.4	5.04	0.9928
swt	**ACC**	67.61	10.45	23	93	65.82	10.31	22	99	
md	**EBV**	-0.1	0.71	-2.53	1.95	-0.11	0.77	-2.75	2.16	0.9977
md	**ACC**	58.46	10.45	19	89	60.32	10.83	20	90	
fd	**EBV**	-0.03	0.37	-0.96	1.52	-0.04	0.34	-0.97	1.48	0.9890
fd	**ACC**	64.06	13.44	21	93	62.92	13.48	20	92	
maternal	**EBV**	-0.01	0.16	-0.52	0.4	-0.01	0.16	-0.52	0.4	1.0000
maternal	**ACC**	22.42	5.84	0	33	22.43	5.84	0	33	
maturesize	**EBV**	0.02	0.12	-0.34	0.34	0.02	0.12	-0.34	0.34	0.9999
maturesize	**ACC**	6.96	1.81	0	10	6.96	1.81	0	10	
lsb	**EBV**	0.01	0.05	-0.1	0.19	0.01	0.05	-0.1	0.19	1.0000
lsb	**ACC**	27.35	6.36	0	38	27.35	6.36	0	38	
ct_lean	**EBV**	-0.07	0.58	-1.99	2.14	-0.08	0.62	-2.09	2.15	0.9947
ct_lean	**ACC**	66.3	10.78	22	93	65.68	10.86	21	92	
ct_fat	**EBV**	-0.04	0.34	-1.1	0.95	-0.05	0.36	-1.13	1.08	0.9908
ct_fat	**ACC**	58.68	10.54	17	89	57.49	10.85	16	88	
ct_musc	**EBV**	-0.23	1.5	-4.83	5.02	-0.31	1.65	-5.26	5.58	0.9882
ct_musc	**ACC**	52.89	12.08	13	86	52.16	12.32	13	85	
index	**index**	93.22	46.3	-50.62	275.48	93.02	46.23	-46.44	261.5	0.9933
index	**ACC**	66.62	10.22	22	92	66.17	10.34	22	97	

Biggest changer for the Index from 2008 Males

Sheep id: 8318219

Trait	Old EBV	Old ACC	New EBV	Old ACC	Diff in EBV	Own Data
8wk	-0.09	66	0.01	66	0.10	Y
swt	-0.69	71	-0.34	68	0.35	Y
md	1.10	61	1.17	63	0.07	Y
fd	-0.95	68	-0.85	64	0.10	Y
maternal	0.10	21	0.10	21	0	
maturesize	-0.01	6	-0.01	6	0	
lsb	-0.03	25	-0.03	25	0	
ct_lean	0.56	68	0.82	67	0.26	N
ct_fat	-0.46	57	-0.35	55	0.11	N
ct_musc	-1.75	47	-1.34	46	0.41	N
index	157.55	69	175.63	68	18	

No extra data from parents or progeny. The biggest changing EBVs are the CT traits. This is logical given that there is no data for this animal and it is dependent on the correlations with other traits and relative's information (of which there is limited CT data). The change in SWT is most likely to be because of slightly stronger correlations found between SWT and other traits. This was the male in 2008 that changed the most; however these changes are relatively small.

Conclusions:

The genetic parameters for the Beltex evaluation could be updated with these revised parameters. The test run showed that there were no major changes. The correlations between the 2 sets of EBVs were essentially 1.0. The average EBVs were similar as were the accuracies of traits. There were small changes to the ranges of EBVs produced – as expected from the different variance components.

To determine which set of parameters is more accurate and reflective of the population is difficult. In the present study only ~900 Beltex animals were used, stringent edits were not possible and parameters were blended with preliminary estimates from Texel animals. Conversely, little is known about the origins of the existing Texel parameters. In either case, the test run has shown that sensible and meaningful EBVs are produced with either set of parameters.