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Towards future genetic evaluations for live weight and carcass composition traits in UK sheep

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Highlights

- Growth and carcass composition traits are highly heritable in sheep and are positively correlated.
- After over 30 years of genetic selection in the UK, variation still exists for all four traits analysed.

- Within-breed analysis for future genetic evaluations for carcass composition traits are recommended in order to achieve high rates of genetic gain.
- Results from this study will be used as part of a further study to produce international genetic evaluations for sheep.

Abstract

The main aim of the current study was to perform a genetic analysis of two live body weight and two carcass composition traits in purebred UK-born Texel, Suffolk and Charollais lambs separately in order to produce future across country evaluations. The two live body weight traits considered were early-life weight (40 to 85 days of age) and scan weight (121 to 180 days of age), and the two carcass composition traits were muscle depth and fat depth. Only records from lambs born between 2010 and 2017 were used in the present study resulting in a total of 132,490 records from 55,155 lambs spread over 374 flocks being included for further analysis. An animal linear mixed model was used to derive (co)variance components for the studied traits, for each breed individually. Fixed effects included in the model were contemporary group, dam age at lamb's birth, dam age at first lambing, a birth type by rearing type of the lamb interaction and a sex by age of the lamb at measurement interaction. Random effects included in the model were the animal additive genetic effect, the dam maternal effect, the litter environment effect and the residual effect. The dam maternal effect applied only to the analysis of early-life weight. Heritability estimates ranged from 0.12 to 0.30 for the two live body weight traits across the three breeds. The two carcass composition traits had heritability estimates ranging from 0.18 to 0.42. Strong positive genetic correlations were observed between all traits analysed. Results from the present study show that genetic variation still exists within breeds for the traits studied indicating that even after over 30 years of genetic selection within the UK they are still amenable to genetic improvement. Furthermore, significant differences in genetic parameters between breeds were observed, especially for carcass composition traits, indicating that genetic evaluations should be calculated separately for each breed.

Keywords

Lamb growth, genetic parameters, muscle depth, fat depth, ultrasound scanning

Introduction

Genetic evaluation and improvement schemes have increasingly been used in the UK sheep industry, particularly in recent years. These schemes have proved to be extremely beneficial with an estimated return of over £15.5 million per year being achieved from genetic improvement within the beef and sheep industries, with much of this economic return attributed to improved growth and carcase traits (Signet, 2019). Much potential exists for further improvement within the UK sheep industry; for example, genetic progress achieved from just 10 years of using a terminal sire breeding programme has led to an economic benefit of £11.5 million to the sheep industry alone (Amer et al., 2007). The opportunity for across-breed evaluations and also that for international collaboration, as is currently the case for dairy (Interbull) and beef (Interbeef) could be a realistic option for the UK sheep industry. For this to happen, firstly trait definition and genetic parameters in respective breeds and countries need to be estimated. Genetic variability has been shown to exist according to the definition of traits and also for the same trait between breeds. This variability tends to be heightened when comparing terminal and maternal traits or terminal and maternal breeds (Safari et al., 2003). High levels of variability across live body weight and carcass composition traits at both a phenotypic and genetic level have been reported, not only in the UK (Simm et al., 2002; Jones et al., 2004; Rius-Vilarrasa et al., 2008), but also in Ireland (McHugh et al., 2017; O'Brien et al., 2017; Fitzmaurice et al., 2020) and elsewhere (Mousa et al., 1999; Safari et al., 2005; Thiruvenkadan et al., *2011*). Previous genetic studies were mostly based on research flocks or other special data subsets that, although useful for the purposes of the specific studies, were not representative of the national flock and sheep population. Furthermore, in the UK, genetic evaluations for sheep are currently conducted on the entire sheep population including multiple breeds and crossbreds.

The aim of the present study was to quantify the genetic variation present in two key live body weight traits and two carcass composition traits within the three most commonly recorded terminal sire breeds in the UK, namely Texel, Suffolk and Charollais. Results from this study will determine if separate within-breed analysis should be considered in future genetic evaluation systems within the UK.

Material and methods

Data

All available data were extracted from the UK National Sheepbreeder Database (AHDB) and subsequently edits were performed to provide a more informative data set. Three breeds were considered for analysis, namely Texel, Suffolk and Charollais and only purebred animals from these three breeds were retained.

Lamb live body weights were recorded at the early-life and scanning stages using weigh-scales. Carcass composition traits were recorded at the same time point as scan weight, post weaning, using ultrasound scanning. Early-life weight was defined as live weight measured between 40 and 85 days of age and weighing between 12 and 45 kg. Scan weight was defined as live weight taken between 121 and 180 days; only lambs weighing between 25 and 75 kg were retained for further analysis. Muscle depth had to measure between 10 and 44 mm to be retained for further analysis. Only fat depth records measuring between 0.5 and 8.0 mm were included in further analyses. For both live body weight traits, average daily gain (ADG) was calculated for all lambs; only lambs with ADG between 100 and 650 g/day were retained.

Additional lamb records were discarded if they had an unknown sire, dam, maternal grandsire or flock of birth. In order for a lamb record to be retained both their sire and maternal grandsire were required to have at least five progeny each. Dams with no known age or aged >9 years had their lamb records discarded; dam age number was then categorised as 1,2,3,4, or ≥5 years. Age at first lambing was defined as the age of the dam at her first lambing and this ranged from 1 to 3 years. Birth type was defined as the number of lambs born per lambing event per ewe. Only lambs with a birth type between 1 (single) and 4 (quadruplets) were included in subsequent analysis. Rearing type was defined as the number of lambs reared per litter per ewe; only lambs with a rearing type of between 1 and 3 were retained. Lambs that were born as a result of embryo transfer, lambs that were artificially reared or not reared by their biological dam were not used as part of the present study. After all previously mentioned edits were performed, lambs were allocated to a contemporary group of breed-by-flock-by-week of weighing. Only contemporary groups with at least five records were retained for further analysis.

After all data edits were completed a total of 132,490 live weight and carcass composition records from 55,155 animals across 374 flocks between the years 2010 and 2017 remained. Trait specific numbers have been included as part of Table 1.

Genetic Analysis

A linear animal mixed model was built for the genetic analysis; each studied trait was analysed separately within breed. The model fitted was:

$$Y_{inhdkljzm} = CG_i + AFL_n + Dam\ age_h + Sex_d * Age + Birth\ type_k * Rearing\ type_l + Animal_j + Dam_z + Litter_m + e_{inhdkljzm}$$

Where $Y_{inhdkljzm}$ = lamb record, CG_i=fixed effect of the i^{th} contemporary group (i=1 to 871), AFL_n = fixed effect of n^{th} age of the dam class at first lambing (1 to 3), Dam age_h = fixed effect of the h^{th} age of the dam at lambing class (1 to 5), Sex_d*Age = the interaction between the d^{th} (1 to 2) sex of the lamb and age of the lamb at record, Birth $type_k$*Rearing $type_l$ = the interaction between the birth type k (1 to 4) and rearing type *l* of the lamb (1 to 3), $Animal_j$ = random additive genetic effect of j^{th} animal (lamb) including all pedigree available, Dam_z = random maternal effect of z^{th} dam of animal *j*, $Litter_m$ = random common environmental effect among lambs in the m^{th} litter, and $e_{inhdkljzm}$= random residual effect.

The above model was built up for each trait and breed separately. Significance of random effects was examined using the log-likelihood ratio test (Ferreira et al., 1999). The random dam maternal effect was an overall collective maternal effect including both a genetic and permanent environment effect of the dam using an identity matrix to link the data to the dams. Early-life weight was the only trait to include all random effects included in the model above. All other traits only included additive genetic and common environmental random effects as no significant dam effect was observed for these traits.

Heritability of each trait was calculated as the proportion of the total phenotypic variance accounted for by the additive genetic effect. The ratios of the maternal and common environmental variances to the total phenotypic variance were also derived in a similar manner. Genetic correlations between traits were estimated using the same model in a series of bivariate analyses of all traits studied.

To ensure accurate estimation of (co)variance components, an informative subset of well-connected flocks was formed, where sires were required to have progeny in at least 2 flocks. Sires were used in a maximum of 56 flocks with 48-60% of sires being used in only 2 flocks. Subsequently, estimated breeding values (EBV) were calculated for each animal and trait on the entire edited dataset using these (co)variance component estimates. Genetic trends for each trait were then derived for sires with at least 10 progeny by regressing the average sire EBV on sire year of birth.

All above-mentioned analyses were performed using the ASReml software (Gilmour et al., 2009). Data was analysed in a similar manner as Fitzmaurice et al. (2020).

Results

Descriptive Statistics

Data after edits used for further genetic analysis is shown in Table 1. The Texel breed had the highest number of records by far across all traits studied. They also had the highest number of sires, dams, maternal grandsires, flocks and contemporary groups. The coefficient of variation suggested that substantial phenotypic variation was present in the studied traits and breeds.

Genetic Parameters

Statistically greater than zero ($P<0.05$) heritability estimates were found for all breeds and traits in Table 2. Heritability estimates for the live body weight traits increased as lambs got older for all breeds. The maternal effect was significant ($P<0.05$) for all breeds for the early-life weight trait. The litter environmental effect accounted for a high proportion of total phenotypic variance for all traits particularly within the Texel breed, where it accounted for up to 22% of total variance. Heritability estimates differed between breeds for the carcass composition traits. The Suffolk breed had a higher heritability estimate ($P<0.05$) for muscle depth compared to all other breeds and Charollais had a significantly higher heritability estimate than the Texel breed for fat depth ($P<0.05$).

Positive genetic correlations were calculated between the additive genetic effects for all traits in all breeds (Table 3). All pairwise correlations were significantly ($P<0.05$) different from zero, except between muscle depth and fat depth for the Charollais breed. Genetic correlations were strongest between the two live body weight traits reaching a maximum of 0.92 (± 0.02) between early-life weight and scan weight in the Texel breed. These strongly positive correlations between the live body weight traits indicate that lambs that grow well early in life will also perform better during subsequent growth phases.

Genetic trends were estimated for all traits and breeds from sire EBVs. In order to increase reliability only sires with ≥10 progeny were included in the trends shown in Figure 1. Significantly positive ($P<0.05$) trends were found for all breeds and traits, with the exception of fat depth in the Charollais breed where no significant trend appeared ($P>0.05$). Substantial variation was observed between breeds for all traits, with the Suffolk breed showing the highest rate of genetic gain for scan weight and muscle depth compared to the other two breeds in the present study.

Discussion

Improved growth and carcass traits due to genetic evaluation and selection schemes in the UK have been shown to be of significant economic benefit to the UK sheep industry (Signet, 2019). In the present study we set out to use national data to estimate within-breed genetic parameters in the UK sheep population after over 30 years of genetic selection had taken place. Results showed that there is still substantial genetic variation present meaning further genetic improvement is attainable and future selection will continue to be successful for live body weight and carcass composition traits.

Heritability estimates calculated in the present study correspond well with the literature for all traits analysed, although the heritability in the Suffolk breed for muscle depth exceeded previous ranges reported for the trait (Safari and Fogarty, 2003). Heritability estimates differed significantly between breeds for both carcass composition traits; however, no significant differences were observed between breeds for the live body weight traits. Genetic variability was highest in the muscle depth trait where the Suffolk breed showed significantly higher heritability compared to the Texel and Charollais breeds. Between breed differences in heritability estimates were also observed for the fat depth trait, where the estimate for the Charollais breed was significantly higher than for the Texel breed, but in all cases this trait can be selected for to effect genetic progress in the future. Differences between breeds also reflect the selection decisions that have been made relating to the different selection indexes placing different emphasis on each breed. In the UK, within breed genetic parameters have previously been reported by Jones et al. (2004) for the same breeds as the present study. The study of Jones et al. (2004) was based on data from research flocks and sire referencing schemes resulting in higher heritability estimates for scan weight, muscle depth and fat depth, particularly for the Texel breed, whereas relatively similar results were obtained for the Suffolk and Charollais breeds. For the Texel breed, substantial differences were observed particularly between the scan weight and fat depth traits; for example, in the present study heritability for fat depth was estimated to be 0.18 whereas Jones et al. (2004) reported a heritability of 0.38 for fat depth. Whilst it is difficult to pinpoint the exact reason for the differences between the studies, we speculate that the discrepancy may be due to differences between the genetic model used or may also be due to changes in genetic variation due to selection over time. In fact, Jones et al. (2004) did not include a common environmental litter effect which may have led to an inflation of the genetic variance (and hence heritability) compared to the present study, where the common environmental effect accounted for a high proportion of the variance. In addition, the data used by Jones et al. (2004) originated from both a research flock and a sire referencing scheme, which would likely have had stronger across-flock genetic linkages leading to higher heritability estimates. Furthermore, previous studies in the UK have reported genetic parameter estimates for the Suffolk breed for all live body weight and carcass composition traits examined in the present study (Maniatis and Pollott, 2002a; Maniatis and Pollott, 2002b; Simm et al., 2002) and observed very similar results to the heritability estimates within the Suffolk breed reported in the present study. Simm et al. (2002) also reported heritability estimates to increase with age, which was found to be the case for the Suffolk and Charollais breeds in the present study.

Genetic parameters were reported for the same three breeds of the present study for scan weight, muscle depth and fat depth in the Irish sheep population (Fitzmaurice et al., 2020). These parameters were estimated using similar genetic models as the present study in order to build towards future international evaluations; however, the resulting heritability estimates still differed. In the Irish study (Fitzmaurice et al., 2020), the highest heritability estimates were derived for the Texel breed for all traits, whereas in the present study highest trait heritability was estimated mostly for the Suffolk breed. Similarly high levels of the common environmental effect were found in both studies with the Irish estimates ranging between 0.15-0.35 for live body weight and carcass composition traits (Fitzmaurice et al., 2020). Other studies in Ireland also estimated heritability estimates for some of the same traits as the present study with O'Brien et al. (2017) reporting estimates to range from 0.22 to 0.28 for lamb live weight, muscle depth and fat depth, although that study included both purebred and crossbred lambs. Throughout the rest of the world there have been numerous similar studies undertaken particularly in Australia (Brown et al. 2016) and New Zealand (Brito et al. 2017). Both of these studies focused on terminal breeds including the Texel and Suffolk breeds and reported substantial genetic variation for all traits analysed, consistently with the results of the present study.

In the present study, the highest genetic correlations were observed between the two live body weight traits, namely early-life and scan weight. This indicates that the two traits are mostly under similar genetic control meaning lambs that are heavier in early-life will also be heavier at a later stage in the growth cycle. Muscle depth was highly correlated with both live body weights in all three breeds indicating that increases in the latter will also lead to an increase in muscle depth in the carcass. Genetic correlation estimates in the present study corresponded relatively well with the literature and results are within the ranges previously reported. Jones et al. (2004) reported similar genetic correlations between scan weight, muscle depth and fat depth for the Texel, Suffolk and Charollais breeds in the UK, although highest estimates were derived for the Texel breed compared to the Suffolk breed in the present study. Simm et al. (2002) reported relatively weaker correlations between the same traits for the Suffolk breed in the UK. Fitzmaurice et al. (2020) estimated genetic correlations for the same three breeds in Ireland and reported similar results for genetic correlations between live body weight and carcass composition traits as in the present study. In general, previous studies throughout the world have reported genetic correlations among similar lamb traits ranging from 0.14 to nearly unity (Safari and Fogarty, 2003). This high level of variation is probably due to the substantially different animal populations, breeds, models of analysis and trait definitions included in the Safari and Fogarty (2003) review. While, for the most part, the positive genetic correlations observed between traits would facilitate genetic improvement, care must be taken when producing selection indices to encourage early live body weight gain and muscle development without detrimentally increasing the fat levels in the carcass or compromising aspects of maternal performance.

Finally, the genetic trends calculated in the present study indicate satisfactory levels of genetic gain achieved from genetic selection on most traits in the three breeds. Desirable positive trends were observed over a nearly 10-year period for live body weights and muscle depth. Stable genetic levels for fat depth were observed in the Charollais breed, which is also desirable, as we do not want to breed animals that are genetically predisposed to being too lean or too fat. Positive genetic trends for fat depth in the other two breeds, however, may raise the issue of revising the respective breeding strategies to ensure future lamb generations do not develop carcasses that are too fat. In order to keep fat depth at an optimal level within a breeding programme, economic weights on relative traits must be adjusted constantly in line with genetic and market trends. Ideally genetic trends for fat depth should remain relatively static rather than increase as is the desire for the other traits analysed. Genetic trends have previously been reported in the UK for hill sheep for similar traits (Conington et al., 2006) and also for the Suffolk breed for live body weight, muscle depth and fat depth (Simm et al., 2002), showing similar positive trends for the first two traits but less so for fat depth, where a greater negative trend was reported. This negative trend may be due to the deliberate relaxing of the original selection index (Simm and Dingwall, 1989) in order to ensure that lambs finish for slaughter at the desired level of fatness. Similar trends have also been observed in Ireland where steady levels of genetic gain in all traits are being achieved (Fitzmaurice et al., 2020). The main disparity that occurs between genetic trends within the two countries is for the fat depth trait. Fitzmaurice et al. (2020) observed an increasing trend for fat depth in both the Suffolk and Charollais breeds while the Texel breed remained stable. The present study however shows increasing fat depth for all breeds apart from the Charollais which is remaining stable. However, this difference may be attributed to contrasting breeder preferences within the two countries. The trends observed in the present study are suggestive of the current genetic selection system in the UK where increased intensity of selection is occurring for higher growth rates in lambs with increased carcass value.

As mentioned previously, Fitzmaurice et al. (2020) have performed similar analysis on Irish data for the same three breeds as the present study. Existing data and high levels of linkage between the two countries as well as similar live weight and carcass composition traits can facilitate across-country genetic evaluations. Implications of the latter would underpin trade of stock and improve accuracy of genetic evaluations between countries.

Conclusion

The four growth and carcass composition traits studied are highly heritable and positively correlated to each other. Results from the present study could be used within the UK sheep industry to support breeding programmes into the future and underpin international cooperation for cross-country genetic evaluations. Significant differences in the estimated genetic parameters for the carcass composition traits were observed between breeds, suggesting that within-breed analysis in future genetic evaluation systems would be recommended in order to achieve high rates of genetic gain. These analyses have also laid the foundation for an across-country genetic evaluation of the studied breeds in the UK and Ireland. The technical aspects of such an analysis are currently being addressed. Overall benefit of across-country genetic evaluations to the respective industries is yet to be determined but it is expected that significant gains at both a genetic and economic level could be achieved.

Declaration of competing interest

The authors declare that there is no conflict of interest regarding the publication of this work.

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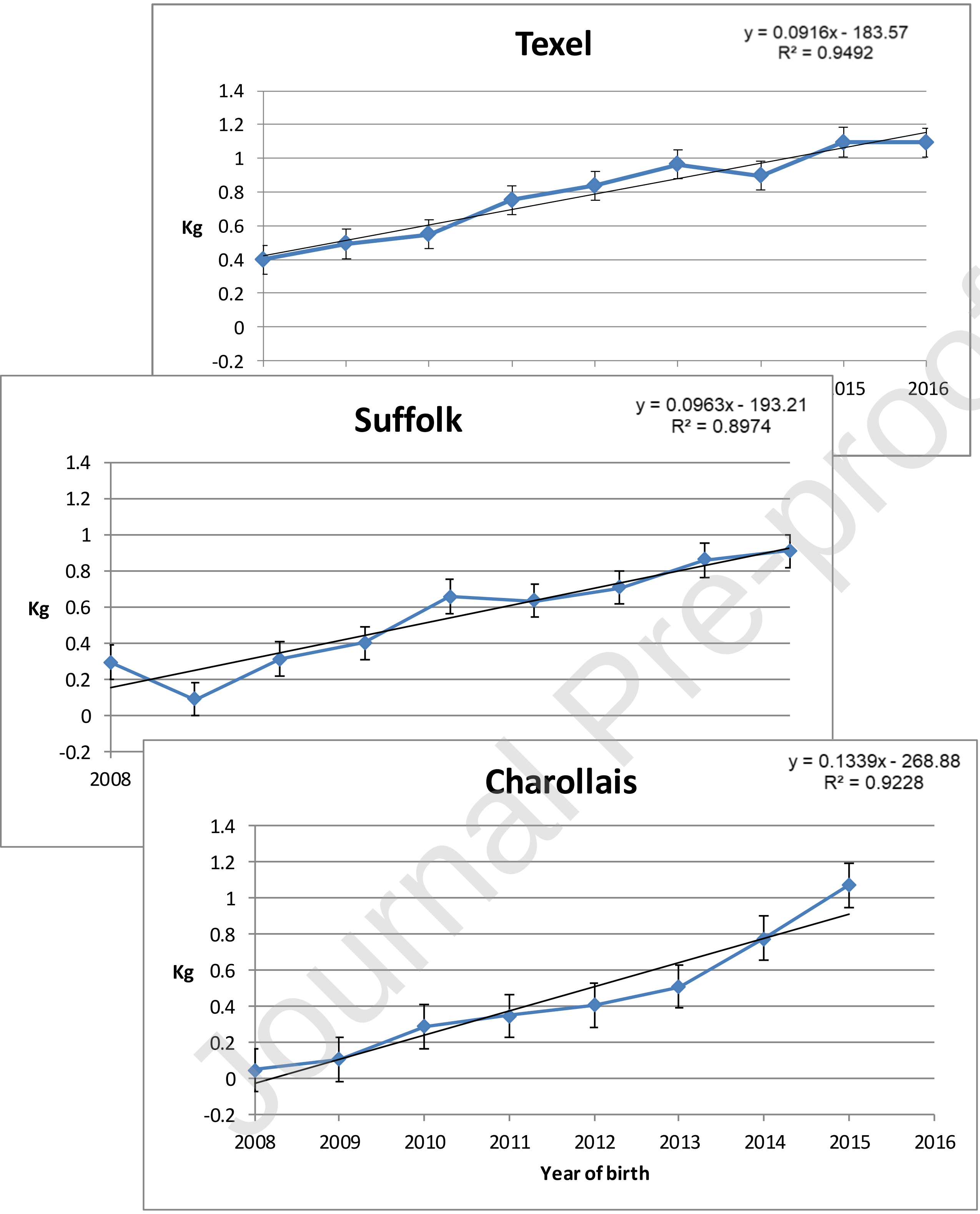
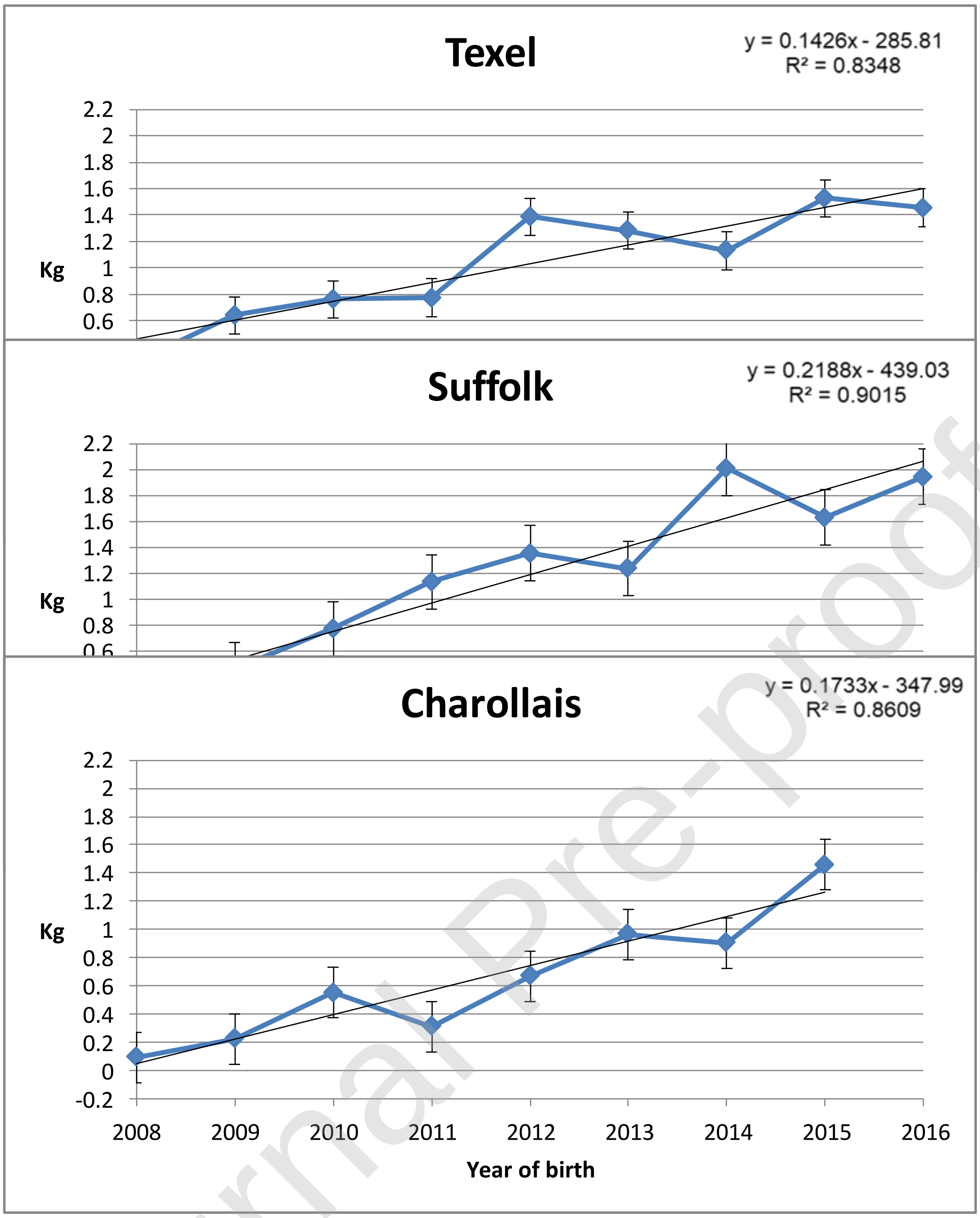
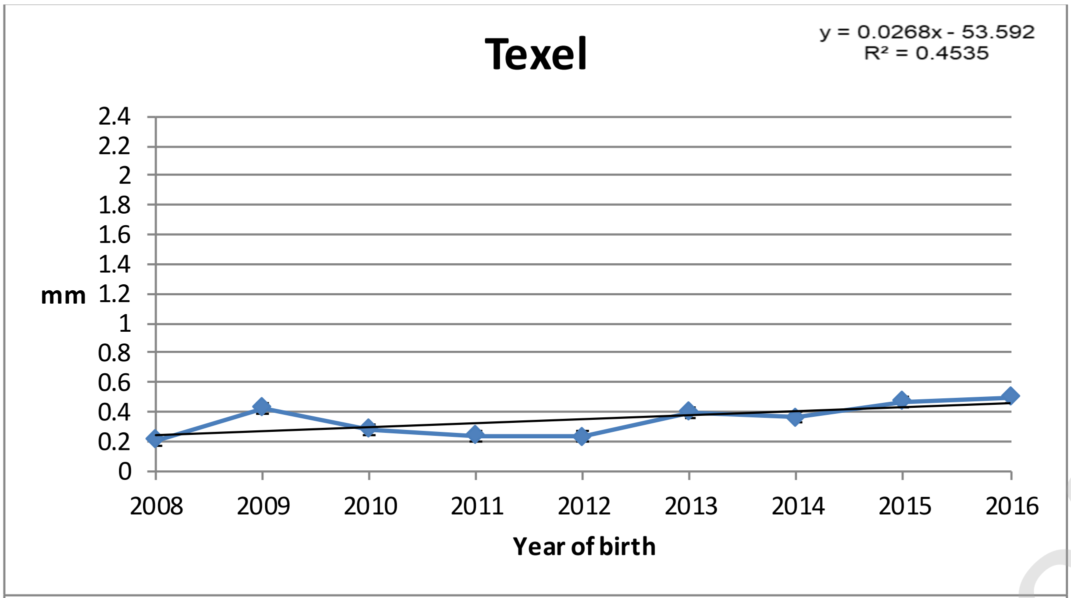
a. **Early life live body weight (kg)**

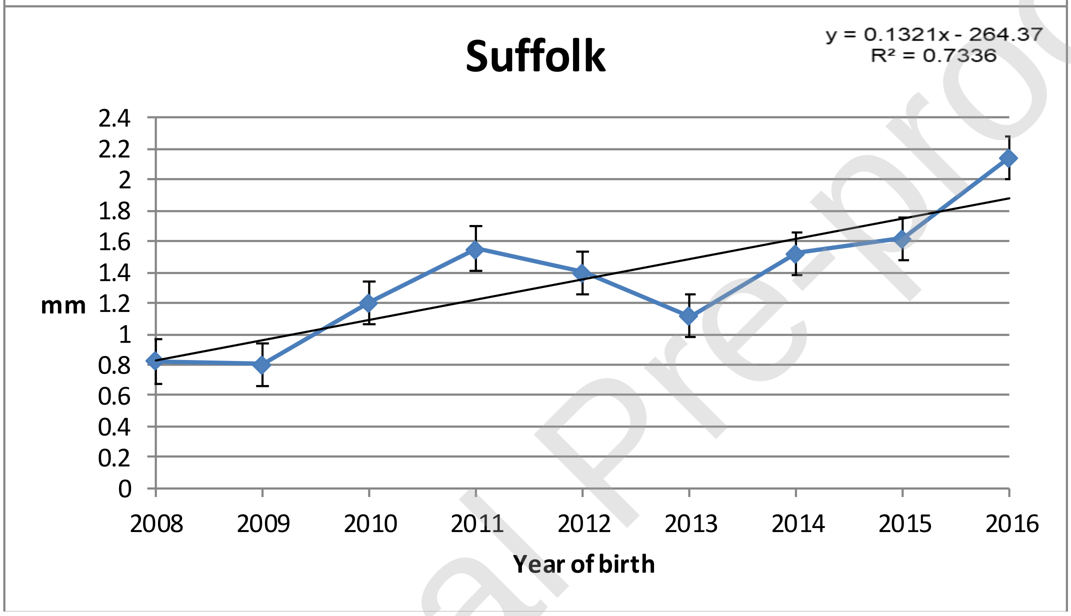


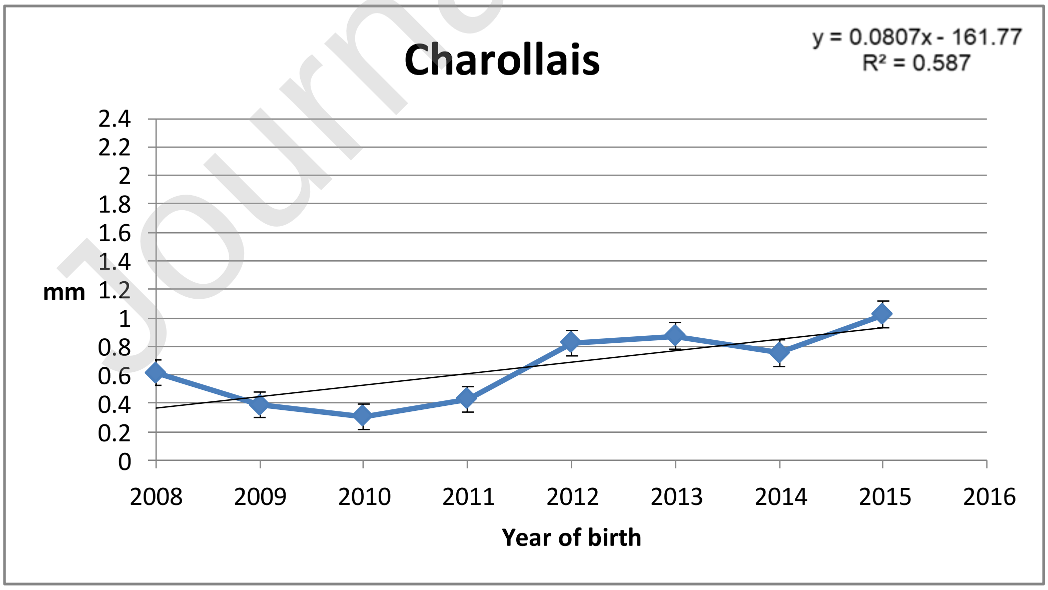
b. **Scan live body weight (kg)**



c. Muscle depth (mm)







d. Fat depth (mm)


Texel
y = 0.0109x - 21.906
R² = 0.7699
0.2
0.15
0.1
0.05
0
-0.05
-0.1
-0.15
-0.2
-0.25
mm
2008
2009
2010
2011
2012
2013
2014
2015
2016
Year of birth
Suffolk
y = 0.0213x - 42.772
R² = 0.674
0.2
0.15
0.1
0.05
0
-0.05
-0.1
-0.15
-0.2
-0.25
mm
2008
2009
2010
2011
2012
2013
2014
2015
2016
Year of birth
0.2
0.15
0.1
0.05
0
-0.05
-0.1
-0.15
-0.2
-0.25
mm
2008
2009
2010
2011
2012
2013
2014
2015
2016
Year of birth

Figure 1. Genetic trends of estimated breeding values of rams (standard errors in bars) for (**a**) early-life live body weight, (**b**) scan live body weight, (**c**) muscle depth and (**d)** fat depth for the Texel, Suffolk and Charollais breeds.

Table 1. Number of lambs (n), trait mean (μ) and standard deviation (SD), corresponding mean lamb age, and number of sires, dams, maternal grandsires (MGS), flocks and contemporary groups (CGs) by trait and breed.

Trait (unit of measurement)	Breed	n	μ (SD)	Age (d)	Sires	Dams	MGS	Flocks	CGs
Early life weight (kg)	Texel	21,480	27.16 (6.48)	65.53	300	10,399	1,475	199	871
	Suffolk	12,302	28.86 (6.95)	66.85	132	5,206	606	73	408
	Charollais	16,452	27.45 (6.20)	66.43	186	6,233	651	81	513
Scan weight (kg)	Texel	13,219	49.00 (9.24)	146.7	192	6,986	1,171	179	627
	Suffolk	7,736	50.14 (11.27)	144.8	95	3,827	498	62	265
	Charollais	7,778	52.01 (9.52)	146.6	120	3,797	463	71	312
Muscle depth (mm)	Texel	12,619	28.69 (4.05)	146.8	180	6,680	1,134	174	594
	Suffolk	7,519	29.62 (5.17)	144.2	88	3,701	486	58	249
	Charollais	6,971	29.43 (3.53)	146.6	105	3,493	445	69	287
Fat depth (mm)	Texel	12,527	2.45 (1.26)	146.8	180	6,650	1,130	174	593
	Suffolk	7,383	3.31 (1.66)	144.2	87	3,649	480	58	244
	Charollais	6,504	4.15 (1.73)	146.6	101	3,317	426	66	274

Table 2. Lamb heritability (h^2), and proportion of the phenotypic variance due to the maternal (m^2) and common environmental (C^2) effect; model of analyses of scan weight, muscle and fat depth did not include a maternal effect; SE=standard error of estimate.

	Breed	h^2 (SE)	m^2 (SE)	C^2 (SE)
Early life weight	Texel	0.18 (0.03)	0.09 (0.01)	0.20 (0.02)
	Suffolk	0.14 (0.03)	0.08 (0.02)	0.17 (0.02)
	Charollais	0.12 (0.02)	0.08 (0.01)	0.19 (0.01)
Scan weight	Texel	0.22 (0.03)		0.22 (0.02)
	Suffolk	0.30 (0.04)		0.14 (0.02)
	Charollais	0.21 (0.03)		0.10 (0.02)
Muscle depth	Texel	0.19 (0.03)		0.17 (0.02)
	Suffolk	0.42 (0.04)		0.08 (0.02)
	Charollais	0.28 (0.04)		0.07 (0.02)
Fat depth	Texel	0.18 (0.03)		0.18 (0.02)
	Suffolk	0.29 (0.04)		0.16 (0.02)
	Charollais	0.32 (0.04)		0.09 (0.02)

Table 3. Correlations (standard error in parentheses) between the additive genetic effects for the studied traits by breed.

Breed	Trait	Early life weight	Scan weight	Muscle depth
Texel	Early life weight			
	Scan weight	0.92 (0.02)		
	Muscle depth	0.45 (0.06)	0.50 (0.05)	
	Fat depth	0.49 (0.06)	0.50 (0.06)	0.35 (0.07)
Suffolk	Early life weight			
	Scan weight	0.90 (0.03)		
	Muscle depth	0.56 (0.06)	0.65 (0.05)	
	Fat depth	0.46 (0.08)	0.39 (0.07)	0.43 (0.06)
Charollais	Early life weight			
	Scan weight	0.81 (0.04)		
	Muscle depth	0.40 (0.08)	0.43 (0.08)	
	Fat depth	0.34 (0.09)	0.38 (0.08)	0.03 (0.10)