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Scotland's Rural College

Genetic analyses of live weight and carcass composition traits in purebred Texel, Suffolk and Charollais lambs

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Genetic analyses of live weight and carcass composition traits in purebred Texel, Suffolk and Charollais lambs

--Manuscript Draft--

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Abstract:	<p>Lamb live weight is one of the key drivers of profitability on sheep farms. Previous studies in Ireland have estimated genetic parameters for live weight and carcass composition traits using a multi breed population rather than on an individual breed basis. The objective of the present study was to undertake genetic analyses of three lamb live weight and two carcass composition traits pertaining to purebred Texel, Suffolk and Charollais lambs born in the Republic of Ireland between 2010 and 2017, inclusive. Traits (with lamb age range in parenthesis) considered in the analyses were: pre weaning weight (20 to 65 days), weaning weight (66 to 120 days), post weaning weight (121 to 180 days), muscle depth (121 to 180 days) and fat depth (121 to 180 days). After data edits, 137 402 records from 50 372 lambs across 416 flocks were analysed. Variance components were derived using animal linear mixed models separately for each breed. Fixed effects included for all traits were contemporary group, age at first lambing of the dam, parity of the dam, a gender by age of the lamb interaction and a birth type by rearing type of the lamb interaction. Random effects investigated in the pre weaning and weaning weight analyses included animal direct additive genetic, dam maternal genetic, litter common environment, dam permanent environment and residual variances. The model of analysis for post weaning, muscle and fat depth included an animal direct additive genetic and litter common environment effect only. Significant direct additive genetic variation existed in all cases. Direct heritability for pre weaning weight ranged from 0.14 to 0.30 across the three breeds. Weaning weight had a direct heritability ranging from 0.17 to 0.27 and post weaning weight had a direct heritability ranging from 0.15 to 0.27. Muscle and fat depth heritability estimates ranged from 0.21 to 0.31 and 0.15 to 0.20, respectively. Positive direct correlations were evident for all traits. Results revealed ample genetic variation among animals for the studied traits and significant differences between breeds to</p>

suggest that genetic evaluations could be conducted on a per breed basis.

21 **Abstract**

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46 traits. Results revealed ample genetic variation among animals for the studied traits
47 and significant differences between breeds to suggest that genetic evaluations could
48 be conducted on a per breed basis.

49

50 **Keywords:** sheep, Ireland, parameters, growth, muscle

51

52 **Implications**

53 This study demonstrated the existence of genetic variation between different breeds
54 of sheep for the three main live weight and two carcass composition traits in the Irish
55 sheep production system suggesting that genetic evaluations should be conducted
56 on a per breed basis. This would allow for more informed and accurate selection
57 decisions on farm, resulting in superior productivity and profitability within Irish sheep
58 flocks.

59

60 **Introduction**

61 Lamb live weight and the rate at which the animal grows have been defined as the
62 key drivers of profitability in Irish (Byrne *et al.*, 2010) and international (Cocks *et al.*,
63 2002; Jones *et al.*, 2004a; Conington *et al.*, 2004) sheep production systems. In
64 Ireland, for example, each additional day a lamb requires to reach its target slaughter
65 weight results in an economic loss of €1.41 per lamb per day (Byrne *et al.*, 2010). In
66 addition to the live weight traits, carcass composition also has an impact on the
67 profitability of sheep production systems with one increase on the EUROP scale for

68 muscle depth leading to an economic gain of €0.35 per lamb and an increase of one
69 point on the fat scale leading to an economic loss of -€0.52 per lamb (Byrne *et al.*,
70 2010). Lamb live weight, weight gain and carcass composition have been shown to
71 vary greatly not only across the various stages of a lambs growth period, such as pre
72 and post weaning (Leymaster and Jenkins, 1993; Djemali *et al.*, 1994; Leeds *et al.*,
73 2012) but also across a plethora of breeds including meat (Osorio-Avalos *et al.*,
74 2012), wool (Safari *et al.*, 2007) and dual purpose (Dixit *et al.*, 2001) breeds.

75 Previous research has shown considerable variability across both pre and
76 post weaning lamb growth rates not only at a phenotypic level (Dixit *et al.*, 2001) but
77 also at a genetic level (Safari *et al.*, 2005; Thiruvankadan *et al.*, 2011), with
78 heritabilities for lamb live weight at different ages ranging from 0.15 to 0.41 (Safari *et*
79 *al.*, 2005). Such studies, however, have tended to focus on small sample sizes,
80 which may not accurately represent the whole sheep population. Furthermore,
81 although some studies have shown that genetic variability exists among breeds
82 (Freking and Leymaster, 2004; Osorio-Avalos *et al.*, 2012), genetic parameters and
83 sheep genetic evaluations in Ireland to date have been developed within a multi-
84 breed population context (Pabiou *et al.*, 2014) and heretofore the genetic variation
85 within individual breeds has not been considered.

86 The objective of the present study therefore was to estimate genetic
87 parameters and breeding values for a range of lamb live weight and carcass
88 composition traits within three breeds commonly recorded in Ireland namely Texel,
89 Suffolk and Charollais. Results from the present study would determine differences
90 between breeds in the genetic evaluations of sheep in Ireland.

93 **Materials and Methods**

94 *Data*

95 A full database was extracted across three breeds, namely Texel, Suffolk and
96 Charollais, from Sheep Ireland, the Irish national database (<http://www.sheep.ie>).
97 Records pertaining to years 2010 to 2017, inclusive, were retained for analyses.
98 Only purebred lambs (as defined by the data records) of the three aforementioned
99 breeds (i.e., Texel, Suffolk and Charollais) were considered in the present study.

100 In Ireland lamb live weights are recorded at three time points post lambing by
101 Irish producers using weigh-scales: pre weaning, at weaning and post weaning, the
102 latter coinciding with muscle and fat ultrasound scanning. Based on the editing
103 criteria used for the national genetic evaluations pre weaning weight was defined as
104 live weight taken between 20 and 65 days of age; only records of lambs weighing
105 between 12.00 and 32.00 kg were retained in the present study. Weaning weight
106 was defined as the live weight recorded between 66 and 120 days of age and
107 weighing between 20.00 and 55.00 kg. Post weaning weight was defined as live
108 weight measured between 121 and 180 days of age; only lambs with live weight
109 records between 25.00 and 75.00 kg were considered for further analysis. Across all
110 live weight measurements average daily gain was calculated for each lamb with a
111 known birth and weigh date at either of the three weight points; only average daily
112 gains between 100 and 650 g/d were retained for each live weight measurement
113 (261 lambs with an erroneous average daily gain were omitted from subsequent
114 analyses). Muscle and fat depth traits were recorded on the same day as post

115 weaning weight in all lambs. Only muscle depth measurements within the range of
116 10 to 44 mm and fat depth measurements ranging within 1 to 23 mm were retained.

117 Live weight and carcass composition measurement records were discarded if
118 flock of birth, sire, dam or maternal grandsire were unknown. Dams with no known
119 parity number or a parity number >10 were discarded; parity number was
120 subsequently categorised as 1, 2, 3, 4, or ≥ 5 . Age at first lambing was defined
121 based on the age of the ewe at first lambing; ewes were either defined as lambing
122 for the first time as ewe lambs (between 8 and 18 months of age) or those that
123 lambed for the first time as hoggets (between ≥ 18 and 28 months of age). Birth type
124 was defined as the number of lambs born per lambing event; only birth types
125 between 1 (singles) and 4 (quadruplets) were retained. Rearing type was defined as
126 the number of lambs reared per litter; only rearing type between 1 and 3 were
127 retained for analysis. Lambs that were recorded as artificially reared or reared by a
128 non-genetic dam were not included for further analysis.

129 For all traits, each lamb was allocated to a contemporary group of breed-by-
130 flock-by-week of weighing. Only contemporary groups containing at least 5 records
131 were retained for analysis. Following all edits described above, 33 721 pre weaning
132 weight records, 32 623 weaning weight records, 28 140 post weaning weight
133 records, 21 468 muscle depth records and 21 442 fat depth records were retained
134 for genetic analysis; the breakdown of records per breed is shown in Table 1.

135 *Genetic Analysis*

136 Variance components were estimated for each lamb live weight trait (i.e., pre
137 weaning, weaning and post weaning weight) and each carcass composition trait (i.e.,

138 muscle depth and fat depth) using linear mixed animal models in ASReml (Gilmour
139 *et al.*, 2009) separately for each breed. The model employed was:

$$140 \quad Y = CG + AFL + Parity + Gender * Age + Birth\ type * Rearing\ type + Animal$$
$$141 \quad \quad \quad + Dam + DamPE + Litter + e$$

142 where Y = lamb live weight or carcass composition record, CG =
143 contemporary group, AFL = age at first lambing of the dam, Parity = parity of the
144 dam, Gender*Age = the interaction between the gender and age of the lamb, Birth
145 type*Rearing type = the interaction between the birth type and rearing type of the
146 lamb, Animal = random animal direct additive genetic effect, Dam = random maternal
147 genetic effect, DamPE = random dam permanent environmental effect associated
148 with multiple lambing records of the same dam, Litter = common environmental
149 effect reflecting the non-genetic covariance among members of the same litter, and e
150 = random residual effect.

151 Each model was progressively built up from including just a residual effect to
152 include a direct genetic, maternal genetic, dam permanent environmental and litter
153 common environmental effect. In the case of post weaning weight, muscle and fat
154 depth the model included a direct genetic and a litter common environmental effect
155 only as there was no significant dam effect. A log likelihood ratio test was used to
156 determine if the additional random terms improved the fit of the data (Ferreira *et al.*,
157 1999). Whilst the maternal genetic and dam permanent environmental effect were
158 not always significant, these effects were kept in the model as the log likelihood ratio
159 test suggested it was the model of best fit.

160 Direct heritability was calculated as the ratio of the direct additive genetic
161 variance to the observed total phenotypic variance. Maternal heritability was

162 estimated as the ratio of the maternal genetic variance to the total phenotypic
163 variance. Common environmental effect was calculated as the ratio of the litter
164 variance to the total phenotypic variance. Dam repeatability was calculated as the
165 ratio of maternal genetic variance plus permanent environment to the total
166 phenotypic variance. The correlation between the direct additive and maternal
167 genetic effects was also estimated where applicable. Genetic correlations between
168 the studied traits were estimated pairwise using the model previously described in a
169 series of bivariate analyses. Estimated breeding values (EBV) were calculated for
170 each trait and genetic trends were produced from these results by estimating the
171 slope of the average ram EBV per year of birth. Genetic trends were only produced
172 for sires with at least 10 progeny and ranged from 3 to 61 sires per year across all
173 traits and breeds.

174

175 **Results**

176 *Phenotypic values and data structure*

177 Edited data used in the genetic analyses are shown in Table 1. The Suffolk breed
178 proved to be heaviest at all three live weight measurements although they were
179 slightly younger at both pre weaning and weaning weights. The Suffolk breed also
180 had the highest muscle and fat depth among the three breeds studied although this
181 may be attributed partly to the higher weight at scanning. Overall the Texel breed
182 had the highest number of records across all five traits and they also had the highest
183 number of flocks. Judging on the coefficient of variation, the greatest variability was
184 observed in fat depth and the least variability was observed for muscle depth, and
185 this was true across all breeds.

186 *Genetic Parameters*

187 Variance components were estimated (Table 2 and heritability estimates were
188 subsequently derived for each trait and breed. All estimates of genetic standard
189 deviation and direct heritability were statistically greater than zero ($P < 0.05$) as shown
190 in Table 3. All traits studied apart from pre weaning weight were most heritable in the
191 Texel breed. Pre weaning weight was most heritable in the Suffolk breed. (□)
192 Maternal heritability was significantly greater than zero for all weight traits in the
193 Texel breed, pre weaning weight in Suffolks and weaning weight in Charollais. The
194 litter common environmental effect accounted for the majority of the total phenotypic
195 variance for most live weight traits and a significant proportion for the carcass
196 composition traits.

197 Negative correlations were estimated between direct additive and maternal
198 genetic effects within trait for all breeds (Table 3). This is an antagonistic correlation
199 suggesting that animals with genetically superior direct additive genetic effect are
200 expected to be maternally inferior. Significant ($P < 0.05$) positive genetic correlations
201 between the direct additive genetic effects on pre weaning and subsequent weights
202 for each of the three breeds were calculated (Table 4). Direct genetic correlations
203 between live weight traits and the two carcass composition traits were also strongly
204 positive reaching a maximum of 0.72 (± 0.04) between weaning weight and muscle
205 depth for the Texel breed (Table 4).

206 *Genetic Trends*

207 Genetic trends based on EBVs of rams with ≥ 10 progeny (Figure 1) indicate that
208 positive genetic gain is occurring in all live weight traits. Significant ($P < 0.05$) trends
209 were observed for all live weight traits in the Texel breed, pre weaning weight in the

210 Suffolk breed and weaning weight in the Charollais breed. Muscle depth had a
211 strong positive significant trend for all breeds, while fat depth had weakly positive
212 significant trends for both the Suffolk and Charollais breeds. There was considerable
213 variation in genetic trends estimated for the same trait among the three studied
214 breeds with higher rates of genetic gain being achieved in the Texel breed for live
215 weight traits and muscle depth in comparison to the other two breeds.

216

217 **Discussion**

218 Live weight measurements on lambs are amongst the key performance indicators in
219 profitable sheep production systems. To date, most genetic studies undertaken in
220 Ireland have tended to estimate genetic parameters for lamb weight and carcass
221 composition traits simultaneously across a range of breeds rather than investigating
222 on an individual breed basis. Therefore, in the present study we investigated if
223 estimates of genetic parameters and breeding values differed between breeds within
224 the Irish sheep population when the breeds were evaluated on a within breed basis.
225 Results showed significant differences in additive genetic variance and direct
226 heritability of each trait between the Texel, Suffolk and Charollais breeds, warranting
227 within-breed genetic analyses.

228 *Phenotypic values*

229 In comparison to previous studies conducted on an Irish sheep population, lamb live
230 weight in the present study was greater for all three live weight traits examined.
231 Previously pre weaning, weaning and post weaning weight in Irish purebred lambs
232 was shown to be 19.64 kg, 33.00 kg and 48.00 kg, respectively (McHugh *et al.*,

233 2016, McHugh *et al.*, 2017). The increased live weight observed in the current study
234 may be attributed to the fact that only terminal purebred lambs were examined
235 whereas maternal and crossbred lambs had been also included in the previous
236 studies. The carcass composition traits in the present study showed similar results to
237 those previously reported in the literature for purebred Irish lambs. An earlier study
238 conducted in Ireland (O'Brien *et al.*, 2017) showed a mean of 33.21 mm and 7.55
239 mm for muscle and fat depth traits, respectively. The first study carried out in the UK
240 on live weight and carcass composition traits in terminal sire sheep was reported by
241 Simm and Dingwall (1989) from which selection indices for terminal sire breeds was
242 implemented in practice for the UK sheep industry and responses to selection
243 reported. Jones *et al.* (2004) reported similar findings to the present study for post
244 weaning weight, muscle depth and fat depth traits for the three breeds studied in
245 terms of breed ranking however fat depth proved to be considerably higher in the
246 present study. Other studies have been reported for crossbred and hill lambs (Jones
247 *et al.*, 1999; Merrell *et al.*, 1990; Conington *et al.*, 2004). Again these findings were
248 very similar to the present study for the post weaning weight and muscle depth
249 values however, fat depth proved to be higher for all breeds in the present study
250 although the ranking of the breeds remained the same. Merrell *et al.* (1990), reported
251 weight at slaughter for Suffolk, Texel and Charollais crossbred lambs in the UK,
252 which was recorded at a similar age to post weaning weight in the present study,
253 ranging from 39.50 kg (Texel) to 41.10 kg (Suffolk). Although these lambs were
254 lighter than those in the present study the ranking of breeds was similar with the
255 Suffolk breed having the highest live weight and the Texel breed having the lowest
256 post weaning live weight. Throughout the rest of the world many studies have
257 recorded live weight in lambs at different time points however few of these studies

258 have focused on the breeds investigated in the current study (Safari and Fogarty,
259 2003) although Shrestha *et al.* (1985) reported similar findings for pre weaning and
260 weaning weights in Canadian Suffolks. Furthermore, a US study of Texel and Suffolk
261 sired crossbred lambs (Leymaster and Jenkins, 1993) showed similar live weight
262 results to the present study with the Suffolk breed proving to be heaviest at both
263 weaning and post weaning weights in comparison to the Texel breed. One contrast
264 observed in Leymaster and Jenkins' (1993) study compared to the present study
265 was that the Suffolk and Texel breeds were recorded to have the same mean weight
266 for pre weaning weight whereas in the present study the Suffolk is considerably
267 heavier for all live weights; however, this may be attributed to the multiple-rearing
268 environment having a greater effect on the growth potential of the Suffolk lambs over
269 the Texel lambs.

270 Many of the studies on carcass composition previously conducted are not
271 comparable to the present study due to different methods used and time points of
272 measurement (Safari and Fogarty, 2003). Many of these studies tended to measure
273 both muscle and fat depth at a later time point with the majority measured when the
274 lamb is between 7 and 16 months of age (Safari and Fogarty, 2003). However one
275 study conducted by Jones *et al.* (2004b) showed very similar results to the present
276 study with the Suffolk breed having the highest muscle and fat depth and the Texel
277 breed having the lowest fat depth out of the three studied breeds.

278 *Genetic Parameters*

279 Direct and maternal heritability estimates reported in the present study for live weight
280 and carcass composition traits are all within the ranges previously reported in the
281 literature. Within the present study with the exception of pre weaning weight and fat

282 depth, direct heritability differed substantially among breeds for all traits analysed
283 with most variability observed in the post weaning weight trait where direct heritability
284 ranged from 0.16 (Suffolk) to 0.32 (Texel). Genetic parameter estimates have not
285 previously been reported in Ireland on a per breed basis. One previous study
286 reported genetic parameter estimates within a multi breed analysis (McHugh *et al.*,
287 2017) including a heritability estimate for pre weaning weight in Irish lambs of 0.09,
288 which is lower than all pre weaning weight estimates in the present study. This may
289 be attributed to the differences between the breeds lowering the heritability in the
290 previous study in comparison to the present study, which was conducted on
291 genetically more homogeneous purebred populations. Higher accuracy of EBVs
292 would also be expected in within breed genetic evaluations as a result of increased
293 direct heritability estimates. Maternal heritability estimates were low for all three live
294 weight traits measured and were not significant for the two carcass composition
295 traits. These results contrast significantly with the study on pre weaning weight by
296 McHugh *et al.* (2017) where a maternal heritability of 0.25 was reported in a multi-
297 breed Irish sheep population. This difference may however be due to different
298 models used in the analysis as much of the variation in the present study was due to
299 the common environmental effect, which was not included in the study of McHugh *et*
300 *al.* (2017). In the UK, previous studies have estimated genetic parameters for the
301 Suffolk breed for all traits analysed in the present study (Maniatis and Pollott, 2002a;
302 Maniatis and Pollott, 2002b; Simm *et al.*, 2002) and results were generally similar.
303 Simm *et al.* (2002) suggested that direct heritability estimates would increase with
304 lamb age due to the lessening maternal influence and increased direct influence.
305 This was indeed the case in the present study for Texel and Charollais breeds. For
306 the Suffolk breed, however, the opposite was true as direct heritability decreased

307 from 0.22 (pre weaning) to 0.16 (post weaning) while maternal heritability also
308 decreased.

309 The strong positive direct genetic correlations among the three live weight
310 traits were as expected, indicating that lambs that are genetically heavier early in life
311 are also more likely to be genetically heavier later on. Whilst these figures
312 corresponded well with the literature, some of the estimates in the present study
313 were outside the ranges previously reported with weaker correlations observed in the
314 present study compared to those previously reported (Safari and Fogarty, 2003).
315 This, however, may be due to the fact that few studies estimated genetic correlations
316 between live weight traits at the specific times that were reported in the present
317 study and may also be due to many of the previous studies being based in Australia
318 or Asia where the studied breeds being differ greatly to those in the current study
319 (Safari and Fogarty, 2003). Many of these studies also tended to have a far greater
320 age spread between weight ages than those reported in the present study. No
321 previous studies have investigated at genetic correlations among growth traits for the
322 Texel or Charollais breeds, individually. However, there was one UK study by Simm
323 *et al.* (2002) that showed the direct and maternal genetic correlations between pre
324 weaning and post weaning weight for the Suffolk breed to be 0.69 and 0.86,
325 respectively. These results were broadly in the range of those reported in the present
326 study although stronger maternal genetic correlations between the traits were
327 recorded in the present study. The difference between the previous study and the
328 present study may be attributed to the fact that the previous study (Simm *et al.*,
329 2002) was based on one flock only whereas the present study includes the entire
330 recorded population.

331 As with the live weight traits, strong positive correlations were also seen
332 among the two carcass composition traits and post weaning weight. Very few
333 previous studies have estimated correlations among these traits at the similar time
334 points to the present study; however, the direct correlations estimated here are
335 broadly within the range previously reported (Atkins *et al.*, 1991; Simm *et al.*, 2002;
336 Ingham *et al.*, 2003). These strong positive correlations indicate that by breeding for
337 heavier lambs we are also breeding for more muscular but also fatter lambs. The
338 former is desirable but the latter undesirable. Although these traits are antagonistic
339 we need to aim to select for animals that are more muscular and less fat while still
340 achieving live weight targets in order to maximise genetic gain and profitability.
341 Appropriate selection indices need to be developed for this matter, optimally
342 combining live weight and carcass traits.

343 For pre weaning and weaning weight, a negative correlation was observed
344 between the direct additive and maternal genetic effects. Although this corresponded
345 with the majority of the literature for growth and live weight traits (Notter, 1998; Safari
346 and Fogarty, 2003; Maxa *et al.*, 2007), previous studies have reported very mixed
347 results with some positive correlations appearing also between live weight traits
348 (Tosh and Kemp, 1994; Nasholm and Danell, 1996; Snyman *et al.*, 1996; Yazdi *et al.*,
349 1997; Rao and Notter, 2000). This variation of results previously reported in the
350 literature may be indicative of differences in data structure but may also be due to
351 breed differences (Maniatis and Pollott, 2002a). The antagonistic correlation reported
352 between direct and maternal effects in the present study suggests that by selecting
353 rams to breed heavier lambs their daughters will have lighter lambs. In order to
354 counteract this, optimal combination of antagonistic traits in a properly developed
355 selection index is needed to support selection decisions.

356 *Genetic trends*

357 To our knowledge, this is the first time genetic trends on Irish sheep are reported for
358 the studied traits. Genetic trends varied between the three breeds for all traits in the
359 present study. From the genetic trends, the Texel breed appears to be achieving the
360 most genetic gain as significantly positive trends were recorded for all live weight
361 traits as well as the muscle depth trait. No significant trend was found for fat depth in
362 the Texels, indicating that this trait is remaining relatively static which is more
363 desirable than the increasing trend observed for the Suffolk and Charollais breeds.
364 The muscle depth trait showed a positive trend for all three breeds. These results are
365 indicative of the on-going genetic selection programme in Ireland based on the
366 emphasis that is being placed on muscle depth for all breeds as well as the increase
367 in genetic gain in live weight that has been seen in all three breeds.

368 **Conclusion**

369 Variance components and genetic parameters derived in the present study for five
370 live weight and carcass traits may be used to support the breeding programme of
371 sheep in Ireland. Considerable differences in genetic analysis results were found
372 between the Texel, Suffolk and Charollais breeds for each of the five traits examined
373 in the present study. Differences were observed in both heritability and genetic
374 correlation estimates suggesting that current genetic improvement systems may
375 benefit by considering these breeds separately in future genetic evaluations.

376

377 **Acknowledgements**

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380 results from the present study have previously been published in abstract form
381 (Fitzmaurice *et al.*, 2019).

382

383 **Declaration of Interest**

384 Authors declare no conflict of interest.

385

386 **Ethics statement**

387 Ethics committee approval was not obtained for the present study as the data were
388 obtained from an existing database provided by Sheep Ireland.

389

390 **Software and data repository resources**

391 None of the data were deposited in an official repository.

392

393 **References**

394 Atkins KD, Murray JI, Gilmour AR, and Luff AL 1991. Genetic variation in liveweight and
395 ultrasonic fat depth in Australian Poll Dorset sheep. Australian Journal of Agricultural
396 Research 42, 629-640.

397 Byrne TJ, Amer PR, Fennessy PF, Cromie AR, Keady TWJ, Hanrahan JP, McHugh MP and
398 Wickham BW 2010. Breeding objectives for sheep in Ireland: A bio-economic approach.
399 *Livestock Science* 132, 135-144.

400 Cocks A, Williams M, Casey M, Brown C, Ware J, Morrison N, Morrison G, Pearce G, Taylor
401 W, Cochrane G, Cochrane J and Harris T 2002. Farmers adopting technology to improve
402 sheep production – a nine year study. *Proceedings of the New Zealand Grassland
403 Association* 64, 49-53.

404 Conington J, Bishop SC, Waterhouse A and Simm G 2004. A bioeconomic approach to
405 derive economic values for pasture-based sheep genetic improvement programs. *Journal of
406 Animal Science* 82, 1290–1304.

407 Dixit SP, Dhillon JS, and Singh G 2001. Genetic and non-genetic parameter estimates for
408 growth traits of Bharat Merino lambs. *Small Ruminant Research* 42, 101-104.

409 Djemali M, Aloulou R and Ben Sassi M, 1994. Adjustment factors and genetic and
410 phenotypic parameters for growth traits of Barbarine lambs in Tunisia. *Small Ruminant
411 Research* 13, 41-47.

412 Ferreira GB, MacNeil MD and Van Vleck LD 1999. Variance components and breeding
413 values for growth traits from different statistical models. *Journal of Animal Science* 77, 2641–
414 2650.

415 Fitzmaurice S, Conington J, Fetherstone N, Pabiou T, McDermott K, Wall E, Banos G and
416 McHugh N 2019. Genetic parameters for live weight traits in purebred Irish Texel, Suffolk
417 and Charollais lambs. *Proceedings of the 75th Annual Conference of the British Society of
418 Animal Science*, 9-11th April 2019, Edinburgh, 098.

419 Freking BA, and Leymaster KA 2004. Evaluation of Dorset, Finnsheep, Romanov, Texel,
420 and Montadale breeds of sheep: IV. Survival, growth, and carcass traits of F1 lambs. *Journal
421 of Animal Science* 82, 3144-3153.

422 Gilmour AR, Gogel BJ, Cullis BR and Thompson R 2009. ASReml User Guide Release 3.0.
423 VSN International Ltd, Hemel Hempstead, UK.

424 Ingham VM, Ponzoni RW, Gilmour AR, and Pitchford W, 2003. Genetic parameters for
425 weight, fat and eye muscle depth in South Australian Merino sheep. Proceedings of the
426 Association for the Advancement of Animal Breeding and Genetics 15, 322-325.

427 Jones HE, Amer PR, Lewis RM and Emmans GC 2004a. Economic values for changes in
428 carcass lean and fat weights at a fixed age for terminal sire breeds of sheep in the UK.
429 Livestock Production Science 89, 1–17.

430 Jones HE, Lewis RM, Young MJ and Simm G 2004b. Genetic parameters for carcass
431 composition and muscularity in sheep measured by X-ray computer tomography, ultrasound
432 and dissection. Livestock Production Science 90, 167-179.

433 Leeds TD, Notter DR, Leymaster KA, Mousel MR, and Lewis GS 2012. Evaluation of
434 Columbia, USMARC-Composite, Suffolk, and Texel rams as terminal sires in an extensive
435 rangeland production system: I. Ewe productivity and crossbred lamb survival and
436 preweaning growth. Journal of Animal Science 90, 2931-2940.

437 Leymaster KA and Jenkins TG 1993. Comparison of Texel- and Suffolk-sired crossbred
438 lambs for survival, growth and compositional traits. Journal of Animal Science 71, 859-869.

439 Maniatis N, and Pollott GE 2002a. Maternal effects on weight and ultrasonically measured
440 traits of lambs in a small closed Suffolk flock. Small Ruminant Research 45, 235-246.

441 Maniatis N, and Pollott GE 2002b. Nuclear, cytoplasmic, and environmental effects on
442 growth, fat, and muscle traits in Suffolk lambs from a sire referencing scheme. Journal of
443 Animal Science 80, 57-67.

444 Maxa J, Norberg E, Berg P and Pedersen J 2007. Genetic parameters for growth traits and
445 litter size in Danish Texel, Shropshire, Oxford Down and Suffolk. *Small Ruminant*
446 *Research* 68, 312-317.

447 McHugh N, Berry D, McParland S, Wall E, and Pabiou T 2016. Irish Sheep Breeding.
448 Current status and future plans. Retrieved on 16th January 2019 from
449 [trhttps://www.teagasc.ie/media/website/animals/sheep/Current_status_future_plans.pdf](https://www.teagasc.ie/media/website/animals/sheep/Current_status_future_plans.pdf)

450 McHugh N, Pabiou T, McDermott K, Wall E and Berry DP 2017. Impact of birth and rearing
451 type, as well as inaccuracy of recording, on pre-weaning lamb phenotypic and genetic merit
452 for live weight. *Translational Animal Science* 1, 137-145.

453 Merrell, B.G., Webster, G.M. and Ellis, M., 1990. A comparison of three terminal sire breeds
454 for crossbred lamb production. 1. Growth performance and carcass classification. *BSAP*
455 *Occasional Publication*, 14, pp.169-172.

456 Nasholm A, and Danell O 1996. Genetic relationships of lamb weight, maternal ability, and
457 mature ewe weight in Swedish finewool sheep. *Journal of Animal Science* 74, 329-339.

458 Notter DR 1998. Genetic parameters for growth traits in Suffolk and Polypay
459 sheep. *Livestock Production Science* 55, 205-213.

460 Osorio-Avalos J, Montaldo HH, Valencia-Posadas M, Castillo-Juárez H and Ulloa-Arvizu R
461 2012. Breed and breed x environment interaction effects for growth traits and survival rate
462 from birth to weaning in crossbred lambs. *Journal of Animal Science* 90, 4239-4247.

463 Pabiou T, Byrne T, Wall E and McHugh N 2014. Genetic improvement of sheep in Ireland.
464 *Proceedings of the 10th World Congress of Genetics Applied to Livestock Production*, 17-
465 22nd August 2014, Vancouver, Canada, 886.

466 Rao S, and Notter DR 2000. Genetic analysis of litter size in Targhee, Suffolk, and Polypay
467 sheep. *Journal of Animal Science* 78, 2113-2120.

468 Safari A., and Fogarty NM 2003. Genetic Parameters for Sheep Production Traits: Estimates
469 from the Literature. Technical Bulletin 49, NSW Agriculture, Orange, Australia.

470 Safari E, Fogarty NM and Gilmour AR 2005. A review of genetic parameter estimates for
471 wool, growth, meat and reproduction traits in sheep. *Livestock Production Science* 92, 271-
472 289.

473 Safari E, Fogarty NM, Gilmour AR, Atkins KD, Mortimer SI, Swan AA, Brien FD, Greef JC
474 and van der Werf JHJ 2007. Across population genetic parameters for wool, growth, and
475 reproduction traits in Australian Merino sheep. 1. Data structure and non-genetic effects.
476 *Australian Journal of Agricultural Research* 58, 169-175.

477 Shrestha JNB, Vesely JA and Chesnais JP 1985. Genetic and phenotypic parameters for
478 daily gain and body weights in Suffolk lambs. *Canadian Journal of Animal Science* 65, 575-
479 582.

480 Simm G and Dingwall WS 1989. Selection indices for lean meat production in
481 sheep. *Livestock production science* 21, 223-233.

482 Simm G, Lewis RM, Grundy B, and Dingwall WS 2002. Responses to selection for lean
483 growth in sheep. *Animal Science* 74, 39-50.

484 Snyman MA, Olivier JJ, and Olivier WJ 1996. Variance components and genetic parameters
485 for body weight and fleece traits of Merino sheep in an arid environment. *South African*
486 *Journal of Animal Science* 26, 11-14.

487 Thiruvankadan AK, Karunanithi K, Muralidharan J and Narendra Babu R 2011. Genetic
488 analysis of pre-weaning and post-weaning growth traits of Mecheri sheep under dry land
489 farming conditions. *Asian-Australasian Journal of Animal Science* 24, 1041-1047.

490 Tosh JJ, and Kemp RA 1994. Estimation of variance components for lamb weights in three
491 sheep populations. *Journal of Animal Science* 72, 1184-1190.

492 Yazdi MH, Engstrom G, Nasholm A, Johansson K, Jorjani H, and Liljedahl LE 1997. Genetic
493 parameters for lamb weight at different ages and wool production in Baluchi sheep. *Animal*
494 *Science* 65, 247-255.

495

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

498

Trait (units of measurement)	Breed	n	μ (SD)	Age	CV	Sires	Dams	MGS	Flocks	CGs
Pre Weaning Weight (kg)	Texel	11 891	20.86 (4.70)	46.59	22.53%	804	5 359	1 093	162	480
	Suffolk	8 783	22.32 (4.85)	45.12	21.73%	541	3 816	759	110	329
	Charollais	13 047	20.58 (4.58)	46.20	22.25%	602	4 965	919	139	456
Weaning Weight (kg)	Texel	12 388	36.69 (7.63)	96.92	20.80%	847	5 688	1 176	161	508
	Suffolk	7 839	40.93 (7.87)	96.31	19.23%	542	3 625	774	107	308
	Charollais	12 396	37.09 (7.40)	96.65	19.95%	607	4 820	913	139	449
Post Weaning Weight (kg)	Texel	12 074	48.70 (9.47)	144.76	19.45%	847	5 746	1 179	161	422
	Suffolk	6 819	56.42 (10.79)	147.24	19.12%	508	3 411	753	96	281
	Charollais	9 247	51.92 (9.91)	148.99	19.09%	567	4 106	844	129	354
Muscle Depth (mm)	Texel	8 810	32.59 (4.09)	146.57	12.55%	662	4 259	916	108	280
	Suffolk	5 589	34.11 (5.01)	151.28	14.69%	402	2 792	621	69	204
	Charollais	7 094	33.23 (3.97)	151.81	11.95%	455	3 344	714	96	252
Fat Depth (mm)	Texel	8 782	6.10 (2.70)	146.63	44.26%	661	4 250	916	108	281
	Suffolk	5 556	8.50 (4.00)	151.42	47.06%	399	2 784	618	69	205
	Charollais	7 087	8.10 (3.80)	151.82	46.91%	455	3 346	712	97	253

499 **Table 2.** Lamb direct genetic variance (V_g^d), maternal genetic variance (V_g^m), variance due to common environmental effect (C_m) and variance
500 due to maternal repeatability (PE_m) per trait and breed; model of analyses of post weaning weight, muscle and fat depth did not include a
501 maternal effect; SE=standard error of estimate.

	Breed	V_g^d (SE)	V_g^m (SE)	C_m (SE)	PE_m (SE)
Pre Weaning Weight	Texel	1.57 (0.27)*	0.58 (0.18)*	2.98 (0.19)*	0.57 (0.19)*
	Suffolk	2.44 (0.40)*	0.56 (0.22)*	3.39 (0.24)*	0.12 (0.23)
	Charollais	1.39 (0.25)*	0.20 (0.13)	3.54 (0.18)*	0.06 (0.16)
Wean Weight	Texel	6.89 (0.81)*	0.98 (0.39)*	6.55 (0.48)*	0.43 (0.43)
	Suffolk	4.79 (1.03)*	0.84 (0.55)	7.85 (0.73)*	0.26 (0.64)
	Charollais	5.77 (0.79)*	0.87 (0.39)*	6.01 (0.45)*	0.18 (0.41)
Post Weaning Weight	Texel	11.94 (1.10)*		8.99 (0.62)*	
	Suffolk	7.42 (1.48)*		11.55 (1.09)*	
	Charollais	6.79 (1.03)*		8.73 (0.74)*	
Muscle Depth	Texel	2.76 (0.28)*		1.39 (0.18)*	
	Suffolk	2.05 (0.35)*		1.48 (0.26)*	
	Charollais	1.70 (0.25)*		1.51 (0.18)*	
Fat Depth	Texel	0.01 (0.00)*		0.01 (0.00)*	
	Suffolk	0.01 (0.00)*		0.02 (0.00)*	
	Charollais	0.01 (0.00)*		0.01 (0.00)*	

502 *Estimates significantly different ($P < 0.05$) from zero.

503

504

505

506 **Table 3.** Lamb direct heritability (h^2_d), maternal heritability (h^2_m), proportion of phenotypic variance due to the common environmental effect
 507 (C^2_m), maternal repeatability (R_m), and the correlation between direct and maternal genetic effects (CORR d/m) per trait and breed; model of
 508 analyses of post weaning weight, muscle and fat depth did not include a maternal effect; SE=standard error of estimate.

	Breed	h^2_d (SE)	h^2_m (SE)	C^2_m (SE)	R_m (SE)	CORR d/m (SE)
Pre Weaning Weight	Texel	0.16 (0.03)*	0.06 (0.02)*	0.30 (0.02)*	0.12 (0.02)*	-0.65 (0.07)*
	Suffolk	0.22 (0.03)*	0.05 (0.02)*	0.31 (0.02)*	0.06 (0.02)*	-0.77 (0.06)*
	Charollais	0.14 (0.02)*	0.02 (0.01)	0.35 (0.02)*	0.03 (0.01)	-0.84 (0.05)*
Wean Weight	Texel	0.27 (0.03)*	0.04 (0.02)*	0.26 (0.02)*	0.06 (0.02)*	-0.61 (0.07)*
	Suffolk	0.17 (0.03)*	0.03 (0.02)	0.27 (0.02)*	0.04 (0.02)	-0.68 (0.09)*
	Charollais	0.23 (0.03)*	0.03 (0.02)*	0.24 (0.02)*	0.04 (0.01)*	-0.71 (0.06)*
Post Weaning Weight	Texel	0.32 (0.03)*		0.24 (0.02)*		
	Suffolk	0.16 (0.03)*		0.25 (0.02)*		
	Charollais	0.18 (0.03)*		0.23 (0.02)*		
Muscle Depth	Texel	0.31 (0.03)*		0.16 (0.02)*		
	Suffolk	0.21 (0.03)*		0.15 (0.03)*		
	Charollais	0.21 (0.03)*		0.19 (0.02)*		
Fat Depth	Texel	0.20 (0.03)*		0.20 (0.02)*		
	Suffolk	0.15 (0.03)*		0.17 (0.03)*		
	Charollais	0.17 (0.03)*		0.17 (0.02)*		

509 *Estimates significantly different ($P < 0.05$) from zero.

510 **Table 4.** Lamb genetic correlations (standard error in parentheses) between the direct additive genetic effects for each trait (below the
 511 diagonal) and the maternal genetic effects for each trait (above the diagonal) by breed; model of analyses of post weaning weight, muscle and
 512 fat depth did not include a maternal effect.

513

514

	Trait	Pre weaning	Weaning	Post weaning	Muscle depth
Texel	Pre weaning		0.95 (0.03)*		
	Weaning	0.76 (0.04)*			
	Post weaning	0.65 (0.07)*	0.94 (0.02)*		
	Muscle depth	0.57 (0.06)*	0.72 (0.04)*	0.69 (0.03)*	
	Fat depth	0.31 (0.08)*	0.49 (0.07)*	0.45 (0.06)*	0.42 (0.06)*
Suffolk	Pre weaning		0.80 (0.06)*		
	Weaning	0.61 (0.09)*			
	Post weaning	0.76 (0.08)*	0.77 (0.07)*		
	Muscle depth	0.41 (0.09)*	0.23 (0.15)	0.61 (0.07)*	
	Fat depth	0.36 (0.11)*	0.27 (0.16)	0.29 (0.12)*	0.48 (0.09)*
Charollais	Pre weaning		0.97 (0.04)*		
	Weaning	0.55 (0.07)*			
	Post weaning	0.63 (0.07)*	0.90 (0.04)*		
	Muscle depth	0.51 (0.08)*	0.63 (0.07)*	0.54 (0.06)*	
	Fat depth	0.18 (0.10)	0.27 (0.10)*	0.26 (0.09)*	0.41 (0.08)*

515 *Estimates significantly different ($P < 0.05$) from zero.

516 **Figure 1.** Significantly different from zero ($P < 0.05$) genetic trends of estimated breeding
517 values of rams (standard errors shown in error bars) for **(a)** pre weaning weight, **(b)** weaning
518 weight **(c)** post weaning weight **(d)** muscle depth and **(e)** fat depth.

519

Figure 1a

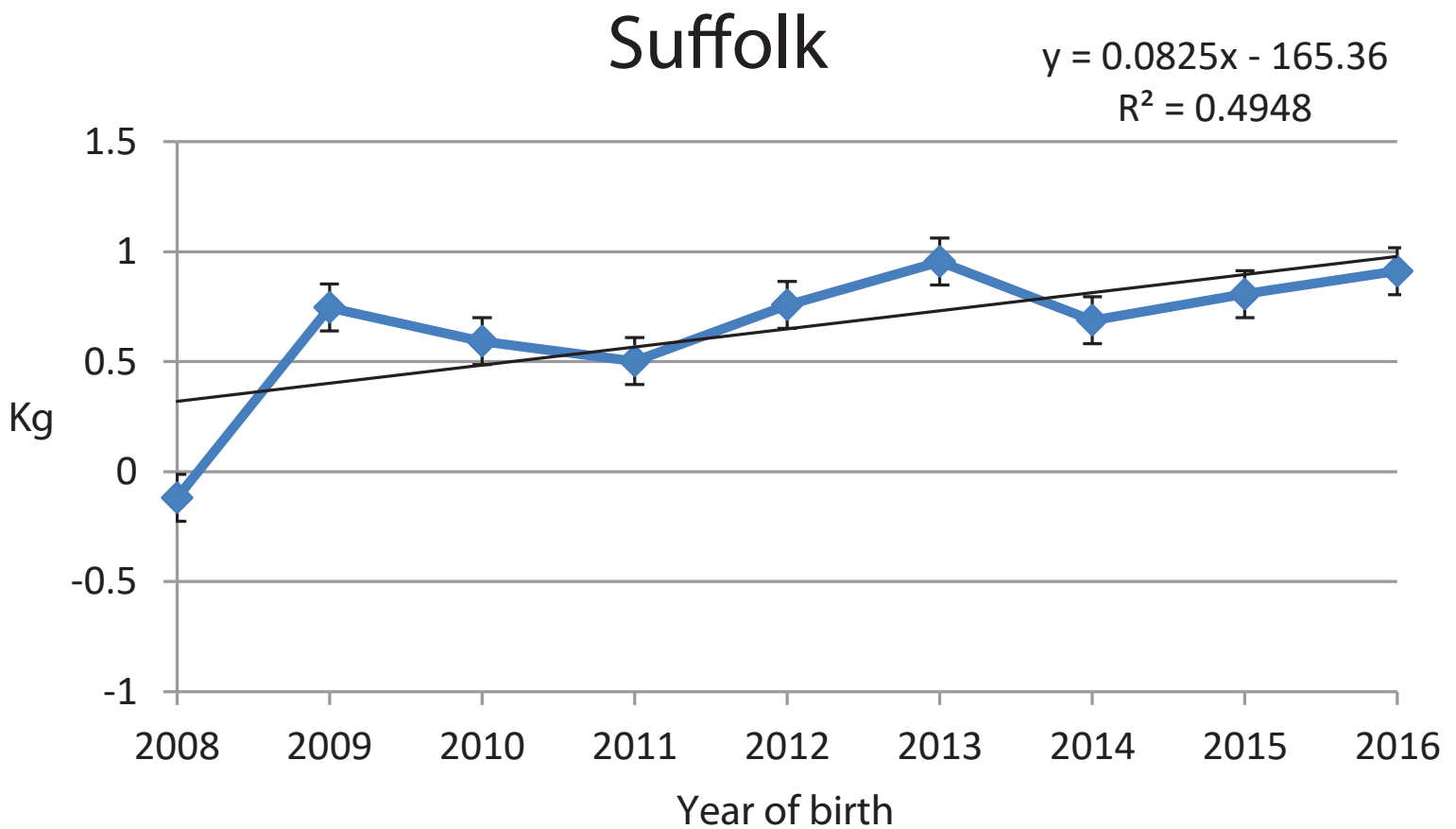
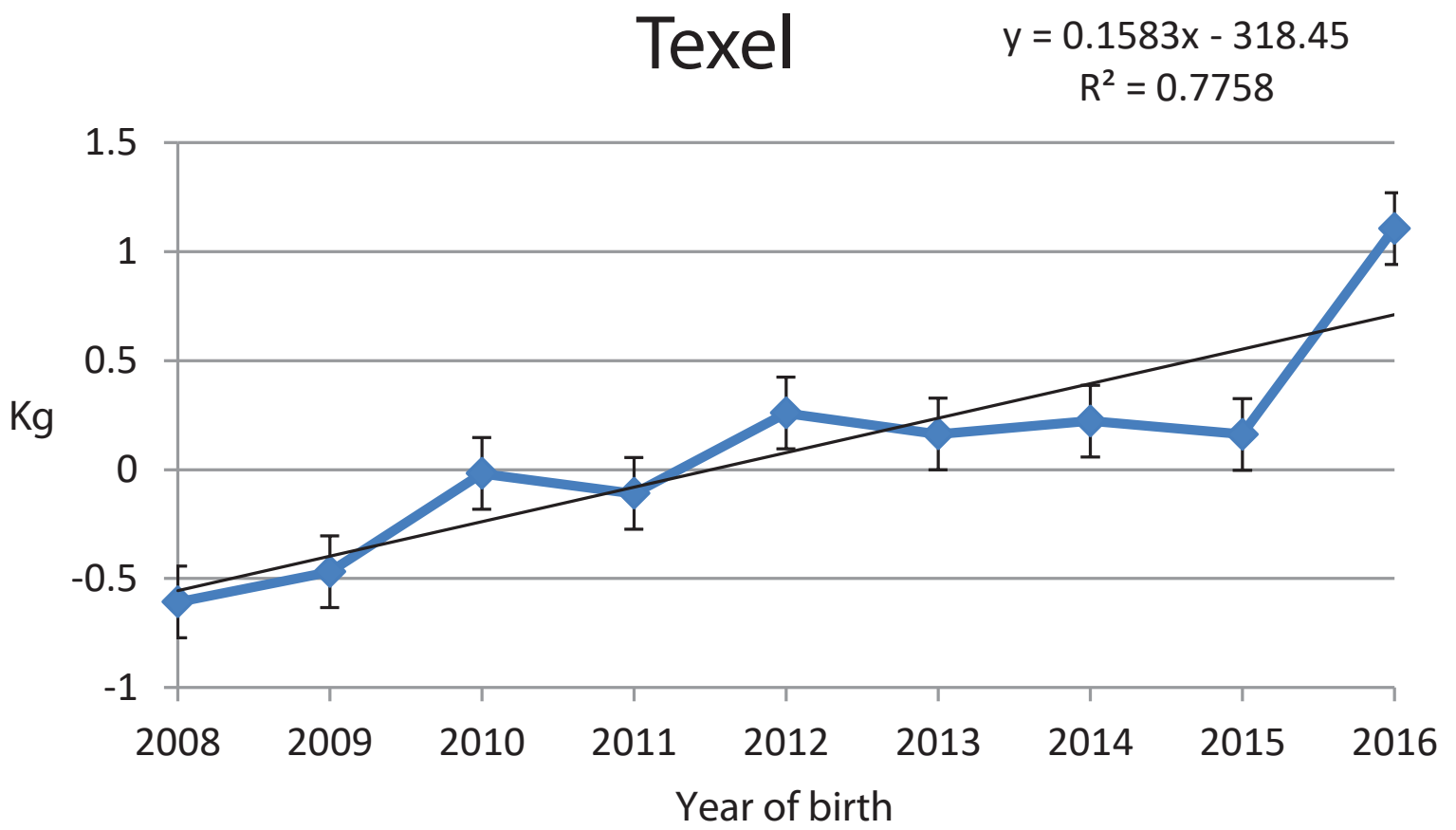
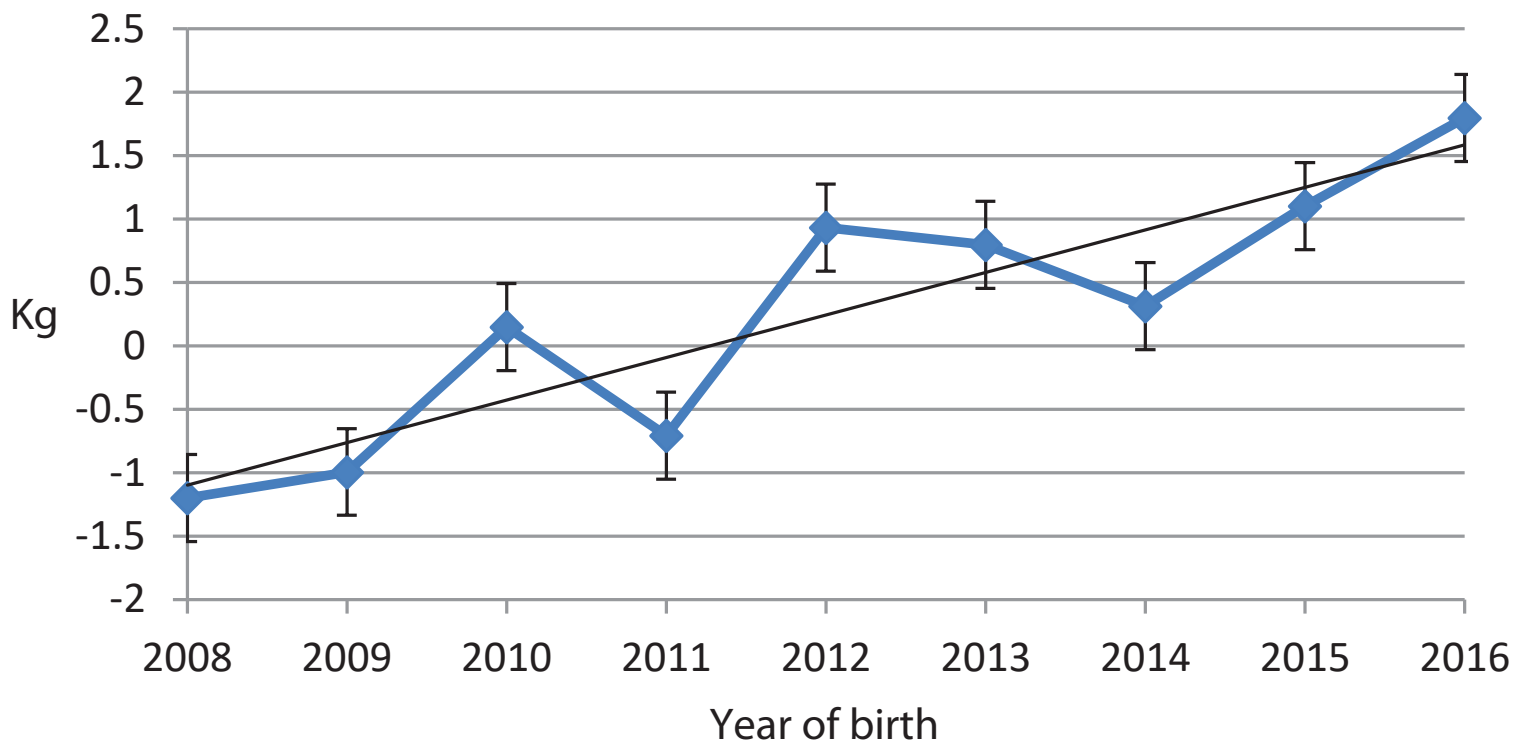


Figure 1b

Texel

$$y = 0.335x - 673.83$$
$$R^2 = 0.7962$$



Charollais

$$y = 0.1903x - 382.66$$
$$R^2 = 0.5581$$

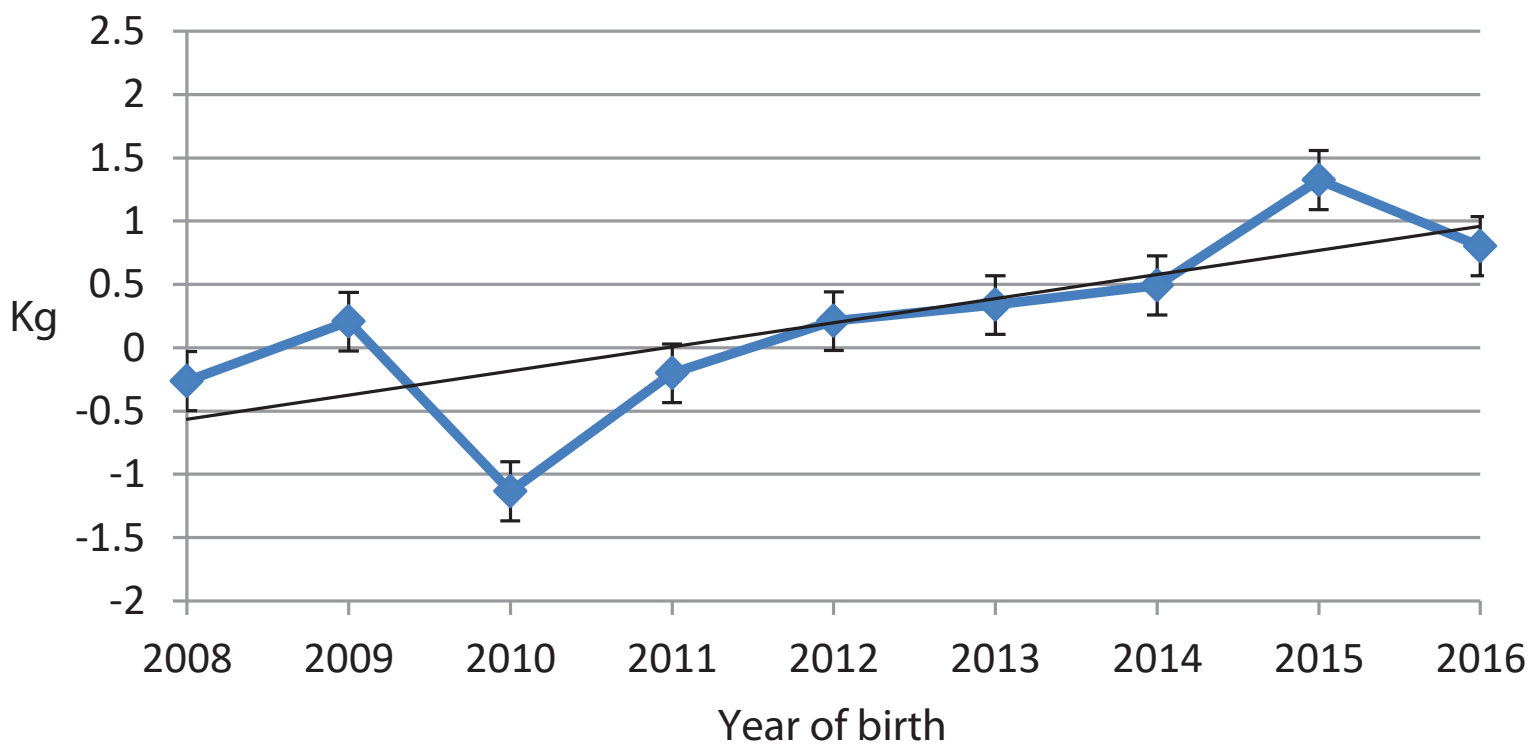


Figure 1c

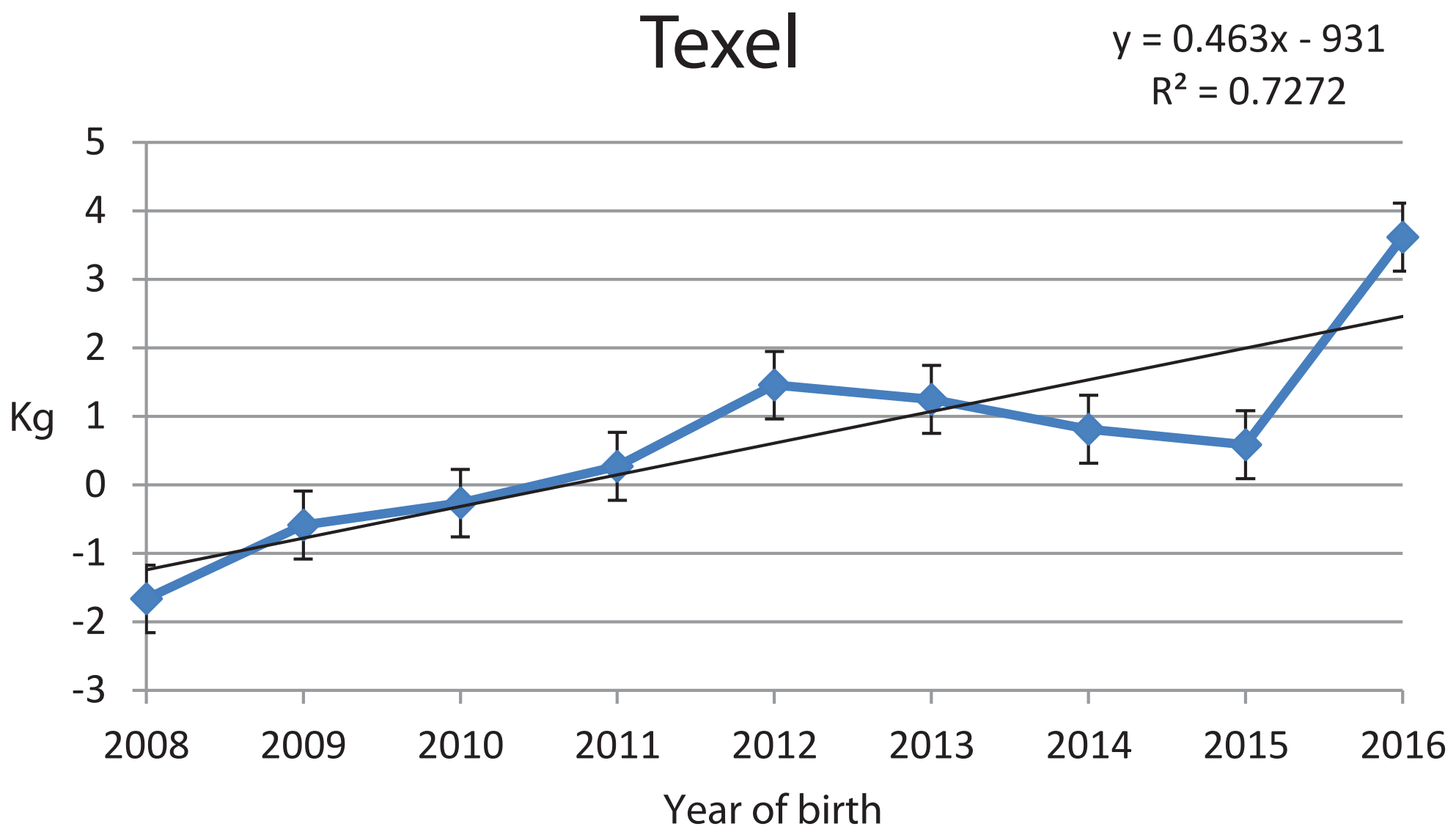


Figure 1d

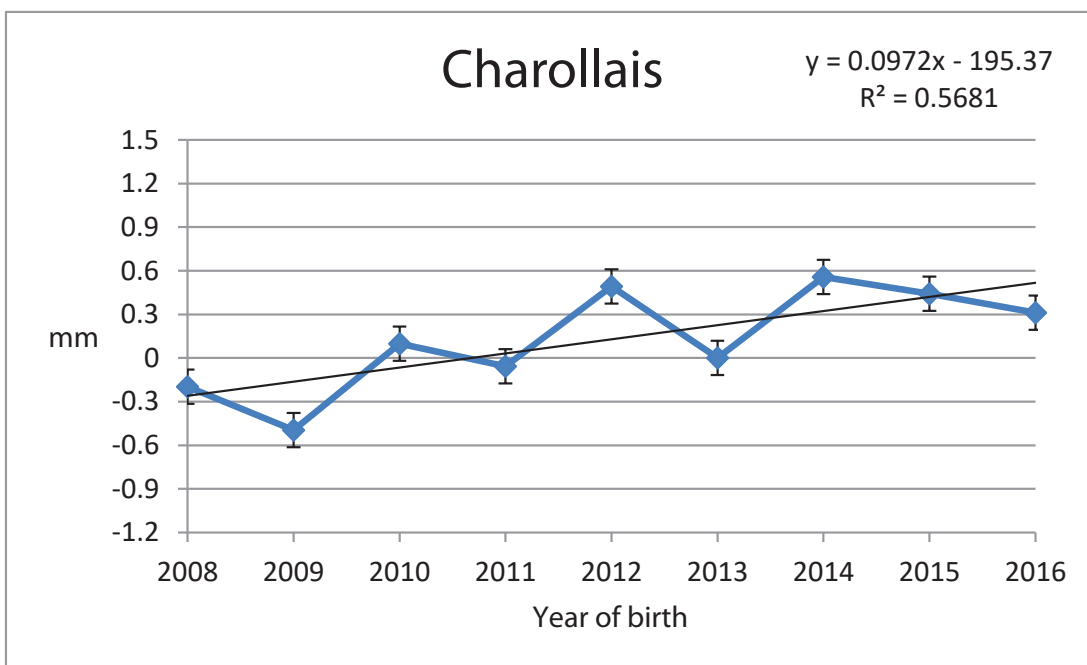
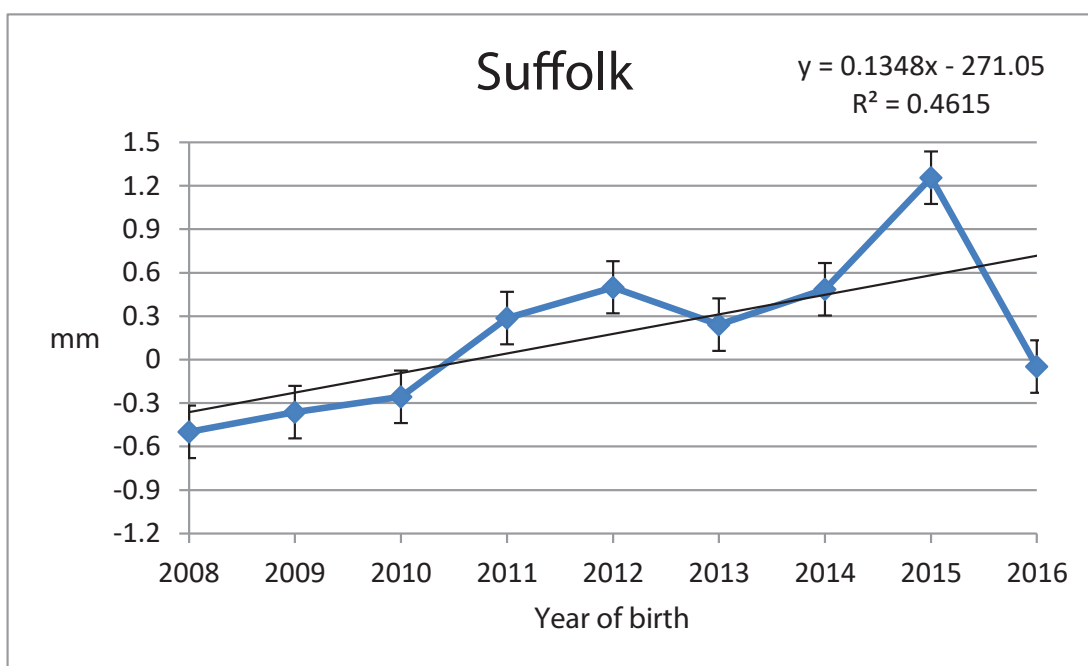
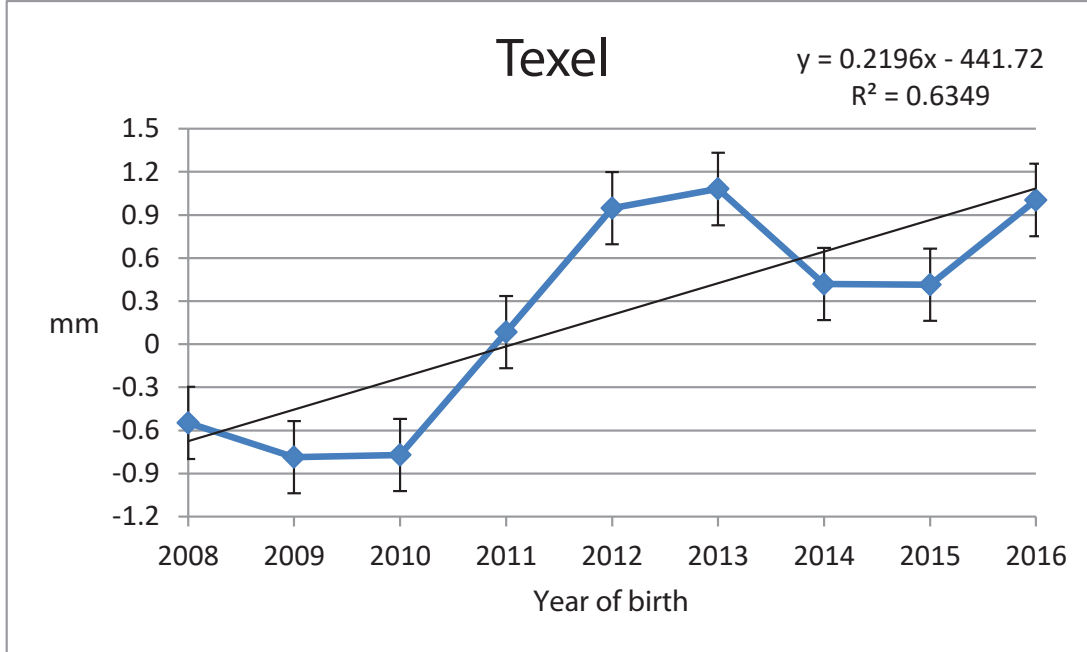
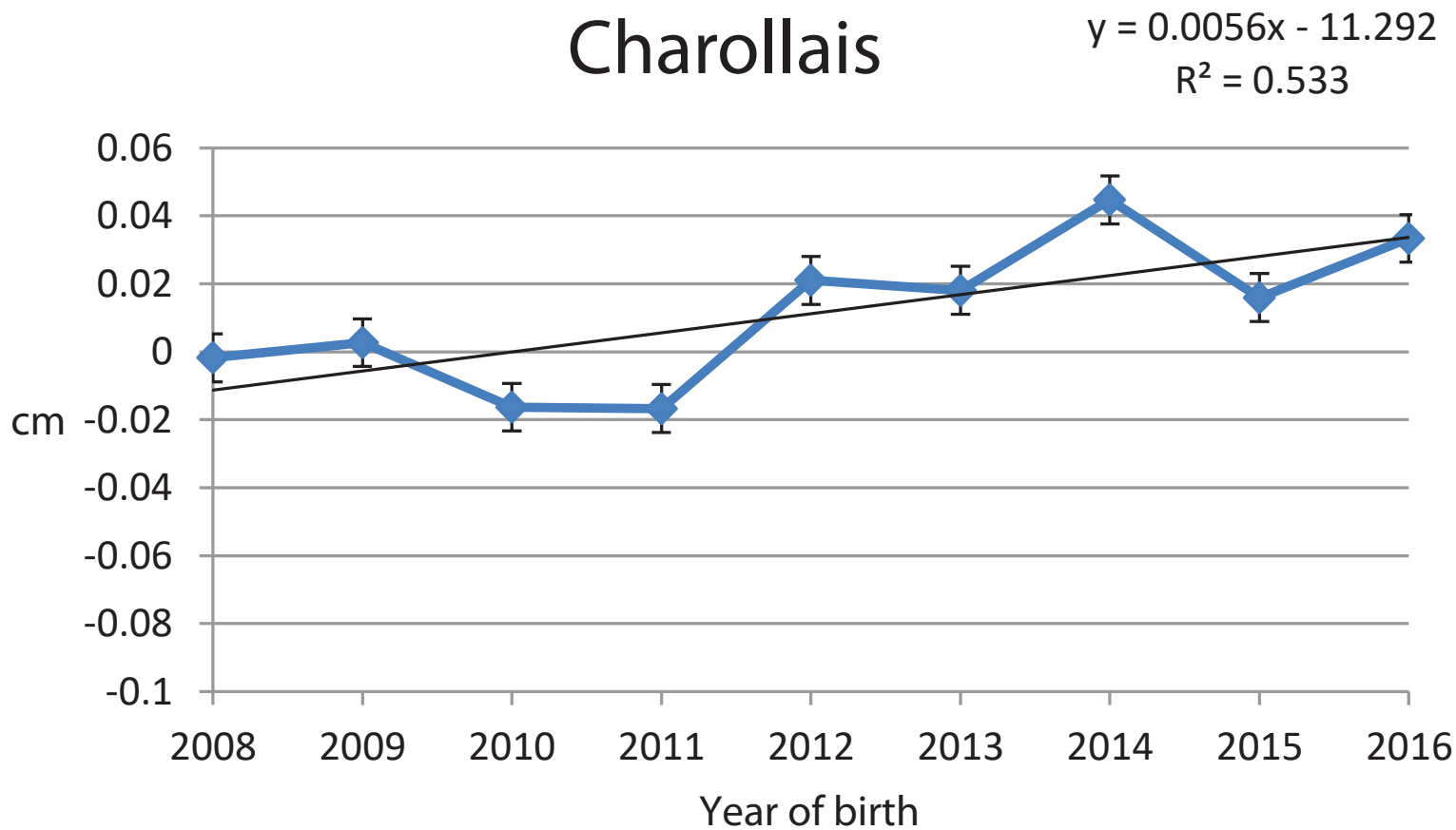
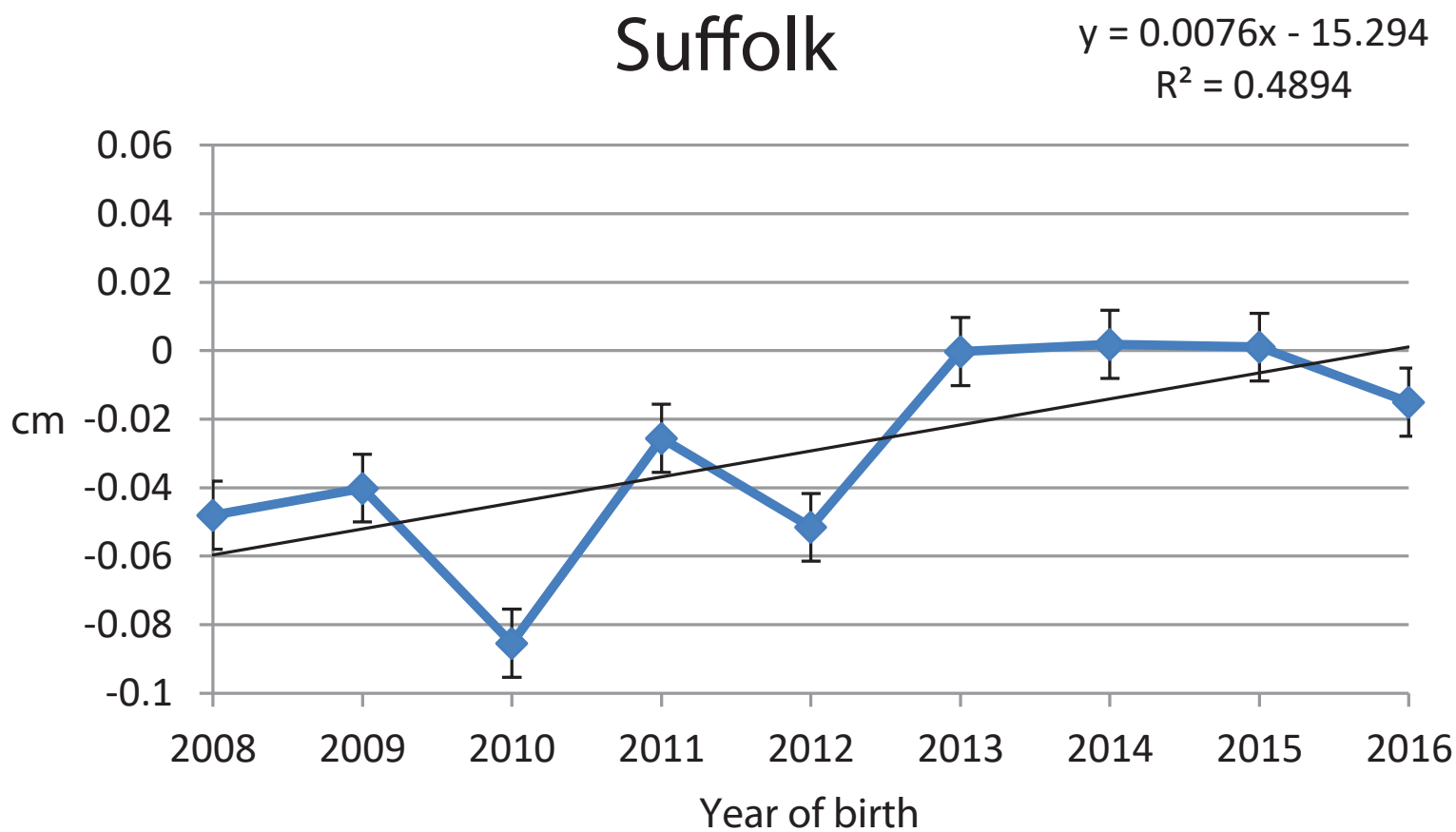


Figure 1e



Manuscript Number: ANIMAL-19-10548

Title: Genetic analyses of live weight and carcass composition traits in purebred Irish Texel, Suffolk and Charollais lambs

Editor's decision: Major Revision

Dear Dr. Rodriguez-Zas,

Enclosed are the responses to the reviewer to the Manuscript Number ANIMAL-19-10548 entitled "genetic analyses of live weight and carcass composition traits in purebred Irish Texel, Suffolk and Charollais lambs ". I feel that the overall objective of the paper has been misunderstood. The aim was never to compare with across breed evaluations but instead to see if major breed differences occurred when within breed evaluations were conducted. The manuscript has been duly revised to clarify this. I hope that the revisions suggested by both editor and reviewer have been sufficiently addressed and the objective of the paper is clear now.

All changes to the text have been highlighted in yellow throughout the text.

Kind regards,
Shauna Fitzmaurice

Section Editor 1: Sandra Luisa Rodriguez-Zas

Comments to Author:

Editor:

Please note the key concerns and limitations of the study noted by a reviewer.

Multiple statements about the goals/objectives of the study and interpretation/conclusions were actually not addressed by the results presented.

The revised manuscript is expected to incorporate results that address the statements to ensure innovative and substantial content of the submission.

Please address each and all the reviewer's comments in the manuscript, provide the location (page and line) in the reply to each comment and highlight all changes in the revision. Failure to follow these guidelines may result in the manuscript being returned to the authors.

Thank you.

AU: We revised the manuscript to ensure consistency between objectives, results and conclusions, and addressed all reviewer's comments.

Reviewer(s)' Comments to Author:

Reviewer: 1

Lines 87-89: This was not accomplished in this paper. See also lines 52-54. No comparison of separate evaluations to the current system was made. Include the relevant results in the revised manuscript.

AU: The main aim of this paper had not been clear in the original manuscript and has now been clarified in the text (Lines 86-87).

Lines 119-122: This is an interesting model effect and worth reporting results for. Add tables or figures in the manuscript

AU: Whilst this is an interesting model effect it has previously been reported in many other previous studies on the Irish sheep population (including on lamb live weight traits) and also is not part of the objectives of this study so does not warrant its own tables/figures. References are included below:

McHugh, N., Berry, D.P., and Pabiou, T. 2016. Risk factors associated with lambing traits. *Animal* 1; 89-95. doi:10.1017/S1751731115001664

McHugh, N., Pabiou, T., Wall, E., McDermott, K., and Berry, D.P. 2017. Impact of alternative definitions of contemporary groups on genetic evaluations of lambing traits. *Journal of Animal Science*. 95:1926-1938. doi:10.2527/jas2016.1344.

O'Brien, A.C., McHugh, N., Wall, E., Pabiou, T., McDermott, K., Randles, S., Fair, S., and Berry, D.P. 2017. Genetic parameters for lameness, mastitis and dagginess in a multi-breed sheep population. *Animal*. 11:911-919. doi: 10.1017/S1751731116002445.

Lines 126-127: Records were discarded instead of lambs. Clarify.

AU: Lambs had all records removed from the dataset if they were artificially reared or reared by a non-genetic dam. This means that they were not used for further analysis for any of the traits analysed in the present study. This has been clarified in the text. (Lines 124-125)

Lines 150-156: Table 3 Maternal repeatability – this term was kept in final models when not different from 0? Justify in the manuscript.

AU: This has been included in the revised manuscript (Lines 152-154).

Lines 166-169: Total records supporting each year of the trend is appropriate to report.

AU: This has now been added in lines 168-169.

Lines 187-189; 193-195; 223-225: The statistical test for this was not described in Materials and Methods. Include in the manuscript.

AU: This has been included in the revised manuscript in lines 161-162.

Lines 221-223: This should be in the introduction. This objective was not accomplished. Add results in the manuscript that will enable to accomplish these objectives. Tables 2 & 3 present the same information. Combine and put SE on estimates of heritability.

AU: This sentence has been restructured so as to fit in to the discussion (Lines 221-223). Table 2 has been kept as a separate table in the manuscript as it presents complementary but not the same results as Table 3. SE has been included with the estimates of heritability in Table 3.

Maxa et al. (2007 *Acta Ag Scand* and *Small Rum Res*), Shrestha et al. (1985 *Can. JAS*); Notter (1998) should be cited for comparison to Texel and Suffolk results.

AU: These papers have been cited in the revised text in lines 258-259, 344, 345.

Revision 2 Comments:

Section Editor 1: Sandra Luisa Rodriguez-Zas
Comments to Author:

Editor:

I share the concern about incorrect comparison of variance estimates (or functions thereof)

expressed by a reviewer. Please consult with an expert in the field of quantitative genetics about statistical methodology to compare (co)variance component estimates (and functions) or remove the sections in the manuscript that correspond to results from the t-test comparison proposed in the R1 manuscript.

Please address the reviewer's comment and indicate the location in R1 that were the lines were removed. In the revised R2 manuscript please highlight the end and start of the sentences surrounding the deleted sections/statements or if you include a different approach to compare estimates, please highlight the changes to the manuscript. Failure to follow these guidelines may result in the manuscript being returned to the authors. Thank you.

AU: All sentences that were removed in R1 have been indicated in the latest version of the manuscript by inserting (□) in their place. Numerous experts in the field of quantitative genetics were consulted and agreed that the method explained below under the reviewers comment and in the manuscript is a feasible method of comparison of variance components.

Reviewer #1: lines 163-164 These parameters cannot be compared statistically this way. Delete this statement and modify the remainder of the results that report statistical comparisons of either variance components or estimates of genetic parameters of different populations accordingly.

AU: The methodology behind these comparisons may have been misunderstood. A 2 two tailed t-test was used to produce 95% confidence intervals based on standard errors for the heritability estimates. If the intervals for different heritability estimates did not overlap then these estimates were significantly different from one another however if they did overlap then the estimates were deemed not to be significantly different from each other.

Revision 3 Comments:

Section Editor 1: Sandra Luisa Rodriguez-Zas
Comments to Author:

From the editor:

The foundation of the minor section of the submission centered on comparing variance component estimates from different populations using t-tests is questionable. The manuscript would be acceptable for publication without this component. If you agree with this recommendation, please remove lines 163 to 167, line 193 and 199 and resubmit your manuscript indicating that these sections were removed.

AU: These lines have now been removed from the manuscript and are indicated by inserting (□).

Minor Technical Revision:

Editor's decision: Editorial Office - Minor Technical Revision

The Editorial Office has viewed your paper on behalf of the Editor in charge of your submission. Minor editorial changes are requested and accessible as described below. Please pay attention to these comments when revising, and highlight the changes made in the revised manuscript.

Your revision is due within 5 working days.

To submit a revision, go to <https://www.editorialmanager.com/animal/> and log in as an Author. You will be able to find your submission in the 'Submission Needing Revision' folder.

AU: All issues have been addressed and highlighted within the manuscript.