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Scotland's Rural College

Genetic parameters of Visual Image Analysis primal cut carcass traits of commercial prime beef slaughter animals

Moore, KL; Mrode, R; Coffey, MP

1   **Genetic parameters of Visual Image Analysis primal cut carcass traits of**
2   **commercial prime beef slaughter animals**

3   K. L. Moore [1], R. Mrode [1] and M. P. Coffey [1]

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5   [1] *Animal and Veterinary Sciences, Scotland's Rural College (SRUC), Peter Wilson*

6   *Building, Kings Buildings, West Mains Road, Edinburgh, EH9 3JG, United Kingdom*

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8   Corresponding author: Kirsty Moore. Email: Kirsty.Moore@sruc.ac.uk

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10   Short title: Genetic parameters of beef primal cuts

11

12   **Abstract**

13   Visual image Analysis (VIA) of carcass traits provides the opportunity to estimate

14   carcass primal cut yields on large numbers of slaughter animals. This allows

15   carcasses to be better differentiated and farmers to be paid based on the primal cut

16   yields. It also creates more accurate genetic selection due to high volumes of data

17   which enables breeders to breed cattle that better meet the abattoir specifications

18   and market requirements. In order to implement genetic evaluations for VIA primal

19   cut yields, genetic parameters must first be estimated and that was the aim of this

20   study. Slaughter records from the UK prime slaughter population for VIA carcass

21   traits was available from two processing plants. After edits, there were 17,765 VIA

22   carcass records for six primal cut traits, carcass weight as well as the EUROP

23   conformation and fat class grades. Heritability estimates after traits were adjusted for

24   age ranged from 0.32 (0.03) for EUROP fat to 0.46 (0.03) for VIA Topside primal cut

25   yield. Adjusting the VIA primal cut yields for carcass weight reduced the heritability

26   estimates, with estimates of primal cut yields ranging from 0.23 (0.03) for Fillet to

27   0.29 (0.03) for Knuckle. Genetic correlations between VIA primal cut yields adjusted

28   for carcass weight were very strong, ranging from 0.40 (0.06) between Fillet and

29   Striploin to 0.92 (0.02) between Topside and Silverside. EUROP conformation was

30   also positively correlated with the VIA primal cuts with genetic correlation estimates

31   ranging from 0.59 to 0.84, while EUROP fat was estimated to have moderate

32   negative correlations with primal cut yields, estimates ranged from -0.11 to -0.46.

33   Based on these genetic parameter estimates, genetic evaluation of VIA primal cut

34   yields can be undertaken to allow the UK beef industry to select carcasses that better

35   meet abattoir specification and market requirements.

36

37   **Keywords:** Visual image Analysis (VIA), genetic parameter estimation, prime
38   slaughter beef cattle, carcass traits

39

40   **Implications**

41   Visual image Analysis primal cut yields are moderately heritable with sufficient

42   genetic variability to allow response to selection. Primal cut yields were estimated to

43   have strong, but not unity, genetic correlations and breeders will be able to

44   genetically select animals that produce carcasses with a greater proportion of the

45   weight in the more valuable primal cuts. This will improve genetic progress for

46   abattoir carcass traits as the EBVs will be based on actual abattoir carcass data,

47   rather than proxy traits as in the pedigree sector. As carcass traits are end of life

48   traits these genetic parameters will also enable genomic selection to be implemented

49   to increase genetic progress estimated early in life.

50

51   **Introduction**

52 Genetic improvement in the UK beef industry has traditionally been implemented in

53 the purebred pedigree sector through voluntary performance recording. Selection for

54 carcass traits has been via Estimated Breeding Values (EBVs) produced from

55 recording proxy traits. Live weight at 400 days of age is a proxy for carcass weight

56 and ultrasound scans for muscle and fat depth are proxies for carcass conformation

57 and fat. However due to the cost of ultrasound scanning, only a relatively small

58 proportion of the purebred population have these carcass traits recorded (Moore *et*

59 *al.*, 2014). Whilst genetic improvement is made in the commercial sector through the

60 purchase of superior purebred bulls, the market signals to pedigree breeders are

61 diluted since commercial farmers are paid based for the carcass on the EUROP

62 classification system.

63

64 In the European Union, beef carcasses are assessed using the EUROP classification

65 system (European Council regulations 1208/81 and 2930/81). Carcasses are valued

66 per kg carcass weight at the base rate price (varies depending on breed, age and the

67 animals type; steer, heifer, cow etc.) with a penalty or premium added based the

68 EUROP conformation and fat class of the carcass. EUROP classification uses letters

69 E (excellent), to P (poor) to grade conformation with particular emphasis on the

70 round, back and shoulder. A five point numeric scale is used to classify the amount of

71 subcutaneous fat on the carcass and in the thoracic cavity, where the number one

72 represents none or low fat cover and number five represents very high fat. Often the

73 EUROP fat scale of five points is subdivided into three subclasses (-, = or +)

74 (MLCSL, 2014).

75

76   Advances in imaging technologies such as Visual Image Analysis (VIA) provide the

77   opportunity to mechanically grade carcasses, at line speed, for the EUROP traits but

78   in addition for individual primal cut yields. This creates the underlying framework to

79   undertake genetic evaluation for these traits using large volumes of commercial

80   abattoir data. In Ireland, VIA carcass traits have been investigated (Pabiou *et al.*,

81   2009; 2011a; 2011b; 2012) and found to have moderate to high heritabilities with

82   strong, but not unity, positive genetic correlations between the VIA primal cuts. In

83   these studies, carcass weight and EUROP traits conformation and fat were also

84   considered and found to have moderate heritability. Carcass weight and EUROP

85   conformation was estimated to have moderate to strong positive genetic correlations

86   with the individual VIA primal cuts, whilst EUROP fat had moderately negative

87   genetic correlations with the individual VIA primal cuts. Given the strong genetic

88   correlations between the VIA primal cuts, Pabiou *et al.* (2011a; 2011b) combined the

89   individual primal cuts into three categories based on the value of the primal cut (high,

90   medium, low). Again moderate to high heritabilities were estimated.

91

92   The objective of this study was to use VIA carcass information from the cross bred

93   UK commercial prime slaughter population to estimate genetic parameters for

94   individual primal cut yields, carcass weight and EUROP conformation and fat class to

95   enable subsequent genetic evaluation of carcass traits.

96

97   **Material and methods**

98   *Data Sources*

99   Carcass data (carcass measurements, animal identification, dates of birth and death,

100 animal breed and type of slaughter animal (i.e. steer or young bull)) was collected

4

101 from two abattoirs fitted with VBS2000 VIA machines (E+V Technology,

102 http://www.eplusv.de/), installed to grade carcases at slaughter. One side of the

103 carcass was positioned on a holding frame while a 2D and 3D image was taken by

104 the VIA machine's mounted digital camera using previously calibrated lighting

105 arrangements. The resulting images are analysed using E+V software and prediction

106 equations to predict six individual primal cuts from the hindquarter; Topside,

107 Silverside, Striploin, Fillet, Knuckle and Rump, as well as carcass weight and the

108 EUROP classification for conformation and fat. The predicted VIA primal cut yields

109 were then multiplied by 2 to represent both sides of the carcass. Carcass weight and

110 all six primal cut yields were estimated in kg, while EUROP conformation and fat was

111 recorded according to EUROP standards and then recoded to a 15 point numerical

112 scale described by Hickey *et al.* (2007). To increase the scale of variation the

113 converted conformation and fat measurements was multiplied by three making the

114 range 1-45.

115

116 Pedigree and additional animal information was obtained from the British Cattle

117 Movement Service (BCMS) database, where it has been compulsory to register all

118 dairy and beef cattle in the UK since 1996. For every animal, the BCMS database

119 records the dam, date of birth, details of each farm movement by the animal, breed,

120 sex and dates of death. In addition the sire can be recorded, but is not compulsory,

121 and is recorded in approximately a third of registered animals. Additional pedigree

122 information was also available from the UK dairy milk recording organizations in the

123 UK as well as the pedigree herd books for a number of different dairy and beef

124 breeds. All sources of pedigree are combined to form a single UK dairy and beef

125 'super pedigree' that contains all known animals in the UK as well as all known

126   pedigree, i.e. if sire is recorded in one data source and dam in another source, the

127   super pedigree is the only pedigree that contains both the sire and the dam.

128

129   *Calculation of proportion of each breed*

130   The animals' breed is supplied in several sources of data. This is usually just a single

131   breed code and does not enable the precise breed make up to be captured,

132   especially of cross breeds, and thus allow breed and hybrid vigour effects to be

133   accounted for. Therefore, for all animals in the super pedigree the proportion of each

134   breed (PEB) is calculated. The PEB of each animal is simply half the PEB of the sire

135   plus half the PEB of the dam. For example, an animal with a sire that is 100%

136   Limousin and a dam that is 50% Holstein Friesian : 50% Limousin will end up with a

137   PEB of 75% Limousin : 25% Holstein Friesian. This approach is iterative, with

138   parents first needing PEB calculated before progeny PEB can be computed. Where

139   one or both parents are unknown a set of assumptions are applied to obtain an

140   estimate of the PEB. When both parents are unknown and if the animal is included in

141   the BASCO database (database storing pedigree and performance recording

142   information for some beef breeds in the UK) with breed make up recorded, then the

143   PEB is set to match the breed make up from BASCO. If the animal is not recorded in

144   BASCO, then it is assumed to be 100% of the breed code supplied in BCMS data. In

145   cases where one parent is known and the other is unknown, the same assumptions

146   as above apply but with the PEB adjusted for the contribution of the known parent.

147   For example, if the breed code in the BCMS data is Limousin, the sire is unknown

148   and the dam is 100% Holstein Frisian then the PEB for the animal would be 50%

149   Limousin : 50% Holstein Frisian.

150

151 *Heterosis and recombination coefficients*

152 To enable the effects of hybrid vigour to be considered in the analysis, heterosis and

153 recombination effects were calculated for a limited number of breed 'type' categories.

154 With such a large number of breeds represented in the data, it was not practical to

155 model heterosis effects for every combination, therefore breeds were grouped into

156 four breed types; dairy, native UK beef breeds, continental beef breeds and

157 remaining breeds (of which there were few). The PEB was then concatenated into

158 these breed types such that a 50% Limousin : 50% Charolais would be 100%

159 continental. For each animal and each combination of breed type (six) heterosis and

160 recombination coefficients were computed where A and B represent the proportion of

161 genes from the two breed types considered and s and d denote sire and dam,

162 respectively (Van der Werf and De Boer, 1989).

163

164 Heterozygosis $_{AB}$ = $A_d . B_s + A_s . B_d$

165 Recombination loss $_{AB}$ = $A_s . B_s + A_d . B_d$

166

167 *Dataset edits*

168 A total of 111,394 prime slaughter commercial carcasses records were available from

169 two abattoir sites. Animals were defined as being prime slaughter if the abattoir

170 classification was one of three categories: heifer (H), steer (S) and young bull (YB).

171 All animals were slaughtered between 2012 and 2014 – although one site only had

172 kill data for a portion of 2014. Records were removed if: the sire was unknown

173 (n=74,844); the age at slaughter was less than 365 days (12 months) (n=13) or

174 greater than 1095 days (36 months) for heifers and steers (n=1,698) and greater than

175 730 (24 months) for young bulls (n=44); the animal was an outlier (defined by ± three

176 standard deviations from the mean within sire breed and category (H;S;YB)) for any

177 of the VIA primal cut yields, carcase weight or EUROP conformation and fat traits

178 (n=886); the sire was not purebred (purebred defined as being 87.5+% of one breed)

179 (n=670); the breed of the sire was from a numerically small breed (defined as breeds

180 with less than 200 animals in the dataset) (n=668); the animal belonged to a paternal

181 half sib family with less than three half sibs (n=4,955); the animal came from a birth

182 herd with less than three records (n=465); the animal was in a finishing herd with less

183 than three records (n=665); there were fewer than three animals in the birth season –

184 herd contemporary group, where season was defined in four month blocks (n=3,314);

185 the animal was in a single sire contemporary group (n=5,296). After the above edits,

186 only 111 records remained from the new VIA abattoir site, so these were removed

187 leaving only one site in the analysis.

188

189 *Final dataset*

190 After edits, 17,765 records remained from one abattoir, covering 11 different sire

191 breeds from 660 birth herds and 668 finishing herds. Of these records there were

192 4,758 heifers, 7,642 steers and 5,365 young bulls. Animals were born between

193 February 2010 and August 2013 and slaughtered between July 2012 and September

194 2014. The population consisted of 1,379 (7.8%) purebred animals and 16,386

195 (92.2%) crossbred animals. Based on the sire breed, the more numerous breeds

196 were Charolais (25.2%), Limousin (18.8%), Simmental (18.6%), Angus (17.7%) and

197 Holstein Frisian (10.7%). The remaining seven breeds combined accounted for 9.3%

198 of the edited dataset. A three generation pedigree (n=87,788) was extracted from the

199 bovine super pedigree for all animals remaining in the edited dataset.

200

201 *Statistical analysis*

202 The statistical model was developed using the PROC MIXED procedure in the SAS

203 software (SAS Institute, 2007). Fixed effects were determined from a sire model

204 using backwards elimination to remove terms that were not significant. Significance

205 was determined using the F test and $P<0.05$. First order interactions were also fitted.

206 The factors considered as fixed class effects were abattoir sex category (H, S or YB),

207 birth season herd contemporary groups (BSH), finishing herd and kill season (defined

208 as four month periods, starting from February). Considered as co-variate effects were

209 age at slaughter (linear and quadratic), dam age in days (linear and quadratic), the

210 percentage of dairy breeds in the dam, and the heterosis and recombination

211 coefficients for each breed type combination (described above).

212

213 For all traits abattoir sex category, BSH, finishing herd, kill season, slaughter age

214 (linear and quadratic), linear dam age and percentage of dairy breeds in the dam

215 were significant. Heterosis effects between the dairy, native beef and continental

216 beef breed types were significant, but not those crosses involving the remaining

217 breed types, most likely due to the small number of animals in the UK that cannot be

218 grouped into the three main breed types. Recombination effects were significant for

219 dairy * native beef breed type crosses, and for most of the traits the native beef *

220 remaining breed type crosses. Significant first order interactions were abattoir sex

221 category with the following terms; kill season, age at slaughter and percentage of

222 dairy in the dam. In addition, interactions with age at slaughter with percentage of

223 dairy in the dam and dam age and the interaction between dam age and the

224 percentage of dairy in the dam were significant.

225

226   Uni-variate co-variance components were estimated using single trait animal models

227   (ASReml; Gilmour *et al.*, 2009). Relationships amongst animals were accounted for

228   using a 5 generation relationship matrix with unknown ancestors assigned to genetic

229   groups as defined by the breed types used to estimate heterosis and recombination

230   co-efficients. The mixed linear model can be written as

231

232   $y = Xb + ZQg + Zu + e$

233

234   where **y** is the vector of observations, **b** is the vector of fixed effects, **g** is the vector

235   of genetic groups, **u** is the vector of random effects, **e** is the vector of residual effects

236   and the **X**, **Z** and **Q** matrices are the respective incidence matrices. The fixed effects

237   included in the model to estimate genetic parameters were those found to be

238   significant as described earlier. To estimate genetic and residual co-variances

239   between the traits a series of bi-variate models were undertaken using ASReml. For

240   the primal cut yield traits; Topside, Silverside, Knuckle, Rump, Striploin and Fillet a

241   separate set of analyses were undertaken using the same methodology but also after

242   adjusting for carcass weight.

243

244   **Results**

245

246   *Phenotypic data*

247   A summary of the phenotypic data is contained in table 1. Animals were slaughtered

248   on average at 627 days (20.5 months) of age with an average carcass weight of 354

249   kg. In total the six VIA primal cut yields sum to 104.72 kg and account for 29.6% of

250   the total carcass weight. The coefficients of variation for all primal cut yields and

251   carcass weight ranged from 0.16 to 0.19. Coefficients of variation for slaughter age,

252   conformation class and fat score were higher ranging from 0.25 to 0.27. Average

253   conformation and fat values were 24.75 and 24.19 respectively, corresponding to a

254   value of R (good muscle development) for EUROP conformation class and to a value

255   of three (average fat cover over the carcass with slight deposits of fat in the thoracic

256   cavity) in the EUROP fat class.

257

258   *Heritability*

259   All carcass traits were moderately heritable with heritability estimates ranging from

260   0.32 for EUROP fat to 0.46 for the Topside primal yield (Table 2). Whilst the

261   heritability estimates were similar for all primal cut yields, there were differences in

262   the variances. The primal cut yield for Fillet has the lowest phenotypic variation at

263   0.43; it was also seen in Table 1 to be the smallest primal cut of those considered in

264   this study. Both Topside and Silverside primal cuts were observed to be the larger

265   primal cuts in the study and also showed the higher phenotypic variances. However,

266   the genetic coefficient of variation for all six primal yields was approximately 0.13.

267   Carcass weight and EUROP conformation and fat class all had higher phenotypic

268   variances estimates and had genetic coefficient of variation of 0.06, 0.11 and 0.15,

269   respectively. When primal cut yields were also adjusted for carcass weight the

270   heritability estimates were lower, but still moderate, ranging from 0.23 for Fillet to

271   0.29 for Knuckle primal cut yield. Phenotypic variances were also reduced.

272

273   *Genetic and phenotypic correlations*

274   Strong positive genetic correlations between carcass weight and all the primal cut

275   yields were estimated when traits were age adjusted (Table 3). These correlations

276   were much reduced and only low to moderate in size when the primal cut yields

277   also adjusted for carcass weight (Table 4). Strong positive phenotypic correlations

278   between these traits were also estimated, but once primal cut yields were adjusted

279   for carcass weight, phenotypic correlations were not significantly different from zero.

280

281   All six primal cut yields had strong positive - almost unity - genetic correlations to

282   each other when adjusted for slaughter age. When the primal cut yields were also

283   adjusted for carcass weight, the strength of the correlations reduced, but was still

284   strong and positive; genetic correlations ranged from 0.40 between Fillet and

285   Striploin to 0.92 between Topside and Silverside. This same trend can be observed

286   with estimates of the phenotypic correlations; when the primal cut yields were

287   adjusted for slaughter age and carcass weight phenotypic correlations ranged from

288   0.22 between Fillet and Striploin to 0.80 between Topside and Silverside.

289

290   EUROP conformation was estimated to have a moderate positive genetic correlation

291   with carcass weight, and strong positive genetic correlations with the primal cut yields

292   (regardless of whether carcass weight was adjusted for). A moderate negative

293   genetic correlation was estimated with EUROP fat. In all cases, EUROP fat was

294   estimated to have low to moderate negative genetic correlations with carcass weight

295   and the primal cut yields. Generally the size of the genetic correlations with primal cut

296   yields increased when they were adjusted for carcass weight. Moderate positive

297   phenotypic trends were estimated between EUROP conformation, and carcass

298   weight and primal cut yields (regardless of whether primal cut yields were adjusted

299   for carcass weight). Generally, the phenotypic correlations between EUROP fat and

300   the other traits were not significantly different from zero or were low and negative.

301   After adjusting for carcass weight, the phenotypic correlations between EUROP fat

302   and the primal cut yields were low and negative. All correlation estimates show that

303   animals that have genetically heavier carcasses will also have increased primal cut

304   yields, increased muscling of the carcass and decreased subcutaneous fat.

305

306   **Discussion**

307   The objective of this study was to estimate genetic parameters for abattoir VIA primal

308   cut yields of UK commercial cross bred animals and determine if the traits are

309   suitable for genetic evaluation. This was the first study in the UK estimating genetic

310   parameters from large numbers of commercial cattle with VIA carcass traits recorded.

311   Outside of the UK, there has only been a small number of studies estimating genetic

312   parameters for individual carcass cut yield (Cantet *et al.*, 2003; Pabiou *et al.*, 2009)

313   or with traits predicted from digital imaging (Pabiou *et al.*, 2011a). With 17,765

314   carcass records, this study is one of the largest studies to consider primal cut yields

315   with most studies having less than 1,000 animals (Cantet *et al.*, 2003, Pabiou *et al.*,

316   2009; 2011b) and only one other sizable data set with Pabiou *et al.* (2011a)

317   analysing 52,722 carcases.

318

319   The UK beef industry consists of many different breeds with 94% of the prime

320   slaughter population being cross bred and through cross breeding, dairy genetics

321   contributes 28% of the genes in the prime slaughter population (Todd *et al.*, 2011).

322   The dataset used in this study was reflective of the prime slaughter population

323   described by Todd *et al.* (2011). In the edited dataset the average carcass weight of

324   354kg was similar to the 2013 national average of 341kg reported by EBLEX (2014).

325

326   Heritability estimates were reported in Table 2. The six primal cut yields were

327   estimated to have moderate heritabilities in both models considered in this study.

328   Adjusting for carcass weight reduced the heritability and phenotypic variance

329   estimates of primal cut yields. However the primal cut yields were adjusted for

330   carcass weight to avoid encouraging the industry to select for larger animals, instead

331   setting a breeding objective of increasing the proportion of weight in valuable primal

332   cut yields for a given carcass weight means more valuable carcasses and not just

333   bigger carcasses. Estimates in this study were comparable to those reported in the

334   literature. Pabiou *et al.* 2009 considered carcass dissection data from an

335   experimental (n=413) and a commercial (n=635) data set similar to the UK data set

336   used in this study. The Primal cut yields were adjusted for age and heritability

337   estimates in the experimental data set ranged from 0.14 (0.16) for Rib roast to 0.86

338   (0.23) for the Round primal cut. Similarly, in the commercial data set heritability of

339   hind quarter cuts ranged from 0.40 (0.19) for Rib roast to 0.63 (0.20) for Fillet. In a

340   much larger commercial data set, Pabiou *et al.* (2011a) estimated heritabilities

341   ranging from 0.17 (0.018) for very high value cuts (Rib roast, Striploin and Fillet) to

342   0.40 (0.024) for high value cuts (Sirloin and the round) predicted from VIA. This same

343   study considered the traits separately for heifers and steers and heritability estimates

344   were generally higher for heifers and showed strong positive genetic correlations

345   between the sexes (correlations ranged from 0.54 (0.14) to 0.76 (0.07)).

346

347   There have been more studies reported for carcass weight and EUROP conformation

348   and fat. The moderate heritability estimated for carcass weight is similar to the

349   average estimate of 0.40 reported by Rios Utrera and Van Vleck (2004) from a

350   review of 56 studies. Hickey *et al.* (2007) reported carcass weight heritability

351   estimates from a number of different breeds in the Irish population ranging from 0.17

352   in Angus and Belgian Blue cattle to 0.65 in Charolais cattle. In a Finland study

353   considering 5 beef cattle breeds, carcass weight heritability estimates ranged from

354   0.39 to 0.48 (Kause *et al.*, 2015). A moderate heritability was estimated for both

355   EUROP conformation and fat class and these estimates are similar to those reported

356   by Pabiou *et al.* (2011a). In a Swedish population, Eriksson *et al.* (2003) estimated

357   heritability for conformation of 0.22 in Hereford and 0.34 in Charolais. In the same

358   study heritability estimates for carcass fat were 0.38 and 0.27 for Charolais and

359   Hereford, respectively. In Finland, Kause *et al.* (2015) estimated heritabilities of

360   between 0.30 to 0.44 for conformation and 0.29 to 0.44 for fat. The study by Hickey

361   *et al.* (2007) showed a wide variation in carcass conformation and fat heritability

362   estimates across the breeds considered. For carcass conformation, heritabilities

363   ranged from 0.04 for Friesian to 0.36 for Limousin. For carcass fat, heritability

364   estimates ranged from 0.00 for Limousin to 0.40 for Simmental.

365

366   This study found that there were moderate to strong genetic correlations between the

367   carcass traits analysed (Table 3 and 4). Carcass weight was found to be strongly

368   positively correlated with carcass conformation (0.53) and negatively correlated with

369   carcass fat (-0.14). Conformation and fat were also had a moderately negative

370   correlation (-0.27). Pabiou *et al.* (2011a) also found these genetic relationships in

371   steers, although with a lower genetic correlation between carcass weight and

372   conformation (0.35). Hickey *et al.* (2007) found positive genetic correlations between

373   carcass weight and conformation (0.11) but, in contrast to our findings, estimated

374   positive genetic correlation between carcass weight and fat (0.26), and between

375   conformation and fat (0.44). Kause *et al.* (2015) also estimated positive correlations

376 between carcass weight and fat with genetic correlation estimates ranging from 0.08

377 to 0.28. In agreement with our results, other studies also found positive genetic

378 correlations between conformation and carcass weight, with values ranging from 0.25

379 to 0.66 (Van der Werf *et al.*, 1989; Hirooka *et al.*, 1996; Liinamo *et al.*, 1999;

380 Parkkonen *et al.*, 2000; Kause *et al.*, 2015) in dairy and dual purpose cattle herds.

381

382 Very strong, almost unity, genetic correlations (0.92+) were estimated between the

383 VIA primal cut yields. Adjusting for carcass weight reduced the correlations with

384 estimates ranging from 0.40 between Fillet and Striploin to 0.92 between Topside

385 and Silverside. These strong positive correlations suggests that selection pressure

386 for a given primal cut will result in increased yields for all six primal cuts, but as

387 carcase weight has been adjusted for in the model, selection will not indirectly select

388 for heavier carcase weights. High positive genetic correlations were also estimated

389 by Pabiou *et al.* (2009) from dissection carcass data with estimates ranging from 0.67

390 between Fillet and Striploin and 0.93 between Fillet and Round. Using predicted

391 yields Pabiou *et al.* (2011a) estimated genetic correlations ranging from 0.45

392 between low value cuts and medium value cuts to 0.89 between high value cuts and

393 very high value cuts.

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453 **Table 1** *Overall mean, standard deviation, minimum, maximum and coefficient of*

454 *variation for Visual Image Analysis (VIA) carcass traits from 17,765 cross bred prime*

455 *slaughter commercial cattle*

Trait[1]	N	Mean	SD	Min	Max	CV
Slaughter age (days)	17765	627.0	157.81	365.0	1095.0	0.25
Carcass Weight (kg)	17765	353.91	55.04	189.10	550.20	0.16
Topside (kg)	17765	23.64	4.01	12.96	37.74	0.17
Silverside (kg)	17765	28.50	5.37	14.86	46.26	0.19
Knuckle (kg)	17765	14.61	2.51	6.80	23.70	0.17
Rump (kg)	17765	15.08	2.65	6.90	23.54	0.18
Striploin (kg)	17765	16.44	2.90	8.02	26.18	0.18
Fillet (kg)	17765	6.46	1.14	3.46	10.92	0.18
Conformation (1-42 scale)	17765	24.75	6.79	3.00	42.00	0.27
Fat (1-42 scale)	17765	24.19	6.46	3.00	42.00	0.27

456 N = Number of animals; Mean = Mean of the trait; SD = Standard deviation of trait; Min = Minimum

457 trait value; Max = Maximum trait value; CV = coefficient of variation

458 [1] Slaughter age is the age of the animal at slaughter; Carcass weight is the weight of the carcass at

459 slaughter; Topside, Silverside, Knuckle, Rump, Striploin and Fillet are all primal cut yields from the

460 total carcass predicted using VIA; Conformation and Fat is the EUROP conformation and fat classes,

461 predicted using VIA and converted to a numerical 1-42 scale; higher values represent more muscular

462 carcasses for conformation and higher levels of fat for fat

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464 **Table 2** *Genetic, residual and phenotypic variances and trait heritability (standard*

465 *errors parenthesis) estimates for Visual Image Analysis (VIA) carcass traits from*

466 *17,765 cross bred prime slaughter commercial cattle*

Trait[1]	σ^2_a	σ^2_e	σ^2_p	h^2
Age adjusted				
Carcass Weight	368.20 (28.96)	481.45 (23.44)	849.66 (11.21)	0.43 (0.03)
Topside	2.31 (0.18)	2.77 (0.14)	5.07 (0.07)	0.46 (0.03)
Silverside	3.63 (0.28)	4.58 (0.23)	8.22 (0.11)	0.44 (0.03)
Knuckle	0.86 (0.07)	1.07 (0.05)	1.93 (0.03)	0.45 (0.03)
Rump	0.91 (0.07)	1.22 (0.06)	2.13 (0.03)	0.43 (0.03)
Striploin	0.92 (0.08)	1.36 (0.06)	2.28 (0.03)	0.40 (0.03)
Fillet	0.18 (0.01)	0.25 (0.01)	0.43 (0.01)	0.42 (0.03)
Conformation	5.53 (0.45)	7.30 (0.36)	12.83 (0.17)	0.43 (0.03)
Fat	6.36 (0.61)	13.58 (0.51)	19.94 (0.25)	0.32 (0.03)
Weight adjusted				
Topside	0.25 (0.03)	0.77 (0.02)	1.02 (0.01)	0.25 (0.03)
Silverside	0.38 (0.04)	1.03 (0.04)	1.42 (0.02)	0.27 (0.03)
Knuckle	0.15 (0.02)	0.37 (0.01)	0.53 (0.01)	0.29 (0.03)
Rump	0.15 (0.02)	0.41 (0.01)	0.57 (0.01)	0.27 (0.03)
Striploin	0.10 (0.01)	0.26 (0.01)	0.37 (0.01)	0.28 (0.03)
Fillet	0.02 (0.003)	0.07 (0.002)	0.09 (0.001)	0.23 (0.03)

467 σ^2_a = Genetic variance component; σ^2_e = Residual variance component; σ^2_p = Phenotypic variance

468 component; h^2 = heritability

469 [1] Carcass weight is the weight (kg) of the carcass at slaughter; Topside, Silverside, Knuckle, Rump,

470 Striploin and Fillet are all primal cut yields(kg) predicted from the total carcass using VIA;

471 Conformation and Fat is the EUROP conformation and fat classes, predicted using VIA and converted

472 to a numerical 1-42 scale; higher values represent more muscular carcasses for conformation and

473 higher levels of fat for fat

Table 3 *Genetic (above diagonal) and phenotypic (below diagonal) correlations estimates (standard errors in parenthesis) for age adjusted Visual Image Analysis (VIA) primal cut yield carcass traits from 17,765 cross bred prime slaughter commercial cattle*

Trait[1]	CWT	TOP	SIL	KNU	RUM	STR	FIL	CON	FAT
CWT		0.95 (0.01)	0.94 (0.01)	0.91 (0.01)	0.91 (0.01)	0.94 (0.01)	0.94 (0.01)	0.53 (0.04)	-0.14 (0.06)
TOP	0.89 (0.002)		0.99 (0.002)	0.98 (0.003)	0.95 (0.01)	0.95 (0.01)	0.98 (0.003)	0.70 (0.03)	-0.26 (0.06)
SIL	0.91 (0.002)	0.96 (0.001)		0.97 (0.004)	0.95 (0.01)	0.95 (0.01)	0.98 (0.003)	0.72 (0.03)	-0.27 (0.06)
KNU	0.85 (0.003)	0.95 (0.001)	0.92 (0.001)		0.96 (0.01)	0.94 (0.01)	0.96 (0.01)	0.73 (0.03)	-0.26 (0.06)
RUM	0.86 (0.002)	0.89 (0.01)	0.87 (0.002)	0.89 (0.002)		0.95 (0.01)	0.94 (0.01)	0.73 (0.03)	-0.21 (0.06)
STR	0.92 (0.002)	0.89 (0.002)	0.89 (0.002)	0.87 (0.002)	0.88 (0.002)		0.93 (0.01)	0.73 (0.03)	-0.16 (0.06)
FIL	0.88 (0.002)	0.95 (0.001)	0.95 (0.001)	0.90 (0.002)	0.84 (0.003)	0.85 (0.003)		0.65 (0.03)	-0.29 (0.06)
CON	0.44 (0.01)	0.56 (0.01)	0.60 (0.01)	0.57 (0.01)	0.60 (0.01)	0.58 (0.01)	0.51 (0.01)		-0.27 (0.05)
FAT	0.17 (0.01)	0.02 (0.01)	0.03 (0.01)	0.02 (0.01)	0.08 (0.01)	0.14 (0.01)	0.03 (0.01)	0.00 (0.01)	

CWT = Carcass weight; TOP = Topside; SIL = Silverside; KNU = Knuckle; RUM = Rump; STR = Striploin; FIL = Fillet; Conformation = Conformation; Fat = Fat

[1] Carcass weight is the weight (kg) of the carcass at slaughter; Topside, Silverside, Knuckle, Rump, Striploin and Fillet are all primal cut yields(kg) predicted from the total carcass using VIA; Conformation and Fat is the EUROP conformation and fat classes, predicted using VIA and converted to a numerical 1-42 scale; higher values represent more muscular carcasses for conformation and higher levels of fat for fat

Table 4 Genetic (above diagonal) and phenotypic (below diagonal) correlations estimates (standard errors in parenthesis) for weight adjusted Visual Image Analysis (VIA) primal cut yield carcass traits from 17,765 cross bred prime slaughter commercial cattle

Trait[1]	CWT	TOP	SIL	KNU	RUM	STR	FIL	CON	FAT
CWT		0.17 (0.06)	0.25 (0.06)	0.28 (0.06)	0.23 (0.06)	0.11 (0.06)	0.22 (0.06)	0.53 (0.04)	-0.14 (0.06)
TOP	-0.09 (0.01)		0.92 (0.02)	0.87 (0.02)	0.69 (0.04)	0.56 (0.05)	0.84 (0.03)	0.78 (0.03)	-0.43 (0.06)
SIL	0.02 (0.01)	0.80 (0.003)		0.85 (0.02)	0.69 (0.04)	0.57 (0.05)	0.82 (0.02)	0.84 (0.02)	-0.44 (0.06)
KNU	0.03 (0.01)	0.78 (0.003)	0.67 (0.01)		0.75 (0.03)	0.60 (0.04)	0.73 (0.04)	0.79 (0.03)	-0.35 (0.06)
RUM	0.02 (0.01)	0.53 (0.01)	0.43 (0.01)	0.58 (0.005)		0.65 (0.04)	0.60 (0.05)	0.77 (0.03)	-0.21 (0.06)
STR	0.01 (0.01)	0.42 (0.01)	0.37 (0.01)	0.40 (0.01)	0.47 (0.01)		0.40 (0.06)	0.81 (0.03)	-0.11 (0.06)
FIL	0.04 (0.01)	0.74 (0.003)	0.75 (0.003)	0.59 (0.01)	0.36 (0.01)	0.22 (0.01)		0.59 (0.04)	-0.46 (0.06)
CON	0.44 (0.01)	0.45 (0.01)	0.56 (0.01)	0.44 (0.01)	0.51 (0.01)	0.53 (0.01)	0.31 (0.01)		-0.27 (0.05)
FAT	0.17 (0.01)	-0.30 (0.01)	-0.30 (0.01)	-0.25 (0.01)	-0.13 (0.01)	-0.03 (0.01)	-0.26 (0.01)	0.00 (0.01)	

CWT = Carcass weight; TOP = Topside; SIL = Silverside; KNU = Knuckle; RUM = Rump; STR = Striploin; FIL = Fillet; Conformation = Conformation; Fat = Fat

[1] Carcass weight is the weight (kg) of the carcass at slaughter; Topside, Silverside, Knuckle, Rump, Striploin and Fillet are all primal cut yields(kg) predicted from the total carcass using VIA; Conformation and Fat is the EUROP conformation and fat classes, predicted using VIA and converted to a numerical 1-42 scale; higher values represent more muscular carcasses for conformation and higher levels of fat for fat

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