Citation for the published paper:
Rius-Vilarrasa, E. et al. (2010) Genetic parameters for carcass dimensional measurements from Video Image Analysis and their association with conformation and fat class scores. *Livestock Science*.
Volume: 128 Number: 1-3, pp 92-100.

http://dx.doi.org/10.1016/j.livsci.2009.11.004

# Genetic parameters for carcass dimensional measurements from Video Image Analysis and their association with conformation and fat class scores

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## Abstract

Data on 630 crossbred lamb carcasses were used to estimate genetic parameters for a number of carcass measures, fitting a multivariate animal model using restricted maximum likelihood. Carcass measures included: cold carcass weight (CCW), EUROP conformation and fat class scores (MLC-CF), primal joint weights predicted using MLC-CF and several carcass linear and area measures obtained by Video Image Analysis (VIA-DM). Heritability estimates for subjective carcass traits (MLC-CF and primal joint weights predicted using MLC-CF) were low (0.05 – 0.17), whereas those for objective carcass traits (linear and area measurements on the carcass from VIA) were moderate to high (0.20 – 0.53). Phenotypic correlations between MLC-CF and VIA-DM were in general low (0.01 – 0.51) and genetic correlations were slightly higher (-0.04 – 0.81), when interpreting their absolute value. The results suggest that selection for shorter carcasses (VIA lengths) will be associated with improved conformation but a reduction of the total CCW. Likewise there was a trend in the genetic correlations between conformation and carcass widths which indicated that conformation could also be improved by selection for wider carcasses as measured by VIA which in turn will also imply an increase in CCW. The genetic correlations between VIA-DM and fat class score were only significantly different from zero for the VIA measurement for the leg area ($r_g$ = -0.73). Length traits were highly correlated with each other, with an average genetic correlation of 0.84. Positive genetic correlations (0.47 – 0.85) were found between widths measured on the shoulders and chest with hind leg widths. The areas measured on the carcass were moderately to highly correlated with each other (0.54 – 0.90). In general, genetic correlations which were found to be significant between areas, lengths and widths were moderate to high and positive. Phenotypic and genetic correlations along with heritabilities of the VIA-DM from crossbred lambs, suggest that using this VIA dimensional information in the evaluation of purebred terminal sire breeds is likely to improve conformation on crossbred lambs.

Keywords: Video Image Analysis, conformation, fat, dimensional measurements, heritability

## 1. Introduction

Carcass quality measurements in slaughter lambs are based on visual appraisal of carcass conformation and fatness, and these criteria are used in payment systems in most European countries (CEC, 2002). The use of these subjective carcass assessments in genetic selection programmes has been found to be of negligible benefit, due to their low heritabilities (Conington et al., 2001), and also because of the positive genetic correlation between these two traits (Pollott et al., 1994; Jones et al., 1999; Conington et al., 2001). This limits their use in sheep breeding programmes that aim to improve conformation without an associated increase in fatness. Despite this, due to the relatively large economic weight of these traits, there are some cases where they are included in selection indexes along with other important traits, such as maternal characteristics (Simm and Dingwall, 1989; Conington et al., 2001). Therefore and because conformation and fat class scores are currently used in sheep breeding programs their genetic and phenotypic correlations with new carcass traits remains of primary importance

Since carcass conformation contributes significantly to the overall value of the slaughter lamb, alternative measures which can describe conformation independently of fatness have recently gained interest in the lamb industry. Measures of muscularity obtained by computer tomography (CT), which by definition are independent of fatness (Navajas et al., 2008), have been suggested as alternative methods to improve carcass conformation by genetic selection in purebred sheep (Navajas et al., 2007). At present, estimated breeding values (EBVs) for *in-vivo* measures of 2D-gigot muscularity obtained by CT (Jones et al., 2002; Navajas et al., 2007) are available in the UK to assist breeders identify terminal sires with better muscularity of the hind legs.

Linear body traits have also been suggested as objective measures of body conformation in sheep (Waldron et al., 1992; Bibe et al., 2002). In these earlier studies, linear measurements were recorded manually and were therefore of restricted use in commercial sheep breeding programs. Conversely, automatic technologies based on Video Image Analysis (VIA) offer the opportunity of recording linear and area traits (dimensional measurements) on the carcass in an objective and automated way, providing a fast and very reliable source of information for genetic improvement programs. The value of using crossbred information in the genetic evaluation of purebreds has been investigated and the results suggest this will increase the rate of genetic responses in crossbred progeny (Wei and Van der Verf, 1994; Bijma and van Arendonk, 1998). In another study, Jones et al. (1999) reported that fat class scores taken on crossbred lambs was positively correlated both with tissue proportions and rations. These findings opened up the possibility to use subjectively assessed scores, such a fat class for improving rates of genetic gain in purebred selection programmes.

The introduction of VIA technology to provide information on a range of linear and area measurements on the carcass could eventually encourage the sheep industry towards a new carcass grading and pricing system based upon payments for individual component joints. This change in the carcass evaluation system would be supported by a general shift from subjective carcass quality measures towards more objective evaluation based on the weight or percentage of meat yields from the different primal joints. In a previous study, Rius-Vilarrasa et al. (2009a) reported genetic parameters for weights of primal carcass cuts predicted using a VIA system. Low to moderate heritabilities were found in that study, suggesting that VIA predictions of primal cut weights, could be used in selection programmes to improve weights of individual carcass cuts. However, while evaluation of carcass quality still relies on the subjective evaluation of conformation and fat class (MLC-CF), genetic parameters of the primal joints weights predicted using the information obtained from these subjective evaluations are also of interest. Prediction models developed to estimate weight of primal meat yields using MLC-CF have high accuracies (expressed as coefficient of determination, $R^2$ values) ranging from 0.82 to 0.95 for primal weights of breast and shoulder, respectively (Rius-Vilarrasa et al., 2009b). Estimates of primal joint weights could be obtained by using the prediction models developed in that previous study along with the MLC-CF scores collected from the present dataset. The predicted primal weights could then be used to estimate genetic parameters for these traits which, to our knowledge, have not yet been investigated. In addition, the possibility to obtain fast and accurate carcass dimensional measurements trough the use of VIA technology could be use to explore the associations between conformation and shape of the carcass. Therefore, the aims of this study were: (1) to estimate genetic parameters for the MLC-CF scores and for primal joint weights predicted from MLC-CF scores, and to compare these results with the results from a previous study (Rius-Vilarrasa et al., 2009a) which used VIA information to predict primal joint weights;

(2) to investigate the associations between MLC-CF scores and VIA-DM; (3) to estimate genetic parameters for VIA-DM.

## 2. Materials and Methods

### *2.1 Animal resource*

The 630 crossbred lambs included in this study were produced by mating crossbred Mule ewes (Bluefaced Leicester x Scottish Blackface), or Welsh Mule (Bluefaced Leicester x Welsh Hardy Speckled Face or Beulah Speckled Face) ewes with three different terminal sire breeds (Charollais, Suffolk and Texel). A total of 18 sires and 385 dams were used to produce the 630 lambs. Pedigree information included individuals who would contribute to variance component estimation by animal model. The software RELAX2 (Strandén and Vuori, 2006), was used for pruning and as a result animals with observations and animals that tie by ancestry animals with observations were included in the pedigree. The complete pedigree comprised 1092 animals.

The lambs were reared at research farms in Wales (Aberystwyth), England (Rosemaund) and Scotland (Edinburgh) where the lambs' birth weight and sex were recorded. Within 48 hours of lambing, the Mule ewes and their lambs were turned out to pasture. Litters were kept as singles or twins and lambs from larger litters were fostered to another ewe when possible. About 80% of the lambs were reared as twins with the remainder reared as singles. Ewes suckling twin lambs were grazed separately from those with singletons and offered supplementary feeding as required in early lactation. Artificially reared lambs were excluded from this study. More information on the production of Mule ewes, as well as the selection of terminal sire rams is available elsewhere (Jones et al., 1999; Simm et al., 2001; Van Heelsum et al., 2003; Van Heelsum et al., 2006).

*2.2 Carcass measurements on crossbred lambs*

The lambs born in 2006 were slaughtered the same year at finished condition (average age 5 months; estimated fat class 3L) at the commercial abattoir of Welsh Country Foods (WCF) in Gaerwen (Wales). Subjective conformation and fat scores were recorded by an expert grader in the abattoir, according to the MLC-CF system. Carcass conformation was assessed using the EUROP five-point scale (where “E” is for excellent and “P” is for poor conformation), and fatness, using a five-point scale from 1 (leaner) to 5 (fatter), with scores 3 and 4 sub-divided into “L” (leaner) and “H” (fatter). These subjective grades were then converted to numeric scales, with conformation coded as E = 5, U = 4, R = 3, O = 2, and P= 1 and fatness transformed to a corresponding estimated subcutaneous fat percentage (1 = 4, 2 = 8, 3L = 11, 3H = 13, 4L = 15, 4H = 17 and 5 = 20) (Kempster *et al.*, 1986). The lamb’s hot carcass weight was recorded just after slaughter and a constant of 0.5 kg deducted as an expected drip loss value to obtain the cold carcass weight (CCW). Prediction equations derived in a previous study by Rius-Vilarrasa et al. (2009b) using MLC-CF scores for the prediction of primal joint weights were used in this study to estimate the weight of LEG, CHUMP, LOIN, BREAST and SHOULDER primal cuts. The prediction models based on MLC-CF were tested and validated in a previous dataset which consisted of 443 observations on dissected primal joint cuts. The dissection of lamb carcasses into primal cuts was done base on industry butchery specifications. The CHUMP joints were separated into boneless chump by cutting through the hipbone and the point end of the chump. The LOIN and BREAST joints were obtained by cutting a parallel cut to the back bone from a point approximately twice the length of the eye muscle at the anterior end of the loin. The LOIN joints were removed by sheet boning the rib bones and half the length of these bones was removed by cutting to a maximum of 35 mm from the chine bone. The SHOULDER joints were separated from the back strap and the knuckle ends. The prediction equations based on the regression of MLC-CF on the different primal joints reported accuracies ranging from 0.82 to 0.95 for BREAST and SHOULDER, respectively (Rius-Vilarrasa et al., 2009b). The following prediction model, together with the regression coefficients found in that previous study for each primal cut, was used in the current study to obtain estimated weights of primal joints which were then used to estimate the genetic parameters of these carcass traits.

$$\hat{Y}_{ijk} = \mu + CONFORMATION_i + FAT_j + b_1(CCW_{ijk}) + e_{ijk}$$

Five prediction models were used to obtained primal joints estimates for each animal *l* ***($\hat{Y}_{ijkl}$)***, from carcass information on ***$CONFORMATION_i$*** (5 classes: 1, poor conformation to 5, excellent conformation) and on ***$FAT_j$*** (7 classes: 1, very lean to 7, very fat). The ***$CCW_{ijk}$*** was used as a linear covariate where ***$b_1$*** represents the regression coefficient of Y on CCW and ***$e_{ijk}$*** represents the residual effects.

After the carcasses were subjectively assessed, lambs were redirected from the main slaughter line to a secondary line specifically designed to steer the carcasses to a VIA station for scanning (VSS2000, E+V Technology GmbH, http://www.eplusv.de/), which was installed offline in the abattoir, but run at the typical line speed. Further details on the VIA system has been reported previously (Rius-Vilarrasa et al., 2009b). Carcass linear and area traits (dimensional measurements) were obtained from the

VIA system by scanning the back and side views of carcasses. Some of the VIA system measurements that were available in the current study included carcass lengths (L1 - L4), widths (W1 - W8) and areas (A1 – A4) and are presented in Figure 1.

### 2.3 Statistical analysis

Restricted maximum likelihood (REML) methods were used to estimate (co)variance components based on an animal model using the ASReml program (Gilmour et al., 2002). The general animal model, used to estimate heritabilities as well as genotypic and phenotypic correlations for MLC-CF (conformation and fat class), primal joint weights and VIA-DM was as follows:

$$Y_{ijkl} = BH_i + DA_j + BR_k + b_1(AS_{ijkl}) + a_l + e_{ijkl},$$

where $\boldsymbol{Y_{ijkl}}$ is the record for animal *l*, $\boldsymbol{BH_i}$ is the combined fixed effect of *i*th year of birth (1 class: 2006), sex (2 classes: male and female) and farm (3 classes: Wales, England and Scotland) and is defined in this paper as batch; $\boldsymbol{DA_j}$ is the effect of *j*th dam age (8 classes: 2 to 8, >8); $\boldsymbol{BR_k}$ is the effect of *k*th sire breed (3 classes: Texel, Charollais or Suffolk); $\boldsymbol{AS}$ is age at slaughter as a covariate where $\boldsymbol{b_1}$ represents the regression coefficient of $\boldsymbol{Y}$ on slaughter age with a mean 145 days and a standard deviation of 41. The random effects $\boldsymbol{a_l}$ and $\boldsymbol{e_{ijkl}}$ represent the direct additive effect of the animal and the residual effects, respectively.

Firstly, univariate analyses were performed to evaluate the significance of different fixed and random effects in the model for the traits listed in Tables 1 and 2. To evaluate the significance of a random effect in the model, a likelihood ratio test was performed that compared reduced and full models, with one degree of freedom, to a critical value from the chi-square distribution. Besides the residual effect, the final models included only the direct additive effect as random effects. The random common environmental effect (litter) was tested but found not to be significant. Following the univariate analysis, multivariate analyses were performed using the most parsimonious model for each trait.

## 3. Results

### *3.1 Heritability estimates*

Heritability estimates and their standard errors for CCW, MLC-CF traits and for MLC-CF based predictions of the primal joints are presented in Table 1. The heritability estimate for CCW was of 0.19 and it was calculated with a relatively high standard error of 0.10. Heritability estimates from MLC-CF traits were low for conformation and fatness (both 0.10). Heritability estimates for weights of primal joints predicted using MLC-CF ranged from 0.05 to 0.17, with the lowest value for the LOIN and the highest for the LEG. All heritabilities, except for the primal LEG, were not significantly different from zero. Heritability estimates for VIA-DM were moderate to high (Table 2). For VIA-DM the lowest heritability estimate of 0.20 was for the width W8, located in the leg region, and the highest of 0.53 was for the area A2, which measures the leg joints.

Heritability estimates for length traits ranged from 0.25 to 0.46, for L1 and L3, respectively. Similar heritabilities were found for carcass width traits with the lowest being 0.20 and the highest 0.39 for width measures near the hind legs, W8 and W5, respectively. In summary, for the VIA-DM, the traits with the highest heritability estimates were those related to measurements in the leg region, such as length trait L2

(0.44), width W5 (0.39) and area A2 (0.53).

### 3.2 Estimates of phenotypic and genetic correlations

Phenotypic and genetic correlations between primal joint weights predicted using MLC-CF were all very high (> 0.84) and are presented in Table 3. The genetic correlation between CHUMP and SHOULDER could not be estimated. Variance structures were set to allow negative parameters to be calculated in the (co)variance matrix leading led to non-positive definite matrices. Restricted positive definite matrices were also tested, which kept variances in the theoretical parameter space so correlation parameters would not exceed ±1. However no standard errors could be estimated. These results suggested that CHUMP and SHOULDER might have a very high linear dependency, thus genetic correlations could not be estimated. Genetic and phenotypic correlations between CCW and the primal joints predicted were all very high and in most of the cases the genetic correlations were not significantly different from 1.

Estimates of genetic and phenotypic correlations between MLC-CF and VIA-DM are presented in Table 4. Phenotypic correlations were negative between VIA carcass lengths and CONF whereas between VIA carcass widths and conformation were all positive ranging from 0.09 to 0.51. The phenotypic correlations between VIA carcass lengths and widths with FAT were in general positive. Looking at the genetic correlations, most of the linear traits were negatively and, in general, strongly correlated with CONF, however only a few were significantly different from zero, due to high standard errors. No significant associations were found between linear traits and FAT. The reasons for this might be a consequence of the sample size and/or the nature of the traits where CONF and FAT class are subjectively asses and VIA dimensional measurements are recorded from a VIA system with room for inaccuracies in both types of measurements. Strong negative correlations were found between carcass lengths (L2, L3 and L4) and CONF, which suggests that selection for longer carcasses will lower the value of the carcass by reducing conformation scores. However it is possible that this would be outweighed by an increase in carcass weight and a possible reduction in fatness, as suggested by the genetic correlations in Table 4, although large standard errors make the correlations non-significant. Selection for wider carcasses could improve carcass conformation, as shown by the trend on the positive genetic correlations between carcass widths (W3 and W4), as measured on the saddle, and CONF. However these associations were also not significantly different from zero. Genetic correlations between CCW with CONF and FAT were associated to high standard errors, whereas phenotypic correlations were both positive.

A significant strong and negative correlation was found between the back area of the legs (A2) with FAT (-0.73) and the same area measure was also negatively correlated with CONF (-0.80). These correlations indicate that selection for an increased leg area (A2) as measured by VIA could result in a reduction of the overall carcass conformation and that could also be accompanied by a reduction of carcass fatness. Phenotypic and genetic correlations among VIA-DM are presented, together with their corresponding standard errors, in Table 5. Most phenotypic correlations were significant, with no standard errors greater than 0.05. However there were large standard errors for several of the genetic correlations, in particular those correlations of low to moderate absolute magnitude. In general, those genetic correlations that were significantly different from zero were higher in their absolute value than the corresponding phenotypic correlations.

Length traits were highly genetically correlated with an average of 0.84. The lowest genetic correlation (0.68) was between L1 and L2 traits and the highest (0.98) between L3 and L4 traits, which indicates a high correlated response for these traits. Positive and moderate to strong genetic correlations (0.47 – 0.85) were found between widths measured on the shoulders and chest areas (W1 and W2) with widths measured on the hind legs (W5, W7 and W8). This implies that selection towards carcasses with wider hind legs could also increase chest and shoulder widths due to a high correlated response between traits. The areas measured on the carcass by VIA were moderately to highly genetically correlated with each other (0.54 – 0.90), which implies that selection to increase any of the carcass areas will increase the rest of the areas as a correlated response.

The lengths were in general lowly to moderately correlated with the widths of the carcass, and most of the estimates with low correlations were not significantly different from zero. The carcass length (L3) measured on the side of the carcass was moderately to highly correlated with W2 (0.51), W5 (0.42), W6 (0.81) and W7 (0.90) widths measured on the back image of the carcass. These correlations are of particular interest for changing the dimension of the carcass by selection. While selection might focus on wider carcasses to improve conformation, the overall carcass length would not reduce. This is of particular interest as a reduction in the length of the carcass would also imply a decrease in CCW as shown by the positive genetic correlations between CCW and the various carcass lengths. The genetic correlation between lengths and areas (Table 5) show that longer carcasses would also have larger surface areas. Additionally, increased carcass surface areas would be expected if selection was focused on wider carcasses as shown by the genetic correlations between widths and areas in Table 5.

## 4. Discussion

In the present study heritabilities for MLC-CF scores and VIA-DM were estimated, along with their phenotypic and genetic correlations. Low heritabilities were found for MLC-CF traits (conformation and fat class) of 0.10, respectively. This is likely to be a reflection of the subjective nature of this assessment, which probably inflates the environmental variance. In addition, categorical traits analysed under the hypothesis of normality distribution might have also influenced the accuracies of the genetic parameter estimates for these traits. Despite CONF and FAT scores observations were classified as normally distributed (Skewness: -0.54 and 1.23 and Kurtosis: 3.17 and 4.0, for CONF and FAT, respectively), the analysis of these categorical traits using Bayesian statistics, particularly for genetic evaluations of traits with discrete and non-normal distributions (Van Tassell et al., 1998; Blasco, 2001) might have provided slightly higher heritability estimates. No references in the literature have been found that used Bayesian statistics on these traits, however several authors have reported genetic parameters for MLC-CF using maximum likelihood methods with a fairly wide range of heritability estimates (Conington et al., 1998; Jones et al., 1999; Puntila et al., 2002; Karamichou et al., 2006; Van Heelsum et al., 2006). At constant subcutaneous fat as the same end point chosen for the analysis of carcass traits in the present paper , Conington et al. (1998), in a study of Scottish Blackface hill lambs, reported similar heritability estimates for fat class (0.09) and EUROP conformation class (0.13) to the present study. Another study where MLC-CF were measured at different slaughter target live weights reported higher heritability estimates, on average of 0.23 and 0.19 for conformation and fat class, respectively (Jones et al., 1999). For lambs slaughtered at fixed age rather than a fixed degree of finish (usual practise in UK sheep industry), Karamichou et al. (2006) reported significantly high heritability estimates of 0.52 and 0.33 for conformation and fat respectively. The authors in this paper also indicate that such high estimates might be the result of large and complex pedigree information.  Although there are limitations to improving carcass conformation through genetic selection, due to its positive correlation with fatness in a wide range of breeds (Lewis et al., 1996; Conington et al., 1998; Jones et al., 1999; Moreno et al., 2001; Bibe et al., 2002; Karamichou et al., 2006), sheep breeders are still interested in improvement of this trait, mainly for its economic impact.

An alternative way to improve carcass conformation could be by indirect selection on measures associated with carcass shape, such as body and carcass linear traits. Moderate to high genetic and phenotypic correlations between carcass shape (conformation) and linear carcass measurements were found in the present study, which were comparable with some found in the literature (Waldron et al., 1992; Bibe et al., 2002). However, they were in disagreement with results reported by Pollott et al. (1994) and Janssens and Vandepitte (2004), where no associations were found between shape, as assessed by conformation scores and body measurements. Improvement of carcass conformation by altering the carcass shape could be due to changes in weight of the muscle relative to a skeletal dimension (length of the bones), defined as muscularity by Purchas et al. (1991). Recent work reported by Navajas et al. (2007) confirmed this association, where strong phenotypic correlations were found between subjective conformation score and muscularity as measured *in-vivo* by CT in lambs from two divergent breeds that are of economic importance in the UK (Texel and Scottish Blackface). Another study by Wolf and Jones (2007) also reported that an improvement of leg shape by a reduction in length of the limb would improve leg muscularity. These changes in leg shape were also expected to give improvements in overall carcass shape (conformation). Collectively, these results are in common with Laville et al. (2004), who found that conformation was strongly influenced by leg muscularity.

While selection for shorter or wider carcasses as measured in the present study could improve carcass conformation, and as a result also increase muscularity of primal cuts, this should be investigated carefully. Base on the genetic correlations between CCW and VIA lengths, the selection for shorter carcasses length could also lead to smaller carcass size with less cold carcass weight, hence resulting in an economic loss for the producer as payments are based mainly on carcass weight. In addition, genetic correlations between VIA-DM and FAT also showed a moderate correlations in the same direction as for CONF, indicating that selection for linear traits to improve carcass CONF could also be associated with an increase in carcass fatness. While these genetic correlations were associated with large standard errors the results have been based on a trend in the data, and therefore further analyses are required to confirm the associations between these carcass traits. However, literature references have been found that support the results found in the present study. Comparable results were reported by Moreno et al. (2001), where selection for shorter carcass length improved carcass conformation accompanied with an increase in fatness (internal fat score), as estimated by kidney fat area. The results in this study indicate that VIA information could help in the improvement of carcass CONF by genetic selection, but the associations between VIA-DM with FAT need to be further investigated because dissected carcass information was not available on these lambs. In addition, future research into the associations between VIA-DM and muscularity measurements are highly relevant, since VIA information from crossbred lambs could be used in current commercial breeding programmes to increase genetic progress to improve muscularity in purebred animals.

There are few published estimates of genetic parameters of linear and area type traits on sheep carcasses and the ones found in the literature are very difficult to compare due to differences in the measures taken. In the present study, heritability estimates for linear and area carcass traits measured on VIA images were moderate to high (0.20 – 0.53) and were within the range of heritability estimates for linear type traits in sheep measured on the carcass and on live animals reported by several authors for sheep (Moreno et al., 2001; Janssens et al., 2004; Gizaw et al., 2008) and also for beef and dairy cattle (Brotherstone, 1994; Mukai et al., 1995). In general, linear traits have been used as indirect measures of relevant economic traits, such as conformation, performance and production traits (Brotherstone, 1994; Janssens and Vandepitte, 2004; Gizaw et al., 2008). However the responses to selection on VIA-DM, as a direct measure of carcass shape with the potential to alter carcass dimensions, were also investigated. The results found in the present study suggested that it would be difficult to select for larger hind legs (longer and wider) without a correlated increase in the length of the whole carcass. The selection of carcasses with larger hind legs would also be accompanied by increasing carcass chest and shoulder width. The latter might be highly undesirable if associations are found with increased incidence of lambing difficulties. In general, it would be difficult to alter the carcass shape by genetic selection based on the group of significant genetic correlations between VIA-DM found in the present study. Further analysis in order to elucidate the associations between VIA-DM and dissected primal weights could also help to provide information on selection for increased dimensions of the most valuable primal cuts as long as these did not result in increased lambing difficulty, but data on the weights of these cuts were not available in these crossbred lambs.

The abattoirs and processing sectors would like to move towards a pricing system based on weight of saleable meat from primal joints. It is possible that VIA systems which can predict weights of primal joints with high accuracies (ranging from 0.86 to 0.97 for dissected primals loin and leg cuts (Rius-Vilarrasa et al., 2009b)) could be introduced in UK lamb abattoirs in the next few years. However, it is unlikely that VIA systems will be simultaneously installed across all lamb abattoirs. Therefore it was of considerable interest to investigate the genetic response that could be achieved by selection for improved weights of primal meat yields predicted using the current EUROP carcass grading. Low heritability estimates (0.05 – 0.17) were found for predicted weights of primal meat yields using the current EUROP conformation and fat scores. Using the same dataset and VIA information to predict the weight of the primal cuts, higher heritability estimates (0.07 – 0.26) were found in a previous study (Rius-Vilarrasa et al., 2009a). These differences in heritability estimates might be due to greater environmental variance associated with subjective measures of carcass quality compared to the objective based measures obtained by VIA (Rius-Vilarrasa et al., 2009b). Additionally, while VIA systems can allow for further improvements in accuracy of prediction of primal weights by re-adjusting the prediction equations with the continuous scanning of carcasses online in abattoirs, MLC-CF have smaller margins for improvement. Therefore, use of primal weights predicted using VIA to improve carcass composition in selection programs would provide an initial faster response to selection, compared to using MLC-CF.

## 5. Conclusions

Carcass quality measures are currently based not only on carcass weight, but also CONF and FAT as visually assessed by an expert grader. However there is the potential that in the near future measures of saleable meat yield could also be used as a measure of carcass quality in the UK abattoirs. Estimates of heritability found in this study for CONF and FAT class and for primal joint weights estimated using MLC-CF, indicate that the additive genetic variability of these traits is low and would lead to a low response to selection for improved carcass quality. On the contrary, heritability estimates found for the VIA-DM suggest that use of these traits in genetic improvement programs could lead to a faster response to selection for improved carcass conformation. Further research is required on the associations between muscularity, which represents a measure of shape that is independent of fatness (De Boer et al., 1974; Purchas et al., 1991), and VIA-DM, since this could provide the means to select for increased meat yield weight without an increase in fatness (Waldron et al., 1992; Jones et al., 2004). Automatic technologies such as VIA can offer a significant opportunity to record very accurate information on carcass characteristics from crossbred lambs with the possibility to feed this information back from the abattoir to the producers and breeders to enable far more information on important carcass traits to be used in genetic evaluations, thereby increasing the accuracy of estimated breeding values (EBVs) and rates of response to selection.

## Acknowledgements

The authors are grateful to sponsors and the partners of this LINK project (Sustainable Livestock Production program): English Beef and Lamb Executive (EBLEX), Hybu Cig Cymru (HCC), Quality Meat Scotland (QMS), the Livestock and Meat Commission for Northern Ireland (LMCNI), Scottish Association of Meat

Wholesalers, CatapultGenetics, Innovis Genetics Ltd, BBSRC, Defra and also to MLC, Genesis Faraday and the Worshipful Company of Woolmen for financial support to ERV. We also thank the companies E+V Technology GmbH and Welsh Country Food for their technical support and collaboration in the project. The assistance provided by the staff of SAC for their collaboration and technical support of the project is gratefully acknowledged.

## References

Bibe, B., Brunel, J.C., Bourdillon, Y., Loradoux, D., Gordy, M.H., Weisbecker, J.L., Bouix, J., 2002. Genetic parameters of growth and carcass quality of lambs at the French progeny-test station Berrytest. Proc. 7th World Congress on Genetics Applied to Livestock Production, Montpellier, France 31, 335-338.

Bijma, P., van Arendonk, J.A.M., 1998. Maximizing genetic gain for the sire line of a crossbreeding scheme utilizing both purebred and crossbred information. Animal Science 66, 529-542.

Blasco, A., 2001. The Bayesian controversy in animal breeding. J. Anim Sci. 79, 2023-2046.

Brotherstone, S., 1994. Genetic and Phenotypic Correlations Between Linear Type Traits and Production Traits in Holstein-Friesian Dairy-Cattle. Animal Production 59, 183-187.

CEC, 2002. Report from the Commission to the Council on the implementation of Council Regulation (EEC) No. 2137/92 concerning the Community scale for the classification of carcasses of ovine animals. <http://europa. eu. int/eur-lex/lex/LexUriServ/site/en/com/2002/com2002_0295en01. pdf>.

Conington, J., Bishop, S.C., Grundy, B., Waterhouse, A., Simm, G., 2001. Multi-trait selection indexes for sustainable UK hill sheep production. Animal Science 73, 413-423.

Conington, J., Bishop, S.C., Waterhouse, A., Simm, G., 1998. A comparison of growth and carcass traits in Scottish Blackface lambs sired by genetically lean or fat rams. Animal Science 67, 299-309.

De Boer, H., Dumont, B.L., Pomeroy, R.W., Weniger, J.H., 1974. Manual on E.A.A.P. reference methods for the assessment of carcass characteristics in cattle. Livestock Production Science 1, 151-164.

Gilmour, A.R., Cullis, B.R., Welham, S.J., Thompson, R., 2002. AsReml, Reference Manual, ASW Agriculture, Orange 2800, Australian. .

Gizaw, S., Komen, H., van Arendonk, J.A.M., 2008. Selection on linear size traits to improve live weight in Menz sheep under nucleus and village breeding programs. Livestock Science 118, 92-98.

Janssens, S., Vandepitte, W., 2004. Genetic parameters for body measurements and linear type traits in Belgian Bleu du Maine, Suffolk and Texel sheep. Small Ruminant Research 54, 13-24.

Janssens, S., Winandy, D., Tylleman, A., Delmotte, C., Van Moeseke, W., Vandepitte, W., 2004. The linear assessment scheme for sheep in Belgium: breed averages and assessor quality. Small Ruminant Research 51, 85-95.

Jones, H.E., Lewis, R.M., Young, M.J., Simm, G., 2004. Genetic parameters for carcass composition and muscularity in sheep measured by X-ray computer tomography, ultrasound and dissection. Livestock Production Science 90, 167-179.

Jones, H.E., Lewis, R.M., Young, M.J., Wolf, B.T., 2002. The use of X-ray computer tomography for measuring the muscularity of live sheep. Animal Science 75, 387-399.

Jones, H.E., Simm, G., Dingwall, W.S., Lewis, R.M., 1999. Genetic relationships between visual and objective measures of carcass composition in crossbred lambs. Animal Science 69, 553-561.

Karamichou, E., Richardson, R.I., Nute, G.R., Mclean, K.A., Bishop, S.C., 2006. Genetic analyses of carcass composition, as assessed by X-ray computer tomography, and meat quality traits in Scottish Blackface sheep. Animal Science 82, 151-162.

Kempster, A. J., Cook, G. L. and Grantley-Smith, M., 1986. National estimates of the body composition of British cattle, sheep and pigs with special reference to trends in fatness. A review. Meat Science 17, 107-138.

Laville, E., Bouix, J., Sayd, T., Bibe, B., Elsen, J.M., Larzul, C., Eychenne, F., Marcq, F., Georges, M., 2004. Effects of a quantitative trait locus for muscle hypertrophy from Belgian Texel sheep on carcass conformation and muscularity. J. Anim Sci. 82, 3128-3137.

Lewis, R.M., Simm, G., Dingwall, W.S., Murphy, S.V., 1996. Selection for lean growth in terminal sire sheep to produce leaner crossbred progeny. Animal Science 63, 133-142.

Moreno, C., Bouix, J., Brunel, J.C., Weisbecker, J.L., Francois, D., Lantier, F., Elsen, J.M., 2001. Genetic parameter estimates for carcass traits in the inra401 composite sheep strain. Livestock Production Science 69, 227-232.

Mukai, F., Oyama, K., Kohno, S., 1995. Genetic relationships between performance test traits and field carcass traits in Japanese Black cattle. Livestock Production Science 44, 199-205.

Navajas, E.A., Lambe, N.R., Fisher, A.V., Nute, G.R., Bünger, L., Simm, G., 2008. Muscularity and eating quality of lambs: Effects of breed, sex and selection of sires using muscularity measurements by computed tomography. Meat Science 79, 105-112.

Navajas, E.A., Lambe, N.R., Mclean, K.A., Glasbey, C.A., Fisher, A.V., Charteris, A.J.L., Bünger, L., Simm, G., 2007. Accuracy of in vivo muscularity indices measured by computed tomography and their association with carcass quality in lambs. Meat Science 75, 533-542.

Pollott, G.E., Guy, D.R., Croston, D., 1994. Genetic parameters of lamb carcass characteristics at three end-points: fat level, age and weight. Animal Production 58, 65-75.

Puntila, M.L., Maki, K., Rintala, O., 2002. Assessment of carcass composition based on ultrasonic measurements and EUROP conformation class of live lambs. Journal of Animal Breeding and Genetics 119, 367-378.

Purchas, R.W., Davies, A.S., Abdullah, A.Y., 1991. An objective measure of muscularity: Changes with animal growth and differences between Genetic lines of southdown sheep. Meat Science 30, 81-94.

Rius-Vilarrasa, E., Bünger L, Brotherstone, S., Matthews, K.R., Haresign, W., Davies, M., Macfarlane, J.M., Roehe, R., 2009a. Genetic parameters for carcass composition and performance data in crossbred lambs measured by Video Image Analysis. Meat Science 82, 94-100.

Rius-Vilarrasa, E., Bünger L, Maltin, C., Matthews, K.R., Roehe, R., 2009b. Evaluation of Video Image Analysis (VIA) technology to predict meat yield of sheep carcasses on-line under UK abattoir conditions. Meat Science 81, 619-625.

Simm, G., Dingwall, W.S., 1989. Selection indices for lean meat production in sheep. Livestock Production Science 21, 223-233.

Simm, G., Lewis, R.M., Collins, J.E., Nieuwhof, G.J., 2001. Use of sire referencing schemes to select for improved carcass composition in sheep. J. Anim Sci. 79, E255-E259.

Strandén, I., Vuori, K., 2006. Relax2: pedigree analysis program. 8th World Congress on Genetics Applied to Livestock Production, August 13-18, 2006, Belo Horizonte, Brazil.

Van Heelsum, A.M., Lewis, R.M., Davies, M.H., Haresign, W., 2003. Growth and carcass characteristics in wether lambs of a crossbred dam line. Animal Science 76, 43-53.

Van Heelsum, A.M., Lewis, R.M., Davies, M.H., Haresign, W., 2006. Genetic relationships among objectively and subjectively assessed traits measured on crossbred (Mule) lambs. Animal Science 82, 141-149.

Van Tassell, C.P., Van Vleck, L.D., Gregory, K.E., 1998. Bayesian analysis of twinning and ovulation rates using a multiple-trait threshold model and Gibbs sampling. J. Anim Sci. 76, 2048-2061.

Waldron, D.F., Clarke, J.N., Rae, A.L., Woods, E.G., 1992. Expected Responses in Carcass Composition to Selection for Muscularity in Sheep. Proceedings of the New Zealand Society of Animal Production, Vol 52 1992 52, 29-31.

Wei, M., Van der Verf, J.H.J., 1994. Maximizing Genetic Response in Crossbreds Using Both Purebred and Crossbred Information. Animal Production 59, 401-413.

Wolf, B.T., Jones, D.A., 2007. Inheritance of an in vivo leg conformation score in Texel lambs and its association with growth, ultrasonic measurements and muscularity. Livestock Science 110, 133-140.

Fig. 1 Dimensional measurements, lengths, widths and areas of back and side views of the carcasses obtained by VIA.