

## Form BEEF

### DATA COLLECTION

<b>Country (or countries)</b>	UK
<b>Trait name</b>	Carcass Conformation (CCO)
<b>Breed(s)</b>	Simmental and Charolais (taken from across breed evaluation including on phenotypes from 89 other breeds)
<b>Trait definition</b>	The carcass is graded under the EUROP system, defined by 5 main classes E, U, R, O, and P. which through European Union regulations allow for 3 further subdivisions (e.g. E+, E, E-) of each conformation, thus 15 classes in total. These classes were converted to numerical values 1 to 15 as shown in Table 19, and multiplied by three to be line with a conversion table supplied by Signet (scale 3 to 45). A 15 point scale with values 1 to 15 as used by Hickey et al (2007 <sup>1</sup> ) would result the same as the values 3 to 45.
<b>Method and frequency of measurement</b>	One measurement per animal
<b>Who does the performance recording?</b>	Abattoir
<b>Method of collecting data</b>	Carcass is scored according to the EUROP grading system
<b>Which animals get recorded?</b>	Any passing through abattoir
<b>Is birthday recorded?</b>	Yes
<b>Is day of recording available?</b>	Yes
<b>Is the data adjusted and/or selected? If yes please describe the methodology applied</b>	<p>All breeds are adjusted to a common variance by scaling the records on an individual for each trait using the following formula where i is the appropriate breed and sex and j is the appropriate sex but breed type=2.</p> $\text{Scaled phenotype} = \text{Average}(i) + [(\text{phenotype} - \text{average}(i)) * (\text{std}(j)/\text{std}(i))]$ <p>Breed types are defined as 1= Dairy, 2=Native beef, 3=Continental beef, 4=Other</p>
<b>Time period for inclusion of data</b>	02/01/2001-19/10/2018
<b>Criteria (data edits) for inclusion of records</b>	<p>Remove duplicates</p> <p>killdate supplied by the abattoir must be within 10 days of BCMS</p> <p>Sex must be recorded</p> <p>Age at slaughter must be recorded and 365&lt;slage&lt;1095</p> <p>Carcass weight&gt;0kg</p> <p>Conformation and fat class recorded and valid EUROP classification</p> <p>Must be a heifer, steer or young bull</p> <p>Dam age&gt;540 days at calving</p> <p>Dam must be present in BCMS</p>

<sup>1</sup> Hickey, J.M., Keane, M.G., Kenny, D.A., Cromie, A.R., and Veerkamp, R.F. 2007. Genetic parameters for EUROP carcass traits within different groups of cattle in Ireland. Journal of Animal Science 85:314-321.

	<p>Dam birthdate missing  Sire and maternal grandsire unknown  Carcass weight within <math>\pm 3sd</math> (for sire-breed, sex and age group)  Average daily carcass gain <math>\pm 3sd</math> (for sire-breed, sex and age group)  BCMS birth recorded  Died in the same herd as born  No location change from birth herd  Last BCMS movement was not death  Finishing herd could not be assigned to be death herd  Must have spent &gt;60days in finishing herd  BCMS kill location was not a slaughter house  Birth herd year season must contain &gt; 3 animals  Kill herd year season must contain &gt; 3 animals</p>
<b>Is embryo transfer applied? How are ET animals identified? Is recipient mother ID recorded?</b>	ET animals removed
<b>How do you treat incomplete data?</b>	Whole record removed if any of the above criteria are not met
<i>MODEL</i>	
<b>Model used for genetic evaluation</b>	MT-AM-FR
<b>Environmental effects</b>	<p>BirthHYS, 242666 (F)  Slage (X)  Sex (F)  Killsite, 7 (F)  KillHYS (F)  Sex*KillHYS, 182750 (F)  Killsite*killHYS, 137750 (F)  Dam age (X)  Once bred heifer, 3 (F)  Dampercentagedairy (X)  Slage2 (X)  Het 1 (X)  Het 2 (X)  Het 3 (X)  Het 4 (X)  Het 5 (X)  Het 6 (X)  Rec 1 (X)  Rec 2 (X)  Rec 3 (X)  Rec 4 (X)  Rec 5 (X)  Rec 6 (X)</p>
<b>Use of genetic groups and relationships</b>	A standard relationship matrix is formed based on available pedigree information. Genetic groups are based on the animal's breed type.

	Breed types are defined as Dairy, Continental beef, Native beef, other.
<b>Genetic parameters in the model</b>	See appendix I
<b>Adjustment for heterogeneous variance in evaluation model</b>	<p>Heterosis and Recombination coefficients were calculated from the breed type proportions of the animal's sire and dam and the formulae are as follows:</p> $[\text{heterosis}]_{ij} = (([\text{sire}]_i * [\text{dam}]_j) + ([\text{sire}]_j * [\text{dam}]_i)) / 100$ $[\text{recombination}]_{ij} = (([\text{sire}]_i * [\text{sire}]_j) + ([\text{dam}]_i * [\text{dam}]_j)) / 100$ <p>Breed types are defined as 1= Dairy, 2=Native beef, 3=Continental beef, 4=Other</p> <p>Het 1 and Rec 1 = breed types 1 and 2  Het 2 and Rec 2 = breed types 1 and 3  Het 3 and Rec 3 = breed types 1 and 4  Het 4 and Rec 4 = breed types 2 and 3  Het 5 and Rec 5 = breed types 2 and 4  Het 6 and Rec 6 = breed types 3 and 4  These 12 terms are then fitted as covariates in the model</p>
<b>System validation</b>	Pre evaluation data quality checks and formation of contemporary groups. Genetic evaluation undertaken using MiX99. Post evaluation checks include adjusting for the genetic base, quality assurance checks and data summaries.
<b>Definition of genetic reference base Next base change</b>	Genetic reference animals are those animals that are born in 2010.
<b>Assessment of index quality (computation of reliability, connection)</b>	Reliabilities are computed using the mix99 software using the Mistztal and Wiggans (1988) calculation method.
<i>PUBLICATION</i>	
<b>Expression of genetic evaluations</b>	EBVs are produced and published on <a href="http://egenes.co.uk/carcassdata/">http://egenes.co.uk/carcassdata/</a> on behalf of AHDB
<b>Criteria for official publication of evaluations</b>	None
<b>Number of evaluations / publications per year</b>	3 times a year
<b>Anticipated changes in the near future</b>	None
<b>Key reference on methodology applied</b>	The mix99 software package is used for the genetic evaluations (Lidauer and Strandén, 1999; Vuori et al., 2006)

**Key organization : contact person,  
address, phone, fax, e-mail, web site**

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## Parameters used in genetic evaluation

Country: United Kingdom

Main trait group: Carcass conformation (CCO)

Breed: Simmental and Charolais

Trait <sup>(1)</sup>	Definition	$h_d^2$	$h_m^2$	$r_{g(d,m)}$	$c^2$	$\sigma_p^2$
CCO	Carcass conformation	0.42	-	-	-	0.97

$h_d^2$  : direct heritability;  $h_m^2$  : maternal heritability;  $r_{g(d,m)}$ : genetic correlation between direct and maternal effects;  $c^2$  : repeatability of (maternal) permanent environmental effects;  $\sigma_p^2$  : phenotypic variance. 1) If you have more than one trait provides the correlations between traits.

**Form BEEF**

**Appendix II BEEF**

Sample of ET animal IDs