

## Form BEEF

### DATA COLLECTION

<b>Country (or countries)</b>	UK
<b>Trait name</b>	Carcass weight (CWE)
<b>Breed(s)</b>	Limousin (taken from across breed evaluation including on phenotypes from 73 other breeds)
<b>Trait definition</b>	The weight of the body of an animal, after the removal of the animal's head, hide, feet/legs, thoracic organs, internal fats, and abdominal organs, dressed according to a defined specification (three specifications exist in the UK namely Standard Specification, EC Reference Specification and UK Specification) followed by chilling (thus also known as cold carcass weight). Cold carcass weight is approximately 2% less than hot carcass weight.
<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 weighed
<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 <math>i</math> is the appropriate breed and sex and <math>j</math> 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            Must be prime slaughter animal            Sex must be recorded            12months&lt;Slaughterage&lt;36 months            Carcass weight&gt;50kg            Dam age must be recorded            Traits must be within <math>\pm 3\text{sd}</math> (for sex)            Birth herd must be recorded            Finishing herd must be recorded            Sire or maternal grandsire must be known            Birth contemporary group&lt;5            Killdate recorded            Birthdate recorded</p>

	killdate supplied by the abattoir must be within 10 days of BCMS
<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>	BirthHYS, 170231 (F) Slage (X) Slage2 (X) Killsite, 11 (F) Sex,3 (F) Finishingherd, 23195 (F) Killseason, 52 (F) Killseasonsex, 156 (F) Dam age (X) Percentagedairy (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) Slagepercentdairy (X) Slagedamage (X) Damagepercentdairy (X) Percentdairysex (X) Slage2sex (X)
<b>Use of genetic groups and relationships</b>	A relationship matrix is formed based on available pedigree and genotype 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>	Heterosis and Recombination coefficients were calculated from the breed type proportions of the animal's sire and dam and the formulae are as follows: $[\text{heterosis}]_{ij} = ([\text{sire}]_i * [\text{dam}]_j) + ([\text{sire}]_j * [\text{dam}]_i)$

	$\frac{[(\text{dam})\_i]}{100}$ $[(\text{recombination})\_ij] = (([(\text{sire})\_i] * [(\text{sire})\_j]) + ([(\text{dam})\_i] * [(\text{dam})\_j])) / 100$ <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 and GEBVs are published for registered animals on <a href="https://www.taurusdata.co.uk/beef">https://www.taurusdata.co.uk/beef</a> on behalf of British Limousin Cattle Society
<b>Criteria for official publication of evaluations</b>	EBVs are published where accuracy > 0.5 If genotyped on or before 01/03/2018 members have the option to publish their GEBVs If genotyped after 01/03/2018 all GEBVs are published
<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)
<b>Key organization : contact person, address, phone, fax, e-mail, web site</b>	Scotland's Rural College (SRUC) contact persons : Abbygail Wells and Samir Id-Lahoucine Roslin Institute Building Bush Estate Penicuik, EH25 9RG abbygail.wells@sruc.ac.uk <a href="mailto:samir.idlahoucine@sruc.ac.uk">samir.idlahoucine@sruc.ac.uk</a> <a href="https://www.sruc.ac.uk">https://www.sruc.ac.uk</a>



**Form BEEF****Appendix I BEEF****Parameters used in genetic evaluation****Country: United Kindgom****Main trait group: Carcass weight (CWE)****Breed: Limousin**

Trait <sup>(1)</sup>	Definition	$h_d^2$	$h_m^2$	$r_{g(d,m)}$	$c^2$	$\sigma_p^2$
CWE	Carcass weight	0.43	-	-	-	849.66

$h_d^2$  : 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