### Form BEEF

**DATA COLLECTION**

<table>
<thead>
<tr>
<th>Country (or countries)</th>
<th>UK</th>
</tr>
</thead>
<tbody>
<tr>
<td>Trait name</td>
<td>Carcass fat (CFA)</td>
</tr>
<tr>
<td>Breed(s)</td>
<td>Limousin (taken from across breed evaluation including on phenotypes from 73 other breeds)</td>
</tr>
</tbody>
</table>

**Trait definition**
The carcass is graded under the EUROP scale with the five main classes (1, 2 ,3 ,4 ,5) but abattoirs differed by the use of both the 7 point and 15 point scale. The 15 point scale was used and converted to a numerical value 1 to 15 and the 7 point and 15 point scales were applied to this as shown in Table 19. A 15 point scale with values 1 to 15 as used by Hickey et al (2007) would result the same as the values 3 to 45.

**Method and frequency of measurement**
One measurement per animal

**Who does the performance recording?**
Abattoir

**Method of collecting data**
Carcass is scored according to the EUROP grading system

**Which animals get recorded?**
Any passing through abattoir

**Is birthday recorded?**
Yes

**Is day of recording available?**
Yes

**Is the data adjusted and/or selected?**
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.

\[
\text{Scaled phenotype} = \text{Average}(i) + [(\text{phenotype} - \text{average}(i)) \times (\text{std}(j)/\text{std}(i))] 
\]

Breed types are defined as 1= Dairy, 2=Native beef, 3=Continental beef, 4=Other

**Time period for inclusion of data**
02/01/2001-19/10/2018

**Criteria (data edits) for inclusion of records**
Remove duplicates
Must be prime slaughter animal
Sex must be recorded
12months<\text{Slaughterage}<36 months
Carcass weight>50kg
Dam age must be recorded
Traits must be within ±3sd (for sex)
Birth herd must be recorded
Finishing herd must be recorded
Sire or maternal grandsire must be known
Birth contemporary group<5
Killdate recorded
Birthdate recorded

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Is embryo transfer applied? How are ET animals identified? Is recipient mother ID recorded? | ET animals removed
---|---
How do you treat incomplete data? | Whole record removed if any of the above criteria are not met

**MODEL**

**Model used for genetic evaluation** | MT-AM-FR

**Environmental effects**

<table>
<thead>
<tr>
<th>BirthHYS, 170231 (F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Slage (X)</td>
</tr>
<tr>
<td>Slage2 (X)</td>
</tr>
<tr>
<td>Killsite, 11 (F)</td>
</tr>
<tr>
<td>Sex,3 (F)</td>
</tr>
<tr>
<td>Finishingherd, 23195 (F)</td>
</tr>
<tr>
<td>Killseason, 52 (F)</td>
</tr>
<tr>
<td>Killseasonsex, 156 (F)</td>
</tr>
<tr>
<td>Dam age (X)</td>
</tr>
<tr>
<td>Percentagedairy (X)</td>
</tr>
<tr>
<td>Het 1 (X)</td>
</tr>
<tr>
<td>Het 2 (X)</td>
</tr>
<tr>
<td>Het 3 (X)</td>
</tr>
<tr>
<td>Het 4 (X)</td>
</tr>
<tr>
<td>Het 5 (X)</td>
</tr>
<tr>
<td>Het 6 (X)</td>
</tr>
<tr>
<td>Rec 1 (X)</td>
</tr>
<tr>
<td>Rec 2 (X)</td>
</tr>
<tr>
<td>Rec 3 (X)</td>
</tr>
<tr>
<td>Rec 4 (X)</td>
</tr>
<tr>
<td>Rec 5 (X)</td>
</tr>
<tr>
<td>Rec 6 (X)</td>
</tr>
<tr>
<td>Slagepercentdairy (X)</td>
</tr>
<tr>
<td>Slagedamage (X)</td>
</tr>
<tr>
<td>Damagepercentdairy (X)</td>
</tr>
<tr>
<td>Percentdairysex (X)</td>
</tr>
<tr>
<td>Slage2sex (X)</td>
</tr>
</tbody>
</table>

**Use of genetic groups and relationships**

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.

**Genetic parameters in the model** | See appendix I

**Adjustment for heterogeneous variance in evaluation model**

Heterosis and Recombination coefficients were calculated from the breed type proportions of the animal’s sire and dam and the formulae are as follows:

\[
\text{heterosis}_{ij} = (\text{sire}_i \cdot \text{dam}_j) + (\text{sire}_j \cdot \text{dam}_i)
\]

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[dam]_i))/100
[recombination]_ij= (([sire]_i* [sire]_j)+([dam]_i* [dam]_j))/100

Breed types are defined as 1=Dairy, 2=Native beef,
3=Continental beef, 4=Other
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.

**System validation**
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.

**Definition of genetic reference base Next base change**
Genetic reference animals are those animals that are born in 2010.

**Assessment of index quality**
Reliabilities are computed using the mix99 software using the Misztal and Wiggans (1988) calculation method.

**PUBLICATION**
**Expression of genetic evaluations**
EBVs and GEBVs are published for registered animals on https://www.taurusdata.co.uk/beef on behalf of British Limousin Cattle Society

**Criteria for official publication of evaluations**
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

**Number of evaluations / publications per year**
3 times a year

**Anticipated changes in the near future**
None

**Key reference on methodology applied**
The mix99 software package is used for the genetic evaluations (Lidauer and Strand, 1999; Vuori et al., 2006)

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

Appendix I BEEF

Parameters used in genetic evaluation

Country: United Kingdom

Main trait group: Carcass fat (CFA)

Breed: Limousin

<table>
<thead>
<tr>
<th>Trait(^{(1)})</th>
<th>Definition</th>
<th>h(d)^2</th>
<th>h(m)^2</th>
<th>r(g(d,m))</th>
<th>c(^2)</th>
<th>(\sigma_P^2)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CFA</td>
<td>Carcass fat</td>
<td>0.32</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>19.94</td>
</tr>
</tbody>
</table>

\(h_d^2\) : 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.
Appendix II BEEF

Sample of ET animal IDs