**STATUS AS OF 07/04/2021**

Form BEEF  
**DESCRIPTION OF BEEF NATIONAL GENETIC EVALUATION SYSTEM**  
Country (or countries): Ireland (IRL)  
Trait group: Carcass conformation

### DATA COLLECTION

<table>
<thead>
<tr>
<th>Breed(s)</th>
<th>All beef breeds</th>
</tr>
</thead>
<tbody>
<tr>
<td>Trait definition</td>
<td>Carcass conformation (score)</td>
</tr>
<tr>
<td>Method and frequency of measurement</td>
<td>Carcass conformation trait is measured in meat factories using automatic (VIA) carcass quality grading. Carcass conformation is scored along the EUROP grid (see <a href="https://ec.europa.eu/food/plants/animal-health/animal-breeding/evaluation/fitness/">Classification of carcasses of bovine animals aged eight months or more (europa.eu)</a>)</td>
</tr>
<tr>
<td>Who does the performance recording?</td>
<td>Recording is done within factories.</td>
</tr>
<tr>
<td>Method of collecting data</td>
<td>All factory data is uploaded to the ICBF database on a weekly basis.</td>
</tr>
<tr>
<td>Which animals get recorded?</td>
<td>All animals slaughtered in Ireland get a conformation score.</td>
</tr>
<tr>
<td>Is birthday recorded?</td>
<td>Yes</td>
</tr>
<tr>
<td>Is day of recording available?</td>
<td>Yes</td>
</tr>
<tr>
<td>Are the data adjusted and/or selected? If yes please describe the methodology applied</td>
<td>No adjustment per-say. However, carcass conformation scores are transformed from a 5-points scale to a linear 15-points scale (Hickey et al., 2007).</td>
</tr>
<tr>
<td>Time period for inclusion of records</td>
<td>No</td>
</tr>
<tr>
<td>Criteria (data edits) for inclusion of records</td>
<td>Age &gt; 12 months</td>
</tr>
<tr>
<td>Is embryo transfer applied? How are ET animals been identified?</td>
<td>‘ET’ recorded in the animal name – Not an issue for this evaluation.</td>
</tr>
<tr>
<td>Is recipient mother ID recorded?</td>
<td>Yes</td>
</tr>
<tr>
<td>How do you treat incomplete data?</td>
<td>Missing data are coded -999 for evaluation.</td>
</tr>
</tbody>
</table>

### MODEL

<table>
<thead>
<tr>
<th>Model used for genetic evaluation</th>
<th>AM-MT + 2-step genomic evaluation</th>
</tr>
</thead>
<tbody>
<tr>
<td>7 traits included in the carcass conformation evaluation: calf quality</td>
<td></td>
</tr>
</tbody>
</table>
### Environmental effects

- Random class effects: HYS of finishing herd, HYS of previous herd
- Random non-genetic effect: Dam P.E.
- Fixed class effects: HYS of finishing herd, HYS of previous herd, dam parity, animal gender (young bull, bull, heifer, steer, cow), birth year, twinning status.
- Fixed regression effects: age within each class of calf live weight, age at slaughter, heterosis coefficients beef x beef and beef x dairy, recombination loss coefficient coefficients beef x beef and beef x dairy.

### Use of genetic groups and relationships

Genetic groups build by breed

### Genetic parameters in the model

- **Non-genetic variances**
  - HYS finishing herd: 0.29 score²
  - HYS previous herd: 0.09 score²
  - Dam P.E.: 0.84 score²

- **Genetic variance**
  - Carcass weight: 0.414 score²

- **Residual variance**: 0.764 score²

### Adjustment for heterogeneous variance in evaluation model

### System validation

- **Definition of genetic reference base**
  - Next base change
  - Base = animals with carcass born 2000-2002; base animals have an average of 315kg across breed.

- **Assessment of index quality (computation of reliability, connection)**

### PUBLICATION

- **Expression of genetic evaluations**
  - Progeny Transmissible Ability

- ** Criteria per official publication of evaluations**
  - none
### Number of evaluations / publications per year

6

### Anticipated changes in the near future

1-step genomic evaluation

### Key reference on methodology applied


### Key organization: Contact person, address, phone, fax, e-mail, website

Ross Evans (revans@icbf.com)

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1. Use Appendix II BEEF for sample ID of ET animals
2a. Use abbreviation listed in the attached list of abbreviation to define the type of model.
2b. Use abbreviation for most common effects as listed in the attached list of abbreviation indicating, also, if the effect is treated as random (R) or fixed (F).
3. Use Appendix I BEEF for heritability/genetic variance estimates.

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### Form BEEF

Appendix I BEEF Parameters used in national genetic evaluation

**Country:**

**Main trait group:**

**Breed:**

<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>
</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 (e.g. AWW at 120d and 210d) provide the correlations between traits.

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### Form BEEF

Appendix II BEEF Sample of ET animal IDs

**Country:**

**Main trait group:**