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

Breed(s)	All beef breeds
Trait definition	Carcass conformation (score)
Method and frequency of measurement	Carcass conformation trait is measures in meat factories using automatic (VIA) carcass quality grading. Carcass conformation is scored along the EUROP grid (see Classification of carcasses of bovine animals aged eight months or more (europa.eu))
Who does the performance recording?	Recording is done within factories.
Method of collecting data	All factory data is uploaded to the ICBF database on a weekly basis.
Which animals get recorded?	All animals slaughtered in Ireland get a conformation score.
Is birthday recorded?	yes
Is day of recording available?	yes
Are the data adjusted and/or selected? If yes please describe the methodology applied	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).
Time period for inclusion of records	No
Criteria (data edits) for inclusion of records	Age > 12months
Is embryo transfer applied? How are ET animals been identified?[1] Is recipient mother ID recorded?	'ET' recorded in the animal name – Not an issue for this evaluation.
How do you treat incomplete data?	Missing data are coded -999 for evaluation.

MODEL

Model used for genetic evaluation[2a]	AM-MT + 2-step genomic evaluation 7 traits included in the carcass conformation evaluation: calf quality

	score, 3 classes of prices: calf price, weanling price, and post-weanling price, muscle development score recorded at weaning,, cull cow conformation, and carcass conformation.
Environmental effects[2b]	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 [3]	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)	Reliability computed using Tier and Meyer approximation (2004)
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	Hickey J., Keane G., Kenny D., Cromie A. and R. Veerkamp (2007) Genetic parameters for EUROP carcass traits within different groups of cattle in Ireland. Journal of Animal Science 85(2):314-21. DOI: 10.2527/jas.2006-263. Tier, B. and Meyer, K. (2004). ”Approximating prediction error covariances among additive genetic effects within animals in multiple-trait and random regression models”. In: J. Anim. Breed. Genet. 121.2, pp. 77–89. DOI: 10.1111/j.1439- 0388.2003. 00444.x
Key organization: Contact person, address, phone, fax, e-mail, website	Ross Evans (revans@icbf.com)

- [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.

Form BEEF

Appendix I BEEF Parameters used in national genetic evaluation Country:

Main trait group:

Breed:

Trait(1)	Definition	h_d^2	h_m^2	$r_{g(d,m)}$	c^2	σ^2_p

- $h_d{}^2$: 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; σ^2_P: 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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Appendix II BEEF Sample of ET animal IDs Country:

Main trait group:

Breed:

ET animal ID