ACCURACY OF GENOMIC PREDICTIONS FOR CARCASS AND MEAT QUALITY TRAITS IN THE URUGUAYAN HEREFORD BREED

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INTRODUCTION





- **Carcass and meat quality traits are economically relevant for beef industry**

- **“Traditional” genetic evaluation**
  - It is limited to in vivo ultrasound measurements, as predictors of quality
  - Post-mortem assessments:
    - Longer generation intervals
    - Expensive and difficult phenotypic recording

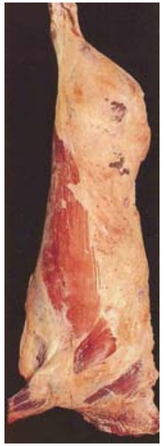
- **Genomic selection**
  - Faster genetic gain due to shorter generation interval
  - Inclusion of specific relevant traits (weight high-value cuts, fatty acids profile)
  - Accuracies depend on the size of training population

OBJECTIVE

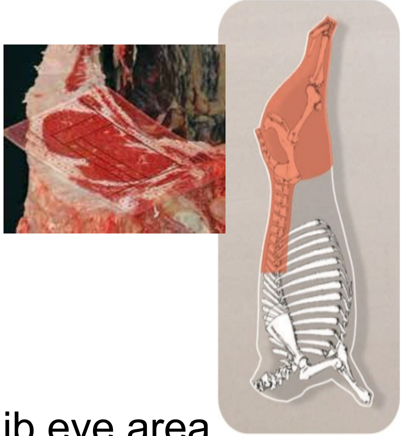
- To evaluate the accuracy of genomic predictions for carcass and meat quality traits in the Uruguayan Hereford breed

MATERIALS AND METHODS

- 747 purebred Hereford steers
- Data recorded in 3 research projects between 2009 and 2015
  - Animals were slaughtered at similar constant live weight (507± 41 kg)
  - Similar protocols for carcass data recording and meat quality analysis
- 64% had identified sire (46 pedigree bulls in genetic evaluation)
  - Pedigree data: 5 generations, 1537 animals
- Genotyped with GGP 80K, GGP 150K and Illumina HD
  - Imputed to 601,339 SNP (Fimpute)



Hot carcass wt



- Rib eye area
- Subcutaneos fat depth
- Pistola hindquarter wt

Pistola retail product
(7 cuts, UK market standard)

- WB Shear force
- Intramuscular fat content

MATERIALS AND METHODS

- Expected progeny differences (EPD) and genomic EPD (GEPD)
- Model:

$$\mathbf{y = Xb + Zu + e}$$

where:
y is the vector of observations
b is the vector of fixed effects: year of slaughter and batch effects as contemporary group and sire class for REA (high, low, unknown)
u is the vector of random animal effects
e is the vector of random residual effects; $e \sim N(0, I\sigma^2 e)$
X and Z are design matrices that relate records to fixed effects and random animal effects, respectively.

BLUP: $u \sim N(0, A\sigma^2 a)$; A = numerator additive relationship matrix; $\sigma^2 a$ polygenic variance,
GBLUP: $u \sim N(0, H\sigma^2 a)$; H = matrix which combines pedigree and genomic information (Aguilar et al., 2010)

- Variance component were estimated using the restricted maximum likelihood method (REML)

MATERIALS AND METHODS

- Accuracy of GEPD assessed by four-fold-crossvalidation:
  - 3 subsets → training population
  - 1 subset → validation

- Two approaches:
  - K-means: minimum relatedness between subset, maximum within subsets
  - Random: random selection of animals, crossvalidation replicated 50 times

- Acc = r (GEPD,P*) / h

  where:
  r = correlation
  P* = phenotypes adjusted by fixed effects
  h = square root of heritability (genomic)
  (Legarra et al., 2008)

RESULTS AND DISCUSSION

Trait	N	Mean ± SD	h^2_P (SE)	h^2_G (SE)
Hot carcass wt. (kg)	740	261.9 ± 22.6	0.41 (0.16)	0.35 (0.09)
Rib Eye Area (cm^2)	701	63.4 ± 6.2	0.36 (0.19)	0.16 (0.08)
Subcutaneous fat depth (mm)	702	7.7 ± 2.3	0.51 (0.17)	0.44 (0.10)
Pistola cut wt. (kg)	740	54.6 ± 4.5	0.48 (0.18)	0.41 (0.09)
Pistola Retail product (kg)	740	39.7 ± 3.5	0.49 (0.18)	0.39 (0.09)
WB Shear Force (kg F)	741	3.8 ± 1.1	0.18 (0.12)	0.26 (0.09)
Intramuscular fat content (%)	735	3.7 ± 1.4	0.31 (0.14)	0.36 (0.10)

- In general: $h^2_P > h^2_G$
  - IMF and WBSF
- h^2_P: larger SE due to scarce pedigree information

Trait	Accuracy	
	Random	k-means
Hot carcass wt.	0.40	0.24
Rib Eye Area	0.32	0.02
Subcutaneous fat depth	0.39	0.28
Pistola cut wt.	0.36	0.26
Pistola Retail product	0.39	0.31
WB Shear Force	0.42	0.37
Intramuscular fat content	0.35	0.27

- Random > k-means
  - Related to the relationship between training and validation population
- Larger h^2_G ➡ higher accuracies
- Encouraging accuracies but need to improve values
  - Impact on genetic improvement
  - Uptake by the industry

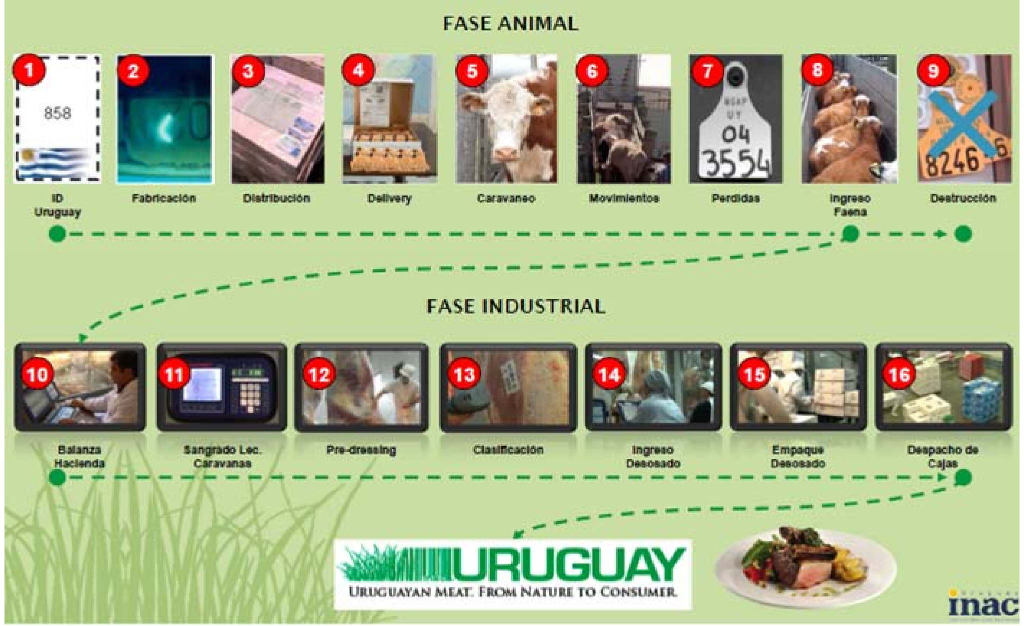
RESULTS AND DISCUSSION

- Larger training populations: cost and difficulties of phenotypic recording is a limitation
  - “research method” (960 steers, 73 sires)
  - sustainable?
- Cost-effective strategies in the case of expensive phenotypes
  - International collaborations
  - Integration of non-invasive novel method for data collection
  - National platforms connecting traceability and data recording at slaughter (Uruguay, Ireland)

✓ All animals are traced from birth to death

✓ Live animal & post-slaughter traceability systems are linked: “ birth to fork”

✓ Automatic recording of key carcass traits in all abattoirs (carcass & pistola cut wt..)



CONCLUSIONS

- **Moderate accuracies of genomic predictions** for carcass and meat quality traits were estimated with **an initial training population of 747 Hereford steers**. Although results are encouraging, **alternatives to assemble larger training populations need to be investigated** to improve the prediction accuracies and uptake by the beef industry.

Acknowledgements

HEREFORD
URUGUAY

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INIA

La población de novillos se dividió en 4 subpoblaciones en base a la matriz de parentesco genómico (matriz G) (Van Raden et al, 2008).

Los grupos se separaron mediante el algoritmo Hartigan-Wong (Hartigan y Wong, 1979) del paquete k-means del software R (R Development Core Team, 2011) que toma como insumos una matriz de distancias, en este caso la matriz G estandarizada:

$$d_{ij} = 1 - \frac{g_{ij}}{\sqrt{g_{ii} g_{jj}}}$$

donde d_{ij} es la distancia entre el individuo i y el individuo j, g_{ij} es el parentesco genómico entre el individuo i y el j y g_{ii} y g_{jj} son elementos de la diagonal para los individuos i y j.

	Grupo 1	**Grupo 2**	**Grupo 3**	**Grupo 4**
N	294	146	154	153
Parentesco máximo promedio dentro de grupos (DE)	0,43 (0,05)	0,36 (0,04)	0,42 (0,04)	0,66 (0,09
Parentesco máximo promedio entre grupos (DE)	0,10 (0,06)	0,10 (0,05)	0,11 (0,05)	0,08 (0,07)