Across-breed genomic evaluation for meat sheep in Ireland

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Sheep Ireland: Profit through science

Background: Irish breeding program

- Trait groups
  - 🐑 Lambing
  - 🐑 Lamb growth
  - 🐑 Lamb carcass
  - 🐑 Lamb health
  - 🐑 Ewe growth
  - 🐑 Ewe health
  - 🐑 Litter size

- Across breed breeding indexes
  - 🐑 TERMINAL INDEX

  - 🐑 REPLACEMENT INDEX
  - 🐑

Background: Genomic research

- EAAP 2016 Belfast

Genomic selection for a multi-breed sheep population

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The Irish Agriculture and Food Development Authority

Objective

- Developing single step across-breed genomic evaluation for meat sheep

- Assessing the accuracy of the genomic evaluation over the current across-breed genetic evaluation
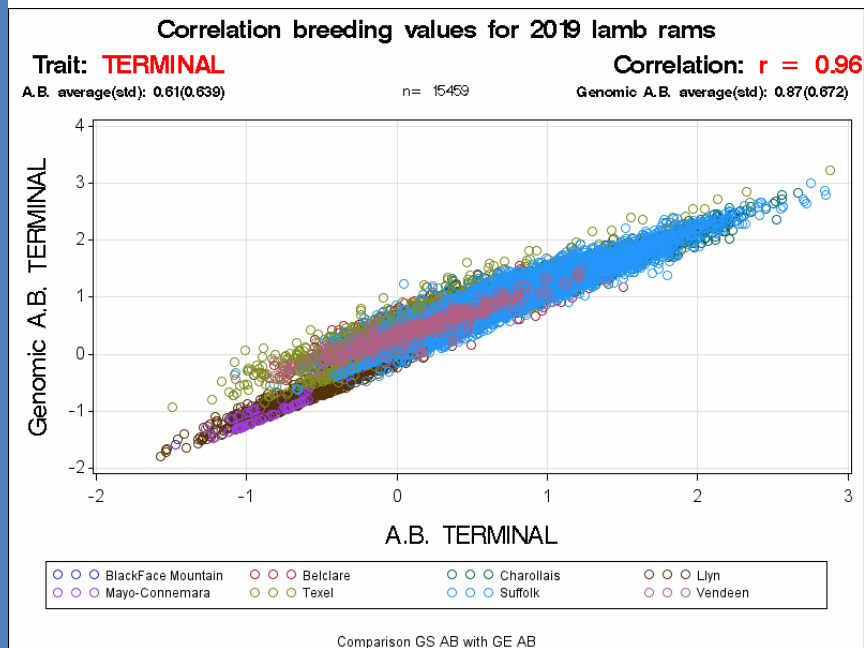
Single step process

- 32,819 animals genotyped across 5 chips (8-11-39-41-49K)
  - ➢ Mainly from 2010 to present

- Imputed to 49K
  - ➢ FImpute (Sargolzaei M., 2014)

- Genomic evaluation across 4 modules
  - ➢ Litter size, Lambing, Growth & Carcass, Health
  - ➢ Single step (SS-GBlup) τ=0.70

$$H_{\tau,\omega}^{-1} := A^{-1} + \begin{pmatrix} 0 & 0 \\ 0 & (\tau G^{-1} - \omega A_{22}^{-1}) \end{pmatrix}$$

- Post-process
  - ➢ Base adjustment
  - ➢ Index construction

Results on breeding values

Correlation breeding values for 2019 lamb rams

Trait: **TERMINAL**   Correlation: **r = 0.96**

A.B. average(std): 0.61(0.639)   n= 15459   Genomic A.B. average(std): 0.87(0.672)

Comparison GS AB with GE AB

Change in mean index for 2019 lamb rams*			
	N	TERMINAL	REPLACEMENT
Belclare	2160	0.27	0.52
Charollais	3819	0.26	0.28
Llyn	1057	-0.05	0.32
Suffolk	2664	0.38	0.78
Texel	5180	0.25	0.63
Vendeen	479	0.30	0.52

Genomic evaluation compared to genetic evaluation

Sheep Ireland: Profit through science

Result on accuracy

Correlation accuracy for 2019 lamb rams

Trait: TERMINAL   Correlation: r = 0.79

A.B. average(std): 0.4(0.075)   n= 15459   Genomic A.B. average(std): 0.43(0.105)

Comparison GS AB with GE AB
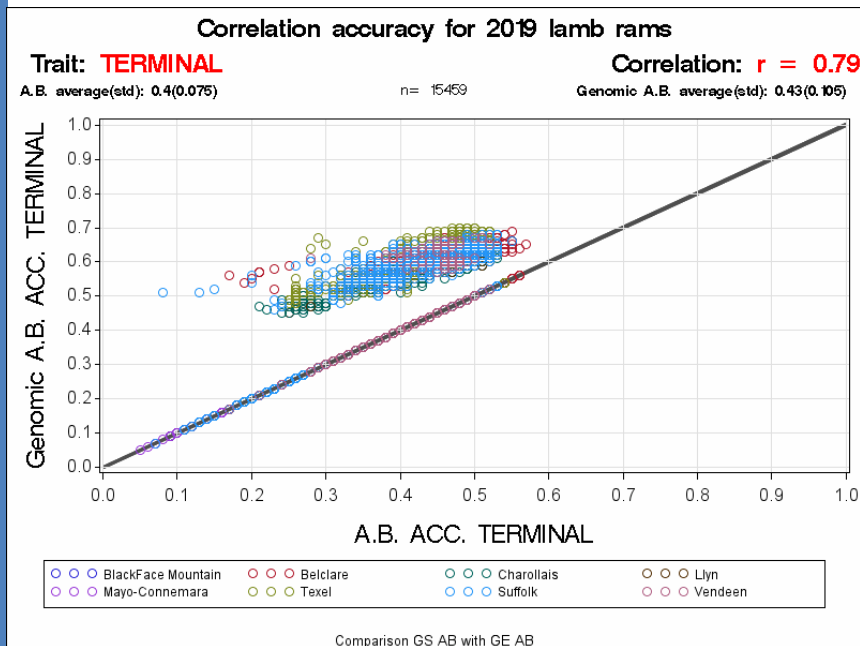
Gain in accuracy for genotyped 2019 lamb rams*			
	N	TERMINAL	REPLACEMENT
Belcalre	679	+16%	+18%
Charollais	444	+15%	+17%
Llyn	44	+13%	+14%
Suffolk	617	+18%	+18%
Texel	901	+16%	+16%
Vendeen	70	+17%	+19%

Genomic evaluation compared to genetic evaluation

Genetic trends

GENETIC TREND - AB TERMINAL INDEX

GENETIC TREND - AB REPLACEMENT INDEX
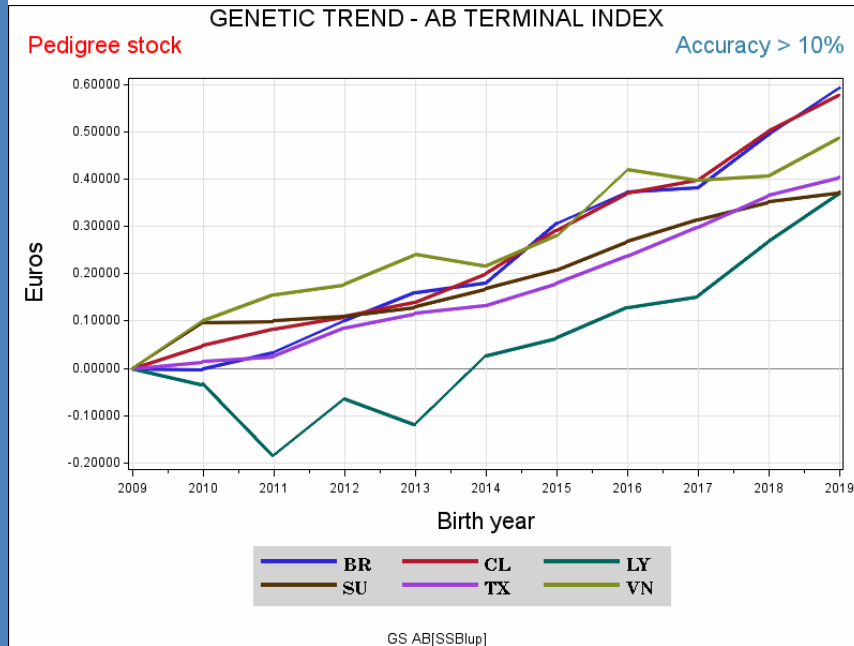
BR = Belclare   CL = Charollais   LY = Llyn
SU = Suffolk   TX = Texel   VN = Vendeen
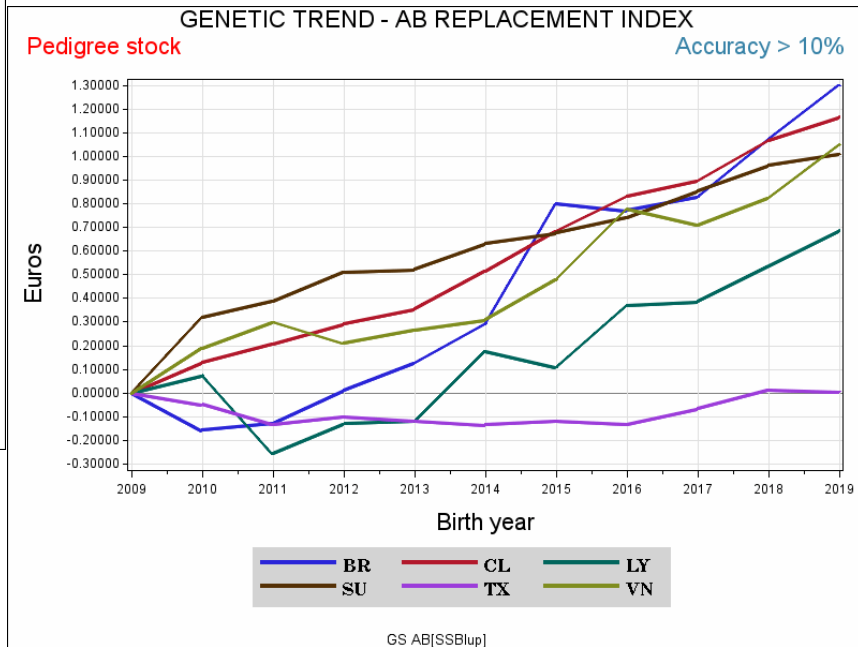
Validation process

- Defining the dataset
  - 🐑 Last 3 years of phenotypes are masked ⇨ validation phenotypes
  - 🐑 Rest ⇨ calibration phenotypes
- Running genetic & genomic eval.
  - 🐑 Validation animals get a parent average genetic merit (PA)
- Computing yield deviations from phenotypes
  - $YD = Y - X\beta$
- Comparing YD and PA
  - Best (★★★★★) & Worst (★) groups of animals
  - Regression of YD on PA

Star validation

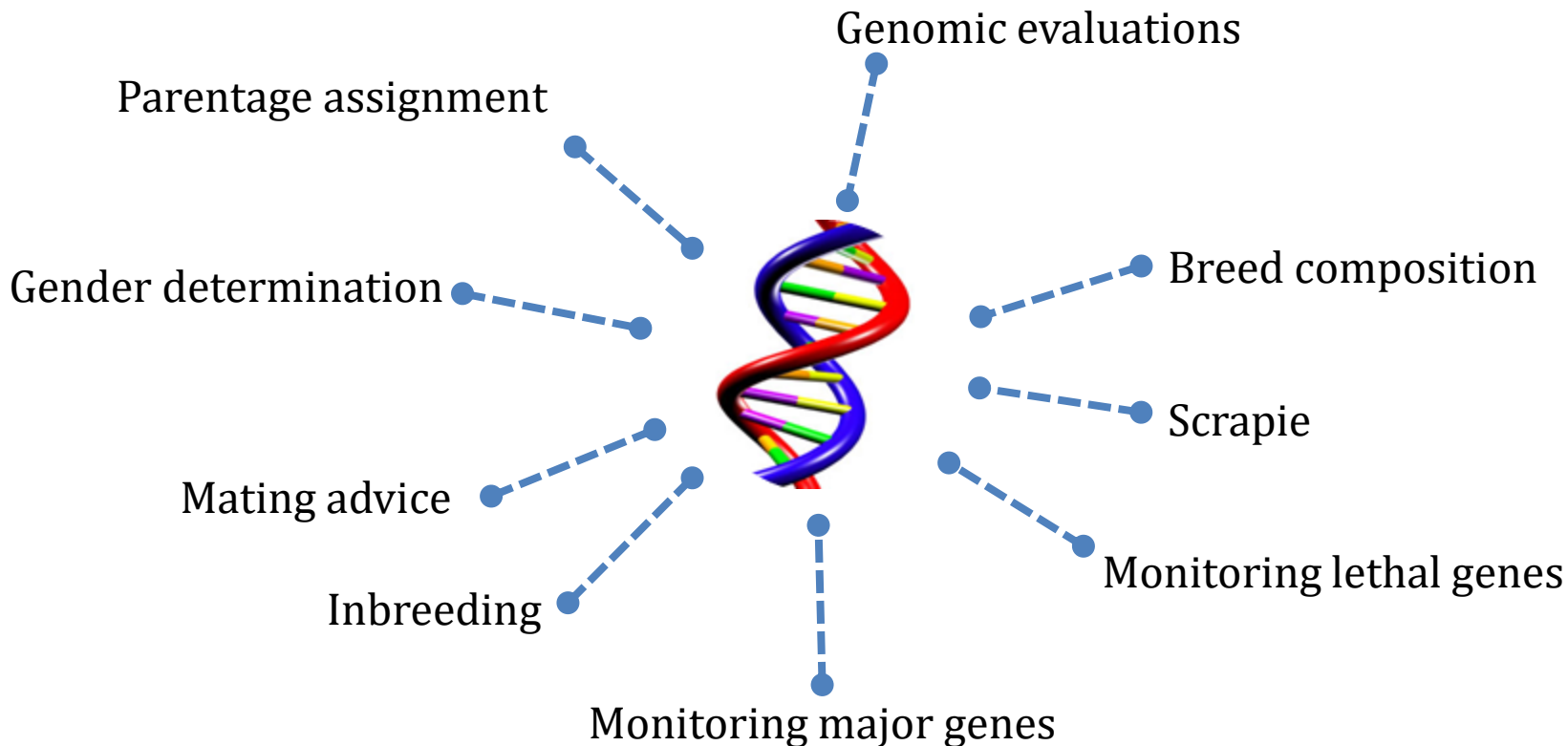|	# validation animals	Difference 5★ - 1★ (s.e)	
		Current genetic eval.	Single step genomic eval.
Litter size	4,565	0.28 (0.025)	0.35 (0.028) ☺
Weaning weight (kg)	15,016	1.4 (0.159)	2.0 (0.147) ☺
Weight @ scan (kg)	8,437	2.4 (0.178)	2.9 (0.195) ☺
Age at slaughter (day)	3,714	-13.9 (2.100)	-12.0 (2.646) 😐
Ewe mature weight (kg)	3,549	-6.2 (0.322)	-6.8 (0.351) ☺
Lamb survival @ birth (%)	21,962	1.8 (0.047)	1.5 (0.053) 😐
Lambing ease multiple (%)	18,406	3.6 (0.086)	4.7 (0.089) ☺

Model validation

	#validation animals	Reg. slope* (s.e.) [rval%]#	
		Current genetic eval.	Single step genomic eval.
Litter size	4,565	1.47 (0.186) [85%]	1.74 (0.215) [85%] ☹
Weaning weight (kg)	15,016	0.67 (0.081) [28%]	0.72 (0.076) [32%] ☺
Weight @ scan (kg)	8,437	0.56 (0.078) [27%]	0.63 (0.076) [32%] ☺
Age at slaughter (day)	3,714	0.71 (0.191) [24%]	0.70 (0.175) [26%] 😐
Ewe mature weight (kg)	3,549	1.59 (0.137) [81%]	1.83 (0.160) [80%] ☹
Lamb survival @ birth (%)	21,962	0.05 (0.029) [22%]	0.05 (0.031) [22%] ☺
Lambing ease multiple (%)	18,406	0.07 (0.022) [12%]	0.10 (0.025) [12%] ☺

Reg. slope = b = regression slope YD = bPA + e*

$$rval^{\#} = r/\sqrt{h^2}$$

More to genomics

Genomic evaluations

Parentage assignment

Gender determination

Breed composition

Scrapie

Mating advice

Monitoring lethal genes

Inbreeding

Monitoring major genes

Conclusion

🐑 Genomic evaluation pipeline in place

🐑 Strong correlations between current and genomic breeding values

🐑 Large gain in accuracy for genotyped animals

🐑 Validation Ok on growth traits

🐑 But (for the sheep industry) there is much more to genomic than genomic evaluations!

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