

Enhancing the hill flock - maintaining momentum without funding

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innovis





Where we were five years ago

- Little genetic progress in hill flocks
 - Amer et al. , 2015
- Few flocks recording performance
- Low use of EBVs when purchasing rams
 - Pollott et al, 2021
- "Rams with EBVs are not available to me.."

HCC attitudes survey and 2021 Breed survey





Hill Ram Scheme – aims

Increase the number of recorded hill flocks in Wales (target 45)

Facilitate genetic improvement in hill environment – DNA parentage

Achieve critical mass of improved sheep

Make it easier to buy and sell recorded rams



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What does Hill Ram Scheme do? RDP funded financial support: 2018-2023

- Setting up and using DNA parentage
- Signet recording and US scanning
- Development of Hill Index and new EBVs
- Training and advice
 - Recording, use of EID etc
 - Use and interpretation of EBVs
 - Marketing rams







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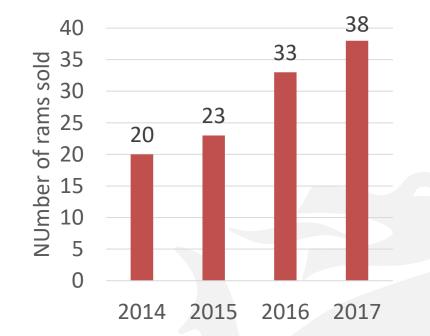
How it started:



How it's going:







Autumn 2021 – Rams sold/retained

Central Sale 75

Off farm 65

Regional sales-91

Retained for future breeding- 88

Total 228



57 DNA flocks2642 ewesgenotyped2541 Lambs

+ 1 manual recorder

0 30 DNA flocks + 8012 ewes genotyped 9175 lambs

+ 5 manual recorders

48 DNA flocks + ~ 9500 ewes genotyped 14 410 lambs

+ 9 manual recorders

202 **40 DNA** + ~ 1796 ewes genotyped **15 027** lambs

+ **16** manual recorders



The future.....

Funding after 2023?

Harnessing the power of genomics

Maintaining critical mass





Genomics data – adding value

- Parentage assignment
- Gene tests
 - e.g yellow fat, scrapie, GDF-9
- Genomic breeding values









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Genotyping GenomNZ

Ewes and lambs genotyped on 17K XT SNP chip (~ 44 000)

Lambs 60K SNP chip (~ 15 000)

Rams genotyped on 600K SNP chip (~630)



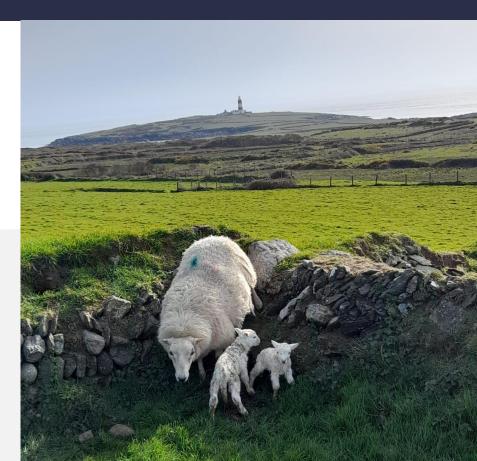


Parentage assignment

Most flocks > 95% assignment

A few flocks < 90% assignment

- unknown ewes
- unknown sires
- incomplete sampling of flock

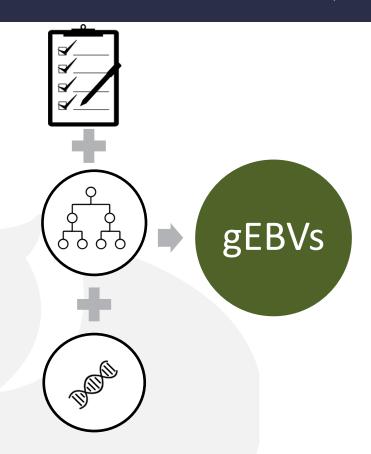




Genomic breeding values ?

Single step genomic evaluation

- uses pedigree + genomic data to estimate genes shared between animals more accurately
- only useful if performance records (phenotypes) available





Why could genomic breeding values add value?

- More accurate selection decisions
 - maternal traits sex limited
 - traits measured over the ewe's lifetime
 - traits that are hard to measure



- Genomic relationships strengthen genetic connectedness (Yu et al, 2017)
 - Shared DNA but not (necessarily) shared parents

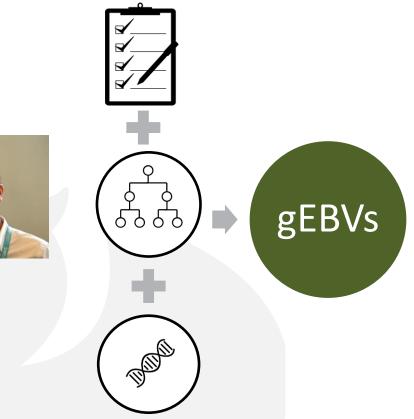


phenotypes on a LOT of lambs + growing number of phenotypes on a LOT of ewes

shallow pedigrees on a LOT of lambs (sire and dam) no pedigrees on a LOT of the ewes deep pedigrees of a few lambs, ewes and rams



A lot of genotypes on rams, ewes and lambs





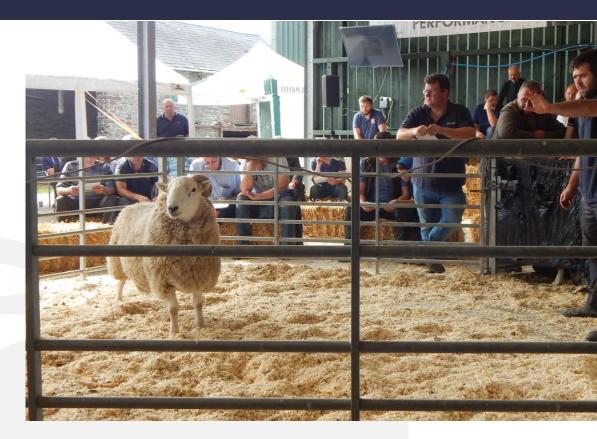
Team Effort on Hill Sheep Genomics

SRUC: Samir Id Lahoucine, Massimiliano Cosso, Abbygail Wells and Ann McLaren, Mike Coffey

HCC: Heather McCalman Innovis: Janet Roden and Kim Hay AHDB/Signet: Kim Matthews, Laura Eyles, Wendy Knight,

Samuel Boon, Marco Winters and Victoria Ashworth

Thanks to SRUC for SBF genotypes and Innovis for Cheviot genotypes





Data used for genomic hill sheep breeding values

Breed	n genotypes
Welsh Mountain	35,408
Hardy Speckle	3,506
North Country Cheviot Hill	1,832
Scotch Blackface	1,037
Brecon Hill Chev	701
Sth Welsh Mountn	570
Beulah	13
North Country Cheviot Park	3

The whole dataset included 910,000 animals.

Breeds: Welsh Mountain, Beulah, Scotch blackface, Roughfell, Herdwick, Hebridean, Hardy Speckle, South Wales Mountain, Swaledale, North Country Cheviot Park, North Country Cheviot Hill, South Country Cheviot, Black Welsh Mountain and Brecon Hill Chev.

Genotypes: 43,070 animals with 53,401 imputed SNPs



Increase % accuracy when adding Genotypes Eight Week Weight (Maternal) 28% Lamb Survival 5% Litter Size Reared 22% Birth Weight 4% Litter Size Born 23% Shearling Weight 24% Fat Depth 20% Muscle Depth 5% Scan Weight 29% Eight Week Weight 28%

Adding genotypes into the genetic evaluation resulted in substantial increases in accuracy





How different are the genomic results?

	Non-Genotyped to 2009 (123,090)	Non-Genotyped from 2010 onwards (45,737)	Genotyped Only (37,157)	
Lamb Survival EBV	0.99	0.87	0.80	
Eight Week Weight EBV	1.00	0.96	0.68	
Litter Size Born EBV	1.00	0.96	0.63	
Maternal Ability EBV	1.00	0.97	0.66	
Mature Size EBV	1.00	0.95	0.68	
Scan Weight EBV No impact on old non-	1.00	0.96	0.68	
Muscle Depth EB genotyped	1.00	0.98	0.00	Most impact
Fat Depth EBV sheep	1.00	0.95	0.72	n genotyped sheep

The correlations between genomic and non-genomic evaluations

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Relationship between EBV and Progeny Data



634 Welsh Mountain rams (>9 scanned progeny)

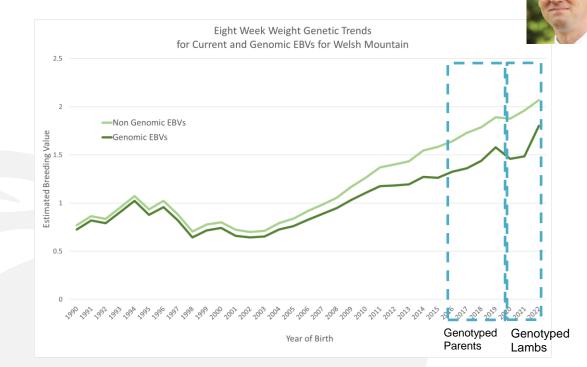
	Correlations between:			
		old EBV and	new EBV and	
	old EBV and new EBV	average progeny phenotype	average progeny phenotype	
Scan weight	0.86	0.30	0.40	
Muscle depth*	0.97	0.26	0.31	
Fat depth*	0.93	0.32	0.41	
	Highly correlated	Genomic BVs more closely related to progeny phenotype	* Weight adjusted to 30kg #PhenotypeIsKing	



• Genomic data may suggest lower rates of gain

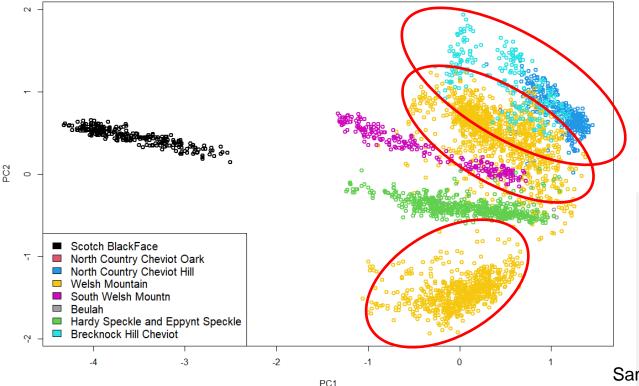
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- Potentially reducing the gap (bias?) between
 - Recorded/unrecorded?
 - Linked/unlinked?
- Will avoiding overprediction increase stability and lead to faster long term gain?





Principal component analysis 1 and 2

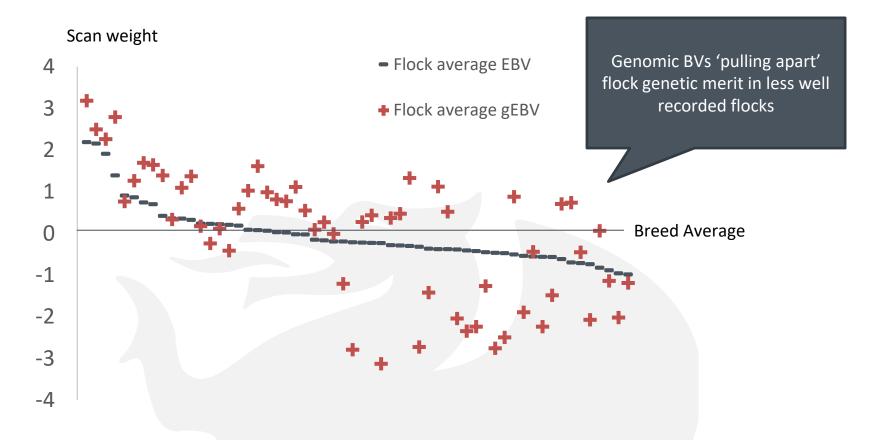


- Clear breed type clusters can be observed, with Cheviot breed types are overlapping.
- Interestingly there are two clusters of Welsh Mountain sheep.
- One tending to be closer to the Cheviot types and the other more distinct.



Samir Id Lahoucine, 2022







HCC Hill Ram scheme – momentum

- Increase in number of recorded flocks
- Recorded rams available for most 'types'
- Increasing number of recorded rams sold



- EBVs and Index fit for the future (few years)
- Huge phenotypic and genomic data resource available
- Genomic values bring the promise of higher rates of progress



Adding value to their hill flocks.....

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Thank You

Diolch yn Fawr

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