

Current status of Nordic purebred beef evaluation

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Nordic Cattle Genetic Evaluation

NAV online workshop 15th September 2026

Last year's priorities — where are we now?

Follow-up on the development priorities agreed at the 2025 workshop



DELIVERED

Genomic reliabilities for growth and carcass traits

Implemented in March 2026



Needs final approval

Harmonized handling of incomplete pedigrees and genetic groups across countries



NEXT

Validation of genomic breeding values for calving traits

In progress work

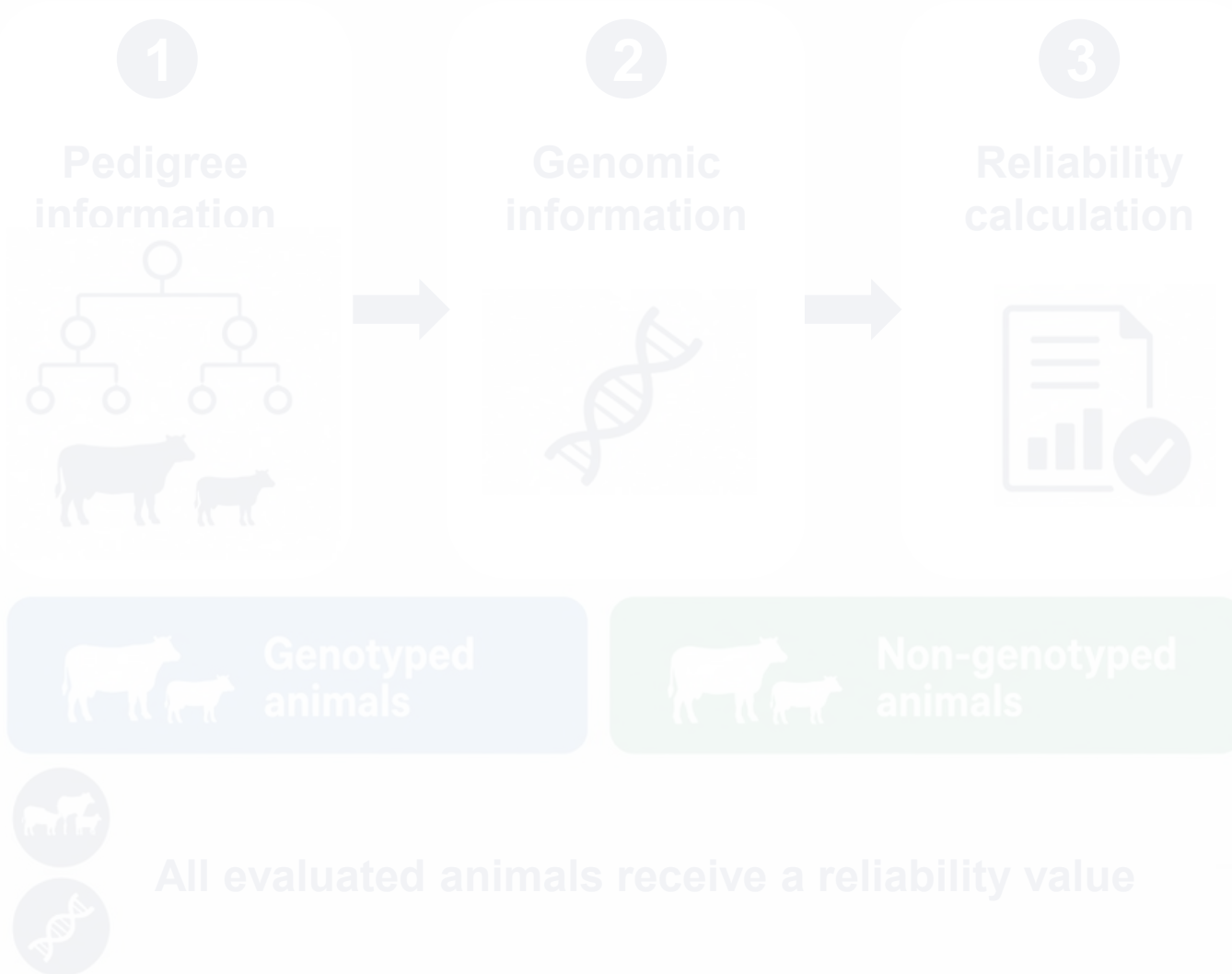


NEXT

Validation of genomic breeding values for BAQ and HLA

In progress work

Genomic reliabilities for growth and carcass traits



What reliability means



1. Reliability shows how certain we are about a breeding value (EBV).



2. Higher reliability means more confidence in the EBV.



3. Genomic information can increase reliability, especially when limited pedigree and phenotypic information is available.

Expectations on gain in genomic reliabilities based on different sources of information for young and older animals

Young animals
(birth year 2024-2026)

Older animals
(birth year < 2024)

No records

With records

No records

With records

Genotyped



Genotypes add
information before own
records are available



Genotypes and
performance information
are combined



Genotypes add
information beyond
pedigree information



Additional genomic gain is
smaller when more
information is already
available



Not genotyped

Benefits through pedigree
relationships



Benefits through pedigree
relationships



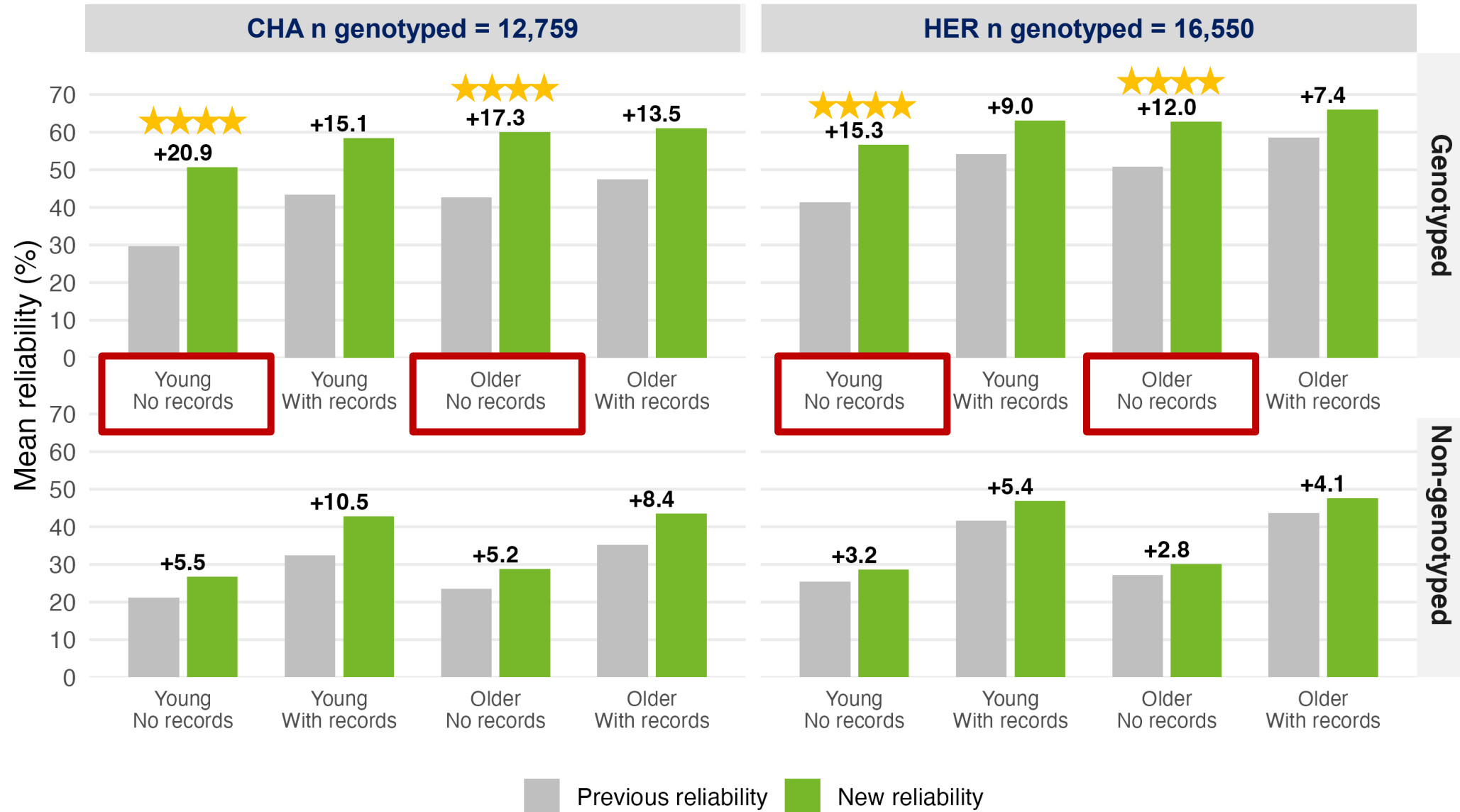
Benefits through
pedigree relationships



Benefits through pedigree
relationships

Reliability increases with the new calculation

Growth index – Charolais and Hereford



Labels above green bars show the change in reliability compared with the previous evaluation.

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How XXX and breed codes are used differently across countries



There is no fully harmonized definition or use of the crossbreed code XXX across Denmark, Sweden and Finland.

As a result, breed codes may not describe the same type of animal in all countries.



Denmark



Breed assignment is mainly reconstructed from pedigree and breed proportions



Repeated backcrossing can make some animals appear purebred



Crossbred background may remain hidden



Sweden



Breed assignment is similar to Denmark



Purebred filtering reduces the problem



Rules are still not fully harmonized across countries



Finland



External breed code is farmer-registered



Crossbred animals may be recorded as a specific breed

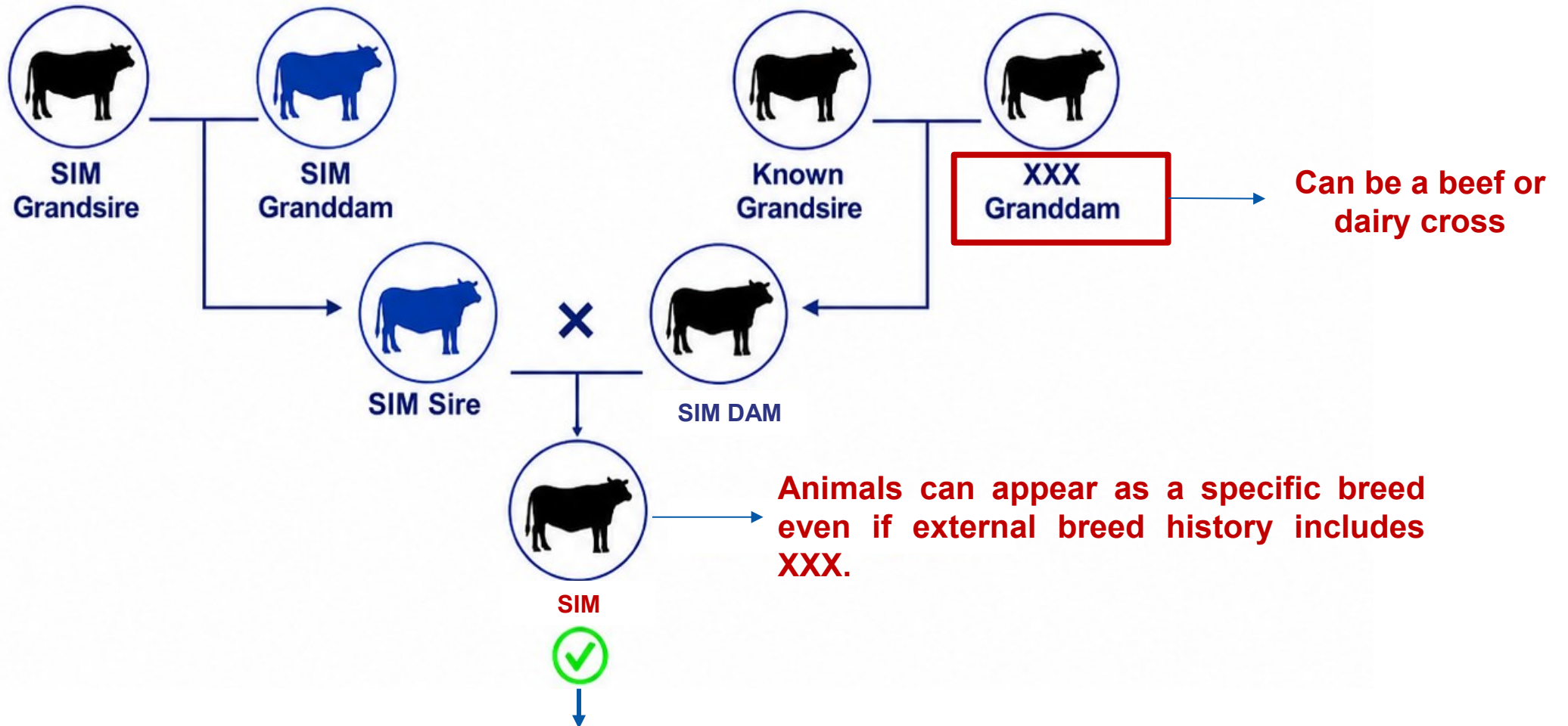


Breed code may not reflect actual breed composition

Why this matters for NAV?

Animals with crossbred background can enter as purebred and lead to problems in the evaluation.

Handling of incomplete pedigree by joint Nordic beef evaluation



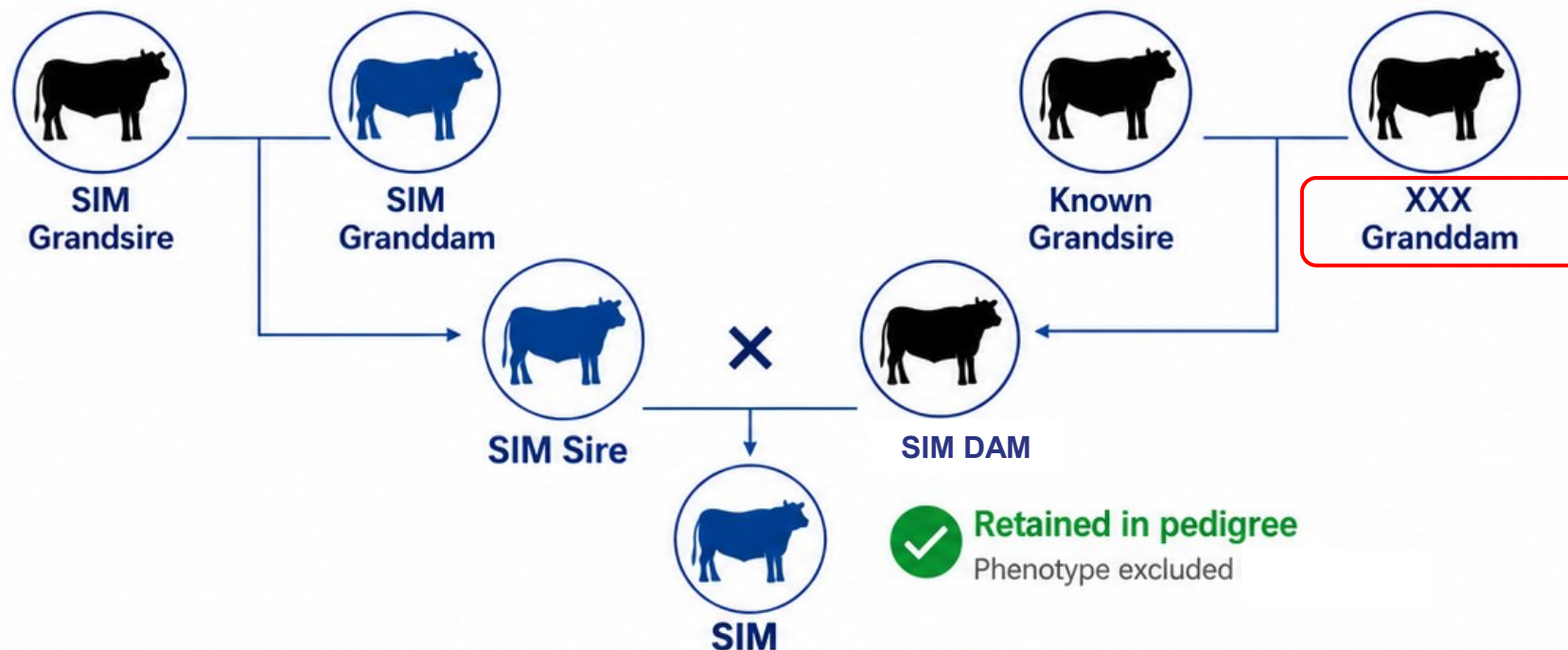
It is difficult to estimate breeding values (extreme estimates)

New handling: we remove the phenotypes of this animals in the evaluation and but kept in the pedigree so we calculate the parent average

Number of animals affected by the MGD = XXX pedigree handling by breed and country

Breed	Denmark			Sweden			Finland		
	Animals	Affected	% affected	Animals	Affected	% affected	Animals	Affected	% affected
LIM	240 305	8 093	3.4	45 759	997	1.1	97 223	4	0.0
SIM	110 581	3 842	3.5	87 101	2 089	2.2	58 557	0	0.0
CHA	88 636	2 931	3.3	214 785	2 427	1.3	101 709	0	0.0
Others	350 570	4 111	1.2	184 447	2 330	2.4	307 110	10	0.0
Total	790 092	18,977	2.4	532 092	7 843	1.5	564 599	14	0.0

The correction resulted in improved breeding values



Before the change

Animal contributed to both pedigree and phenotype

Trait	EBV	Reliability
Direct calving ease	Stable (74)	22
Maternal calving ease	Low (59)	20

After the change

Animal retained in pedigree, phenotype excluded

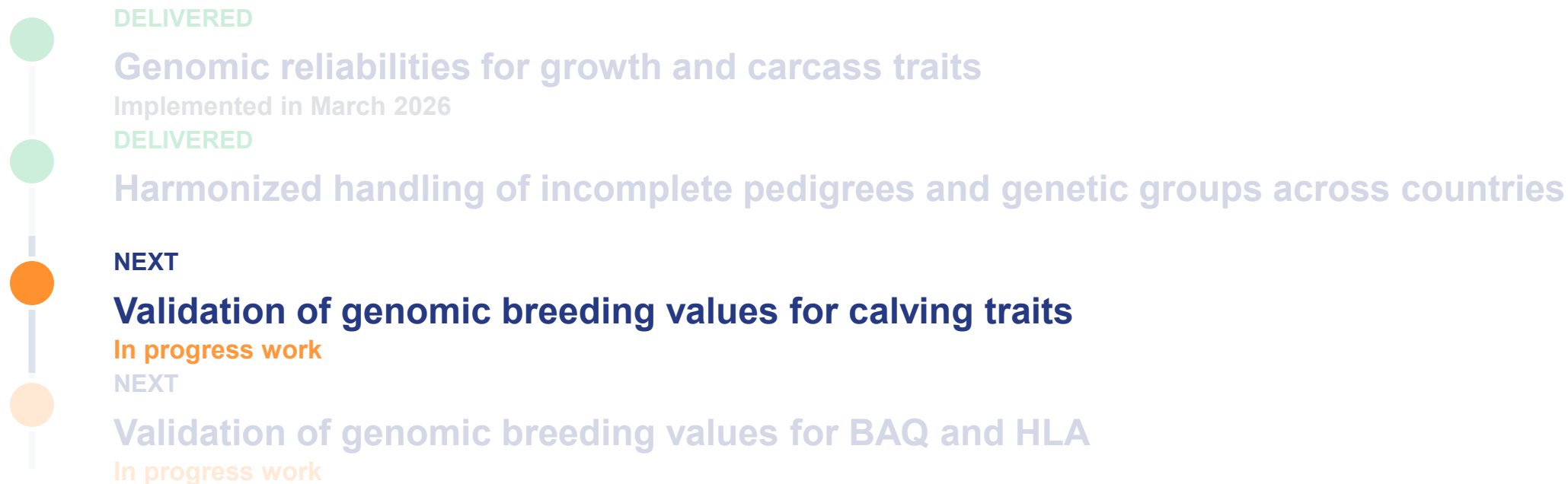
Trait	EBV	Reliability
Direct calving ease	Stable (74)	23
Maternal calving ease	Parent average (89)	18



Direct effects remained unchanged, while maternal effects moved toward parent average

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Calving traits in ssGBLUP: key challenges

Why calving ease and stillbirth need careful validation before routine publication

Selective genotyping in calving traits

Only some animals are genotyped



Dead calves are rarely genotyped



1

Only a part of the population is genotyped

2

Genotyped animals are mostly those born alive

3

Extreme calving outcomes may be underrepresented

4

Cow calving breeding values are based mainly on successful calvings

5

This can lead to bias and lower reliability



Take-home message: ssGBLUP is promising for calving traits, but careful validation is still needed because genotyped animals may not represent the full calving population.



Validation of genomic breeding values for calving traits

Legarra-Reverter (LR) validation

Validation principle

**1. Reduced evaluation
(historical data only)**



2. Predict breeding values



3. Compare predictions with



**4. Full evaluation
(reference with all data)**

Interpretation

Key LR statistics

R^2 / reliability
Higher is better

Slope
Ideal = 1

Bias
Ideal = 0

LR validation asks: can old data predict the full evaluation without systematic bias or over/under-estimation?

First validation results for genomic calving traits

Maternal traits, genotyped animals, results are in unit of GEBVs for Charolais

Birth weight was used as a control trait

Trait	R ² (higher is better)		Slope (Ideal = 1)		Bias (Ideal = 0)	
	ssGBLUP	PBLUP	ssGBLUP	PBLUP	ssGBLUP	PBLUP
Maternal birth weigh	0.68	0.63	0.99	0.95	-1.04	-1.34
Maternal calving ease	0.75	0.76	0.94	0.89	-0.30	-0.37
Maternal stillbirth	0.72	0.72	0.92	0.90	-0.07	-0.03

Keynote

- ✓ **Maternal birth weight supports the ssGBLUP implementation**

Caution note

Calving ease and stillbirth need continued validation:

- ✓ results are comparable, but not clearly better for all traits
- ✓ stillbirth is affected by selective genotyping
- ✓ validation should continue across breeds, countries and consecutive evaluations

ssGBLUP improved genetic connectedness between countries

For **Charolais**, genotyped animals:

- ❖ **ssGBLUP genetic trend was 2.5–5 EBV units higher** than pedigree BLUP for **Birth index** and **Calving index**
- ❖ **ssGBLUP deviation in EBVs is smaller** than in pedigree BLUP

Populations	Mean Relationships (A22)	Mean Relationships (G)
FIN x DNK	0.005 	0.339 
FIN x SWE	0.016 	0.343 
SWE x DNK	0.006 	0.338 
 Pedigree-based relationship are very low indicating weak recorded pedigree links between countries		 Genomic relationship are high improves genetic connectedness between countries and reduced population-structure effects

Next steps - development priorities for 2026/2027

- **Harmonized handling of incomplete pedigrees and genetic groups across countries**
Target: Implementation in the NAV routine evaluation 2027
- **Genomic breeding values for calving traits and indices**
 1. Continue stability checks across consecutive evaluations
 2. Validation of the results
 4. Evaluate results by breed and country
 5. Target: Expected implementation 2027
- **Genomic reliabilities for calving traits and indices**
Target: implementation in 2027, pending validation
- **Validation of genomic breeding values for BAQ and HLA**
 1. Focus on growth, carcass and slaughter traits and indices.
 2. Compare ssGBLUP with pedigree BLUP
 3. Validation of the results
 4. Monitor genetic trends and EBV stability across evaluations
 5. Target: Expected implementation in early 2027, pending final validation



Thank you!

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