

# AUTHENTICATING CATTLE BREEDS USING GENOMIC INFORMATION

An animal's breed composition is usually assumed to be the average of its parents' breed proportions. However, due to chromosomal recombination during gametogenesis, offspring from crossbred parents may deviate from these expectations. The INTAQT project evaluated the accuracy of genomic methods for predicting the breed composition of breeds of cattle with limited numbers of purebreds and to compare its performance to that of a commonly used approach. An additional objective was to investigate the impact of including data from 13 well-represented breeds on the accuracy of breed composition predictions for breeds with limited numbers.

The approach leveraged a large a reference database containing almost DNA markers on several thousand animals from 19 different cattle breeds and their crosses. The key here was access to the crossbred animals. Before developing the method, the breed composition of the purebred animals was firstly verified using principal component analysis of just the purebred animals

A genomic tool was developed to quantify the breed composition of individual cattle of unknown breed composition. The approach was developed using almost 50,000 DNA markers on over 15,000 cattle including 19 beef and dairy breeds and their crosses. Validation results demonstrated a high level of accuracy in determining the breed composition of even crossbred animals of multiple breeds. The open access tool can be very useful for individual breeders but also producers to know the true breed composition of their animals and, from that, make more informed decisions in breeding.

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one quality

Two methods were compared: **SNP-BLUP**, the statistical approach already used in genomic evaluations, and **Admixture**, a widely used stand-alone software. Using SNP-BLUP means breed prediction can slot straight into existing genetic evaluation pipelines.



**Fig 1: Crossbred cattle of different breed compositions (Source: Teagasc)**

## Key results

Of the purebred animals explored, it was possible to accurately assign 98% of the individual to their correct breed – this result was the same as that achieving using a bespoke software. The advantage of the approach developed here, however, was that the estimate of the DNA effect were generated like as is the case in the national genetic evaluations; hence, any new genotype can easily and rapidly be compared against these estimates and a breed composition estimate rapidly generated.

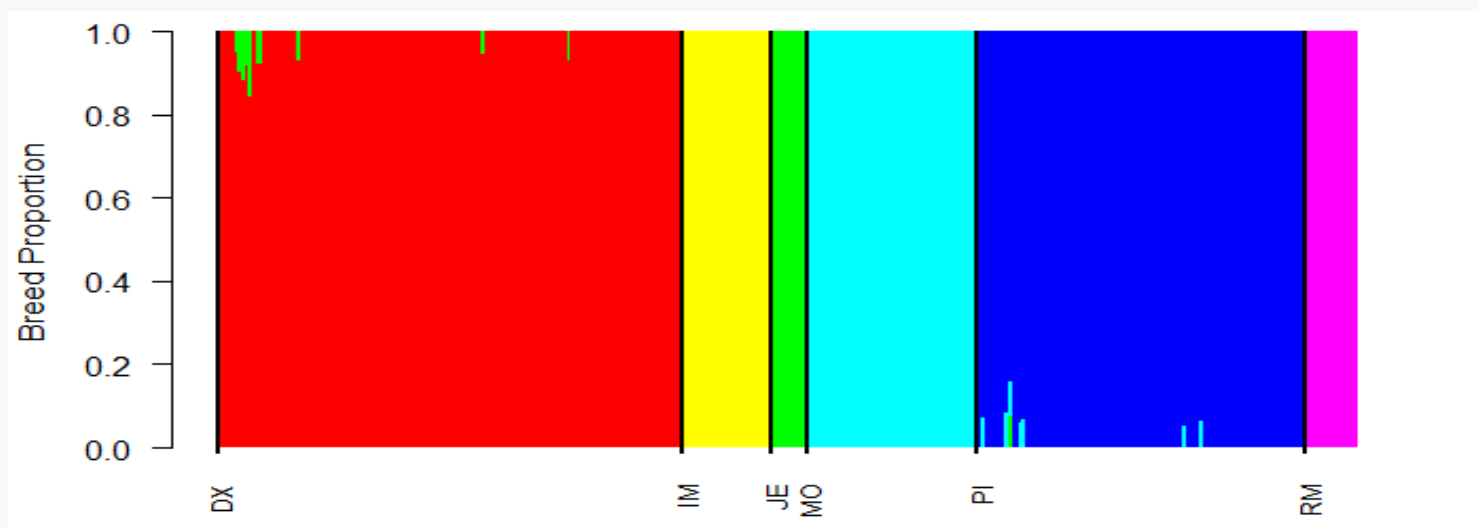


**Fig 2: Breed composition, estimated with Admixture, of purebred validation animals from the six breeds with limited numbers. Each vertical line is one animal and each colour one inferred population (here equivalent to a breed). DX = Dexter, IM = Irish Maol, JE = Jersey, MO = Montbéliarde, PI = Piedmontese, RM = Romagnola.**

### Box 1. Simplified workflow for breed determination

#### 1. Sample collection



#### 2. Genotyping



#### 3. Compare with breed SNP effects



#### 4. Breed determination



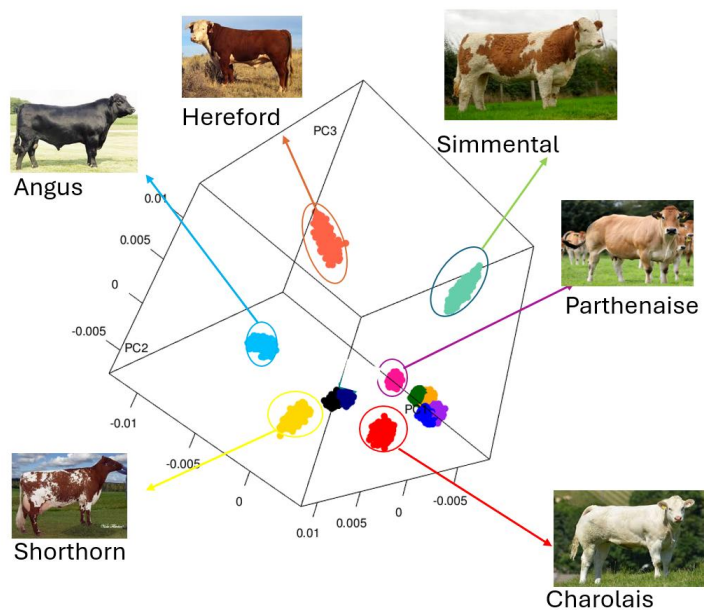


**Fig 3: Principal component analysis showing clear separation between a selection of the breeds studied**

**19**

beef and dairy breeds

**50,000**

DNA markers (SNPs) per animal

**15,000+**

genotyped cattle, purebred and crossbred

## Why breed composition matters

- **Crossbreeding** – knowing the true breed make-up of crossbred and composite animals helps exploit hybrid vigour (heterosis).
- **Herdbooks** – breed societies can verify an animal's breed before registration, protecting the integrity of the herdbook.
- **Product authenticity** – milk and meat from some breeds command premium prices, and rare-breed conservation is often financially supported. Genomic verification underpins consumer confidence and rare-breed purity.
- **Genetic evaluations** – breed composition is used as a correction factor in multi-breed genetic evaluations.
- **Quality control** – predicting the breed of a batch of genotyped samples can flag sample mix-ups or genotyping errors before any further analysis.

## Conclusions

Although additional work is underway using real commercial samples, these results demonstrate that genetic authentication can become a powerful complement to conventional traceability systems. By providing an independent scientific verification of the genetic origin of Label Rouge poultry, this approach could help strengthen consumer confidence, support certification bodies, and improve fraud prevention throughout premium poultry supply chains. Future developments may also adapt the method for routine testing of production batches while keeping analytical costs under control.

## Using the open-access tool

The INTAQT database provides SNP effects for each breed, a SNP map, reference genotypes and a user guide. For any genotyped animal:

1. Align its genotypes (0, 1, 2) to the SNP map
2. Multiply each genotype by each breed's SNP effect
3. Sum across all SNPs to give a score per breed
4. Set scores  $\leq 0.05$  to 0 and  $\geq 0.95$  to 1, then rescale so they sum to 1

## References

Ryan, C.A. (2025) Evaluating the accuracy of SNP-BLUP and Admixture for breed composition prediction in limited and well-represented cattle breeds. *Proc. Assoc. Advmt. Anim. Breed. Genet.* 26: 90–93.

Ryan, C.A., Berry, D.P., O'Brien, A., Pabiou, T. and Purfield, D.C. (2023) Evaluating the use of statistical and machine learning methods for estimating breed composition of purebred and crossbred animals in thirteen cattle breeds using genomic information. *Front. Genet.* 14: 1120312.

**Authors:** Cliona A. Ryan and Donagh P. Berry, Teagasc Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Co. Cork, Ireland.