

Logistics and value of recording field data for an international genomic reference population to improve beef cow resource use efficiency

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Introduction

Improving efficiency and reducing emissions is a challenge faced by all industries and genetic selection has been identified as a key tool to help beef industries world-wide meet this challenge (Shang *et al.*, 2026). Genomic selection is now widely deployed in developed countries, and with an appropriate reference population, provides a deployable commercialization path to reduce methane emissions. The challenge with establishing the required reference populations for selection for reduced methane is the complex nature of the trait and difficulty in accurate recording.

To overcome this challenge several major beef producing countries (AU, NZ, UK, IE and US), who exchange genetic material in the form of semen and embryos, have come together to form an alliance to develop a joint genomic prediction reference population in the belief that, individually, these datasets would be limited in prediction power but by sharing data and resources, the development of large and relevant reference populations will be accelerated.

A key challenge is the choice of measurement techniques and class of animal to measure. The target animal for methane reduction is the mature dam as it has been estimated to contribute 3/4 of the total emissions attributable to beef production (Rotz *et al.*, 2019).

The objective of this study was to practically evaluate four potential measurement technologies: 1) an in-field gas flux measure which would be akin to the GreenFeed (C-Lock Inc., Rapid City, SD, USA) and is used in Ireland and Australia 2) an accumulation chamber which is based on the approach developed by AgResearch (Bilton *et al.* 2025) and follows the successful deployment of accumulation chambers for genetic selection in sheep (Conington *et al.*, 2024), 3) an infield sniffer based on the Agscent/Optiweigh technology that is emerging as a practical method (Agscent and Optiweigh 2026), and 4) a biomarker predicted phenotype. Regarding option 4), while no commercial product is yet available, the potential of a lower cost/accuracy method using biomarkers as a proxy is on the horizon (McInerney *et al.*, 2026). Traits were evaluated not just for their individual heritability estimates but for their contribution to genomic prediction accuracy and ease of recording at scale. Accounting for the cost and ease of measurement may provide a legitimate case for the lower cost measures which

take advantage of more phenotypes for given investment, but this will need to be balanced by the degree of association with the goal trait of methane production in mature grazing beef cows.

Materials & Methods

Potential recording technologies for measuring methane in mature beef cows were evaluated based on expected accuracy of genomic prediction given a level of investment. This framework assumed a linear relationship between recording costs and number of animals recorded. The level of investment considered was a combined investment of 2,050,982 USD for a single breed's reference population in line with the current investment in the alliance. Recording methods considered along with costs in different scenarios are presented in Table 1.

Table 1. Genomic prediction accuracy potential among alternative methane measurement technologies in beef cattle.

Methane Measurement Technology	Heritability	Cost (USD) ³	N	Accuracy
Gas Flux in field	0.40 ¹	2,050,982	3,453	0.51
Accumulation Chamber	0.20 ¹	2,050,982	9,263	0.55
Accumulation Chamber	0.16 ⁴	2,050,982	9,263	0.51
Sniffer in field	0.10 ²	2,050,982	23,259	0.57
Sniffer in field	0.10 ²	1,408,000	16,000 ⁴	0.51
Sniffer in field	0.07 ⁴	2,050,982	23,259	0.51
Molecular phenotype	0.05 ²	2,050,982	68,366	0.62
Molecular phenotype	0.03 ⁴	2,050,982	68,366	0.51

¹ Based on available estimates

² Hypothetical

³ Estimated total reference cost based on \$594, \$221, \$88 and \$30 per record for gas flux, accumulation chamber, sniffer and biomarker, respectively

⁴ Value reduced to provide 0.51 accuracy

The genomic prediction accuracy was determined as a function of trait heritability, number of animals phenotyped (N) and the effective number of chromosome segments (Me) using equations and parameters ($Me/N=1603.5N^{-0.892}$) for Angus cattle (Moore *et al.*, 2026). The expected genomic prediction accuracy was for the measured trait, which may not be the goal trait. To illustrate the impact of measuring a correlated trait, the accuracy of a goal trait, in this case the mature cow, was determined as a product of the assumed genetic correlation and the genomic prediction accuracy of the measured trait.

Results & Discussion

The expected genomic prediction accuracy from using measurement methods with a range of heritability and cost per animal phenotype are provided in Table 1. With the level of investment constant at 2,050,982 USD for an international Angus reference, the lower cost technologies, which also happened to be lower heritability, resulted in more phenotypes, directly impacting accuracy. The heritability measures modelled were indicative but based on current information where available. Recent experience amongst the authors with gas flux for grazing beef females (Madsen *et al.* 2025), growing stock (Ryan *et al.* 2025), accumulation chambers for cattle (Bilton *et al.* 2025) and sheep (Conington *et al.*, 2024) provided realistic heritability estimates. There are insufficient sniffer records from grazing beef cattle to provide a heritability estimate, so a conservative value was used from the lower end of estimates from dairy cattle, being the most similar alternative trait available (van Breukelen *et al.* 2023). The biomarker phenotype was based on emerging technology and therefore does not have a heritability available. The traits chosen represented the very real trade-off between accuracy and cost.

Although all technologies are predicted to provide a satisfactory accuracy (0.51 to 0.62) at this level of investment, the measurement method with the highest heritability did not result in the highest genomic prediction accuracy. Although the differences in accuracy between approaches is marginal, the trend was that the lower cost measures provided enough additional records to overcome the lower heritability. Any reduction in the genetic correlation between the measured traits and the goal trait would erode these prediction accuracies. Given the gas flux technique is the most widely applied among project partners at the moment, using the resulting 0.51 accuracy as a standard, other measurement techniques can be compared at this same accuracy. For the accumulation chamber, sniffer and biomarker techniques the realised heritabilities can reduce to 0.16, 0.07, and 0.03 to obtain the same accuracy for the same level of monetary investment. These lower required heritability estimates appear quite achievable. This conclusion, however, assumes a similar genetic correlation between the individual methods and the goal trait but also, due to the international nature of this initiative, the extent of genotype-by-environment across jurisdictions are assumed equal for each technology.

The type of animal to target for methane reduction was the mature grazing cow and was considered as the goal trait. Measurement technologies which can be applied to mature grazing cows directly will have a genetic correlation of 1 with the goal trait, as modelled here. Measurements on correlated animal classes such as steers in a feedlot on a concentrate diet will require additional records to obtain the same accuracy of the goal trait. Assuming gas flux in the feedlot had a genetic correlation of 0.8 or 0.6 and a similar heritability to the goal trait, the resulting accuracy in the target mature cows would be 0.41 and 0.31, respectively, compared to 0.51 if the same number of mature cows were measured directly with the gas flux technology. There are no heritabilities available for methane production in mature beef cows, but we could expect this heritability to be lower than estimates from growing animals, due to more residual variation expected. To obtain the 0.51 accuracy in mature cows, the number of records would have to increase in the growing feedlot animals from 3,453 to 7,400 and 32,000 at the genetic correlations of 0.8 and 0.6, respectively. This required increase in records comes at a higher cost, with the genetic correlation of 0.6 scenario resulting in close to a 10-fold increase in investment required. Alternatively, sniffer measurements in the feedlot would require a greater number of records, estimated at 34,000 and 150,000, assuming a genetic correlation with grazing cow methane emissions of 0.8 and 0.6, respectively. This increase in the number of records required as the genetic correlation weakens illustrates the importance of not only choosing the technology, but also the type of animal to measure.

The gas flux, accumulation chamber and sniffer technologies were chosen as they are amenable to measures on mature grazing cows, which is the goal trait. The biomarker phenotype, although preliminary at this stage, is unlikely to be a direct measure of methane in mature grazing cows and can be expected to have a lower genetic correlation with the goal trait. To obtain the 0.51 accuracy possible with gas flux measures in grazing cows, the genetic correlation between the molecular phenotype and the target trait would need to be at least 0.82. If the correlation was 0.6, the number of molecular phenotypes required would be 320,000 which would result in 5 times the cost. Not only does measuring a correlated trait put a cap on the possible accuracy, equal to the genetic correlation, it can result in the number of records required to achieve the same accuracy being orders of magnitude greater.

The cost of measurement was considered, but this may not have completely captured the true cost. For example, assume the biomarker phenotype costs \$30 USD. In some scenarios, the number of records required was large, with 68,000 samples in the base scenario. Access to this many animals and collection and processing of this large number of samples is something that needs to be practically considered. One of the benefits of the infield sniffer is the ease of use as it is somewhat of a passive approach. The lower cost enabled more animals to be measured but this too needs practical consideration. To accomplish a similar accuracy to what is possible

with the more costly and involved gas flux measurements, over 4 times more measurements will be needed. This will require logistics with more producers and more animals and will be more difficult in partner countries like Ireland and the UK where herd sizes are smaller. The added benefit of measuring more animals across more environments is the ability to capture more genetic variation and potential investigations into genotype by environment interactions. Although this study compared individual technologies, the implementation in practice will see a combination of technologies. Both Australia and Ireland have already developed significant reference populations with GreenFeed units, and New Zealand has embarked on a significant phenotyping initiative using accumulation chambers. Besides a mix of measurement technologies, a combination of animal types will be required as historic datasets are combined with measures on steers in a feedlot setting along with heifers and cows in grazing environments likely being combined. Appropriate analyses models will need to combine multiple correlated traits across animal type, measurement technology and potentially environments with the goal of a limited number of breeding values reported. The results of this study demonstrate the potential value of in-field sniffer measurement technology as an added measurement technique. At conservative heritability estimates combined with the relatively low cost and the ability to measure the target trait in mature cows, the technology will contribute to the reference being developed.

Conclusions

Less accurate and cheaper technology can result in more reliable genomic predictions as the lower cost per record enables more records for a given investment. The heritability of the lower cost measurement technologies evaluated can be lower to achieve similar outcomes in genomic prediction accuracy compared to in-field gas flux methods. As the genetic correlation between the measured trait and the target trait is reduced, more records are needed to obtain the same accuracy, with proportional additional costs, which can be substantial.

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