Predicted economic and greenhouse gas benefits from using improved maternal genetics in UK beef cattle

C. Quinton[1], P. Amer[1], T. Kirk[1] & E. Wall[2]

[1] *AbacusBio Ltd., 442 Moray Place, P.O. Box 5585, 9058 Dunedin, New Zealand*
cquinton@abacusbio.co.nz *(Corresponding Author)*
[2] *SRUC, Kings Buildings, West Mains Road, EH9 3JG, UK*

Summary

A gene flow model was used to predict the economic and greenhouse gas emissions (GHG) effects of using improved maternal trait genetics in a UK beef herd expressed over 20 years. Maternal traits in a dual-purpose index were partitioned out into a Maternal sub-index (M) containing mature weight, calving interval, age at first calving, longevity, gestation length and calving ease. Economic and GHG effects of changes in each trait in response to change in M were calculated. The expressions of these traits in calves, heifers and cows over 20 years were modelled for the current M sub-index genetic trend, and for scenarios that modelled selecting high maternal value sires to breed herd replacements over short (5 years) and long (20 years) terms. Selecting high maternal value sires was predicted to reverse current trends of declining overall maternal economic value and rising GHG emissions, mainly through improvements in mature weight and calving interval. For example, long-term selection of AI proven sires with M genetic value £30 above sire mean was predicted to generate a cumulative economic increase of £47/cow calving with a GHG reduction of 95 kgCO_2e/cow after 5 years, and an increase of £344 /cow calving with a reduction of 2009 kgCO_2e/cow calving after 20 years. These results indicate that genetic improvement of beef maternal traits through selection of high maternal-value sires can have substantial economic benefits while reducing GHG emissions.

Keywords: beef, cattle, selection, economic index, greenhouse gas, environment

Introduction

The Beef Efficiency Scheme (**BES**) is a program to improve the efficiency of Scottish beef suckler herds, with the goal to improve herd profitability and reduce greenhouse gas (**GHG**) emissions. A major strategy is genetic improvement through increased use of elite maternal genotypes and genomic selection. For the BES, there is a need to quantify the effects of genetic change on beef herd profitability and GHG emissions, and predict a timeframe for when these effects will be realized.

Genetic change in Scottish beef can be measured through the Maternal Dual-Purpose index, which contains maternal and carcass traits (Roughsedge et al. 2005). Genetic trends for maternal traits have shown improvements in age at first calving and gestation length, but unfavourable trends of increasing mature weight, lengthening calving interval and reduced calving ease (Amer et al. 2015). Several of these traits also influence GHG emissions (Wall et al. 2010).

In this study, a gene flow model was used to predict the economic and GHG effects of using improved maternal trait genetics in a beef herd that are expressed over 20 years in

calves, heifers, and breeding cows. The objectives were: 1) construct a gene flow model to predict expression of maternal index traits and resultant economic and GHG emissions effects over 20 years, and 2) predict genetic, economic and GHG change over time from a commercial farmer sourcing improved maternal trait genotypes to breed herd replacements.

Methods

Index effects on economics and greenhouse gas emissions

The Dual-Purpose index maternal traits were partitioned out into a Maternal sub-index (**M**) containing mature weight (**MWT** for annual cow, heifer and cull cow), calving interval (**CI**), age at first calving (**AFC**), longevity (**LG**), gestation length (**GL**) and calving ease (**CE**). Trait genetic, economic and GHG values and trends are summarised in Table 1. Genetic trends in M traits (based on Amer et al. 2015) were multiplied by trait economic values (based on Roughsedge et al. (2005) scaled to 2013 values as per Amer et al. (2015)) to generate trait-specific economic trends; the sum of these was an overall M trend of -£0.722/cow calving/year. The trait-specific economic effects of the M sub-index (change in £/£ increase in M) were then calculated as the regression of the trait's economic trend on the total M trend. Trait-specific effects on GHG emissions (kg CO_2 equivalents/trait unit) were based on estimates by Wall et al. (2010), except the GHG effect of LG was based on an estimate for cow survival by Quinton et al. (2017), assuming 0.038% survival per year herd life. The relationships of GHG with GL and CE are unclear and were assumed to be zero. GHG values were then multiplied by trait genetic trends to calculate trait-specific GHG trends; the sum of these was an overall M trend of 3.15 $kgCO_2e$/breeding cow/cow calving/year. Trait-specific GHG effects of the M sub-index (change in $kgCO_2e$/£ increase in M) were then calculated as the regression of the trait's GHG trend on the total M trend.

Gene flow model

A spreadsheet gene flow model was built to simulate a herd of cows aged from 2 to 11 years, over 20 years, and expression of M traits in calves, heifers, breeding cows, and cull cows. Herd proportions were based on Roughsedge et al. (2005). Gene flow was modelled as annual M sub-index values in sires, dams and calves for years 0 to 20. As a base point, the herd cow (dam) genetic value at year 0 was set to £0. Sire genetic values were assumed to be following the M genetic trends described above with a genetic lag between sires and cows of approximately 10 years; therefore, at year 0 sire genetic value was -£7.52/cow calving. The model assumed that each year, sires were selected for mating to herd cows whose genetic value was based on the M trend described above. Herd cow genetic merit each year was the average M value of their birth year weighted according to the proportion of each age class. Genetic merit of calves was the average of sire and dam genetic merit and daughters entered the herd as replacements.

In the base scenario, sire genetic values in years 1 to 20 were assumed to follow the same M genetic trend described above. This gene flow was adapted in test scenarios to simulate a farmer selecting only top maternal value sires in year 1 and after. Scenarios tested were: use of AI proven sires, young sires, proven sires with genomics, and young sires with genomics, where these were assumed to respectively have M values 30, 20, 40, and 35 £/cow calving higher than population average bulls at year 1, with M values increasing by £1/year subsequently. Scenarios tested effects of short (5 year) and long (20 year) terms of sire

selection.

Economic and greenhouse gas emission expression

Economic and GHG effects were modelled through expression of traits in different herd groups over time. Genetic value was expressed at birth by calves through traits GL and CE; expressed at age 2 by replacement heifers through MWT, AFC and LG; expressed annually from ages 2 to 11 by cows through MWT, CI and LG; and expressed by cull cows after their last year in the herd through MWT. For each group, coefficients representing the changes in economic and GHG expression per unit increase in the M sub-index were calculated as the regression of the group's sums of economic or GHG changes on the total M trend (Table 1). Therefore, economic coefficients for calves born, replacement heifers, annual cows and cull cows were 0.3238, 0.2651, 1.1501 and -0.7612 £/£ sub-index, respectively; and GHG coefficients were 0, -0.9455, -3.4168 and 0 kgCO$_2$e/£ sub-index, respectively. For each group, these coefficients were multiplied by annual genetic values to obtain annual economic and GHG expression in the herd. Cumulative economic expressions were calculated as net present value (NPV) discounting values at years t by a factor of $1/(1+0.05)^t$ and then summing over 5, 10 and 20 years. Cumulative GHG expressions were also calculated over these years.

Results and Discussion

Predicted annual maternal genetic values in sires, dams and calves, and expressed economic value and GHG in the herd for years 0 to 20 are shown in Figures 1, 2 and 3. These figures present predictions for the base model scenario, and scenarios of a maternal AI proven sire (M value £30 above sire average) selected for 5 or 20 years. Other sire selection scenarios followed similar patterns scaled according to sires' M values. Cumulative economic and GHG effects of all scenarios are presented in Table 2 as deviations from the base scenario.

When high maternal value sires were selected, their improved daughters entered the herd, causing maternal genetic value of dams to rise starting in year 3, compared with the base scenario where M value continued to decline (Figure 1). For short-term (5y) sire selection, dam M value increased until year 7, after which it declined back to starting level by year 13. For long-term (20y) sire selection, dam M value continued to increase in line with sire gains.

Effects on expressed economic value

In the base model, calves, cows and replacement heifers all lost value (£/cow calving) over time due to expression of increasing MWT for heifers and cows, lengthening CI, increasing AFC, and reduced CE; only cull cows increased in value due to higher MWT (Figure 2). The losses outweighed gains, therefore total maternal value expressed (sum of all groups) was -£3.48/cow calving at year 0 and decreased over time. After 5 years, cumulative NPV was a loss of £27/cow calving due to expressed maternal traits, and after 20 years, a cumulative NPV loss of £125/cow calving. These results reflect an industry concern that over-emphasis on growth and carcass conformation has been a detriment to maternal ability.

Selection of high maternal-value sires generally reversed these economic trends (Figure 2). With short-term selection, overall maternal trait expression increased toward a peak of £11.56/cow calving at year 5, driven by gains expressed in most groups, except cull cows which lost value slightly due to decreasing MWT. After year 5, when superior genetics

stopped being used, calves born declined in value, with effects flowing to replacement heifers and cows in the following 2 years. After year 10, total value returned to negative values. For long-term sire selection, overall expressed trait value continued to increase in line with sire gains. There was always a trade-off of value expressed by cull cows versus other maternal traits, but gains in expression by annual cows outweighed cull losses. Compared with the base scenario, the scenarios for a maternal AI proven sire resulted in cumulative NPV increase of £47/cow calving after 5 years, and after 20 years, increases of 109 and 344 £/cow calving for short- and long-term selection, respectively (Table 2).

Effects on greenhouse gas emissions

In the base model, overall GHG emissions (kg CO_2e/breeding cow/cow calving) rose over time due to expression of increasing MWT for heifers and cows, and lengthening CI (Figure 3). Higher MWT increases GHG through increased maintenance feed required by larger animals, and longer CI increases GHG though greater number of empty (non-producing) days fed (Wall et al. 2010). After 5 years, cumulative GHG emissions were 60 kgCO_2e/cow calving due to expressed maternal traits, and after 20 years, 707 kgCO_2e/cow calving.

Selection of high maternal-value sires reversed these GHG trends (Figure 3). Short-term selection reduced annual overall GHG emissions by 40 kgCO_2e/cow calving at year 7, driven by improvements in MWT and CI which reduce maintenance feed requirements and number of empty days. After year 7, the effect of superior maternal genetics began to be lost as GHG emissions rose and by year 12 emissions returned to starting levels. For long-term sire selection, overall GHG emissions continued to reduce. In these models, selection affected GHG emissions from heifers and mature cows; changes in traits expressed by calves and cull cows were assumed not to influence GHG. Compared with the base scenario, the scenarios for a maternal AI proven sire resulted in cumulative reduction of 95 kgCO_2e/cow calving after 5 years, and after 20 years, reductions of 623 and 2009 kgCO_2e/cow calving for short- and long-term selection, respectively (Table 2).

The results of this study indicate that genetic improvement of maternal traits through selection of high maternal-value sires can have substantial economic benefits while reducing greenhouse gas emissions in UK beef farms.

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Table 1. Maternal sub-index (M) trait genetic trends, and economic (£/cow calving) and greenhouse gas (GHG, kgCO₂e/breeding cow/cow calving) values (change/trait unit), trends (change/year) and M index effects (change/£ M sub-index).

		Economic (£)			GHG (kgCO$_2$e)		
Trait[1] (unit)	Genetic trend[2] (units/cow calving/y)	Value[3] (Δ/unit)	Trend[4] (Δ/y)	M effect[5] (Δ/£ M)	Value[6] (Δ/unit)	Trend[7] (Δ/y)	M effect[8] (Δ/£ M)
MWT-cow (kg)	2.1284	-0.35	-0.743	1.0286	0.878	1.869	-2.532
MWT-heif (kg)	0.3618	-0.84	-0.305	0.4217	1.89	0.684	-0.927
MWT-cull (kg)	0.3618	1.52	0.550	-0.7612	0	0	0
CI (d)	0.0802	-1.29	-0.104	0.1437	7.46	0.598	-0.811
AFC (d)	-0.0003	-348.95	0.097	-0.1344	3.85	-0.001	0.002
LG (y)	0.0010	94.46	0.016	-0.0222	-0.625	-0.0001	0.0001
GL (d)	-0.0145	-2.05	0.030	-0.0411	0	0	0
CE (%)	-0.0520	5.07	-0.264	0.3649	0	0	0
Sum =			-0.722			3.150	

[1] MWT=mature weight of annual cow, heifer and cull cow; CI=calving interval; AFC=age at first calving; LG=longevity; GL=gestation length; CE=calving ease.
[2] Based on Amer et al. (2015).
[3] Economic value based on Roughsedge et al. (2005) scaled to 2013 value as per Amer et al. (2015).
[4] Economic trend = unit genetic trend × economic value.
[5] Economic effect of M sub-index = regression of trait economic trend on total M trend.
[6] GHG value based on Wall et al. (2010), except LG which is based on Quinton et al. (2017) survival value.
[7] GHG trend = unit genetic trend × GHG value.
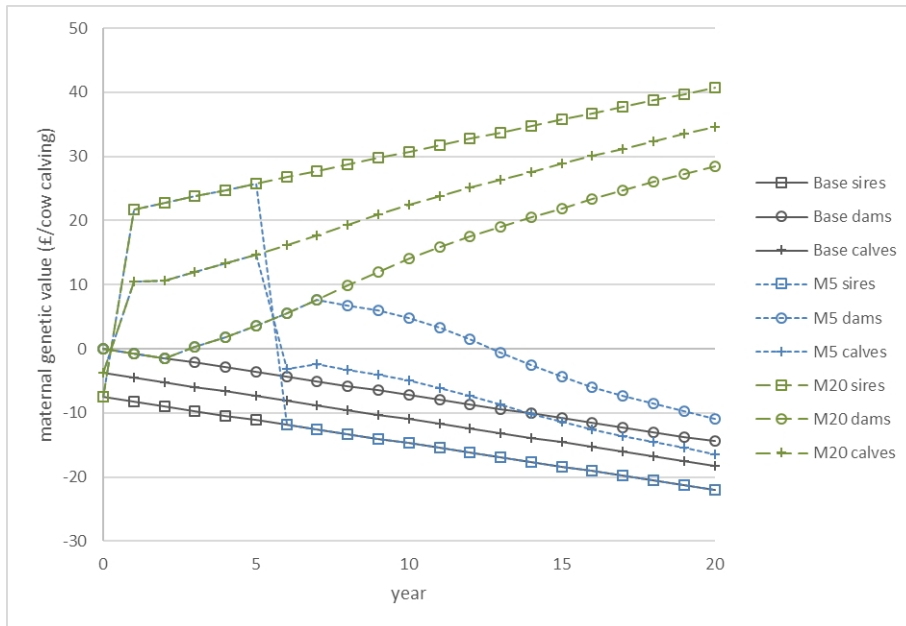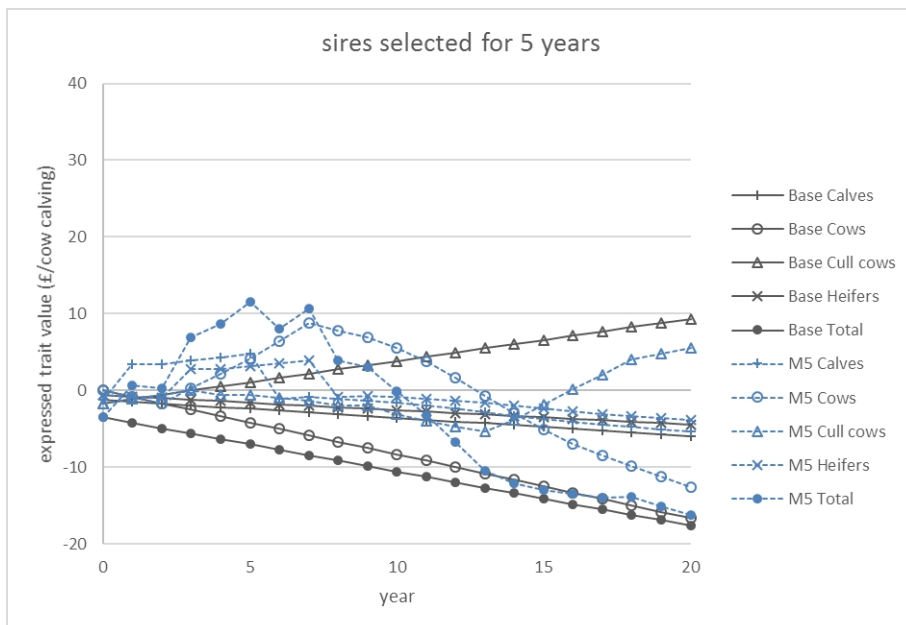[8] GHG effect of M sub-index = regression of trait GHG trend on total M trend.

Figure 1. Maternal sub-index (M) genetic values (£/cow calving) of sires (□), dams (○) and calves (+) in base scenario (solid black lines), and scenarios selecting sire genotypes £30 above population mean M for 5 years (short dash blue lines) and for 20 years (long dash green lines).
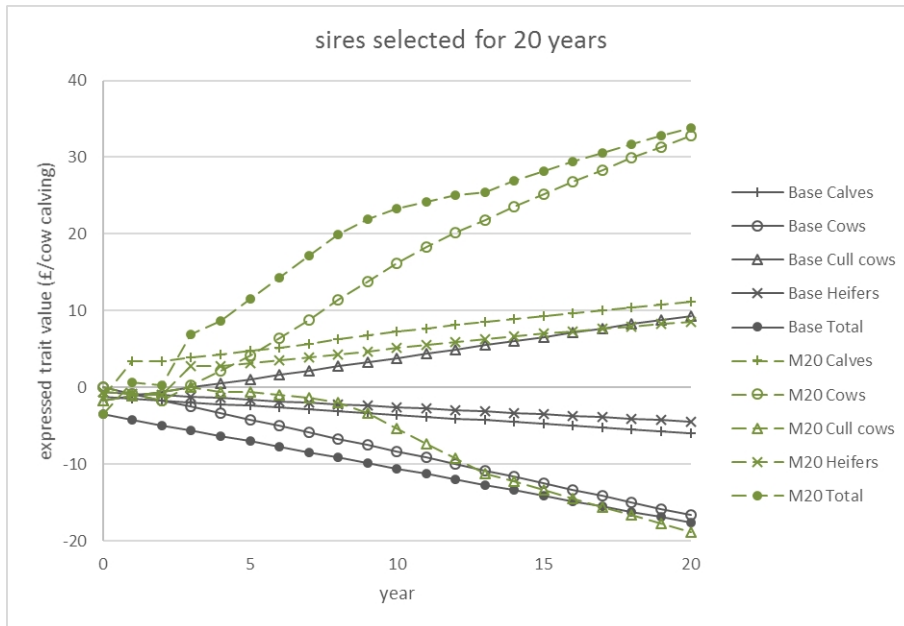
Figure 2. Expressed economic value (£/cow calving) of calves (+), cows (O), cull cows (Δ) and replacement heifers (×), and total (●) in base scenario (solid black lines), and scenarios selecting sire genotypes £30 above sire mean maternal sub-index value for 5 years (top, blue lines) and for 20 years (bottom, green lines).
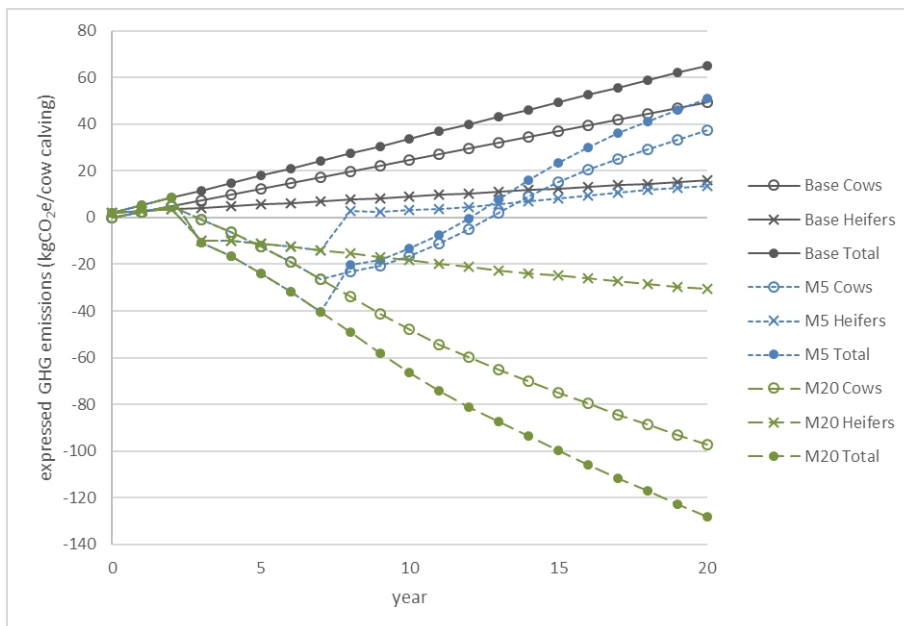

Figure 3. Expressed GHG emissions (kgCO$_2$e/cow calving) of cows (O) and replacement heifers (×), and total (●) in base scenario (solid black lines), and scenarios selecting sire genotypes £30 above sire mean maternal sub-index value for 5 years (short dash blue lines) and for 20 years (long dash green lines).

Table 2. Predicted cumulative discounted economic value expressed, and cumulative GHG emissions expressed after 5, 10 and 20 years in scenarios selecting high maternal value sires for 5 or 20 years. Values are deviations from base scenario.

Selection term,	Economic (£/cow calving)			GHG (kgCO$_2$e/cow calving)		
Sire type	5y	10y	20y	5y	10y	20y
5, AI proven	47	96	109	-95	-356	-623
5, Young	32	67	77	-65	-248	-436
5, Genomic	62	125	142	-126	-464	-809
5, Genomic young	54	110	126	-111	-410	-716
20, AI proven	47	143	344	-95	-478	-2009
20, Young	32	102	261	-65	-339	-1524
20, Genomic	62	183	427	-126	-616	-2494
20, Genomic young	54	163	385	-111	-547	-2251

[1] AI proven sires, young sires, proven sires with genomics, and young sires with genomics assumed to have maternal sub-index values 30, 20, 40, and 35 £/cow calving higher than population average sire, respectively.