



Project Partners

Beef Feed Efficiency Programme Consortium Update

October 2018

The Beef Feed Efficiency Programme (BFEP) is nearing the end of its data collection phase, and is it is progressing well in relation to achieving its major milestones, having expanded in the summer of 2017 in response to an additional injection of funding from the Scottish Government and ABP Ltd. The programme aims to demonstrate the ability to measure and select for feed efficiency traits in beef cattle in a UK commercial environment. Four specially equipped commercial farms across the UK have been measuring individual feed intake in growing beef cattle since July 2016, with over 2340 records collected. The output will include genetic parameters required for the development of breeding values for traits associated with feed efficiency. Initially, the programme has targeted Limousin bred cattle, but has also added Aberdeen Angus, and aims to extend to other breeds in the future. EBVs for the Limousin breed will be produced and incorporated into a revised selection index aimed to be rolled out by summer 2019.

Cattle recorded at the SRUC facility

Records for just over 500 cattle, across 5 batches, were initially collected at Scotland's Rural College (SRUC) Easter Howgate facility. Pure and crossbred cattle were sourced in sire groups, representing a wide range of genetic merit within the population, and their intake and performance records will form the basis of the genetic evaluation.

Commercial feed recording units

GrowSafe feed recording equipment has been installed on 4 commercial farms across the UK. The unit furthest south, in Dorset, is currently sourcing its seventh batch of cattle, and has submitted 534 records thus far. Dorset has contributed some 175 Angus sired records and 359 Limousin sired records. A host unit in Yorkshire recorded 205 records, and was then replaced with two "half size" recording farms in North Wales and North Yorkshire, with 60 places each. The two new units were installed in November 2017 with the aim of collecting 240 records each by end December 2018. Both are well on their way to achieving their respective targets, having put through 363 cattle between them to date.

Having a recording unit in Scotland has allowed the programme greater flexibility in its search for suitable cattle in terms of both geography and capacity, and has allowed an expansion in scope to incorporate Angus



sired progeny. This unit is in its 5th batch of cattle and by the end of the current batch will have measured 720 cattle, meeting its target for both numbers and timing.

In total the programme has recorded over 2340 records (by 26th October 2018). This represents 1928 Limousin bred animals and 412 Aberdeen Angus bred animals. There have been 309 Limousin sire groups recorded along with 85 Aberdeen Angus sire groups. The programme has exceeded its targeted 1800 Limousin records, sufficient for creation of the parameters required to develop an EBV for feed efficiency. Table 1 below demonstrates where the programme currently sits in relation to records collected across the UK.







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	Actual							Predicted to end 2018			
	B1	B2	B3	B4	B5	B6	Totals	B4	B5	B7	Total
Dorset	46	109	98	89	106	86	534			120	654
Yorkshire	87	118					205				205
SRUC	99	119	131	41	128		518				518
Scotland	135	165	165	121	134		720				720
County Durham	62	64	57				183	60			243
North Wales	58	61	61				180	60			240
							2340				2580

Table 1 BFEP actual and predicted records collected to end December 2018

Initial Correlations

Interim results for all completed batches were reported in the May 2018 consortium update. Since then further work has been done to produce correlations and heritabilities from the data collected thus far. A summary of this information is shown below.

Trait	Heritability	Genetic variance	Residual variance	
Growth rate	0.43 (0.16)	0.01	0.01	
Mean fat	0.22 (0.14)	0.21	0.78	
DMI	0.39 (0.16)	0.14	0.21	
RFI	0.24 (0.15)	0.08	0.24	
FCR	0.46 (0.17)	0.34	0.40	

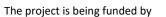
Table 2. Preliminary results of the univariate analyses of the beef feed efficiency data

Table 2 shows the results of the univariate analyses of growth rate, mean fat, DMI, RFI and FCR. Heritabilities are in line with those from other studies and populations. However, the standard error is high for some of the heritability estimates and therefore we do not have enough records for those traits to have complete confidence in the estimate (fat and RFI) at this stage.

Growth rate		Growth rate	Mean fat	DMI	RFI	Res corr
	Mean fat	0.44 (0.16)	0.13 (0.24)			-0.27 (0.22)
	DMI	0.43 (0.16)		<u>0.65 (0.23)</u>		0.10 (0.18)
Mean fat	RFI	0.49 (0.16)			0.08 (0.36)	-0.26 (0.16)
	Growth rate	-0.06 (0.04)	0.60 (0.11)			-0.27 (0.22)
	DMI		0.28 (0.14)	0.29 (0.44)		-0.59 (0.11)
DMI	RFI		0.22 (0.14)		0.10 (0.43)	-0.12 (0.12)
	Growth rate	<u>0.33 (0.03)</u>		0.41 (0.16)		0.10 (0.18)
RFI	Mean fat		-0.34 (0.03)	0.28 (0.15)		-0.59 (0.11)
	Growth rate	<u>-0.14 (0.03)</u>			0.24 (0.15)	-0.26 (0.16)

Table 3. Results of bivariate analyses beef efficiency data (significant heritability estimates in bold, significant correlation estimate in italics and underlined)

Table 3 shows the results of the bivariate analyses, which helps to estimate the genetic relationship between the traits affecting feed efficiency and improve the information used to estimate all genetic









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parameters. Fixed effects used varied between the analyses and traits. Models were based on the univariate models and were kept as close as possible to these models.

- Heritabilities were mostly in agreement between the bivariate models and the univariate. However, mean fat heritability estimated from the univariate analysis fluctuated in scale depending on the correlated traits included in the analysis (h² fat = 0.60 (0.11)) with growth rate between 0.22 (0.14) to 0.28 (0.14) for the other bivariate analyses). This will help to inform us if we include fat as a separate trait in the genetic evaluation of feed efficiency or include it as an explanatory variable in the models of other traits.
- For mean growth rate in a bivariate model with RFI, the proportion of UK beef and other breed were significant. The heterosis coefficient between native and continental beef breed types was significant. Recombination coefficients were found to be significant for dairy breed and other breed crosses, and for continental beef and other breed crosses. The significance of these factors highlight the importance of including the crossbred and original breed effects in analysing crossbred data.
- For RFI in a bivariate model with growth rate, the proportion of native breed type was significant. For RFI in a bivariate model with mean fat, the proportion of UK beef and other breed were significant. The heterosis coefficient between dairy breed and other breed types, between UK beef and continental beef breed types and UK beef and other breed types was significant. Recombination coefficients were found to be significant for dairy breed and continental beef and other breed and continental beef crosses, for dairy breed and other breed crosses, and for continental beef and other breed crosses.
- For DMI in a bivariate model with growth rate, the proportion of dairy breed was significant.

Table 4 shows the heritabilities (on-diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal).

Table 4. Results of the trivariate analysis of the beef efficiency data (significant heritability estimates									
in bold, significant heritability	/ estimates	in	bold <u>,</u>	significant	correlation	estimate	in	italics	and
<u>underlined)</u>									

	Growth rate	Mean fat	DMI
Growth rate	0.46 (0.16)	0.24 (0.36)	<u>0.70 (0.27)</u>
Mean fat	0.03 (0.03)	0.21 (0.14)	0.22 (0.49)
DMI	<u>0.31 (0.03)</u>	<u>-0.36 (0.03)</u>	0.27 (0.15)

- Heritabilities were in agreement with heritabilities resulting from the bivariate analyses, except for mean fat (discussed earlier)
- The only significant genetic correlation (se) estimated was between growth rate and DMI was 0.65 (0.23) for the bivariate and 0.70 (0.27) for the trivariate analysis, which was in agreement. The other genetic correlations that involved fat were not significantly different from zero.
- The phenotypic correlation (se) between growth rate and DMI was 0.33 (0.03) for the bivariate and 0.31 (0.03) for the trivariate analysis, which was in agreement. The phenotypic correlation between mean fat and DMI was -0.34 (0.03) for the bivariate and -0.36 (0.03) for the trivariate analysis.
- Some of the proportion of each breed (PEB), heterosis and recombination coefficient terms were significant for the bivariate and trivariate analyses. However, when included in the trivariate model ASReml failed to fit all fixed effects included in the model. Therefore, PEB, heterosis and recombination coefficient terms were not included in the final trivariate model.





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• For the bivariate analysis between growth rate and DMI the proportion of dairy breed was significant.

Business planning & knowledge exchange (KE)

The business planning and KE group have transferred their activity to the Project Management Group having submitted a report to Defra on options for taking the programme forward. The members of the business planning group felt that more progress could be made having individual conversations with the supply chain partners, rather than in a group format. Progress to secure funding to continue recording feed efficiency traits to roll out across a wider proportion of the industry has been slow. Currently no firm plans are in place. The project management group meets regularly and is monitoring progress on several of the activities that the business planning group initiated.

a. Contract for commercial unit(s)

The current contract with the commercial units finishes at the end of December 2018 and a new draft covering the Legacy period has been circulated. The aim of the contract is to allow for continuation of this work, but with flexibility for the host units.

b. Leaflet

A leaflet that advertises the facilities and capabilities has been produced. Circulation to interested parties and more widely through AHDB channels is imminent.

c. Alternative funding sources

Both SRUC and AHDB are attempting to utilise external funding bodies to source partial funding to continue to measure feed intake in the UK, with the aim of creating parameters for genetic selection. Further, both SRUC and AHDB are encouraging breed societies to recognise the requirement and opportunity for external funding, and providing partnership options for these applications.

d. Knowledge Exchange

A series of open meetings were held on the commercial units in early summer 2018. The meetings were well attended and considerable interest was shown in the industry benefits that recording feed efficiency across multiple breeds could bring. Follow up activity has seen breed specific meetings convened to discuss in more detail the options available through the programme and the estimated costs. There are a few focus group visits planned over the autumn, which increase awareness of the programme and prepare the industry for introduction of feed efficiency EBVs in 2019. The recording units are very willing to host visits by groups wishing to come and learn about the work they are doing so if you have a group wishing to visit please contact natalie.cormack@ahdb.org.uk.

Alongside breeder facing communication, industry wide knowledge exchange activity has aimed to promote the progress of the programme and demonstrate the scope for breed improvement by showing the variation seen in preliminary data sets. Two case studies which showcase breeders that have contributed calves for data measurement have been developed to do this. Regular updates of the project are provided to industry via the AHDB e-newsletter 'Feeding Club', producer bulletins, press releases, presentations to farmer groups, and through partner communications e.g. AHDB Dairy, British Limousin Cattle Society, and the Aberdeen Angus Cattle Society. The programme has also featured on the AHDB Beef & Lamb stand at shows over the summer including Beef Expo. AHDB communications team have created a blog focussed on each individual host farm over a series of posts.





