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ACCURACY OF GENOMIC SELECTION FOR RESIDUAL FEED INTAKE AND 250-DAY LIVEWEIGHT IN DAIRY HEIFERS USING HIGH DENSITY (630K) SNP

J.E. Pryce[1], J. Arias[2], P.J. Bowman[1], K.A. Macdonald[3], G.C.Waghorn[3], Y.J. Williams[4], W.J. Wales[5], R.J. Spelman[2] and B.J. Hayes[1]

[1]Department of Primary Industries, 1 Park Drive, Bundoora, VIC 3083, Australia
[2]LIC, Private Bag 3016, Hamilton 3240, New Zealand
[3]DairyNZ, Private Bag 3221, Hamilton 3240, New Zealand
[4]Department of Primary Industries, 255 Ferguson Rd, Tatura, VIC,3616, Australia
[5]Department of Primary Industries, 1301 Hazeldean Rd, Ellinbank, VIC 3820 Australia

SUMMARY

Using data from almost 2,000 Holstein-Friesian dairy heifers measured for growth rate and feed intake in both Australia and New Zealand (NZ), we demonstrated substantial variation in residual feed intake (RFI) and 250-day-liveweight (LWT250d). The respective heritabilities of RFI and LWT250d were 0.25 and 0.31 in Australian data and 0.41 and 0.25 in NZ data. Further, using around 630,000 SNP markers, genomic breeding values for RFI and LWT250d could be predicted with a moderate degree of accuracy (RFI: 0.41 and 0.31 in Australian and NZ data respectively; LWT250d: 0.41 and 0.25 in Australian and NZ data respectively).

INTRODUCTION

Residual feed intake (RFI) is usually defined as the difference between an animal's actual feed intake and its expected feed intake based on its size and growth over a specific period. In growing beef cattle, significant genetic variation in RFI of up to 30% has been demonstrated (Arthur *et al*. 2004). However the genetic variation seen in beef cattle cannot be assumed to be the same in dairy cattle for two reasons. Firstly, long-term selection objectives in dairy cows are very different from beef cattle – namely selection for high milk production. Secondly, in lactating dairy cattle the calculation of RFI is complicated by the dynamic changes in liveweight and body condition which occur annually and which need to be accurately accounted for if RFI is to be accurately determined. Therefore, although RFI has been examined in lactating dairy cows, the amount of true genetic variation and its heritability has not been resolved (see the review of McNaughton and Pryce 2007). The challenge is that a large number of lactating cows must be tested to get accurate estimates of the genetic parameters – a simulation study carried out to determine the number of animals required to estimate the heritability of RFI showed that 2,000-10,000 animals were needed to ensure the estimate was close to the true value and the error around the estimate was small (McNaughton and Pryce 2007). Unfortunately testing so many cows is likely to be both very expensive and logistically difficult. A possible alternative approach is to measure a large number of growing heifers for RFI, select the extremes and then confirm the ranking of these extreme animals for RFI in a lactating cow test. There is some evidence to show that selection for RFI in growing animals is correlated to RFI in mature, breeding and lactating animals (Nieuwhof *et al.* 1992). Therefore, measuring RFI in growing heifers as opposed to lactating cows is attractive as the problems associated with negative energy balance due to mobilisation of body tissue generally do not exist in non-lactating dairy heifers.

The traits considered in this study were RFI and 250-day-liveweight (LWT250d), which is an indicator of heifer growth. The aim was to calculate the accuracy of genomic selection to predict RFI and LWT250d using a reference population of heifers from Australia and NZ and validation populations of cohorts of these animals excluded from the reference population.

MATERIALS AND METHODS

Animals and facilities. With a collaborative effort between research organisations in Australia and NZ, resources were available to take measurements required to calculate RFI on 2,000 Holstein-Friesian heifer calves, approximately 1,000 in each country. The Australian trial was carried out over 2 years in Rutherglen, Victoria and included 2 × Spring and 1 × Autumn born cohorts of calves. The NZ trial was carried out at Hawera, Taranaki over 3 years (Spring born calves) and 3 cohorts (in the last 2 years these were divided into 2 groups run consecutively). In both countries calves were on-test when they were approximately 6-8 months old.

The feed offered to the calves was Lucerne cubes offered *ad libitum*. Both Australian and NZ trials used electronic feed intake measuring devices made by Gallagher Animal Management Systems, Hamilton, NZ. The feed intake units were hard wired to data loggers, so data was relayed continually 24 hours a day for the duration of the trial. Williams *et al.* (2011) present full details of the phenotype data collection and data editing techniques (Australia only).

Phenotypes. Both countries calculated the phenotypes of RFI and LWT250d independently within cohorts. RFI was calculated by fitting growth rate, average liveweight and age to dry matter intake (Williams *et al.* 2011). RFI was the residual term from the fitted model. Additionally farm of origin was fitted to the Australian data, as Australian heifers were leased from their owners, while NZ heifers were purchased at a week of age. Compared to their age-group contemporaries, NZ heifers were high genetic merit, while Australian heifers were average. The Australian and NZ heifers were sired by 167 and 47 different bulls respectively. One bull sired heifers from both countries, although there were more ancestors in common further generations back. Heritabilities were estimated within country for RFI and LWT250d and genetic correlations were calculated for the same trait measured in each country using ASReml (Gilmour *et al.* 2006).

Genotype data quality control. 903 Australian heifers and 1034 NZ heifers were genotyped with the Illumina High Density Bovine SNP chip, which has 780,000 SNP markers. Stringent quality control procedures were applied to the data. These included the use of the Illumina Genetrain (GC) score (>0.6), which describes the performance of genotyping each SNP in each individual. There were 16,316 SNPs that had minor allele frequencies <0.5% and these were removed. We also checked for Hardy Weinberg equilibrium, as SNPs out of Hardy Weinberg equilibrium can indicate genotyping errors. There were 624,930 SNPs that passed all criteria, and 1920 animals.

Methods for predicting genomic breeding values (GEBVs). Three methods were used to predict GEBVs. They were GBLUP (Hayes *et al.* 2009), BayesA (Meuwissen *et al.* 2001) and BayesR (a modified version of Bayesian SSVS; Verbyla *et al.* 2009). While GBLUP assumes a normal distribution of SNP effects, BayesA assumes a t-distribution of SNP effects, allowing a higher probability of moderate to large effects than GBLUP. In BayesR the assumption was that many SNP effects had no effect, as they are not in linkage disequilibrium with any of the mutations that explain the variation in RFI or LWT250d. In this method, 90% of the SNPs were assumed to have no effect.

A cohort (AU1, AU2 or AU3 for the 3 Australian cohorts, NZ1, NZ2 or NZ3 for the New Zealand cohorts) was removed from the data. The SNP effects for either RFI or LWT250d were calculated using the methods above in the remaining data. Using the SNP effects, a vector of genomic estimated breeding values (GEBV) was calculated for the heifers in the trial that was set aside. Ideally, the accuracy of GEBV should be the correlation between the GEBV and the true breeding value (TBV). The TBVs for each animal were approximated as the phenotype (i.e. RFI or LWT250d) divided by the square-root of the respective heritability.

RESULTS AND DISCUSSION

Table 1. Phenotypic standard deviations (SD) and heritability (h^2) estimates with standard errors (s.e.) in brackets for RFI and LWT250d in Australian (AU) and New Zealand (NZ) and the genetic correlation (ra) of the same trait measured in each country

Country	Trait	SD (kg)	h^2 (s.e.)	ra
AU	RFI	0.42	0.25 (0.12)	0.95
NZ	RFI	0.50	0.41 (0.14)	
AU	LWT250d	42.0	0.31 (0.12)	0.73
NZ	LWT250d	17.9	0.25 (0.11)	

The heritability estimates of LWT250d and RFI are presented in Table 1. The genetic correlation between RFI measured in Australia and NZ was 0.95. This is encouraging for genomics research, as it demonstrates that RFI is essentially the same trait in Australia and NZ. In theory at least, this should improve the chances of genomic predictions of RFI across countries. On the other hand, the genetic correlation of LWT250d between Australia and NZ was estimated to be 0.73. This correlation is substantially less than unity and implies that liveweight in Australia and NZ is not the same trait. This could reflect differences in rearing environment or be a result of differing body composition across the two populations.

Table 2. Accuracies of genomic estimated breeding values (GEBVs) and residual feed intake for each validation cohort, when heifers in a cohort were left out of the group of animals used to estimate the marker effects i.e. AU1 is where Australian cohort 1 is the validation dataset

Validation	N (reference)	N (validation)	GBLUP	BayesA	BayesR
AU1	1504	278	0.28	0.40	0.41
AU2	1516	266	0.31	0.40	0.39
AU3	1483	299	0.29	0.42	0.42
Average			0.29	0.41	0.41
NZ1	1670	112	0.67	0.67	0.63
NZ2	1371	411	0.22	0.20	0.19
NZ3	1366	416	0.29	0.33	0.33
Average			0.31	0.31	0.31

Table 3. Accuracies of genomic estimated breeding values (GEBVS) and 250-day-liveweight for each validation cohort, when heifers in a cohort were left out of the group of animals used to estimate the marker effects i.e. AU1 is where Australian cohort 1 is the validation dataset

Validation	N (reference)	N (validation)	GBLUP	BayesA	BayesR
AU1	1504	278	0.50	0.55	0.55
AU2	1516	266	0.22	0.23	0.23
AU3	1483	299	0.40	0.44	0.43
Average			0.38	0.41	0.40
NZ1	1670	112	0.61	0.60	0.59
NZ2	1371	411	0.25	0.27	0.27
NZ3	1366	416	0.13	0.14	0.13
Average			0.24	0.25	0.25

The accuracy of GEBV for RFI was moderate in the Australian data, and significantly different to zero, at 0.41(0.02), when averaged across the three validation cohorts (Table 2). The accuracy of GEBVs in the NZ data was slightly lower. The same pattern was seen for LWT250d with higher accuracies observed for Australian compared to NZ GEBVs. Genomic relationships (calculated for GBLUP) were generally stronger among Australian heifers, which could be why the accuracy of prediction was higher in Australian data. Although there was little difference between methods for NZ GEBVs (Tables 2 and 3), the superiority of the Bayesian methods over GBLUP for predicting Australian GEBVs could demonstrate that when high density SNP data are used, having a model that allows the sizes of SNP effects to vary is advantageous.

Improving the accuracy of GEBVs for RFI is desirable, as the genetic gain that can be achieved is directly proportional to this accuracy. The accuracy of GEBVs can be improved by increasing the size of the reference population where the SNP effects are estimated (in our case even more genotyped heifers with RFI phenotypes), so the SNP effects can be estimated more accurately (Hayes *et al*. 2009). The most cost effective way to increase the size of the reference population is to collaborate with other groups who are also measuring RFI, and exchange data.

The next phase of this work is to establish whether RFI is the same trait in lactating cows (as growing heifers). This will be achieved by evaluating RFI of the 60 highest (in Australia) and 40 highest (in NZ) and the equivalent number of lowest performing heifers in a lactation trial. Also, before RFI can be included in a breeding programme it is important to understand the genetic relationship of RFI with other traits of importance, especially health and fertility traits.

CONCLUSIONS

We have demonstrated that genomic selection of RFI (and LWT250d) is achievable with moderate accuracies in growing heifers. Further work to understand the intricate relationships of this trait with health and fertility traits are required in addition to demonstrating that the trait is repeatable in lactating cows.

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REFERENCES

Arthur P.F., Archer J.A. and Herd R.M. (2004) *Aust. J. Exp. Agric*. **44**:361.

Gilmour A.R., Gogel B.J., Cullis B.R. and Thompson R. (2006) ASReml User Guide Release 2.0. VSN International Ltd, Hemel Hempstead, HP1 1ES, UK.

Hayes B.J., Bowman P.J., Chamberlain A.J. and Goddard M.E. (2009) *J. Dairy Sci*. **92**:433.

Meuwissen T.H.E., Hayes B.J. and Goddard M.E. (2001) *Genetics* **157**:1819.

McNaughton L.R., and Pryce,J.E. (2007) *Proc. NZ Soc. Anim. Prod*. **67**: 392.

Nieuwhof, G. J., van Arendonk, J.A.M., Vos, H. and Korver S. (1992) *Livest. Prod. Sci*. **32**:189.

Verbyla K.L., Hayes B.J., Bowman P.J. and Goddard, M.E. (2009) *Genet. Res.* **91**:307.

Williams Y.J. Pryce J.E., Grainger C., Wales W.J., Linden N., Porker M., and Hayes B.J. (2011) *J. Dairy Sci.* (submitted)