

58. Lifetime feed efficiency and deep phenotypes from scarce feed intake records using the mechanistic LiGAPS-Dairy model

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Abstract

Ideally, selection for feed efficiency requires deep phenotyping of net efficiency, or lifetime recording of intake and all energy sinks across environments. However, recording of feed intake is scarce. Therefore, net efficiency is often defined as a simplistic linear equation, e.g. RFI. We tested the use of the mechanistic LiGAPS-Dairy model to derive nine deep phenotypes with a dataset for 1,228 dairy cows, combining feed intake, yield and liveweight data, with ration, weather, cow and farm data. Mismatch between data recording and model assumptions made this process time consuming, but allowing for missing parities and further automation should improve this quickly. We managed for 206 cows to estimate the deep phenotypes. Heritability and phenotypic correlations between the nine traits were estimated. When the pipeline is finished, the mechanistic LiGAPS-Dairy model will enable us to derive a more comprehensive breeding goal, more closely resembling net efficiency, whilst utilising scarce records.

Introduction

Extending breeding goals require more and more scarcely recorded data to be included in animal breeding. For example, breeding values for feed efficiency should be based on a full lactation or even a full lifetime of many cows, and across many different environments. However, in practice feed intake has been recorded for limited numbers of cows, during part of their lifetime, and on cows that are mostly kept indoors in intensive feeding systems. Also, feed efficiency is a composite trait containing many elements: energy uses for milk production, gestation, maintenance and growth, all with their own net efficiency (Veerkamp and Emmans, 1995). Ideally, animal breeding should target these net efficiencies (e.g. digestibility or converting net energy to yield) rather than partitioning energy away from essential functions towards production. However, net efficiencies are even more difficult to measure than feed intake, and therefore, often simple approximations, like residual feed intake (RFI), are used. A potential solution to make the step from scarcely recorded traits, with limited data per animal in selective circumstances, towards more plausible breeding goals is to use mechanistic models to standardise or derive new traits that can be used in breeding values estimation.

The mechanistic model LiGAPS-Dairy can assess the performance of cows in different environments and in different farm types and uses recorded phenotypes to simulate the performance of dairy cows over their entire lifetime with a time step of one day. Inputs required for this model are parameters that represent the animals' traits, outside weather temperature, information on feed quality and available feed quantity, and livestock management. The feeding strategy implemented can be precisely set and the model has been evaluated under Dutch conditions (van der Linden *et al.*, 2021).

The model genotype (in contrast to the DNA genotype that animal breeders use) of an animal is included in the LiGAPS-Dairy model as a set of different parameters that represent the individual animal's traits, i.e. traits that otherwise need deep phenotyping. Parameter values of individual cows can be determined by model calibration with measured data for milk production, feed intake and liveweight. Using these deeper

phenotypes, the model simulates milk production, feed intake and liveweight across the lifetime of a cow and therefore allows for new definitions of feed efficiency for dairy cows outside the space where data were recorded, e.g. a full lifetime efficiency or in different environments, on top of selecting for the deeper phenotypes directly. For example, a recent pilot study used data from indoor-housed cows at a commercial farm of CRV (milk production, feed intake and live weight) with input model parameters (feed quality and feed availability, weather conditions and livestock management) to calibrate nine parameters (or deep phenotypes) for 101 individual cows, and simulated feed efficiency of these cows in an outdoor grazing system.

The objective of this study was to get estimates for nine deep phenotypes, and to assess their heritability and correlations. We report on work in progress to expand the LiGAPS-Dairy pipeline on a more complex (more herds and years and different recording strategies) and larger dataset (~1,228 dairy cows).

Materials & methods

A dataset was available on 1,228 cows from Dairy Campus and other experimental farms with weekly records on dry matter intake (DMI), fat- and protein-corrected milk (FPCM) and liveweight (LW) recorded in 3,701 lactations and 605 different experimental treatments between 1991 and 2021. For the weekly records there were at least 25 records for DMI, 9 records for kg of milk and 9 records for LW per cow. A cow should have records for at least 2 lactations (the first lactation often differs from the second or third). All cows in the feed efficiency experiments were housed indoors. Birth and calving dates were used as model input to resemble the life of cows in the experiments.

Weather data were obtained for de Bilt, the Netherlands (52.2°N, 5.2°E) and were assumed to be representative for the locations of the experimental farms. Feed quality was not available for individual experiments. The average feed quality of the diets was used from the study by Zom *et al.* (2012), where the average proportion of concentrates was 37% of the dry matter (DM) intake; Crude protein (CP) of concentrates was 188 g/kg DM, digestible Organic Matter (dOM) was 829 g/kg DM, and CP of roughage was 136 g/kg DM, and dOM was 700 g/kg DM.

The LiGAPS-Dairy model, written in R, was subsequently ran for each individual cow with Azure Databricks on the Microsoft Azure platform with inputs from the cow and farm. The model produced outputs that included FPCM, DMI, and LW. During calibration of the deep phenotypes, the simulated FPCM, LW and DMI were compared with the measured data for individual cows, and the difference was expressed as the root mean squared error (RMSE). The RMSEs for FPCM, DMI, and LW were added up and used as input for a genetic algorithm from the R-package 'GA'. This algorithm selected the combination of the nine deep phenotypes that resulted in the lowest sum of RMSE for each cow by iterating the model.

The deep phenotypes of the LiGAPS-Dairy model resulted in nine newly derived feed efficiency traits, together with DMI, FPCM and LW. Heritabilities and genetic correlations were estimated with ASReml (Gilmour *et al.*, 2015) and the model included only the mean and the additive genetic effect using the pedigree relationship matrix for each animal.

Results

The dataset used at the start is described in Table 1. Since it was the first time that the LiGAPS-Dairy model was used with this large dataset, optimising the model was very time consuming. At the time of writing, missing lactations and cows with parity above 5 created model failures, and needed to be excluded. After this selection, data on nearly all cows tested converged, and we were able to estimate the nine deep phenotypes for a cow in about 50 minutes, a task that could be parallelized by using Databricks. In total,

data on 206 cows converged and a small percentage failed due to mismatches between cow data and model assumptions. Solving these mismatches, and further automation and parallelisation is needed to make this process more efficient, and eventually get data on more animals converged. The summary statistics for the nine deep phenotypes are given in Table 2.

Using the 206 animals available just now, only five of the nine heritability estimates converged, albeit with large standard errors (Table 3). The low number of generations used in GA (n=2) might have reduced accuracy of the phenotypes and therefore the heritability. Phenotypic correlations were large between maintenance requirements and milk efficiency, contrary to what was expected when gross efficiency was used. Also, the correlations between the two milk efficiency traits and two Wood curve parameters were high.

Discussion

We reported research in progress on the development of the LiGAPS-Dairy model to derive nine deep phenotypes for scarcely recorded data on cows. Time needed to fit the sparse data was more than expected, and most effort was, and is, on automation of parallelisation and model adjustments to fit the data.

When efficient data fitting is resolved, in the near future, further steps required are to add more animals for the genetic parameter estimation, and to investigate the model fit per cow. Especially how model fit is affected by the records available for a cow, and the number of generations and base population size assumed in the genetic algorithm. These are likely to improve estimation of the heritability, since minimal

Table 1. Summary statistics of the data used.

# cows	1,228		
# lactations	3,701		
Average parity (sd)	2.99 (1.67)		
	FPCM (kg/day)	LW (kg/cow)	DMI (kg/day)
# records	50,364	58,491	62,375
Mean	18.7	609.5	21.3
stdev	7.0	112.5	4.2

Table 2. Average (Avg), standard deviation (sd), minimum (min) and maximum (max) values of nine deep phenotypes in Holstein-Friesian cows (initial n=206).

Description deep phenotypes	Units	Min	Avg	Max	sd
Energy requirements for maintenance	kJ NE/kg ^{0.75} /day	256.9	360.3	420.9	49.4
Maximum intake capacity	Fill units/kg ^{0.75} /day	105.7	120.9	134.4	6.8
Maximum body weight	kg	550.2	651.5	812.1	72.5
Woods curve parameter 1 ¹	-	2,387	3,109	3,562	255
Woods curve parameter 2 ¹	-	11.1	16.5	30.0	2.4
Woods curve parameter 3 ¹	-	0.19	0.28	0.40	0.04
Net energy efficiency for milk	%	0.77	0.89	0.97	0.06
Protein efficiency for milk	%	0.42	0.62	0.70	0.08
Protein requirements per unit NE	g per kJ NE	1.88	2.03	2.20	0.10

¹ Woods curve parameter 1, 2 and 3 indicate the first, second, and third parameter of Woods curve multiplied by 100, describing jointly deeper phenotypes for the genetic potential for milk production in LiGAPS-Dairy.

Table 3. Heritability (diagonal), and phenotypic correlations, with standard errors in brackets for the nine deep phenotypes in Holstein-Friesian cows (initial n=206).

	1	2	3	4	5	6	7	8	9
1 Energy requirements maintenance	0.10 (0.14)	0.34 (0.06)	0.19 (0.07)	0.33 (0.06)	-0.04 (0.07)	-0.05 (0.07)	0.68 (0.04)	0.40 (0.06)	-0.30 (0.06)
2 Maximum intake capacity		0.28 (0.23)	0.18 (0.07)	-0.16 (0.07)	0.16 (0.07)	0.11 (0.07)	0.12 (0.07)	-0.01 (0.07)	-0.18 (0.07)
3 Maximum body weight			0.14 (0.19)	0.11 (0.07)	-0.02 (0.07)	0.19 (0.07)	-0.08 (0.07)	-0.20 (0.07)	-0.08 (0.07)
4 Woods curve 1				0.00 (0.12)	-0.62 (0.04)	-0.31 (0.06)	0.39 (0.06)	0.55 (0.05)	-0.21 (0.07)
5 Woods curve 2					0.00 (0.15)	-0.12 (0.07)	-0.29 (0.06)	-0.08 (0.07)	-0.12 (0.07)
6 Woods curve 3						0.00 (0.09)	-0.36 (0.06)	-0.15 (0.07)	-0.36 (0.06)
7 Net energy efficiency milk							0.00 (0.14)	0.45 (0.06)	-0.13 (0.07)
8 Protein efficiency milk								0.73 (0.18)	-0.12 (0.07)
9 Protein per unit NE									0.10 (0.17)

criteria (two generations and the base population of 40 animals) were used. With a large dataset, the genomic predictions for the nine deep phenotypes can be subsequently used through the mechanistic LiGAPS-Dairy model to derive a more comprehensive feed efficiency breeding goal, more closely than RFI resembling net efficiency or lifetime efficiency, whilst still utilising scarce records for feed intake, FPCM and LW. Furthermore, through this mechanistic model the impact of selection can be estimated in different environments, i.e. indoor versus outdoor systems, or different climates.

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