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Genomic-polygenic and polygenic evaluations for milk yield and fat percentage using random regression models with Legendre polynomials in a Thai multibreed dairy population

Danai Jattawa [a], Mauricio A. Elzo [b], Skorn Koonawootrittriron [a,*], Thanathip Suwanasopee [a]

[a] Department of Animal Science, Kasetsart University, Bangkok 10900, Thailand
[b] Department of Animal Sciences, University of Florida, Gainesville, FL 32611-0910, USA

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ABSTRACT

The objectives of this research were to compare estimates of variance components, genetic parameters, prediction accuracies, and rankings of animals for 305-d milk yield (305-d MY) and 305-d fat percentage (305-d FP) from random regression genomic-polygenic (RRGM) and random regression polygenic (RRPM) models. In addition, RRGM and RRPM prediction accuracies and rankings were compared with those from a standard cumulative 305-d genomic-polygenic model (SCGM). The dataset contained first-lactation monthly test-day records (69,029 for MY and 29,878 for FY) from 7206 Holstein-upgraded cows located in 761 Thai farms. Genotypic data included 74,144 actual and imputed SNP from 1661 animals. Variance components and genetic parameters were estimated using REML procedures. The RRGM and RRPM included contemporary group (herd-year-season), calving age, heterosis, and third-order Legendre population regression coefficients. Random effects were animal additive genetic third-order Legendre regression coefficients, permanent environment third-order Legendre regression coefficients, and residual. The SCGM contained contemporary group (herd-year-season), calving age and heterosis as fixed effects, and additive genetic and residual as random effects. The RRGM yielded higher additive genetic variances and heritabilities for 305-d MY and 305-d FP than RRPM, whereas correlations between MY and FY were similar in both models. The highest prediction accuracies for both traits were for RRGM, followed by RRPM, and the lowest ones were from SCGM. Similarly, the highest rank correlations were between animal EBV for 305-d MY and 305-d FP from RRGM and RRPM, followed by those between RRGM and SCGM, and the lowest ones were between RRPM and SCGM. The higher heritability estimates and higher prediction accuracies for RRGM than for RRPM and SCGM indicated that higher selection responses for 305-d MY and 305-d FP may be achieved in this Thai dairy population by utilizing a random-regression model and genotypic information in addition to phenotypes and pedigree.

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1. Introduction

Random regression models (RRM; Schaeffer and Dekkers, 1994; Jamrozik and Schaeffer, 1997) are the method of choice for genetic evaluation with test-day phenotypic records in dairy cattle. Advantages of RRM over standard cumulative 305-d models include more precise accounting of environmental factors affecting milk production throughout the lactation (Ptak and Schaeffer, 1993; Schaeffer et al., 2000), and in some cases inclusion of animals with incomplete lactations in genetic evaluations (Jensen, 2001). Dairy genetic evaluations for 305-d MY with RRM were found to be more accurate than with standard cumulative 305-d models (Schaeffer et al., 2000; Santos et al., 2014a; 2014b). The advantages of RRM over 305-d models led to their wide utilization for national dairy genetic evaluations in many countries across the world (Interbull, 2007).

The original implementation of RRM for dairy genetic evaluations utilized only test-day phenotypic records and pedigree data. Advances in genotyping technology have made information on thousands of genotypes per animal available for dairy genetic evaluations. The combination of genomic information with phenotypes and pedigree (Meuwissen et al., 2001) increased accuracy of prediction (VanRaden et al., 2009; Wiggans et al., 2011; Thomasen et al., 2012; Přibyl et al., 2014) and rate of selection progress for dairy traits in cattle populations (de Roos et al., 2011; Buch et al., 2012). Several genomic evaluation approaches have been developed and implemented to date. The first implementation of a

* Correspondence to: Department of Animal Science, Faculty of Agriculture, Kasetsart University, Bangkok 10900, Thailand.
E-mail address: agrskk@ku.ac.th (S. Koonawootrittriron).

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national genomic evaluation in dairy cattle utilized a multi-step approach (VanRaden, 2008). However, this approach is somewhat complex and difficult to implement, especially in multiple-trait model and RRM (Misztal et al., 2013; Silva et al., 2014). Thus, a single-step approach was subsequently developed that was easier to implement and more accurate for genomic evaluation than multi-step procedures (Misztal et al., 2009, 2013; Aguilar et al., 2010). Single-step genomic-polygenic EBV for milk and fat yield with a standard cumulative 305-d model yielded prediction accuracies that were, on the average, 7.2%, higher than from a polygenic model in the Holstein-upgraded Thai population (Jattawa et al., 2015). However, evaluation of animals in this population with either polygenic or single-step genomic-polygenic RRM has yet to be done. This action is crucial for the development of a national dairy cattle genomic evaluation program in Thailand. Thus, the objectives of this research were: 1) to estimate variance components and genetic parameters for 305-d milk yield and 305-d fat percentage using random regression single-step genomic-polygenic and polygenic models, and 2) to compare prediction accuracies and rankings of animals for 305-d milk yield and 305-d fat percentage from random regression single-step genomic-polygenic and polygenic models, and also with prediction accuracies and rankings from a standard cumulative 305-d genomic-polygenic model in the Holstein-upgraded dairy cattle population in Thailand.

2. Materials and methods

2.1. Animals, datasets, and traits

Animals in the dataset belonged to the Holstein-upgraded Thai dairy population. The dataset included 7206 first-lactation cows that were the progeny of 933 sires and 6145 dams. Animals in this population were produced through upgrading from various breeds (Brahman, Jersey, Brown Swiss, Red Dane, Red Sindhi, Sahiwal and Thai Native) to Holstein (Koonawootrittriron et al., 2009). Approximately 90% of cows, 93% of sires, and 78% of dams were 75% Holstein or higher.

Cows were from 761 farms located across five regions in Thailand (North, Northeastern, Western, Central, and Southern). Cows had their first calving between 1997 and 2014. Phenotypic records were collected once a month starting on the fifth day after calving until completion of lactation. Only cows that had their first test-day record before 40 days and had at least 4 test-day records were used. The last test-day record used here was the eleventh record (collected between 296 d and 340 d in milk). A total of 69,029 monthly test-day records from 7206 cows that met these criteria were used in this research.

Two separate phenotypic datasets were prepared for genetic evaluations with the random regression and the standard cumulative 305-d model. Random regression models utilized a phenotypic dataset with monthly test-day records of 69,029 milk yield (MY) and 29,878 fat percentages (FP). The standard cumulative 305 – d model used a phenotypic dataset with accumulated 305-d milk yields (305-d MY) and average 305-d fat percentages (305-d FP) computed using the collected monthly test-day records. The 305-d MY records were computed using the test interval method (Sargent et al., 1968; Koonawootrittriron et al., 2001). Numbers of records, means, and SD per trait for each dataset are shown in Table 1.

Table 1
Description of datasets used for the two random regression models and the standard cumulative 305-d model.

Item	n	Mean	SD
Random regression models			
Cows	7206		
Milk yield, kg	69029	13.8	4.9
Fat percentage, %	29878	3.5	0.9
Standard cumulative 305 – d model			
Cows	7206		
305-d Milk yield, kg	7206	4243	1112
305-d Fat percentage, %	3264	3.5	0.7

2.2. Genotypic data

Tissue samples (blood and semen) were collected from 2661 animals (89 sires and 2572 cows). All sires had daughters with pedigree and phenotypes and all cows had pedigree and phenotypes. The tissue samples were DNA extracted using a MasterPure™ DNA Purification Kit (Epicentre®, Madison, WI, USA). A NanoDrop™ 2000 Spectrophotometer (Thermo Fisher Scientific Inc., Wilmington, DE, USA) was used to assess the quality of the extracted DNA. A DNA sample was considered acceptable if it had a concentration higher than 15 ng/μl and an absorbance ratio (i.e., absorbance at 260 nm divided by absorbance at 280 nm) of approximately 1.8. Acceptable DNA samples were sent to GeneSeek (GeneSeek Inc., Lincoln, NE, USA) for genotyping with genomic profiler chips (1412 with GGP9K, 570 with GGP20K, 540 with GGP26K, and 139 with GGP80K). Numbers of SNP genotypes per chip were 8590 for the GGP9K, 19,616 for the GGP20K, 25,979 for the GGP26K, and 76,694 for the GGP80K. Animals genotyped with GGP9K, GGP20K, and GGP26K chips were imputed to GGP80K using FImpute 2.2 (Sargolzaei et al., 2014). Actual and imputed SNP genotypes with minor allele frequencies lower than 0.04 (n = 2375) or call rates lower than 0.9 (n = 175) were removed. The resulting genotype file after these edits contained 74,144 actual and imputed SNP markers.

2.3. Estimation of variance and covariance components

Estimates of variance and covariance components for MY and FP were obtained using bivariate random regression genomic-polygenic (RRGM) and random regression polygenic models (RRPM). The RRGM was a single-step model (Misztal et al., 2009; Aguilar et al., 2010) that utilized phenotypic, genotypic, and pedigree information, whereas the RRPM utilized only phenotypic and pedigree information. Contemporary groups for RRGM and RRPM were defined as herd-year-seasons because of the extremely low number of cows within herd-test-day subclasses (1 or 2). This resulted in a total of 2208 contemporary groups with a minimum size of 4 cows and a maximum size of 36 cows per contemporary group. In matrix notation, the RRGM and RRPM can be described as follows:

$$y = Xb + Z_a a_a + Z_p p_a + e,$$

where y was a vector of MY and FP monthly test-day phenotypic records, b was a vector of fixed contemporary group (herd-year-season) subclass effects, calving age regression coefficient effects, heterosis regression coefficient effects, and third-order Legendre population regression coefficient effects, a_a was a vector of random animal additive genetic third-order Legendre regression coefficient effects, p_a was a vector of random permanent environment third-order Legendre regression coefficient effects, e was a vector of residuals, X, Z_a, and Z_p were incident matrices relating elements of y to elements of b, a_a, and p_a. Columns of X related phenotypic records to: a) contemporary group effects through ones and zeroes, b) calving age regression coefficient effects through calving ages (mo), c) heterosis regression coefficient effect through animal heterozygosities (i.e., probabilities of one Holstein allele and one

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