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Animal Reproduction Science xxx (xxxx) xxx-xxx



Contents lists available at ScienceDirect

Animal Reproduction Science



journal homepage: www.elsevier.com/locate/anireprosci

Genetic parameters, predictions, and rankings for semen production traits in a Thailand multi-breed dairy population using genomic-polygenic and polygenic models

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ARTICLE INFO

Keywords: Dairy bull Genomic Polygenic Semen production Tropical

ABSTRACT

The objectives were to compare estimates of variance components, genetic parameters, prediction accuracies, and rankings of bulls for semen volume (VOL), number of sperm (NS), and motility (MOT) using genomic-polygenic (GPRM) and polygenic repeatability models (PRM). The dataset comprised 13,535 VOL, 12,773 NS, and 12,660 MOT from 131 bulls collected from 2001 to 2017 in the Semen Production and Dairy Genetic Evaluation Center of the Dairy Farming Promotion Organization of Thailand. Genotypic data encompassed 76,519 actual and imputed SNP from 72 animals. The three-trait GPRM and PRM included the fixed effects of contemporary group, ejaculate order, age of bull, ambient temperature, and heterosis. Random effects were animal additive genetic, permanent environmental, and residual. Variance components and genetic parameters were estimated using AIREMLF90. GPRM heritabilities were slightly greater than PRM for MOT (0.27 compared with 0.24), and slightly less for VOL (0.11 compared with 0.12), and NS (0.17 compared with 0.19). Repeatabilities were slightly less for GPRM than PRM (0.44 compared with 0.45 for MOT, 0.26 compared with 0.28 for NS, and 0.20 compared with 0.21 for VOL). Additive genetic correlations were high between NS and MOT (GPRM: 0.76, PRM: 0.78), moderate between VOL and NS (GPRM: 0.43, PRM: 0.55), and near zero between VOL and MOT (GPRM: -0.13, PRM: 0.04). Rank correlations between GPRM and PRM estimated breeding values (EBV) were high for all traits. The similarity between GPRM and PRM results suggested that SNP data from the small number of genotyped animals had a minimal impact on genetic predictions in this population.

1. Introduction

Artificial insemination (AI) is an essential technique for genetic improvement of milk production traits in Thailand dairy population. Holstein frozen semen from countries with high-producing Holstein populations (Canada, USA, Australia, Japan; Department of Livestock Development, 2015) has been introduced to genetically improve these traits in Thailand. Crossbreeding was initially used to combine the high milk producing capacity of Holstein with the desirable fertility and tropical adaptability of local cattle. These crossbred animals, however, could not produce enough milk to meet Thailand's demand. Thus, a national upgrading system was implemented to produce animals with a greater Holstein percentage breeding while retaining tropical adaptability. Both

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https://doi.org/10.1016/j.anireprosci.2018.05.008

Received 19 March 2018; Received in revised form 24 April 2018; Accepted 9 May 2018

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purebred and crossbred Holstein sires were used. The outcome of this mating system was a multi-breed dairy population composed of animals of a variety of percentages of Holstein and various other breeds (Brown Swiss, Jersey, Red Dane, Brahman, Red Sindhi, Sahiwal and Thai Native; Koonawootrittriron et al., 2009).

Semen traits are economically important for dairy producers because female AI conception rates are highly dependent on semen quantity and quality (Swanson and Herman, 1944; Seidel and Schenk, 2008). Quantity and quality of semen are assessed through semen volume (VOL), number of sperm (NS), and motility (MOT). Heritabilities for these traits ranged from moderate to high and the genetic correlations ranged from low to high in temperate regions (Taylor et al., 1985; Druet et al., 2009; Karoui et al., 2011; Atagi et al., 2017). Currently, there is neither a genomic-polygenic nor a polygenic evaluation for semen traits in the Thailand dairy multibreed populations. There, however, is historical information available on VOL, NS, and MOT at the Semen Production and Dairy Genetic Evaluation Center of the Dairy Farming Promotion Organization of Thailand (DPO). This information could be used to obtain the estimates of variance components and genetic parameters needed to predict genetic values and rank sires for selection and mating purposes. Further, assessing the impact of genomic information on the accuracy of genomic-polygenic relative to polygenic predictions and bull rankings also needs to be determined. Thus, the objectives of this research were 1) to estimate variance components, genetic parameters, and genetic predictions for VOL, NS, and MOT using genomic-polygenic and polygenic repeatability models, and 2) to compare the rankings of genomic-polygenic and polygenic EBV for VOL, NS, and MOT from AI sires in the top 5%, 10%, 15%, 20% and all sires in the DPO dataset.

2. Materials and methods

2.1. Data, animals and traits

Data were collected by the Semen Production and Dairy Genetic Evaluation Center of the DPO (Muaklek, Saraburi province, in Central of Thailand, 14°38′24.7″ latitude North, 101°11′57.2″ longitude East] from October 2001 to July 2017. Semen traits were: volume (VOL, ml), number of sperm (NS; million), and motility (MOT, %). Semen volume was the quantity of semen per ejaculation as measured in a scaled tube. Number of sperm per ejaculate was calculated by multiplying semen volume by sperm concentration. Sperm motility referred to the percentage of active motile sperm (average of two repeated measures of percentage of spermatozoa moving forward) analyzed with an optical microscope by a single trained technician. Bull identification, collection date and time, ejaculation number, ambient temperature (°C), and collector's name were recorded at each semen collection. The phenotypic data file contained records from 131 bulls (13,533 VOL, 12,773 NS, and 12,660 MOT). Bulls were the progeny of 62 sires and 112 dams. The pedigree file included 304 bulls, sires, and dams. Numbers of records, means, SD, minima, and maxima for VOL, NS, and MOT are presented in Table 1.

Most bulls in the DPO dataset were Holstein crossbreds (95%), and the remaining 5% were purebred H. Bull Holstein percentage ranged from 62.5% to 100% (average = 92%). Bull non-Holstein fractions were composed of various percentages of other breeds (Brown Swiss, Jersey, Red Dane, Brahman, Red Sindhi, Sahiwal and Thai Native breeds; Koonawootrittriron et al., 2009). Young bulls were trained for semen collection when bulls were between 10 and 18 mo of age. Semen was collected to produce frozen semen when bulls were older than 18 mo, once a week for bulls younger than 60 mo, and twice a week for bulls 60 mo or older. Semen continued to be collected from each bull until 25,000 doses of frozen semen were produced or when a bull reached approximately 108 mo of age.

2.2. Climate, nutrition and management

Table 1

Weather in Central of Thailand is influenced by the southwestern (May to October) and northeastern monsoons (October to February). The average temperature during the years of the study was 22.3 °C (average minimum = 15 °C and average maximum = 34 °C), the average relative humidity (RH) was 69.3% (average minimum = 33% and average maximum = 97%), and the average rainfall was 1243.1 mm (average minimum = 934 mm and average maximum = 1615 mm). Monthly average temperatures, relative humidity, and rainfall were 24.3 °C, 63.3%, and 19.6 mm in January, 24.6 °C, 63.2%, and 29.3 mm in February, 30.9 °C, 67.2%, and 207.9 mm in March, 32.4 °C, 70.5%, and 304.4 mm in April, 31.4 °C, 75.5%, and 378.0 mm in May, 30.4 °C, 74.8%, and 317.2 mm in June, 27.6 °C, 74.5%, and 706.7 mm in July, 27.1 °C, 76.8%, and 852.3 mm in August, 26.6 °C, 81.4%, and 677.1 mm in September, 26.2 °C, 79.3%, and 691.9 mm in October, 25.6 °C, 71.3%, and 31.5 mm in November, and 23.7 °C, 65.1%, and 13.5 mm in December (Thai Meteorological Department, 2018).

Bulls were kept in open barn stalls until they were assessed to be ready for semen collection. Bulls were fed 4–6 kg/d of concentrate (16% of CP, 2% fat, 14% fiber, and 13% moisture; Charoen Pokphand Foods, Bangkok, Thailand) and 50–60 kg/d of

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Traits	n	Mean	SD	Min	Max
Semen volume (ml)	13,535	5.8	2.0	1.5	12.0
Number of sperm (million)	12,773	6,012	2,175	1,600	11,000
Motility (%)	12,660	47.2	13.9	30.0	80.0

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