

1 Comparison of genetic evaluations for milk yield and fat yield using a polygenic model and
2 three genomic-polygenic models with different sets of SNP genotypes in Thai multibreed
3 dairy cattle

4 Danai Jattawa^a, Mauricio A. Elzo^b, Skorn Koonawootrittriron^{a*}, and Thanathip
5 Suwanasopee^a

6

7 ^aDepartment of Animal Science, Faculty of Agriculture, Kasetsart University, Bangkok
8 10900, Thailand

9 ^bDepartment of Animal Sciences, University of Florida, Gainesville, FL 32611-0910, USA

* Corresponding author: Department of Animal Science, Faculty of Agriculture, Kasetsart University, Bangkok 10900, Thailand; Tel: +66 2 5791120; Fax: +66 2 5791120; Email: agrskk@ku.ac.th (Skorn Koonawootrittriron)

10 **Abstract**

11 The objectives of this research were to compare variance components, genetic
12 parameters, prediction accuracies, and ranking of animals for 305-day milk yield (MY) and
13 305-day fat yield (FY) using a polygenic and three genomic-polygenic models in a Thai
14 multibreed dairy population. The genomic-polygenic models utilized 7,656 SNP (GM7K),
15 74,144 actual and imputed 80K SNP from FImpute (GM80K-FI), and 73,600 actual and
16 imputed 80K SNP from Findhap (GM80K-FH). Traits were gathered from 8,361 first-
17 lactation cows in 810 farms that had their first calving between 1989 and 2014. Variance
18 components and genetic parameters were estimated using REML procedures. Fixed effects
19 included contemporary group (herd-year-season), calving age and heterosis. Random
20 effects were animal additive genetic and residual. Estimates of variance components,
21 heritabilities and prediction accuracies for MY and FY from GM80K-FI and GM80K-FH
22 were similar. They were also the highest, followed by those from GM7K, and the lowest
23 were those from the polygenic model. Correlations estimates between MY and FY were
24 similar across models. Different MY and FY EBV rankings existed across models. The
25 highest rank correlations were those between rankings from GM80K-FI and GM80K-FH.
26 The second highest rank correlations between rankings from GM7K and GM80K-FI, and
27 GM7K and GM80K-FH. The lowest rank correlations were between rankings from the
28 polygenic model and the three genomic-polygenic models. Rank correlations indicated that
29 selection response would differ when choosing replacement animals based on rankings
30 from polygenic and genomic-polygenic EBV. Accuracy of EBV indicated that the highest
31 expected selection responses for MY and FY would be achieved by utilizing EBV from
32 GM80K-FI and GM80K-FH. Lastly, the similarity between results from GM80K-FI and

33 GM80K-FH suggested that genotype imputation with either FImpute or Findhap would be
34 appropriate for this Thai multibreed dairy population.

35

36 **Key words:** Dairy cattle, Genomic, Imputation, Milk yield, Fat yield, Multibreed

37

38 **1. Introduction**

39 The availability of thousands of genotypes across the genome has provided valuable
40 information for the characterization and evaluation of livestock animals. Genomic
41 evaluations that utilize pedigree, phenotypes, and genotypes have increased accuracies of
42 prediction and rates of genetic progress in animal breeding programs (VanRaden et al.,
43 2009; de Roos et al., 2011). Currently, genomic evaluation is widely utilized in the
44 livestock industry, especially in dairy cattle (Schenkel et al., 2009; VanRaden et al., 2009;
45 de Roos et al., 2011; Wiggans et al., 2011). Conversely, dairy cattle in Thailand are
46 genetically evaluated using only pedigree and phenotypic information. The main trait of
47 the Thai genetic evaluation is milk yield, the most important trait economically for Thai
48 dairy producers. To improve the accuracy of genetic evaluation and speed up selection
49 response for milk yield, fat yield, and other dairy traits, a national project for the
50 development of a national genomic-polygenic evaluation system in Thailand was started in
51 2012 (Koonawootrittriron et al., 2012).

52 Utilization of high density genotypic data can increase the effectiveness of genomic
53 evaluation (VanRaden et al., 2011; Mulder et al., 2012). However, budgetary restrictions
54 determined that only a fraction of animals in the Thai genomic-polygenic evaluation project
55 would be genotyped with a high-density chip, whereas the rest would be genotyped with
56 cheaper lower density chips, followed by imputation from the low density chips to the high

57 density chip. Two of the most frequently used imputation programs in dairy cattle are
58 FImpute (Sargolzaei et al., 2014) and Findhap (VanRaden and Sun, 2014). FImpute uses
59 pedigree information to impute unknown genotypes using known relationships among
60 animals followed by a population algorithm (overlapping sliding windows) to find shared
61 haplotype segments assuming that all animals are related to each other. Findhap uses a
62 population algorithm to construct a library of haplotypes, then it matches haplotypes from
63 target animals with those in the library using first a population algorithm followed by a
64 population-pedigree algorithm. These two programs have yielded imputation accuracies of
65 93% to 99% in various dairy cattle populations (Ma et al., 2013; VanRaden et al., 2013;
66 Sargolzaei et al., 2014; He et al., 2015). To develop a national genomic-polygenic
67 evaluation system, variance components, genetic parameters, prediction accuracies, and
68 ranking of animals need to be compared among polygenic and genomic-polygenic
69 prediction models using Thai dairy information. In addition, the impact of FImpute and
70 Findhap on estimates of genetic parameters, prediction accuracies, and animal rankings
71 from genomic-polygenic models also needs to be assessed in the Thai dairy population.
72 Thus, the objectives of this research were to compare variance components, genetic
73 parameters, prediction accuracies, and ranking of animals for 305-day milk yield and 305-
74 day fat yield using a polygenic model, a genomic-polygenic model with 7K SNP, a
75 genomic-polygenic model with actual and imputed 80K SNP from FImpute, and a
76 genomic-polygenic model with actual and imputed 80K SNP from Findhap, in a Thai
77 multibreed dairy cattle population.

78

79 **2. Materials and methods**

80 *2.1. Animals, management, and traits*

81 Animals used in this research were 8,361 first-lactation cows from 810 farms
82 located across five regions in Thailand (North, Northeastern, Western, Central, and
83 Southern). These cows were the progeny of 1,210 sires and 6,992 dams, and had their first
84 calving between 1989 and 2014. The Thai multibreed population was generated through
85 upgrading of cattle from various breeds (Brahman, Jersey, Brown Swiss, Red Dane, Red
86 Sindhi, Sahiwal and Thai Native) to Holstein (Koonawootrittriron et al., 2009).
87 Approximately 88% of all animals in the dataset were 75% Holstein and above, and 94% of
88 sires and 73% of dams were 75% Holstein or higher. Climate was tropical with
89 temperatures ranging from 15° to 36° Celsius and relative humidity ranging from 29 to
90 99%. Seasons are winter (November to February; average temperature of 26° Celsius and
91 average relative humidity of 69%), summer (March to June; average temperature of 29°
92 Celsius and average relative humidity of 72%), and rainy (July to October; average
93 temperature of 28° Celsius and average relative humidity of 80%). Cows were kept in open
94 barns with free access to mineral supplement. Concentrate (14 to 22% of CP, 63 to 83% of
95 NFE; approximately 1 kg of concentrate per 2 kg of milk) was fed to cows during milking
96 times (5 am and 3 pm). Roughage fed to cows consisted of grasses (*Penisetum purpurium*,
97 *Brachiaria mutica*, and *Penicum maximum*), crop-residues (rice straw, corn stover, and
98 sugarcane), or agricultural by-products (cassava pulp, and bagasse).

99 Traits were 305-day milk yield (MY) and 305-day fat yield (FY). Monthly test-day
100 fat yield was equal to the product of test-day milk yield and fat content, which were
101 collected monthly after calving until the end of lactation. Monthly test-day milk yield and
102 fat yield were used to compute MY and FY using the test interval method (Sargent et al.,
103 1968; Koonawootrittriron et al., 2001).

104

105 2.2. Genotypic data

106 Blood or semen samples were collected from 2,661 animals (89 sires and 2,572
107 cows) for DNA extraction with a MasterPure™ DNA Purification Kit (Epicentre®,
108 Madison, WI, USA). The quality of DNA samples was measured using a NanoDrop™
109 2000 Spectrophotometer (Thermo Fisher Scientific Inc., Wilmington, DE, USA). Only
110 DNA that had a ratio of absorbance at 260 nm to absorbance at 280 nm (purity ratio) of
111 approximately 1.8, and concentration higher than 15 ng/μl were forwarded to GeneSeek
112 (GeneSeek, Lincoln, NE, USA) for genotyping with GeneSeek genomic profiler (GGP) 9K
113 (n = 1,412), 20K (n = 570), 26K (n = 540), and 80K (n = 139) chips.

114 The numbers of SNP markers from autosomal chromosomes and the X chromosome
115 were 8,590 for the GGP9K, 19,616 for the GGP20K, 25,979 for the GGP26K, and 76,694
116 for the GGP80K. These actual SNP markers were used to construct three sets of SNP for
117 genomic-polygenic comparisons that included: 1) actual 7K SNP markers (SNP set 1), 2)
118 actual and imputed 80K SNP markers from FImpute (SNP set 2) and, 3) actual and imputed
119 80K SNP markers from Findhap (SNP set 3). The SNP markers in common among the
120 GGP9K, GGP20K, GGP26K, and GGP80K chips (n = 7,667) were used to represent SNP
121 set 1. Construction of SNP sets 2 and 3 was accomplished by imputation from GGP9K,
122 GGP20K, and GGP26K to GGP80K using FImpute 2.2 (Sargolzaei et al., 2014) and
123 Findhap 4 (VanRaden and Sun, 2014), respectively. Actual and imputed SNP markers with
124 minor allele frequencies lower than 0.04 or call rates lower than 0.9 were removed. After
125 these quality checks, 7,656, 74,144, and 73,600 SNP markers were kept to represent the
126 genotypic information for SNP sets 1, set 2, and set 3.

127

128 2.3 Estimation of variance and covariance components

129 Estimates of variance and covariance components for MY and FY were obtained
 130 using a bivariate polygenic model and three bivariate single-step genomic-polygenic
 131 models (Aguilar et al., 2010), namely: 1) GM7K model that used pedigree, phenotypes, and
 132 SNP set 1 genotypes, 2) GM80K-FI model that used pedigree, phenotypes, and SNP set 2
 133 genotypes, and 3) GM80K-FH model that used pedigree, phenotype, SNP set 3 genotypes.
 134 Fixed effects for the polygenic model and genomic-polygenic models included
 135 contemporary group (herd-year-season), calving age, and heterosis (as a function of
 136 Holstein-Other Breeds heterozygosity, i.e., as a function of the probability of having an
 137 allele from Holstein and an allele from Other Breeds in 1 locus). Random effects were
 138 animal additive genetic and residual. The mean for random effects was assumed to be zero
 139 in all models. The variance-covariance matrix among additive genetic effects for the
 140 polygenic model was equal to $A * \sigma_a^2$, where A was the additive relationship matrix among
 141 all animals in the population, “*” was the Kronecker product, and σ_a^2 was the additive
 142 genetic variance. The variance-covariance matrix among additive genetic effects for all
 143 genomic-polygenic models was equal to:

$$144 \begin{bmatrix} A_{11} + A_{12}A_{22}^{-1}(G_{22} - A_{22})A_{22}^{-1}G_{21} & A_{12}A_{22}^{-1}G_{22} \\ G_{22}A_{22}^{-1}A_{21} & G_{22} \end{bmatrix} * \sigma_a^2,$$

145 where A_{11} was the additive relationship submatrix among all non-genotyped animals, A_{12}
 146 was the additive relationship submatrix among non-genotyped and genotyped animals,
 147 A_{22}^{-1} was inverse of the additive relationship submatrix for genotyped animals, G_{22} was the
 148 matrix of genomic relationships for genotyped animals (VanRaden, 2008; Aguilar et al.,
 149 2010). Matrix G_{22} was computed as $ZZ'/2 \sum p_j (1 - p_j)$, where p_j = frequency of allele 2
 150 in locus j in the Thai dairy population, $z_{ij} = (0 - 2p_j)$ for genotype = 11 in locus j , $z_{ij} =$
 151 $(1 - 2p_j)$ for genotype = 12 or 21 in locus j , and $z_{ij} = (2 - 2p_j)$ for genotype = 22 in

152 locus j . Matrix G_{22} was scaled based on matrix A_{22} using the default rule of program
153 PREGSF90 from the BLUPF90 family programs (Misztal et al., 2002), i.e., that the mean of
154 the diagonal elements of G_{22} = mean of the diagonal elements of A_{22} , and that the mean of the
155 off-diagonal elements of G_{22} = mean of the off-diagonal elements of A_{22} .

156 The BLUPF90 family programs (Misztal et al., 2002) was utilized to estimate
157 variance components and genetic parameters for MY and FY. Variance components were
158 estimated using an average information restricted maximum likelihood algorithm using
159 AIREMLF90 (Tsuruta, 2014). Standard errors for additive genetic, and environmental
160 variances and covariances were computed as square roots of the diagonal elements of the
161 inverse of the average information matrix. The repeated sampling approach of
162 Meyer and Houle (2013) was used to estimate phenotypic variances and covariances,
163 heritabilities, and their standard deviations. Phenotypic, genetic, and environmental
164 correlations including their standard deviations for MY and FY were also estimated using
165 the repeated sampling approach. Statistical tests to determine the significance of
166 differences between variance components and genetic parameters across polygenic and
167 genomic-polygenic models were beyond the scope of this research. Thus, comparisons
168 among estimates of variance components and genetic parameters here represent
169 comparative descriptions of values obtained with the polygenic and genomic-polygenic
170 models in the Thai multibreed dairy population.

171

172 *2.4. Prediction accuracies and animals rankings*

173 Animal EBV for MY and FY were computed using the polygenic and the three
174 genomic-polygenic models (GM7K, GM80K-FI, and GM80K-FH). Prediction accuracies

175 for each EBV was obtained as $\sqrt{1 - \frac{PEV}{\sigma_a^2}}$, where PEV was the prediction error variance.

176 Rankings of animal EBV for MY and FY were compared using Spearman's rank
177 correlations using the CORR procedure of SAS (SAS, 2003). Rank correlations were
178 computed for each trait for all animals in the population, only sires (top 5%, 15%, 25%, and
179 all sires), and only cows (top 5%, 15%, 25%, and all cows).

180

181 **3. Results and discussion**

182 *3.1. Variance components and genetic parameters*

183 The scaling strategy used for matrix G_{22} worked well for the Thai population. The
184 statistics of the diagonal and off-diagonal elements of matrices A_{22} and matrices G_{22} for the
185 GM7K, GM80K-FI, and GM80K-FH models indicated that these two matrices were similar
186 (Table 1). In particular, the means of their diagonal elements were all equal to 1 and the
187 mean of their off-diagonal elements were equal to zero, ensuring that estimates of variance
188 components and genetic parameters as well as additive genetic predictions from genomic-
189 polygenic models would be unbiased (Chen et al., 2011; Forni et al., 2011; Simeone et al.,
190 2012).

191 Estimates of variances and covariances for MY and FY from the polygenic model
192 and the three genomic-polygenic models are shown in Table 2 for additive genetic effects,
193 in Table 3 for environmental effects, and in Table 4 for phenotypic effects. Estimates of
194 phenotypic variances and covariances were similar across models. However, estimates of
195 additive genetic variances and covariances for MY and FY were larger for the GM7K
196 model (12%), and the GM80K-FI (46%) and GM80K-FH (46%) models than
197 corresponding values from the polygenic model. Conversely, estimates of environmental

198 variances and covariances for all genomic-polygenic models were lower (2% for GM7K,
199 7% for GM80K-FI and 7% for GM80K-FH) than those from the polygenic model. These
200 results indicated that the inclusion of genotypes in addition to pedigree and phenotypes in
201 genomic-polygenic models accounted for substantially larger amounts of additive genetic
202 variation than by using only pedigree and phenotypic information in the polygenic model.

203 Similarly, additive genetic variances and covariances were larger for the GM80K-FI
204 (29%) and GM80K-FH (29%) models than for the GM7K model, whereas environmental
205 variances and covariances were lower for the GM80K-FI (6%) and GM80K-FH (6%)
206 models than for the GM7K model. This indicated that the additional SNP used by the
207 GM80K-FI (74,144 SNP) and GM80K-FH (73,600 SNP) models explained nearly 30%
208 more additive genetic variation for MY and FY than that accounted for by the 7,656 SNP in
209 the GM7K model.

210 Variance and covariance components for MY and FY obtained with the GM80K-FI
211 and GM80K-FH models were nearly identical, except for the additive genetic variance for
212 FY (229.9 kg^2 for GM80K-FI and 196.1 kg^2 for GM80K-FH; Table 2). The additive
213 genetic variance for FY computed with the GM80K-FI model was 17% higher than the
214 estimate from GM80K-FH. This higher value may have been due to the larger SNP
215 markers were used in GM80K-FI ($n = 74,144$) than GM80K-FH ($n = 73,600$). Perhaps the
216 imputed SNP genotypes from FImpute managed to extract additional additive genetic
217 variability for FY beyond that uncovered by the set of imputed SNP from Findhap.

218 Table 5 shows estimates of heritabilities and correlations for MY and FY obtained
219 using the polygenic model and the three genomic-polygenic models (GM7K, GM80K-FI,
220 and GM80K-FH). The heritabilities from the polygenic model were the lowest for both
221 MY (0.15) and FY (0.14). Heritabilities estimates for MY tended to increase with the

222 number of SNP included in the model (from 0.19 for GM7K to 0.26 for GM80K-FI and
223 GM80K-FH). This trend was less noticeable for FY, where heritabilities increased from
224 0.15 for GM7K to 0.18 for GM80K-FI and 0.16 for GM80K-FH. Heritability estimates for
225 MY and FY from the GM80K-FI and GM80K-FH models were on the average 25% higher
226 than estimates from the GM7K model, and 47% higher than estimates from the polygenic
227 model. This indicated that genomic-polygenic models likely accounted for additive genetic
228 relationships among animals in the Thai population more accurately resulting in higher
229 additive genetic variances and heritabilities than those from polygenic models. Nearly
230 identical environmental and phenotypic correlations were obtained across models, but
231 estimates of genetic correlations between MY and FY using the polygenic and GM80K-FH
232 models were slightly higher than estimates computed using the GM7K and GM80K-FI
233 models. The similarity of correlations estimates between MY and FY among the four
234 models indicated that all models accounted for correlations between these two traits to a
235 similar extent.

236 The heritabilities estimated here for MY and FY with all models were somewhat
237 lower than those estimated in various Thai multibreed populations using polygenic models
238 (0.31 to 0.38 for MY: Koonawootrittriron et al., 2009; Sarakul et al., 2011; Jattawa et al.,
239 2012; Endris et al., 2013, and 0.25 for FY: Koonawootrittriron et al., 2009). Heritabilities
240 estimated here for MY using the GM80K-FI and GM80K-FH models were within the range
241 of estimates of genomic heritabilities for Holstein cattle from temperate regions (0.23 to
242 0.30; Gao et al., 2012; Rodríguez-Ramilo et al., 2014; Tsuruta et al, 2014; Bauer et al.,
243 2015), but heritabilities for FY were somewhat lower (0.28 to 0.30; Gao et al., 2012;
244 Rodríguez-Ramilo et al., 2014). Higher estimates of heritability for MY and FY with
245 GM80K-FI and GM80K-FH models will increase the accuracy of genetic predictions

246 resulting in a more reliable identification of the superior sires and cows in this Thai dairy
247 population. Continued use of genotyping with high-density and medium-density chips
248 coupled with genomic-polygenic evaluations and extensive use of top ranking sires and
249 cows should accelerate the rate of genetic progress for MY and FY in this population.

250 Similar variance components and genetic parameters were estimated by the
251 GM80K-FI and GM80K-FH models reflecting a high degree of similarity between the
252 imputed genotypes from FImpute and Findhap. This was likely due to the algorithmic
253 resemblance of these two programs (both use population and pedigree information to
254 impute genotypes) and their high level of imputation accuracy. Imputation accuracy for
255 FImpute and Findhap was found to be high in several dairy populations (Ma et al., 2013;
256 VanRaden et al., 2013; Sargolzaei et al., 2014; He et al., 2015). Accuracies from low
257 density to 50K chips have ranged from 95% to 99% for FImpute and from 93% to 99% for
258 Findhap. Further, the highest additive genetic variances and heritabilities obtained here
259 were from genomic-polygenic programs using actual and imputed SNP from 80K chips
260 (GM80K-FI and GM80K-FH), indicating that genomic imputation can be a reasonable
261 alternative to increase the effectiveness of genetic evaluation and selection under tropical
262 conditions in Thailand.

263

264 *3.2. Accuracy of polygenic and genomic-polygenic EBV*

265 Fig. 1 shows the EBV accuracies for MY and FY computed from the polygenic
266 model and the three genomic-polygenic models (GM7K, GM80K-FI, and GM80K-FH).
267 The GM80K-FI and GM80K-FH models had the highest EBV accuracies (average of
268 38.8% for MY and 32.5% for FY), GM7K model was second (36.7% for MY, and 31.4%
269 for FY), and the least accurate was the polygenic model (31.5% for MY, and 24.4% for

270 FY). Gains in EBV accuracies were 5.2% between the polygenic and the GM7K models
271 and 7.2% between the polygenic and the GM80K-FI and GM80K-FH models. The
272 increase in EBV accuracy between the low density GM7K and the high density GM80K-FI
273 and GM80K-FH models was only 2%. This indicated that a strategy to keep genotyping
274 costs reasonably low in this population would be to genotype animals that are highly
275 connected in the population (i.e., most sires and some dams) with high density chips, and
276 use low density chips with the rest of the population.

277

278 The higher prediction accuracies obtained here with the GM80K-FI and GM80K-
279 FH models was in agreement with previous studies that found that higher number of SNP in
280 genomic evaluation yielded higher levels of prediction accuracies for MY and FY in dairy
281 cattle (VanRaden et al., 2009; Mulder et al., 2012). However, the gains in EBV accuracy in
282 the Thai multibreed population (5.2% to 7.2%) were lower than the accuracy gains obtained
283 in various Holstein dairy populations (23% to 32%; de Roos et al., 2009; Schenkel et al.,
284 2009; VanRaden et al., 2009; Wiggans et al., 2011). Previous studies have indicated that
285 the larger the number of genotyped animals the higher the prediction accuracies in a
286 population (Goddard, 2009; VanRaden et al., 2011; Mulder et al., 2012). Thus, the lower
287 EBV accuracy gains obtained here may have been partly due to the small number of
288 animals genotyped in this population (2,661) compared to the Holstein populations in other
289 studies (5,335 to 63,615). Consequently, prediction accuracies of genomic-polygenic
290 evaluations in Thailand will likely increase as higher numbers of dairy animals are
291 genotyped in the future.

292 Using super high density chips (777K) have been proposed to increase prediction
293 accuracies in genomic evaluation (Su et al., 2012; VanRaden et al., 2013). However,

294 prediction accuracies substantially increased as numbers of SNP increased from low (3K)
295 to high density chips (50K; VanRaden et al., 2011; Mulder et al., 2012), but increased only
296 slightly from high density (50K) to super high density chips (777K; Harris et al., 2011;
297 VanRaden et al., 2011; Erbe et al., 2012; Su et al., 2012). This indicates that genotyping
298 animals with high density chips (50K, 80K) would produce genomic-polygenic EBV of
299 sufficient accuracy to rank animals appropriately for genetic selection. VanRaden et al.
300 (2011) also indicated that prediction accuracies were found to be more affected by numbers
301 of genotyped animals than number of SNP markers. Thus, prediction accuracies will
302 continue to increase as numbers of genotyped animals increase over time. As mentioned
303 above, genotyping costs could be kept low if only highly related animals were genotyped
304 with high density chips (mostly sires) and the remaining animals (mostly cows) were
305 genotyped with low density chips and subsequently imputed to a high density chip.

306

307 *3.3. Ranking of animals from polygenic and three genomic-polygenic models*

308 Spearman rank correlations between rankings of all animal EBV from the polygenic
309 model and the three genomic-polygenic models ranged from 0.80 to 0.96 for MY and 0.80
310 to 0.93 for FY (Table 6). Rankings between animal EBV from GM80K-FI and GM80K-
311 FH had the highest correlations (0.96 for MY, and 0.93 for FY). Rank correlations between
312 animal EBV from the low density GM7K and the high density models (GM80K-FI: 0.90
313 for MY, and 0.91 for FY; GM80K-FH: 0.89 for MY, and 0.86 for FY) were the second
314 highest. The lowest rank correlations were between animal EBV from the three genomic-
315 polygenic models (GM7K, GM80K-FI and GM80K-FH), and the polygenic model (0.80 to
316 0.84 for MY, and 0.79 to 0.83 for FY).

317 Spearman rank correlations between polygenic and three genomic-polygenic models
318 were also computed for sires only (top 5%, 15%, 25%, and all sires; Table 7) and for cows
319 only (top 5%, 15%, 25%, and all cows; Table 8). The lowest rank correlations were those
320 for the top 5% of sires and cows. Rank correlations for the top 5% of sires ranged from
321 0.50 between the polygenic and GM7K models to 0.87 between GM80K-FI and GM80K-
322 FH for MY, and from 0.61 between the polygenic and GM80K-FH models to 0.76 between
323 GM80K-FI and GM80K-FH for FY. Rank correlations for the top 5% of cows ranged from
324 0.64 between the polygenic and GM80K-FI models to 0.90 between GM80K-FI and
325 GM80K-FH for MY, and from 0.59 between the polygenic and GM80K-FH models to 0.79
326 between GM7K and GM80K-FI for FY. Rank correlations tended to increase as the
327 fraction of sires (or cows) increased from the top 5% to the top 15% to the top 25% to all
328 sires (or all cows).

329 Rank correlations for all sires and for all cows from the polygenic model and the
330 three genomic-polygenic models followed the same pattern as rank correlations for all
331 animals in the population. The highest rank correlations for MY and FY were between
332 EBV from GM80K-FI and GM80K-FH (0.92 to 0.94 for all sires and 0.93 to 0.96 for all
333 cows). The second highest rank correlations between MY and FY were those between
334 EBV from GM7K and from GM80K-FI and GM80K-FH (0.87 to 0.93 for all sires and 0.86
335 to 0.91 for all cows). The lowest rank correlations for MY and FY were between animal
336 EBV from GM7K, GM80K-FI and GM80K-FH and animal EBV from polygenic model
337 (0.80 to 0.88 for all sires and 0.79 to 0.84 for all cows).

338 As expected, sires and cows in the top 5%, 15%, and 25% differed across models.
339 Percentages of animals in common in the top 5%, 15%, and 25% for pairs of models are
340 shown in Table 7 for sires and in Table 8 for cows. Most percentages of animals in

341 common in the top 5%, 15%, and 25% between pairs of models were higher for EBV
342 rankings for MY and FY from models using high density chips (GM80K-FI and GM80K-
343 FH), followed by percentages of animals in common between EBV from the model using
344 the low density (GM7K) and the models using a high density chip (GM80K-FI and
345 GM80K-FH), and lastly by percentages of animals in common between EBV from the
346 polygenic model and all genomic-polygenic models (GM7K, GM80K-FI, and GM80K-
347 FH). As an illustration, consider the top 5% for MY. The highest percentages of animals
348 in common across models in the top 5% for MY occurred between rankings from GM80K-
349 FI and GM80K-FH (87% of sires; 89% of cows), followed by percentages of animals in
350 common between GM7K and the high density genomic-polygenic models (76% to 79% for
351 sires; 74% to 75% for cows). The lowest percentages of animals in common in the top 5%
352 for MY occurred between the polygenic model and all genomic-polygenic models (71% to
353 74% for sires; 66% to 69% for cows). Considering the similarity between the GM80K-FI
354 and GM80K-FH in terms of their estimates of genetic variances, heritabilities, and
355 prediction accuracies for MY and FY, either one of these models would be suitable for
356 genetic evaluation in this Thai multibreed population.

357

358 **4. Conclusions**

359 Estimates of additive genetic variances, heritabilities, and prediction accuracies for
360 MY and FY from genomic-polygenic models were higher than those from the polygenic
361 model. Additive genetic variances, heritabilities, and prediction accuracies tended to
362 increase as the number of SNP increased. Animal rankings from high density genomic-
363 polygenic models should be preferred because they were based on EBV of higher accuracy
364 than the polygenic and low density genomic-polygenic model. Faster selection responses

365 for MY and FY would be expected from high density genomic models. FImpute and
366 Findhap performed similarly, thus either program would be appropriate for the Thai
367 multibreed population.

368

369 **Conflict of interest**

370 No conflicts of interest influenced this research.

371

372 **Acknowledgements**

373 The authors would like to thank the Royal Golden Jubilee Ph.D. Program (RGJ) of
374 the Thailand Research Fund (TRF) for giving the scholarship to first author, the University
375 of Florida for supporting the training of the first author as a research scholar, and the
376 National Science and Technology Development Agency (NSTDA), Kasetsart University
377 (KU), and the Dairy Farming Promotion Organization of Thailand (D.P.O.) for supporting
378 genomic SNP information used in this research. We also appreciate the Thai dairy farmers,
379 dairy cooperatives, and dairy related organizations for their participation and support of this
380 investigation.

381

382 **References**

- 383 Aguilar, I., Misztal, I., Johnson, D.L., Legarra, A., Tsuruta, S., Lawlor, T.J., 2010. Hot
384 topic: A unified approach to utilize phenotypic, full pedigree, and genomic
385 information for genetic evaluation of Holstein final score. *J. Dairy Sci.* 93, 743-752.
- 386 Bauer, J., Přibyl, J., Vostrý, L., 2015. Short communication: Reliability of single-step
387 genomic BLUP breeding values by multi-trait test-day model analysis. *J. Dairy Sci.*
388 98, 1-5.

- 389 Chen, C.Y., Misztal, I., Aguilar, I., Legarra, A., Muir, W.M., 2011. Effect of different
390 genomic relationship matrices on accuracy and scale. *J. Anim. Sci.* 89, 2673-2679.
- 391 de Roos, A.P.W., Schrooten, C., Veerkamp, R.F., van Arendonk, J.A.M., 2011. Effects of
392 genomic selection on genetic improvement, inbreeding, and merit of young versus
393 proven bulls. *J. Dairy Sci.* 94, 1559-1567.
- 394 de Roos, A.P.W., Schrooten, C., Mullaart, E., van der Beek, S., de Jong, G., Voskamp, W.,
395 2009. Genomic selection at CRV. In: Proceedings of the Interbull technical
396 workshop – genomic information in genetic evaluation, Uppsala, Sweden.
- 397 Endris, M., Tumwasorn, S., Sopannarath, P., Prasanpanich, S., 2013. Genotype by region
398 interaction on milk production traits of Holstein crossbred dairy in Thailand.
399 *Kasetsart J.* 47, 228-237.
- 400 Erbe, M., Hayes, B.J., Matukumalli, L.K., Goswami, S., Bowman, P.J., Reich, C.M.,
401 Mason, B.A., Goddard, M.E., 2012. Improving accuracy of genomic predictions
402 within and between dairy cattle breeds with imputed high-density single nucleotide
403 polymorphism panels. *J Dairy Sci.* 95, 4114-4129.
- 404 Forni, S., Aguilar, I., Misztal, I., 2011. Different genomic relationship matrices for single-
405 step analysis using phenotypic, pedigree and genomic information. *Genet. Sel. Evol.*
406 43, 1.
- 407 Gao, H., Christensen, O.F., Madsen, P., Nielsen, U.S., Zhang, Y., Lund, M.S., Su, G., 2012.
408 Comparison on genomic predictions using three GBLUP methods and two single-
409 step blending methods in the Nordic Holstein population. *Genet. Sel. Evol.* 44, 1-8.
- 410 Goddard, M., 2009. Genomic selection: prediction of accuracy and maximization of long
411 term response. *Genetica* 136, 245-257.

- 412 Harris, B.L., Creagh, F.E., Winkelman, A.M., Johnson, D.L., 2011. Experiences with the
413 Illumina high density bovine beadchip. In: Proceeding of the 2011 Interbull
414 meeting, Stavanger, Norway.
- 415 He, S., Wang, S., Fu, W., Ding, X., Zhang, Q., 2015. Imputation of missing genotypes from
416 low- to high-density SNP panel in different population designs. *Anim. Genet.* 46, 1-
417 7.
- 418 Jattawa, D., Koonawootrittriron, S., Elzo, M.A., Suwanasopee, T., 2012. Somatic cells
419 count and its genetic association with milk yield in dairy cattle raised under Thai
420 tropical environmental condition. *Asian-Aust. J. Anim. Sci.* 25, 1216-1222.
- 421 Koonawootrittriron, S., Elzo, M.A., Thongprapi, T., 2009. Genetic trends in a Holstein ×
422 other breeds multibreed dairy population in Central Thailand. *Livest. Sci.* 122, 186-
423 192.
- 424 Koonawootrittriron, S., Elzo, M.A., Tumwasorn, S., Sintala, W., 2001. Prediction of 100-
425 d and 305-d milk yields in a multibreed dairy herd in Thailand using monthly test-
426 day records. *Thai J. Agric. Sci.* 34, 163-174.
- 427 Koonawootrittriron, S., Suwanasopee, T., Elzo, M.A., 2012. Development of a Dairy
428 Genetic Genomic Evaluation System in Thailand. National Science and Technology
429 Development Agency, Thailand.
- 430 Lund, M.S., Su, G., Janss, L., Guldbbrandtsen, B., Brøndum, R.F., 2014. Genomic
431 evaluation of cattle in a multi-breed context. *Livest. Sci.* 166, 101-110.
- 432 Ma, P., Brøndum, R.F., Zhang, Q., Lund, M.S., Su, G., 2013. Comparison of different
433 methods for imputing genome-wide marker genotypes in Swedish and Finnish Red
434 Cattle. *J. Dairy Sci.* 96, 4666-4677.

- 435 Meyer, K., Houle, D., 2013. Sampling based approximation of confidence intervals for
436 functions of genetic covariance matrices. In: Proceedings of the 20th conference of
437 the association for advances in animal breeding, Napier, New Zealand.
- 438 Misztal, I., 1999. Complex models, more data: simpler programming. *Interbull Bull.* 20,
439 33–42.
- 440 Misztal, I., Tsuruta, S., Strabel, T., Auvray, B., Druet, T., Lee, D. H., 2002. BLUPF90 and
441 related programs (BGF90). In: Proceeding of 7th world congress on genetic applied
442 to livestock production, Montpellier, France.
- 443 Mulder, H.A., Calus, M.P.L., Druet, T., Schrooten, C., 2012. Imputation of genotypes with
444 low-density chips and its effect on reliability of direct genomic value in Dutch
445 Holstein cattle. *J. Dairy Sci.* 95, 876-889.
- 446 Rodríguez-Ramilo, S.T., García-Cortés, L.A., González-Recio, Ó., 2014. Combining
447 genomic and genealogical information in a reproducing Kernel Hilbert spaces
448 regression Model for genome-enabled predictions in dairy cattle. *PLoS ONE*, 9,
449 e93424. Available at:
450 <http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0093424>.
- 451 Sarakul, M., Koonawootrittriron, S., Elzo, M.A., Suwanasopee, T., 2011. Factors
452 influencing genetic change for milk yield within farm in Central Thailand. *Asian-*
453 *Aust. J. Anim. Sci.* 24, 1031-1040.
- 454 Sargent, F.D., Lytton, V.H., Wall Jr., O.G., 1968. Test interval method of calculating Dairy
455 Herd Improvement Association records. *J. Dairy Sci.* 51, 170-179.
- 456 Sargolzaei, M., Chesnais, J.P., Schenkel, F.S., 2014. A new approach for efficient genotype
457 imputation using information from relatives. *BMC Genomics*, 15, 478.
- 458 SAS, 2003. SAS OnlineDoc 9.1.3. SAS institute Inc., Cary, North Carolina, USA.

- 459 Schenkel, F.S., Sargolzaei, M., Kistemaker, G., Jansen, G.B., Sullivan, P., Van Doormaal,
460 B.J., VanRaden, P.M., Wiggans, G.R., 2009. Reliability of genomic evaluation of
461 Holstein cattle in Canada. In: Proceedings of the Interbull international workshop,
462 Uppsala, Sweden.
- 463 Simeone, R., Misztal, I., Aguilar, I., Vitezica, Z.G., 2012. Evaluation of a multi-line broiler
464 chicken population using a single-step genomic evaluation procedure. *J. Anim.*
465 *Breed. Genet.* 129, 3-10.
- 466 Su, G., Brøndum, R.F., Ma, P, Guldbbrandtsen, B., Aamand, G.P., Lund, M.S., 2012.
467 Comparison of genomic predictions using medium-density (~54,000) and high-
468 density (~777,000) single nucleotide polymorphism marker panels in Nordic
469 Holstein and Red dairy cattle populations. *J. Dairy Sci.* 95, 4657-4665.
- 470 Tsuruta, S., 2014. Average Information REML with several options including EM-REML
471 and heterogeneous residual variances. Available at:
472 http://nce.ads.uga.edu/wiki/doku.php?id=application_programs.
- 473 Tsuruta, S., Misztal, I., Aguilar, I., Lawlor, T.J., 2014. Genome wide association study on
474 cow mortality in three US regions. In: Proceeding of 10th World Congress of
475 genetics applied to livestock production, Vancouver, Canada.
- 476 VanRaden, P.M., 2008. Efficient methods to compute genomic predictions. *J. Dairy Sci.*
477 91, 4414-4423.
- 478 VanRaden, P.M., Sun, C., 2014. Fast imputation using medium- or low-coverage sequence
479 data. In: Proceeding of 10th World Congress of genetics applied to livestock
480 production, Vancouver, Canada.
- 481 VanRaden, P.M., Null, D.J., Sargolzaei, M., Wiggans, G.R., Tooker, M.E., Cole, J.B.,
482 Sonstegard, T.S., Connor, E.E., Winters, M., van Kaam, J.B.C.H.M., Valentini, A.,

- 483 Van Doormaal., B.J., Faust, M.A., Doak, G.A., 2013. Genomic imputation and
484 evaluation using high-density Holstein genotypes. *J. Dairy Sci.* 96, 668-678.
- 485 VanRaden, P.M., O'Connell, J.R., Wiggans, G.R., Weigel, K.A., 2011. Genomic
486 evaluations with many more genotypes. *Genet. Sel. Evol.* 43, 10.
- 487 VanRaden, P.M., Van Tassell, C.P., Wiggans, G.R., Sonstegard, T.S., Schnabel, R.D.,
488 Taylor, J.F., Schenkel, F.S., 2009. Invited review: Reliability of genomic
489 predictions for North American Holstein bulls. *J. Dairy Sci.* 92, 16-24.
- 490 Wiggans, G.R., VanRaden, P.M., Cooper, T.A., 2011. The genomic evaluation system in
491 United States: Past, present, future. *J. Dairy Sci.* 94, 3202-3211.
- 492

493 **Table 1**

494 Statistics for diagonal and off-diagonal elements of the pedigree and genomic relationship
 495 matrices

Matrix ^a	Mean	Minimum	Maximum	Variance
Diagonal elements				
A ₂₂	1.000	1.000	1.250	0.000
G ₂₂ (GM7K)	1.002	0.837	1.432	0.011
G ₂₂ (GM80K-FI)	1.000	0.721	1.599	0.003
G ₂₂ (GM80K-FH)	1.000	0.488	2.354	0.010
Off-diagonal elements				
A ₂₂	0.003	0.000	0.750	0.001
G ₂₂ (GM7K)	0.003	-0.145	1.218	0.006
G ₂₂ (GM80K-FI)	0.003	-0.079	1.025	0.003
G ₂₂ (GM80K-FH)	0.003	-0.091	1.258	0.002

496 ^aA₂₂ = additive relationship matrix for genotyped animals; G₂₂ = genomic relationship
 497 matrix for genotyped animals; GM7K = Genomic-polygenic model with actual 7K SNP;
 498 GM80K-FI = Genomic-polygenic model with actual and imputed 80K SNP using FImpute;
 499 GM80K-FH = Genomic-polygenic model with actual and imputed 80K SNP using Findhap.
 500

501 **Table 2**

502 Additive genetic variances and covariances for 305-d milk yield (MY) and 305-d fat yield (FY) estimated using a polygenic model and
 503 three genomic-polygenic models with different sets of SNP genotypes

Variance Component	Model ^a							
	PM	SE	GM7K	SE	GM80K-FI	SE	GM80K-FH	SE
Var (MY), kg ²	100,030.0	25,447.0	126,480.0	24,023.0	172,190.0	30,558.0	174,600.0	29,971.0
Cov (MY, FY), kg ²	3,057.1	1,000.6	3,264.1	949.6	4,147.6	1,176.1	4,645.8	1,139.6
Var (FY), kg ²	176.5	55.3	183.7	53.5	229.9	64.5	196.1	59.5

504 ^a PM = Polygenic model; GM7K = Genomic-polygenic model with actual 7K SNP information; GM80K-FI = Genomic-polygenic
 505 model with actual and imputed 80K SNP information using FImpute; GM80K-FH = Genomic-polygenic model with actual and
 506 imputed 80K SNP information using Findhap.

507

508 **Table 3**

509 Environmental variances and covariances for 305-d milk yield (MY) and 305-d fat yield (FY) estimated using a polygenic model and
 510 three genomic-polygenic models with different sets of SNP genotypes

Variance Component	Model ^a							
	PM	SE	GM7K	SE	GM80K-FI	SE	GM80K-FH	SE
Var (MY), kg ²	565,990.0	25,164.0	542,750.0	22,912.0	500,420.0	27,936.0	496,730.0	29,971.0
Cov (MY, FY), kg ²	17,099.0	1,011.4	16,955.0	942.1	16,125.0	1,117.4	15,624.0	1,139.6
Var (FY), kg ²	1,085.4	56.7	1,082.5	54.2	1,039.0	62.8	1,067.7	59.5

511 ^a PM = Polygenic model; GM7K = Genomic-polygenic model with actual 7K SNP information; GM80K-FI = Genomic-polygenic
 512 model with actual and imputed 80K SNP information using FImpute; GM80K-FH = Genomic-polygenic model with actual and
 513 imputed 80K SNP information using Findhap.

514

515 **Table 4**

516 Phenotypic variances and covariances for 305-d milk yield (MY) and 305-d fat yield (FY) estimated using a polygenic model and three
 517 genomic-polygenic models with different sets of SNP genotypes

Variance Component	Model ^a							
	PM	SD ^b	GM7K	SD	GM80K-FI	SD	GM80K-FH	SD
Var (MY), kg ²	666,030.0	14,472.0	669,230.0	14,749.0	672,610.0	14,943.0	671,330.0	14,867.0
Cov (MY, FY), kg ²	20,156.0	603.5	20,219.0	610.8	20,273.0	615.2	20,270.0	611.2
Var (FY), kg ²	1,261.9	34.3	1,266.2	34.6	1,268.9	34.8	1,263.8	34.3

518 ^a PM = Polygenic model; GM7K = Genomic-polygenic model with actual 7K SNP information; GM80K-FI = Genomic-polygenic
 519 model with actual and imputed 80K SNP information using FImpute; GM80K-FH = Genomic-polygenic model with actual and
 520 imputed 80K SNP information using Findhap.

521 ^b Repeated sampling approach of Meyer and Houle (2013).

522 **Table 5**

523 Heritabilities and correlations for 305-d milk yield (MY) and 305-d fat yield (FY) estimated using a polygenic model and three
 524 genomic-polygenic models with different sets of SNP genotypes

Parameter	Model ^a							
	PM	SD ^b	GM7K	SD	GM80K-FI	SD	GM80K-FH	SD
Heritability (MY)	0.15	0.04	0.19	0.03	0.26	0.04	0.26	0.04
Heritability (FY)	0.14	0.04	0.15	0.04	0.18	0.05	0.16	0.05
Genetic correlation (MY, FY)	0.73	0.13	0.68	0.11	0.66	0.11	0.79	0.11
Environmental correlation (MY, FY)	0.69	0.02	0.70	0.02	0.71	0.02	0.68	0.02
Phenotypic correlation (MY, FY)	0.70	0.01	0.69	0.01	0.69	0.01	0.70	0.01

525 ^a PM = Polygenic model; GM7K = Genomic-polygenic model with actual 7K SNP information; GM80K-FI = Genomic-polygenic
 526 model with actual and imputed 80K SNP information using FImpute; GM80K-FH = Genomic-polygenic model with actual and
 527 imputed 80K SNP information using Findhap.

528 ^b Repeated sampling approach of Meyer and Houle (2013).

529

530 **Table 6**

531 Rank correlations between animal EBV for 305-d milk yield and fat yield evaluated using a polygenic model and three genomic-
 532 polygenic models with different sets of SNP genotypes

Trait	Rank correlations ^a					
	PM, GM7K	PM, GM80K-FI	PM, GM80K-FH	GM7K, GM80K-FI	GM7K, GM80K-FH	GM80K-FI, GM80K-FH
MY	0.80	0.84	0.84	0.90	0.89	0.96
FY	0.80	0.83	0.79	0.91	0.86	0.93

533 ^a PM = Polygenic model; GM7K = Genomic-polygenic model with actual 7K SNP information; GM80K-FI = Genomic-polygenic
 534 model with actual and imputed 80K SNP information using FImpute; GM80K-FH = Genomic-polygenic model with actual and
 535 imputed 80K SNP information using Findhap; All rank correlations were significant at $P < 0.0001$.

536

537 **Table 7**

538 Rank correlations between sire EBV for 305-d milk yield (MY) and fat yield (FY) evaluated using a polygenic model and three
 539 genomic-polygenic models with different sets of SNP genotypes

Trait	Sires ^b	Rank correlations ^a					
		PM, GM7K	PM, GM80K-FI	PM, GM80K-FH	GM7K, GM80K-FI	GM7K, GM80K-FH	GM80K-FI, GM80K-FH
MY	top 5% (62)	0.50 (74)	0.55 (71)	0.57 (74)	0.78 (79)	0.69 (76)	0.87 (87)
	top 15% (186)	0.78 (75)	0.79 (80)	0.78 (78)	0.83 (82)	0.80 (77)	0.92 (92)
	top 25% (309)	0.77 (80)	0.82 (85)	0.86 (83)	0.83 (85)	0.86 (82)	0.94 (90)
	100% (1,236)	0.82	0.88	0.85	0.92	0.88	0.94
FY	top 5% (62)	0.72 (79)	0.68 (82)	0.61 (63)	0.70 (81)	0.62 (68)	0.76 (76)
	top 15% (186)	0.88 (74)	0.89 (81)	0.78 (69)	0.88 (83)	0.76 (72)	0.84 (81)
	top 25% (309)	0.79 (81)	0.85 (83)	0.70 (77)	0.83 (86)	0.71 (81)	0.78 (88)
	100% (1,236)	0.83	0.87	0.80	0.93	0.87	0.92

540 ^a PM = Polygenic model; GM7K = Genomic-polygenic model with actual 7K SNP information; GM80K-FI = Genomic-polygenic
 541 model with actual and imputed 80K SNP information using FImpute; GM80K-FH = Genomic-polygenic model with actual and
 542 imputed 80K SNP information using Findhap; All rank correlations were significant at $P < 0.0001$, except for top 5% between PM and
 543 GMLD that was significant at $P < 0.0005$; numbers in brackets are percentage of animals in common between pairs of models.

544 ^b Numbers in brackets are numbers of sires. ² Numbers in brackets are numbers of sires.

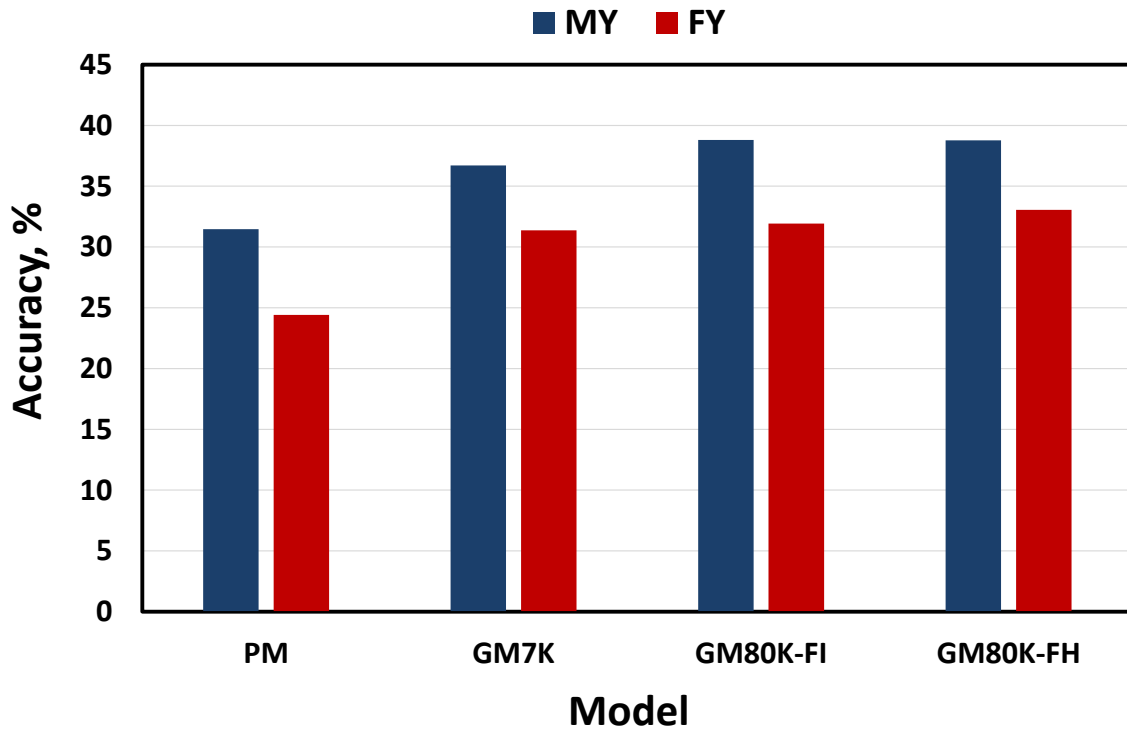
545 **Table 8**

546 Rank correlations between cow EBV for 305-d milk yield (MY) and fat yield (FY) evaluated using a polygenic model and three
 547 genomic-polygenic models with different sets of SNP genotypes

Trait	Cows ^b	Rank correlations ^a					
		PM, GM7K	PM, GM80K-FI	PM, GM80K-FH	GM7K, GM80K-FI	GM7K, GM80K-FH	GM80K-FI, GM80K-FH
MY	top 5% (706)	0.68 (68)	0.64 (66)	0.67 (69)	0.71 (74)	0.71 (75)	0.90 (89)
	top 15% (2,117)	0.70 (74)	0.67 (73)	0.68 (74)	0.76 (79)	0.75 (79)	0.91 (88)
	top 25% (3,529)	0.74 (77)	0.72 (79)	0.74 (78)	0.79 (84)	0.79 (84)	0.90 (89)
	100% (14,113)	0.80	0.84	0.84	0.90	0.89	0.96
FY	top 5% (706)	0.78 (65)	0.76 (69)	0.59 (61)	0.79 (75)	0.67 (68)	0.77 (76)
	top 15% (2,117)	0.67 (74)	0.68 (76)	0.61 (69)	0.75 (81)	0.68 (76)	0.78 (83)
	top 25% (3,529)	0.75 (76)	0.77 (78)	0.66 (73)	0.81 (85)	0.71 (80)	0.81 (85)
	100% (14,113)	0.79	0.83	0.79	0.91	0.86	0.93

548 ^a PM = Polygenic model; GM7K = Genomic-polygenic model with actual 7K SNP information; GM80K-FI = Genomic-polygenic
 549 model with actual and imputed 80K SNP information using FImpute; GM80K-FH = Genomic-polygenic model with actual and
 550 imputed 80K SNP information using Findhap; All rank correlations were significant at $P < 0.0001$; numbers in brackets are percentage
 551 of animals in common between pairs of models.

552 ^b Numbers in brackets are numbers of cows.



553

554 **Fig. 1.** Accuracy of estimated breeding values for 305-d milk yield and 305-d fat yield in a
 555 Thai multibreed population using polygenic models (PM), genomic-polygenic models with
 556 actual 7K SNP information (GM7K), genomic-polygenic models with actual and imputed
 557 80K SNP information from FImpute (GM80K-FI), and genomic-polygenic models with
 558 actual and imputed 80K SNP information from Findhap (GM80K-FH)

559