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# Adjusting for heterogeneity of experimental data in genetic evaluation of dry matter intake in dairy cattle

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European Master in  Animal Breeding and Genetics

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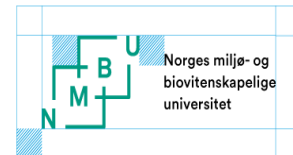
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# Preface

The author carried out this thesis as a part of his European Master in Animal Breeding and Genetics (EMABG) program at the Department of Animal and Aquacultural Sciences of Norwegian University of Life Sciences, Norway. In this report, an in-depth and complete study was performed i) to get the best fitted models for dry matter intake data from nutritional experiment sources and ii) to have better estimate of the genetic parameters and better genetic evaluations.

At first, the author expresses his deepest sense of gratefulness to the Almighty Allah who has enabled the author to complete this study and to prepare the report.

The author would like to express his profound gratitude to his thesis supervisor to Professor Dr. Theodorus Meuwissen for his talented expert guidance, monitoring, encouragement and appreciations during thesis period. His comments, valuable suggestions and constructive criticisms helped the author a lot to improve this report. The author expects and hopes that the findings of this study will be helpful for better genetic evaluation of dairy animals for dry matter intake.

The author also would like to give his special thanks to Professor Dr. Ir. Roel Veerkamp for providing data otherwise it would be impossible to conduct this study. He also helped to solve the ASReml problems and made constructive criticisms, valuable suggestions and appreciations.

Finally, the author wants to express warmest gratitude to his beloved wife Sheuly, parents and friends especially Akhter, Lusa and Rahul for showing their love, affection, encouragement and support during this period.

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# Abstract

Feed cost is the major cost for dairying. So, improving feed efficiency could make dairy farming economically more profitable and environmentally viable by reducing methane emission. But, measuring feed intake in dairy animals is not only difficult but also expensive. So, feed efficiency traits were not considered in the dairy breeding program in past decades. One of the solutions of this problem might be the use of feed intake data from nutritional experiments. The objectives of the present study were i) to find the best fitted model for repeatedly measured daily dry matter intake (DMI) data obtained from different herds and experiments across lactations and ii) to get better estimates of the genetic parameters and better genetic evaluations. After editing, there were 572512 daily DMI records of 3495 animals from 11 different herds across 13 lactations and animals were under 110 different nutritional experiments. The fitted model for this dataset was a univariate repeated measure animal model in which additive genetic and permanent environmental (within and across lactations) effects were fitted as random. Two different models were fitted based on different fixed effects. For unscaled data, each model was fitted as homoscedastic (HOM) model at first and then heteroscedastic (HET) model. After that, data were scaled by multiplying with particular herd's scaling factors which were calculated by accounting for heterogeneity of phenotypic within herd variances. Models were selected based on cross-validation and prediction accuracy results. Scaling factors were re-estimated to see the effectiveness of accounting herd heterogeneity. Variance components and respective heritability and repeatability were estimated based on pedigree based relationship matrix. Spearman's rank correlations of EBVs between scaled and unscaled DMI were also calculated. All the analyses were performed using ASReml software package. Results indicated that HOM model for scaled data showed better fit than the models (HOM or HET) fitted for unscaled data. The heritability and repeatability estimates of daily DMI for the final model (HOM model 3 fitted for scaled data) were 0.08 and 0.51, respectively. The re-estimated scaling factor after accounting for heterogeneity of residual variances was close to 1.0 indicating the stabilization of residual variances and herd accounted for most of the heterogeneity. The rank correlation of estimated breeding values (EBVs) between scaled and unscaled data ranged from 0.96 to 0.97.

**Keywords:** Dry Matter Intake, Heterogeneity, Heritability, Repeatability, Genetic Evaluation, Dairy Cattle

**Chapter 1: Introduction**

Feed cost is one of the major recurring costs of dairy farming. It comprises 43 -67% of total farming cost found in different countries (Simm et al., 1994, Shalloo et al., 2004, Ho et al., 2005). It is even higher (about 80% of the total recurring cost) if we consider only milk production cost (Board, 1990). So, genetic improvement of feed efficiency traits could make the dairy farming economically more profitable and viable. Moreover, the more the cow is efficient, the less methane she emits (Hegarty et al., 2007)**.** Although feed efficiency is a complex trait in almost all farm animals however it can be still considered in selection program for beef cattle, pig and poultry during growing period. But for dairy cattle, it is even more complex because many physiological processes such as milk production, reproduction, maintenance of health and body and growth in young cows happen simultaneously in dairy cows. Moreover, it is expensive and difficult to measure individual feed intake of dairy animals (Veerkamp and Emmans, 1995, Arthur et al., 2004) and feed intake data are not easily recorded in commercial dairy herds**.** So, most of the previous estimates of the genetic parameters for feed intake and feed efficiency traits were based on small dataset which makes the estimates biased due to large sampling error (Pech et al., 2014). For this reason, the traits that were emphasized in selection strategy for dairy development in the past decades were mainly related with production and health of dairy cows (Weigel).

With the invention of genomic selection (GS) (Meuwissen et al., 2001) tool, feed efficiency trait has become of research interest and been considered in selection program. Because in GS, only reference population (sometimes called training population) need to have both phenotypic and genotypic information and genomic estimated breeding values (GEBVs) can be estimated for candidate animals having only genotypic information without phenotype (Meuwissen, 2007) **.** So, GS would be the perfect choice for difficult and expensive to measure traits like feed intake and feed efficiency traits (Pryce et al., 2014). To achieve satisfactory genetic gain from GS, accuracy of GEBVs is very important. So far, many research have been conducted to evaluate the accuracy of GEBVs (Khansefid et al., 2013). Past research results and theories reveal that the numbers of animals genotyped and precision of the phenotype measured are the most important factors affecting the reliability of GEBVs (VanRaden et al., 2009). One could increase accuracy

of GEBVs by increasing the size of reference population. Incorporation of multi-breed animals having genotype and phenotypic information is one of the options to increase the size of reference population. But multi-breed reference populations did not work well to increase the accuracy of GS (Khansefid et al., 2013) because of i) breed $\times$ quantitative trait loci (QTL) interaction ii) variation of linkage disequilibrium (LD) between QTL and single nucleotide polymorphisms (SNPs) among breeds and iii) low LD across the breeds and it is even limited to SNPs that are closed to QTL. Another way to increase reference population size is combining data from different populations from several countries because each country has a small reference population that is not enough to get satisfactory level of accuracy (Verbyla et al., 2010). Major problems of combining phenotypic data from different countries are genotype $\times$ environment interaction and definition of traits varies among countries as well (De Haas et al., 2012). There is very limited opportunity to get enough and accurate phenotypic data for difficult-to-measure traits like feed intake. So for feed intake, another option of increasing the reference population size might be the use of historical nutritional experiment's data in which people have already recorded the difficult to measure and expensive trait like individual feed intake and DMI on dairy animals (Banos et al., 2012, Pryce et al., 2012, Veerkamp et al., 2012). For example, the global Dry Matter Initiative (gDMI) was formed to increase the size of the reference population by combining international research animal's phenotype and genotype (Berry, 2013, Veerkamp, 2013). The main challenge of using experimental data is the wide variability of the phenotypes measured from different nutritional experiments mainly due to different treatments used in those experiments and animals are from different herds and parities. An approach was developed by Banos et al. (2012) who described in details of combining phenotypic data of dairy cattle collected from experimental sources in three different countries. These data were successfully used for genome-wide association study (GWAS) by Veerkamp et al. (2012) to detect the significant QTL of feed intake. But they used only first parity data. The objectives of the present study were i) to find the best fitted model suitable for repeatedly measure DMI data originated from multiple nutritional experiments across herds, years and parities in the Netherlands and ii) to get better estimates of the genetic parameters and better genetic evaluation of the animals.

## Chapter 2: Materials and Methods

**2.1 Data Description and Editing**

Original dataset consisted of 637471 records repeatedly measured on 3771 Holstein cows from 11 herds across 13 parities in Netherlands. Cows were under 110 different nutritional experiments subjected to different treatments in those experiments. Data were collected from 1991 to 2015 on cows calved between 1990 to 2015. Cows having at least single daily DMI record were kept in the dataset for further analysis and cows with missing DMI records were removed from the dataset. In addition to feed intake data, other related information on individual cows such as daily milk yield, live weight, calving interval etc. were also available but these data were not sufficient to use. As data collection were not performed specifically for the present study, so there were some extreme values in the dataset and some of the values were even beyond the biological limit. To remove extreme data, editing was performed manually by setting certain biological limits for the different variables or traits as proposed by Banos et al. (2012) (Table 1).

Table 1 Biological limits set for editing the original records

| Trait/Variable | Unit of Measurement | Acceptable Range |
|---|---|---|
| DMI | Kg/d | 0.89 to 65 |
| Days in milk (DIM) | Days | 1 to 400 |
| Live weight | Kg | 400 to 1200 |
| Milk Yield | Kg/d | 3 to 100 |
| No. of lactation | Number | 1 to 13 |

After editing, there were 572512 daily DMI records from 3495 cows across 11 herds and each cow has at least a single DMI record. Average number of daily DMI records per cow was 168.8. After editing, there were 109 experiments retained subjected to 467 different treatments in those experiments. Average (mean ± SD) daily DMI of the cows was 17.95 ± 6.49 kg/d. Data retained after editing have been summarized in Table 2.

Table 2 Data summary after editing

| Variable | Class Size/Range/Average |
|---|---|
| Total number of DMI records | 572512 |
| Number of cows having at least single records | 3495 |
| Average number of records per cow | 168.80 (1 to 1076) |
| Number of herds | 11 |
| Number of experiments | 109 |
| Number of treatments | 467 |
| Lactation Number (LN) | 1 to 13 |
| Year of recording | 1991 to 2015 |
| Calving year | 1990 to 2015 |
| Average DMI (SD*) Kg/d | 17.95 (6.49) |
| Average age at recording in months | 52.64 (21 to 189) |
| Average age at calving in months | 47.76 (19 to 175) |
| Average days in milk (DIM) | 126.6 |

* SD stands for standard deviation

## 2.2 Pedigree Information

Traditional relationship matrix (A-matrix) was generated based on the pedigree information available. The pedigree file consisted of 18566 animals and among which 15867 animals were the parents.

## 2.3 Model Fitting

A univariate repeated measure animal model was fitted for this dataset and the model is given below in matrix notation.

$$y = Xb + Z_1p + Z_2a + e \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \quad 1$$

Where, $y$ = Vector of n observations; $b$ = Vector of fixed effects; $p$ = Vector of permanent environmental effects; $a$ = Vector of additive genetic effects; $e$ = Vector of random residual variances; $X$, $Z_1$ and $Z_2$ are incidence matrices which relate $b$, $p$ and $a$ to $y$, respectively. The assumptions of random effects of the model are shown below.

$$\begin{bmatrix} a \\ p \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I_d\sigma_c^2 & 0 \\ 0 & 0 & I_n\sigma_e^2 \end{bmatrix} = \begin{bmatrix} G & 0 \\ 0 & R \end{bmatrix} \quad G = \begin{bmatrix} A\sigma_a^2 & 0 \\ 0 & I_d\sigma_c^2 \end{bmatrix}$$

where, $\sigma_a^2$ = additive genetic variance; $\sigma_c^2$ = variance due to permanent environment; and $\sigma_e^2$ = residual variance; phenotypic variance ($\sigma_p^2$) is the sum of these three variance components; A =

Pedigree based relationship matrix, $I_d$ is the identity matrix equal to the number of animals included in the pedigree and $I_n$ is the identity matrix equal to the number of observations.

Usually best fitted models have relatively more parameters but available data do not always support the complex model in terms of convergence. There were a number of models tried from simple to complex by exploratory exercises but two models (called model 2 and 3) were compared and these are shown below in model terms.

DMI = μ + a + p + pol(DIM,3).Herd + TD + Treat/EXP + lin(LN)/pol(Age_cal,2) + e…………………………… 2 (model 2)

DMI = μ + a + p + pol(DIM,3).Herd + TD.Herd + Treat/EXP + lin(LN)/pol(Age_cal,2) + e……………….. …….3 (model 3)


Where, DMI is the daily DMI observations; μ is the overall mean; a is the random additive genetic effect; p is the random term for combined permanent environmental effect (within and across lactations); pol(DIM,3).Herd is fixed effect for third order polynomial of DIM interact with Herd; TD (Test day) is fixed effect; TD.Herd is fixed effect of test day interact with Herds; Treat/EXP is the fixed effect of treatment nested within experiment; lin(LN)/pol(Age_cal,2) is fixed effect of LN fitted as co-variate and nested in second order polynomial of age at calving in months; e is the random residual error.

### 2.3.1 First stage

At first it was assumed that the residual variances for all the observations are homogeneous. So, the diagonal elements of matrix R in equation 1 was equal for all observations i.e. $\sigma_e^2$ and the fitted model is called homoscedastic model (HOM). As DMI was recorded on animals from 11 different herds across 13 lactations over 25 years (1991 to 2015) and animals were under different nutritional experiments, so it was not realistic to assume the residual variances as homogeneous. That is why we also fitted the heteroscedastic model (HET) where we assumed different diagonal elements of matrix R for different herds. For example, $\sigma_{ei}^2$ is the residual variances to the particular herd of $i^{th}$ different herds. Based on homogeneity or heterogeneity of residual variances, we fitted model 2 as two distinct models namely 2A and 2B as HOM and HET model, respectively.

**2.3.2 Second stage**

In the second step, we fitted HET model 2B for herds but excluding additive and permanent environmental effect. From these models, we got the residual variances for each herd and weighting factor ($f_i$) for each herd was calculated based on the estimated herd residual variances as shown in Equation 4.

$$f_i = \sqrt{\frac{V_i}{V_i}} \dots\dots\dots\dots\dots\dots\dots\dots\dots \dots\dots\dots\dots\dots\dots\dots 4$$

Where, $f_i$ = weighting factor for observations of ith herd (i = 1, 2 …………11); $\sqrt{Vi}$ = Square root of average residual variances for all herds; $\sqrt{Vi}$ = Square root of residual variances for i[th] herd;

Observations of each herd were then multiplied by respective weighting factor to get scaled observations. Scaled observations were fitted as homoscedastic model in model 2 which is called model 2C. Finally, model 2A, 2B and 2C were compared themselves based on model selection criteria (described below).

Same procedure was followed for model 3 and fitted models were named as model 3A (HOM model), 3B (HET model) and 3C (HOM for scaled DMI data).

Heterogeneous herd residual variances and scaling factors were re-estimated in the similar manner for the scaled data to see the effectiveness of scaling for herd heterogeneity.

**2.4 Cross-validation and other selection criteria for comparing models**

Initially Akaike Information Criterion (AIC) and the Bayesian Information Criterion (BIC) were used to select better fitted models. Then prediction accuracy (correlation between DMI observations or scaled DMI and predicted DMI) was calculated. Model giving highest correlation was considered as the best predictable model. Additionally and finally, 10-fold cross-validation was performed for comparing the models. For this purpose, the whole dataset were equally and randomly divided into 10-subsets (disjoint). Each time, 9-subsets were considered as training dataset and the remaining one was called testing set. After training the model in the training set, the model was validated using testing set and mean squared error (MSE) of each testing fold were recorded for the models. Then, the MSE of the testing folds were averaged

across all 10 testing sets. The model giving the lowest average MSE was considered as the best model.

**2.5 Estimation of Variance Components and Genetic Parameters**

Additive genetic ($\sigma_a^2$), permanent environmental ($\sigma_c^2$) and residual ($\sigma_e^2$) variance components were estimated for all the models. Relationship matrix used in these models was based on pedigree information. Respective heritability ($h^2$) and repeatability (t) were calculated based on the estimated variance components.

$$\hat{h}^2 = \hat{\sigma_a^2} / (\hat{\sigma_a^2} + \hat{\sigma_c^2} + \hat{\sigma_e^2}) = \hat{\sigma_a^2} / \hat{\sigma_p^2} \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots 5$$

$$\hat{t} = (\hat{\sigma_a^2} + \hat{\sigma_c^2}) / (\hat{\sigma_a^2} + \hat{\sigma_c^2} + \hat{\sigma_e^2}) = (\hat{\sigma_a^2} + \hat{\sigma_c^2}) / \hat{\sigma_p^2} \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots 6$$

## 2.6 Comparing ranking of animals based on EBVs

We also compared the ranking of the animals based on estimated EBVs between different models. Ranking was done by calculating Spearman's rank correlation using SPSS software package.

All the analyses performed were based on the REML method and the software package used for analysis was ASReml 4.1 (Gilmour et al., 2014) except for Spearman's rank correlation. Heteroscedastic models were fitted by 'sat' function of ASReml 4.1 package e.g. 'residual sat(Herd).idv(units)' is a function used to partition heterogeneous residual variances by herd.

## Chapter 3: Results

**3.1 Model Comparison**

AIC, BIC, average MSE of prediction, and prediction accuracy for all fitted models are shown in Table 3. For unscaled data, HET model showed a better fit than HOM model according to AIC, BIC and average MSE criteria, and similar trend was found both for model 2 and 3 (Table 3). But, the prediction accuracy of unscaled data was same for both the HOM and HET models. Although AIC and BIC criteria did not favour HOM model fitted for scaled data but based on average MSE and prediction accuracy, HOM model for scaled data was found as best fitted model. Scaling of data improved prediction accuracy noticeably regardless of fitting either model 2 or model 3 but same MSE and prediction accuracy were obtained for model 2 and 3 when fitted for scaled data (Table 3).

Table 3 AIC, BIC, average MSE and prediction accuracy of the models

| Model | Type of model | Data type | AIC | BIC | Average MSE of prediction | Prediction accuracy |
|---|---|---|---|---|---|---|
| 2A | HOM | unscaled | 194518.2 | 194545 | 14.36 | 0.81 |
| 2B | HET | unscaled | 189020.6 | 189074.3 | 13.68 | 0.81 |
| 2C | HOM | scaled | 192158.4 | 192185.2 | 10.46 | 0.85 |
| 3A | HOM | unscaled | 194466.4 | 194493.3 | 14.36 | 0.81 |
| 3B | HET | unscaled | 188995.6 | 189049.3 | 13.84 | 0.81 |
| 3C | HOM | scaled | 192019.5 | 192046.4 | 10.46 | 0.85 |

**3.2 Variance Components**

Estimates of the variance components and respective standard errors (se) are presented in Table 4. In case of unscaled data, estimate of additive genetic variance ($\hat{\sigma}_a^2$) was slightly higher for HET model than HOM model (Table 4). On contrary when HOM model was fitted for scaled data, the estimate of the $\hat{\sigma}_a^2$ was approximately 2.5 times higher than unscaled data in case of model 2. For model 3, there was also a substantial increase of $\hat{\sigma}_a^2$ but increment was lower in comparison to model 2. On the other hand, permanent environmental variance ($\hat{\sigma}_c^2$) showed an opposite trend for both model 2 and 3. For unscaled data, estimate of the $\hat{\sigma}_c^2$ was lower for HET than HOM model and it was even lower for scaled data (Table 4). Residual error variance ($\hat{\sigma}_e^2$) also showed the similar trend likewise $\hat{\sigma}_c^2$.

Table 4 Variance components and respective standard errors (within parenthesis) estimates of unscaled and scaled data for different HOM and HET models

| Model | Type of model | Data type | $\hat{\sigma}_a^2$ (se) | $\hat{\sigma}_c^2$ (se) | $\hat{\sigma}_e^2$ (se) | $\hat{\sigma}_p^2$ (se) |
|---|---|---|---|---|---|---|
| 2A | HOM | unscaled | 3.22 (0.30) | 11.53 (0.26) | 14.68 (0.02) | 29.43 (0.30) |
| 2B | HET | unscaled | 3.83 (0.33) | 11.31 (0.26) | 10.72 (0.19) | 25.86 (0.40) |
| 2C | HOM | scaled | 8.42 (0.46) | 9.42 (0.23) | 10.69 (0.02) | 28.53 (0.43) |
| 3A | HOM | unscaled | 1.29 (0.19) | 10.84 (0.23) | 14.67 (0.02) | 26.80 (0.62) |
| 3B | HET | unscaled | 1.45 (0.19) | 10.61 (0.23) | 10.67 (0.18) | 22.72 (0.33) |
| 3C | HOM | scaled | 1.69 (0.20) | 9.32 (0.21) | 10.68 (0.02) | 21.69 (0.62) |

**3.3 Heritability and Repeatability**

Both the heritability and repeatability estimates of model 2 were higher for HET model than HOM model in case of unscaled data and it was even higher when HOM model fitted for scaled data (Figure 1). Model 3 showed almost similar trend but the estimates of the heritability for model 3 were much lower compared to model 2. Estimates of the $\hat{h}^2$(se) for model 2A, 2B and 2C were 0.11 (0.009), 0.15 (0.01) and 0.30 (0.01), respectively. Heritability estimates were 0.05 (0.07), 0.07 (0.008) and 0.08 (0.008), respectively for model 3A, 3B and 3C. Repeatability estimates were almost similar between model 2 and 3 and it ranged from 0.45 to 0.63.
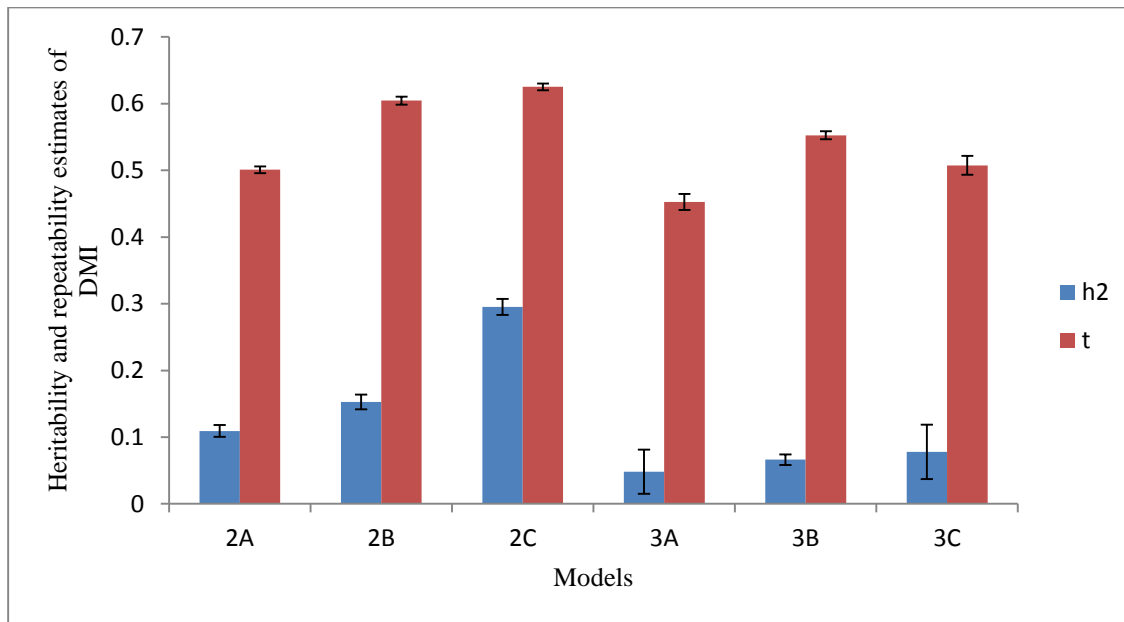


Figure 1 Heritability and repeatability estimates from different models

From HET model 2B and 3B, within herd $\hat{h}^2$ and $\hat{t}$ were obtained and it has been shown in Figure 2. Although the trend of $\hat{h}^2$ and $\hat{t}$ across herds were similar for both models but estimates of model 2B was higher for both the heritability and repeatability. Estimates of $\hat{h}^2$ ranged from 0.11-0.21 and 0.05 -0.09 for model 2B and 3B, respectively. Repeatability estimates ranged from 0.40 to 0.80.

Figure 2 Within herd heritability and repeatability estimates from unscaled data (model 2B & 3B)

### 3.4 Rank Correlations of EBVs

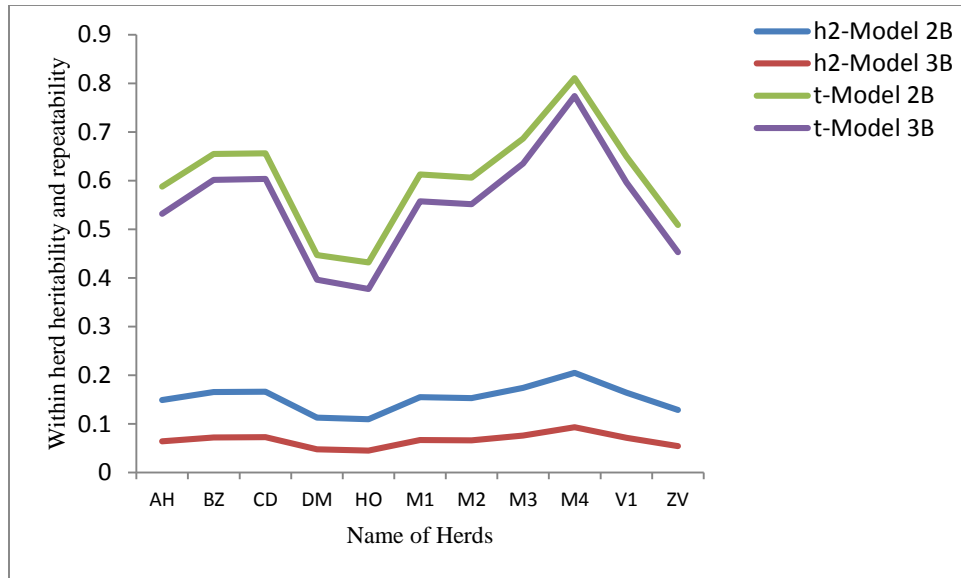Table 5 shows the Spearman's rank correlations of EBVs among different models. Rank correlation of EBVs between model 2A and 2B or model 3A and 3B was approximately 1.0 indicating similar ranking of animals between HOM and HET models fitted for unscaled data (Table 5). But EBV ranking of the animals changed after scaling data. Rank correlations for EBVs between scaled and unscaled data were 0.91-0.92 for model 2 and 0.96-0.97 for model 3.

Table 5 Spearman's rank correlation of EBVs

| Models | Spearman's rank correlations | | | | | |
| | 2A | 2B | 2C | 3A | 3B | 3C |
|---|---|---|---|---|---|---|
| 2A | 1.0 | 0.99** | 0.92** | 0.77** | 0.73** | 0.74** |
| 2B | 0.99** | 1.0 | 0.91** | 0.74** | 0.72** | 0.73** |
| 2C | 0.92** | 0.91** | 1.0 | 0.63** | 0.61** | 0.68** |
| 3A | 0.77** | 0.74** | 0.63** | 1.0 | 0.99** | 0.96** |
| 3B | 0.73** | 0.72** | 0.61** | 0.99** | 1.0 | 0.97** |
| 3C | 0.74** | 0.73** | 0.68** | 0.96** | 0.97** | 1.0 |

** Level of significance at 1%

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**3.5 Comparison of heterogeneous residual herd variance before and after scaling data**

Heterogeneous residual variances by herds before and after scaling the data are presented in Figure 3. Before scaling the data, there was a wide variability of residual variances across herds found for both models (Figure 3). For scaled data, although there was a little bit variability of residual variances but it seemed to be similar across herds for both models indicating the stabilization of heterogeneous herd residual variances (Figure 3).
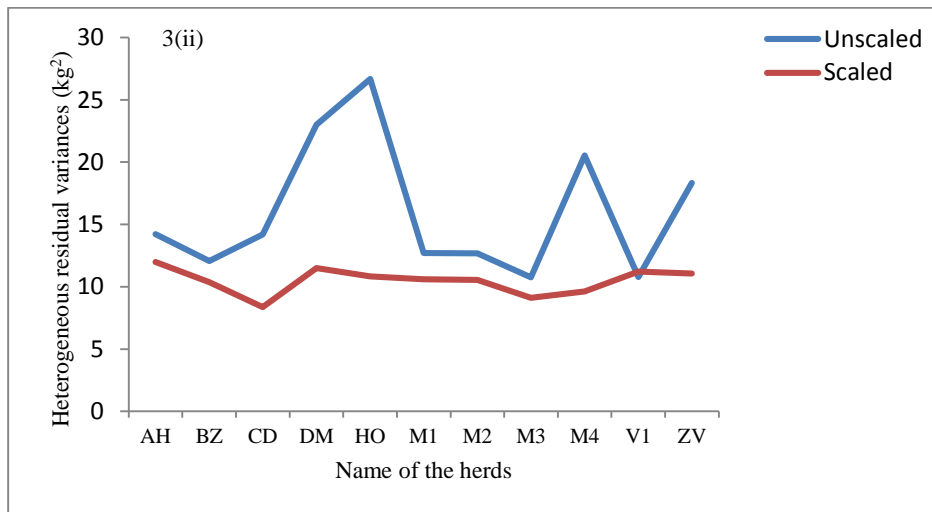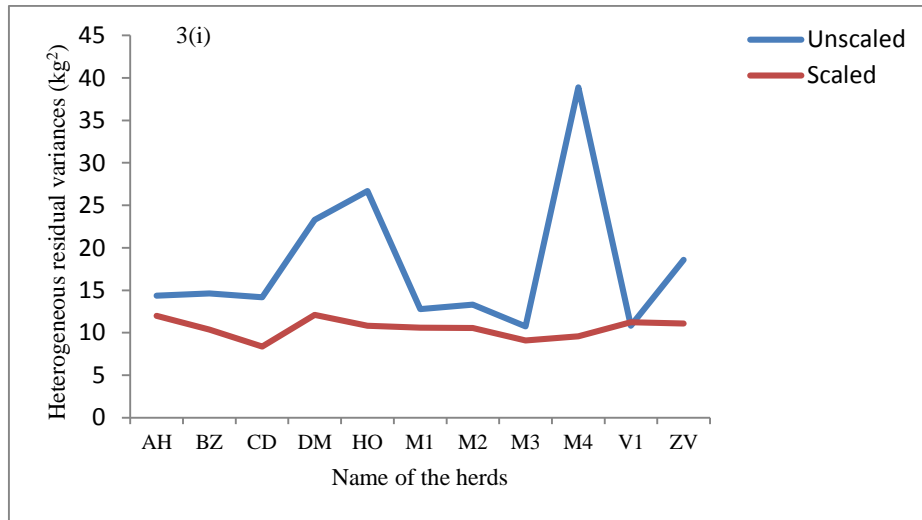


Figure 3 Heterogeneous residual variances by herd before and after scaling of data for (i) model 2 and (ii) model 3

# Chapter 4: Discussion

## 4.1 Model Selection

For unscaled data, HET model fitted slightly better than HOM model based on AIC, BIC and average MSE criteria but the prediction accuracy was same for both HOM and HET model (Table 3). Similar trends were noticed for both model 2 and 3. The findings of a previous study on body weight traits in beef cattle by Neves et al. (2012) disagree with our results i.e. they found HOM model is better than HET model according to BIC and average MSE criteria. But they also found better fit of the HET model than HOM model when considered AIC as selection criteria. Moreover, when fitted sex specific model they also found the higher predictive ability (lower average MSE) of HET model than HOM model for body weight in female. Although scaling slightly increased AIC and BIC values for HOM model fitted for scaled data but scaling of data decreased the average MSE and increased prediction accuracy of the model. Increase of prediction accuracy was not surprising. Because it was expected that scaled data will fit better than unscaled data. Clearly it indicates that HOM models fitted for scaled data were the best fitted models. From a past study with swine body weight and backfat thickness trait, it was concluded that the scaled data accounting for heterogeneous herd variances fit better than unscaled data which is in consistent with our findings (MR et al., 1998)

## 4.2 Estimation of Variance Components

In case of unscaled data, the estimates of variance components were almost similar for HOM and HET model. Neves et al. (2012) also found the similar estimates of variance components for HOM and HET model for body weight traits in Nellore beef cattle. After scaling data, there was a slight increase of additive genetic variances for model 3 but the increment was triple for model 2 (Table 4). In model 2, fixed effect of TD (Test Day) was fitted within herd which might be one of the reasons of getting higher estimate of additive genetic variance in this model. On contrary, TD-by-Herd interaction effect was included as fixed term in model 3 which is more realistic because TD effect varies from herd to herd. Another reason of getting model sensitive estimates might be that models had faced difficulty in separating fixed effect, permanent environmental effect and additive genetic effect due to lack of connectedness between TD and Herd. Previous study also pointed a slight increase of variance components estimate for weight trait of swine after scaling the data which is in complete agreement with the results of model 3 (MR et al., 1998). On the other hand, estimates of both permanent environmental and residual variance

components decreased after accounting for heterogeneity of herd variances indicating a better fit of the model for scaled data (Table 4).

**4.3 Heritability and Repeatability**

Increase of heritability was double to triple for both model 2 and 3 after scaling data but repeatability estimates were almost similar for both scaled and unscaled data. For the final model (i.e. HOM model with scaled data), the estimate of the heritability from model 3 (0.08) was much lower than model 2 (0.30). It may be due to the same reasons as explained for estimates of additive genetic variances in previous paragraph. The heritability estimates of model 2 are consistent with the past estimate (0.27 to 0.34) reported by Berry (2013). Although heritability estimate of model 3 was much lower but it falls still in the range of within country heritability estimates (0.08 to 0.52) which was also documented by Berry (2013). Banos et al. (2012) found the heritability ranging from 0.15 to 0.22 for daily DMI in dairy cows but they estimated using first lactation DMI records. When only first lactation DMI data were included in our analysis, estimates of heritability increased slightly. The heritability estimates for final model (i.e. HOM model fitted for first lactation scaled DMI) were 0.39 and 0.10 for model 2 and model 3, respectively. Berry (2013) also reported the substantial increase of DMI heritability from 0.08 to 0.16 when pedigree based relationship matrix was replaced by combined pedigree and genomic relationship matrix indicating the potentiality of using genomic information to improve heritability.

In our study, repeatability (within and across lactations) estimates ranged from 0.51 to 0.63 for the final model (i.e. HOM model with scaled DMI). When within and across lactations repeatability was separated, it did not affect the estimates of repeatability and heritability (Table 7 in Appendix I). Although there is not much information available for across lactations DMI repeatability but our finding agrees with the previous repeatability (across lactations) estimate of 0.51 reported by Søndergaard et al. (2002) in Denmark for 293 dairy cows from three different breeds. Findings of Berry (2013) was also consistent to our results and they found across lactations  repeatability of 0.66 (ranging from 0.46 to 0.84) using experimental DMI data collated from 9 different countries of 6957 dairy cows. They also reported identical repeatability estimates using either only pedigree information or combined pedigree and genomic information for generating relationship matrix.

**4.4 Scaling of Data**

Estimated scaling factor for 11 different herds varied from 0.68 to 1.29 for model 2 and 0.77 to 1.22 for model 3 indicating a wide variability among herds. This signifies the necessity of taking into account the herd heterogeneity in consideration. Re-estimated within herd residual variances of scaled DMI were almost similar across herds and this is reflecting the variability stabilization due to adjustment for herd heterogeneity (Table 6 in Appendix I). In other words, one could say that most of the heterogeneity came from herds. In fact, re-estimated scaling factors using scaled DMI were close to 1.0 which is the proof of the effectiveness of data scaling.

**4.5 Comparison of EBV ranking of cows**

For unscaled data, the spearman's rank correlation between EBVs of HOM and HET model was 0.99 (close to 1.0). This indicates that there were not much changes of overall EBV ranking due to fitting HOM or HET model. But, the rank correlations between EBVs before and after scaling the data were 0.92 for model 2 and 0.97 for model 3. This means that the EBV ranking of cows' changes due to scaling of data and the change was more prominent in model 2 than in model 3. The rank correlation of EBVs before and after scaling the data for swine production traits was 0.98 and this result is in agreement with the results of model 3 in our study (MR et al., 1998). The results also suggest that the scaling of data accounting for heterogeneity of residual herd variances reduces the biasness of genetic evaluation of dairy cows.

**4.6 Conclusions**

Although HET model fitted better than HOM model in case of unscaled data but HOM models for scaled data were the best fitted models. As the estimate of model 2 was not stable, so HOM model 3 fitted for scaled data was considered as the final model for this dataset. The heritability and repeatability estimates of the final model were 0.08 and 0.51, respectively which agree with the previous findings found in literature. The re-estimated scaling factor after accounting for heterogeneity of residual variances was close to 1.0 which indicates the stabilization of residual variances and herd accounted for most of the heterogeneous variances. The rank correlation of EBVs between scaled and unscaled data ranged from 0.96 to 0.97 which means a bit change of ranking of the animals. So, scaling data accounted for heterogeneity of herd variances may reduce the biasness of genetic evaluations.

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# Appendix I

Table 6 Estimates of heterogeneous residual variances within herd for model 2 and 3 before and after scaling data

| Herd | Model 2 | | Model 3 | |
|------|---------|---------|---------|---------|
| | Before scaling | After scaling | Before scaling | After scaling |
| AH | 14.35 | 11.98 | 14.21 | 11.99 |
| BZ | 14.65 | 10.38 | 12.06 | 10.36 |
| CD | 14.19 | 8.37 | 14.19 | 8.37 |
| DM | 23.29 | 12.1 | 23.00 | 11.1 |
| HO | 26.66 | 10.82 | 26.67 | 10.83 |
| M1 | 12.77 | 10.59 | 12.69 | 10.59 |
| M2 | 13.30 | 10.58 | 12.68 | 10.55 |
| M3 | 10.75 | 9.11 | 10.75 | 9.12 |
| M4 | 38.90 | 9.57 | 20.53 | 9.62 |
| V1 | 10.82 | 11.23 | 10.79 | 11.22 |
| ZV | 18.58 | 11.09 | 18.33 | 11.05 |

Table 7 Estimates of heritability and repeatability with respective standard errors (within parenthesis) when within and across lactations permanent environment effects were separated for final models i.e. HOM model fitted for scaled DMI

| Parameters | Model 2 | Model 3 |
|------------|---------|---------|
| Heritability | 0.30 (0.012) | 0.07 (0.011) |
| Repeatability | | |
| i) Within lactation | 0.30 (0.012) | 0.081 (0.008) |
| ii) Across lactations | 0.63 (0.005) | 0.50 (0.012) |