

Estimation of genetic parameters for udder traits using a Random Regression Model on age at classification for Holsteins in Japan

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Introduction

Genetic evaluation for type traits in Japan

- Single traits animal model.
- Record at first lactation.

Improvement

- Type traits, especially **udder traits**, can vary with aging.
- Contains all classification records from various ages and lactations.
- Consider change of genetic variances on age at classification using a random regression model.

Objective

To estimate genetic parameters for the udder traits using Random Regression model on age at classification.

Materials and Methods

Data

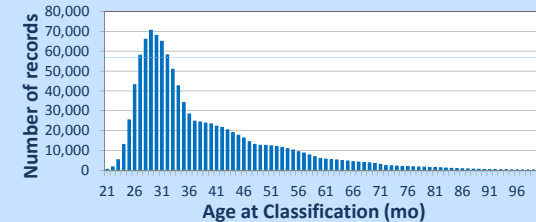
- **1,006,185** records from **818,488** cows provided by The Holstein Cattle Association of Japan.
- 1st -5th parity and 21 to 100 mo of age at classification.

Udder traits

- Overall Udder (**UDDER**), Fore Udder (**FU**), Rear Udder Height (**RUH**), Rear Udder Width (**RUW**), Udder Support (**US**), Udder Depth (**UD**) and Front Teat Placement (**FTP**)

Description of the data (Mean ± SD)

Parity	1 st	2 nd	3 rd	4 th	5 th
Number of records	674,543	234,435	102,919	39,976	14,312
Age at classification (mo)	30.7 ± 3.9	44.1 ± 3.9	56.6 ± 5.4	69.4 ± 6.0	82.7 ± 6.6
UDDER	79.3 ± 2.3	81.9 ± 3.0	83.4 ± 3.3	84.1 ± 3.4	84.1 ± 3.6
FU	5.9 ± 1.1	6.1 ± 1.2	6.1 ± 1.2	6.1 ± 1.3	6.0 ± 1.3
RUH	6.2 ± 1.2	6.5 ± 1.3	6.6 ± 1.3	6.5 ± 1.3	6.4 ± 1.3
RUW	5.5 ± 1.1	6.8 ± 1.1	7.3 ± 1.0	7.4 ± 1.0	7.4 ± 1.0
US	6.0 ± 1.2	6.1 ± 1.3	6.0 ± 1.3	6.0 ± 1.3	5.9 ± 1.4
UD	6.1 ± 1.3	4.8 ± 1.2	4.1 ± 1.0	3.7 ± 0.9	3.4 ± 0.9
FTP	4.9 ± 1.1	5.0 ± 1.2	5.0 ± 1.2	4.9 ± 1.2	4.8 ± 1.2



Number of records by age at classification

Random Regression (RR) model

$$y_{ijklmn} = hcd_i + pa_j + sl_k + \sum_{l=0}^2 a_{lm} z_{lm} + \sum_{l=0}^2 pe_{lm} z_{lm} + e_{ijklmn}$$

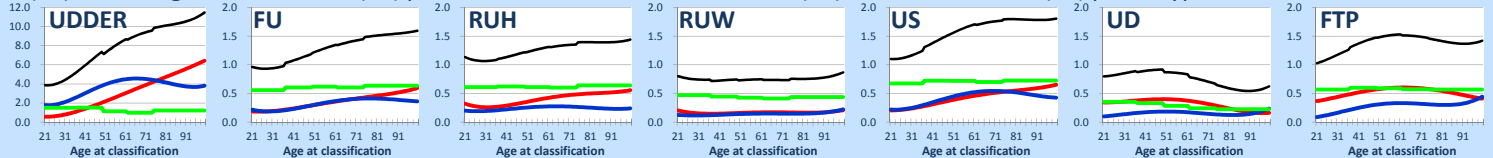
- hcd_i = fixed effects of Herd-classifier-date at classification i
- pa_j = fixed effects of parity-age group at classification j
- sl_k = fixed effects of stage of lactation k
- a_{lm} = RR on age at classification l for additive genetic effects of cow m
- pe_{lm} = RR on age at classification l for permanent environmental effects of cow m
- z_{lm} = second-order Legendre polynomials
- e_{ijklmn} = Heterogeneous residual effects with 5 groups (21-36, 37-49, 50-61, 62-74 and 75-100 mo of age at classification)

GIBBS3f90 program used (Miszta *et al.* 2002)

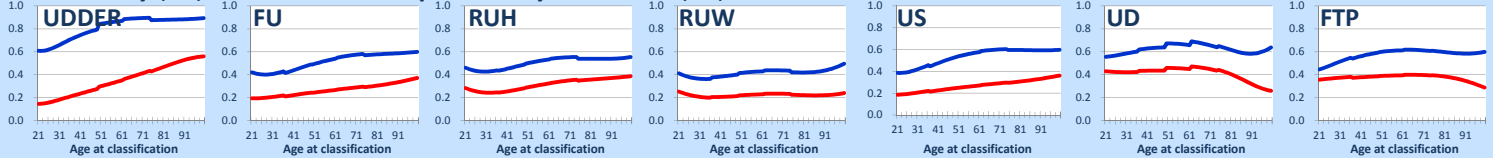
Results

Variance components

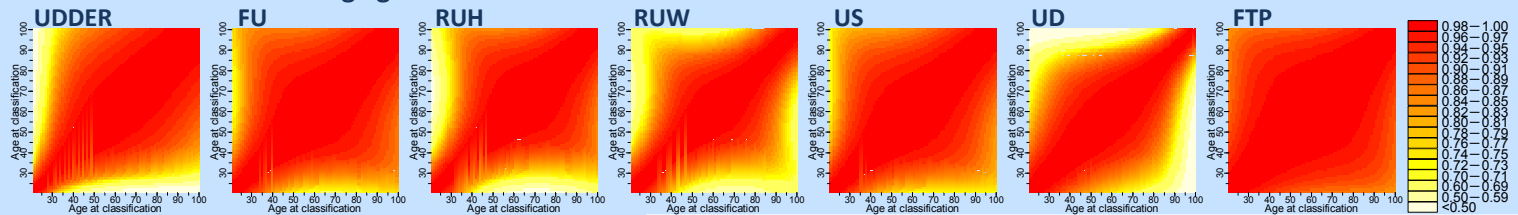
(—) additive genetic variance, (—) permanent environmental variance, (—) residual variance, (—) phenotypic variance



Heritability (—) estimates and Repeatability estimates (—)



Genetic correlations among ages at classification



Genetic correlations between 29 and 42-81 mo of age at classification

Traits	42 mo	55 mo	69 mo	81 mo
UDDER	0.92	0.84	0.78	0.74
FU	0.95	0.89	0.87	0.86
RUH	0.90	0.77	0.72	0.72
RUW	0.91	0.79	0.74	0.74
US	0.96	0.91	0.88	0.87
UD	0.96	0.91	0.84	0.76
FTP	0.98	0.96	0.94	0.93

Conclusions

Heritability estimates

- UDDER, FU, RUH, and US increased dramatically with cow's age.
- UD and FTP decreased after 65 mo of age.

Genetic correlations

- FU, US, and FTP showed high correlations throughout the age.
- In contrast, UDDER, RUH, RUW, and UD presented a weak decline with distance between ages.

↓↓↓

RR model could appropriately use classification records from various ages.