THE USE OF MONTHLY EGG PRODUCTION RECORDS FOR GENETIC EVALUATION OF LAYING HENS

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ABSTRACT

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This research addresses the possibilities of using monthly production records for genetic evaluation of laying hens with four different models and different data sets. The data were collected from a pure line of Lohmann Tierzucht GmbH at Cuxhaven in Germany for two generations from 1998 to 1999 with pedigree being traced back one generation. In total of 9735 hens from 220 sires and 1879 dams were analysed. The evaluated models were: (1) Cumulative Model (*CM*), (2) Multiple Trait Model (*MTM*), (3) Fixed Regression Model (*FRM*), and Random Regression Model (*RRM*). Variance components were estimated using Animal Model with REML and breeding values were predicted using BLUP Animal Model. The *RRM* is an interesting model for the evaluation. The *RRM* agrees with the laying curve over the whole evaluated period from the first to eleventh month production. Selection for an increased total production based on the first six month production with the *RRM* may not be useful. The integration of full year performance from the parent in a selection on the first six month production with the *RRM* improved the shape of the curve and increased the correlation with the full performance considerably. In addition, genetic evaluation of total production based on odd month production is sufficient for an efficiency of recording system.

Key words: Laying hens, cumulative model, multiple trait model, fixed regression model, random regression model

ABSTRAK

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Penelitian ini bertujuan untuk mempelajari kemungkinan penggunaan catatan produksi telur bulanan untuk evaluasi genetik ayam petelur dengan empat model dan komposisi data yang berbeda. Data berasal dari salah satu galur murni Lohmann Breeding Company di Cuxhaven Jerman. Hanya ayam-ayam yang bertelur dari bulan ke satu sampai bulan ke sebelas yang dipertimbangkan dalam analisis. Produksi telur dari 9735 ayam betina yang berasal dari 220 pejantan dan 1879 induk dari dua generasi mulai tahun 1998 sampai 1999, dengan pedigree satu generasi kebelakang dianalisis. Model-model utama yang dievaluasi adalah: (1) Model Kumulatif (*CM*), (2) Model Multiple Trait (*MTM*), (3) Model Regresi Tetap (*FRM*), dan Model Regressi Random (*RRM*). Varian komponen diduga dengan Animal Model REML dan nilai pemuliaan dengan Animal Model BLUP. Hasil analisis menunjukan bahwa *RRM* adalah model yang menarik untuk evaluasi, tapi untuk evaluasi dengan *RRM* perlu standard kurva produksi telur mulai bulan ke satu sampai ke sebelas. Evaluasi genetik berdasarkan catatan enam bulan pertama dengan *RRM* mungkin kurang baik. Penggabungan catatan penuh dari tetua dalam suatu seleksi berdasarkan catatan enam bulan pertama dengan *RRM* membantu memperbaiki bentuk kurva dan dapat meningkatkan korelasi nilai pemuliaan dengan catatan penuh lebih tinggi dibandingkan dengan model-model lainnya. Sebagai tambahan bahwa evaluasi genetik untuk produksi penuh berdasarkan catatan produksi bulan ganjil dianjurkan untuk effisiensi pencatatan.

Kata Kunci: Ayam petelur, model kumulatif, model multiple trait, model regresi tetap, model regressi random

INTRODUCTION

Genetic evaluation of egg production in laying hens is normally based on cumulative part record (up to 40 weeks of age). he use of monthly egg production records for genetic evaluation was rarely studied. There are two possibilities of analysing monthly records: firstly, they are treated as different traits and secondly they are analysed as repeated measurements of the same trait. The possibilities of using monthly records treated as different traits have been studied, for example, by Preisinger and Savas (1997), Savas *et al*. (1998), and Anang *et al*. (2000a). The second method is that the monthly egg production records are analysed as repeated measurements of the same trait by accounting for egg production curve as covariates in the mixed

model analyses. The curve can be considered as two sets of regression: the regression common to all animals (fixed regression) and the regression fitted to each animal (random regression). The possibilities of genetic evaluation using fixed and random regression models, applied to experimental data on laying hens have been studied by ANANG *et al.* (2000b), ANANG *et al.* (2001a), and ANANG *et al.* (2001b). This paper addresses the possibility of using monthly egg production records for genetic evaluation of laying hens with four different models, including Cumulative Model, Multiple Trait Model, Fixed Regression Model and Random Regression Model, applied to the data from commercial breeding programmes.

MATERIALS AND METHODS

The data were collected from a pure line of Lohmann Tierzucht GmbH at Cuxhaven in Germany for two generations from 1998 to 1999 with pedigree being traced back one generation. The laying period stretched from 20th to 60th weeks of age. Because of management system, only the survival hens from 1st to 11th month productions were considered in the analyses. In total of 9735 hens from 220 sires and 1879 dams were analysed. The structures of the data are given in Table 1.

Table 1. Structure of data

Period	$\overline{x}$	sd	cv (%)
M1	17.20	10.99	63.94
M2	24.46	5.01	20.71
M3	26.45	2.12	8.02
M4	26.62	1.97	7.38
M5	26.48	1.98	7.47
M6	26.07	2.22	8.54
M7	25.78	2.20	8.55
M8	25.76	3.19	12.39
M9	24.49	3.87	15.87
M10	23.72	4.56	19.23
M11	23.12	5.01	21.65

M=month, $\overline{x}$ = average, sd=standard deviation, and cv=coefficient of variation

The evaluated models were Cumulative Model (*CM*), Multiple Trait Model (*MTM*), Fixed Regression Model (*FRM*) and Random Regression Model (*RRM*). The models can be summarised as follows:

Cumulative model (CM)

$y_{ij} = YHCT_i + a_j + e_{ij}$, where: y_{ij} = cumulative records, $YHCT_i$ = fixed effect of year-hatch-

cage(house)-tier, a_j = animal additive genetic effect (random effect), and e_{ij} = residual effect.

Multiple trait model (MTM)

$y_{ijk}* = YHCT_{ik} + a_{jk} + e_{ijk}$,where: y_{ijk}^* = record of hen *j* in month *k*, $YHCT_i$ = fixed effect of year-hatch-cage(house)-tier in month *k*, a_{jk} = animal additive genetic effect (random effect) in month *k*, and e_{ijk} = residual effect in month *k* (random effect).

Fixed regression model (FRM)

$$y_{ijkl}^* = YHCT_i + a_j + pe_j + YM_k + \sum_{m=1}^{4} b_{im} x_{jml} + e_{ijkl}$$

where: y_{ijkl}^* = monthly records, $YHCT_i$ = fixed effect of year-hatch-cage(house)-tier, YM_k = year-moving cage effect (fixed effect), a_j = animal additive genetic effect (random effect), pe_j = permanent environmental effect (random effect), and e_{ijkl} = residual effect (random effect). $\sum_{m=1}^{4} b_{im} x_{jml}$ = a function of four covariates derived from the regression of ALI and SCHAEFFER (1987). $x_1 = \frac{1}{11}$, $x_2 = \left(\frac{1}{11}\right)^2$, $x_3 = \ln(\frac{11}{t})$, and $x_4 = \ln^2(\frac{11}{t})$. *t* was monthly records and set from 1 for first month production to 11 for eleventh month production. 11 was total monthly records used in the analyses.

Random regression model (RRM)

$$y_{ijk}^* = MYHCT_i + \sum_{m=0}^{4} \alpha_{jm} z_{jkm} + \sum_{m=0}^{4} pe_{jm} z_{jkm} + e_{ijk}$$

where: y_{ijk}^* = monthly records, $MYHCT_i$ = fixed effect of moving cage-year-hatch-cage(house)-tier, e_{ijk} = residual effect (random effect),

$\alpha_j^{'} = \left(\alpha_{j0}, ..., \alpha_{j4}\right)$ = vector of additive genetic effects or coefficients of regression for additive genetic effects.

$pe_j^{'} = \left(pe_{j0}, ..., pe_{j4}\right)$ = vector of permanent environment or coefficients of regression for permanent environment

$z_{jk}^{'} = \left(z_{jk0}, ..., z_{jk4}\right)$ = vector of covariates

Let the covariates be presented as

$z_{jk}^{'} = \left(1, \quad c, \quad c^2, \quad d, \quad d^2\right)$

with $c = \dfrac{t_{jk}}{11}$; $d = \ln\left(\dfrac{1}{c}\right)$,

in which t_{jk} was monthly records and set from 1 for first month to 11 for eleventh month of production. 11 was total monthly records used in the analyses.

The data evaluated are presented in Table 2. Genetic and phenotypic parameter for *CM*, *MTM* and *FRM* were estimated by REML with VCE 4 (GROENEVELD, 1998) and breeding values were predicted with PEST package (GROENEVELD, 1990). The genetic and phenotypic parameters for the *RRM* were estimated by REML using a random regression Animal Model with the DXMRR (MEYER, 1998). In addition, the correlation of breeding values were calculated using Spearman rank with SAS 6.03.

Table 2. Evaluated data

Data	Remark
P1-11	Production from first to eleventh month
Podd	Production of odd month (1,3,5,...,11)
Peven	Production of even month (2,4,6,...,10)
P1-6	Production from first to sixth month

RESULTS AND DISCUSSION

Spearman rank correlations of animal breeding values among the four evaluated models by considering the full record (first to eleventh month) are given in Table 3.

Table 3. Spearman rank correlation of animal breeding values among the evaluated models by considering the full record

Model	RRM	FRM	MTM	CM
RRM	1.00	0.81	0.83	0.81
FRM		1.00	0.95	0.97
MTM			1.00	0.97
CM				1.00

The correlations among *CM, MTM* and *FRM* were generally high, ranging from 0.95 to 0.97, whereas the correlations among *CM, MTM, FRM* and *RRM* were lower, ranging from 0.81 to 0.83. The choice of *FRM, MTM* or *CM* for the evaluation may not be important, but the use of *RRM* must be considered carefully.

Spearman rank correlations of animal breeding value between the full and part records within the four evaluated models are given in Table 4.

The correlations of breeding values between *P1-11* and *Podd* were generally high, ranging from 0.91 to 0.96. The use of *Podd* in a selection for increased total

egg production (*P-11*) may be sufficient for an efficiency of recording.

The *RRM* produced the lowest correlations. The correlation of breeding values between *P-11* and *P1-6*, for example, was 0.60. It is likely that the *RRM* is very sensible with the egg production curve over eleven-month production. Each animal with the *RRM* had five genetic effects as a function from the regression. Fitting the first six-month production in the analyses resulted in different estimates of regression coefficients. Consequently, the correlations of breeding value were low. The prediction of total breeding values (from first to eleventh month production) from *P1-6* did not improve the correlation.

Table 4. Spearman rank correlations of animal breeding value between full and part records within the four evaluated models

Model	*Podd*	*Peven*	*P1-6*
RRM	0.91	0.82	0.60
FRM	0.94	0.92	0.71
MTM	0.92	0.88	0.76
CM	0.96	0.93	0.74

The part record of egg production from first to sixth month production (*P1-6*) is of interest to animal breeder because it is able to maintain short generation interval and annual production (PREISINGER and SAVAS, 1997). The correlations between the part record *P1-6* and *P1-11* resulting from the four evaluated models ranged from 0.60 to 0.76. A selection of hens based only on *P1-6* to increase the total egg production (P*1-11*) may not be satisfactory. An extension of the record may be able to increase the correlation but it results in increased generation interval. The generation interval can be maintained one year with the use of *P1-6* in a selection.

The last of this paper discusses the possibility of an integration of the full performance (*P1-11*) from the parent in a selection on part record (*P1-6*) of the offspring. Three models were evaluated: *MTM, FRM,* and *RRM*. The *CM* fell in summing the full cumulative record of selected hens (offspring). Spearman rank Correlations of breeding values of the full performance (*P1-11*), predicted from *P1-6* from the offspring and *P1-11* only from the parent are given in Table 5.

Table 5. Spearman rank correlations of breeding values for *P1-11*, predicted from *P1-6* from the offspring and *P1-11* only from the parent

Model	*r*
MTM	0.91
FRM	0.84
RRM	0.93

The integration of *P1-11* from the parent in a selection on *P1-6* of the offspring increased the correlation of breeding value with the full data performance. With the *RRM*, the correlation increased considerably from 0.60 to 0.93. It is likely that the *RRM* agreed with the regression curve over all evaluated periods from 1st to 11th month productions. The use of *P1-6* only for selection of full performance with *RRM* may not be useful. The integration of full performance from the parent in a selection on part record of the offspring with *RRM* increased the correlation to full performance considerably.

The comparison of the models seems to be difficult as the four evaluated models define strictly different traits. The *CM* analyses directly on the trait as a selection objective. The *FRM* expresses actually only the additive genetic effect for the mean of laying performance per monthly period. Consequently, the hens whose high mean of egg production from 1st to 11th month production had also high total cumulative production. The *MTM* treats the monthly production as different traits. The sum of breeding values resulting from the each single month-production represents the total breeding value for total production. With the *RRM*, every interval time along the laying period is declared as breeding value, described through the covariates typical to each animal. The breeding value can be calculated with the help of the regression coefficients and the covariates as a function from the regression ALI and SCHAEFFER (1987). For each monthly period, the breeding values can be derived. The sum of the predicted breeding values from 1st to 11th monthly production represents the total breeding value.

We evaluate here 11 traits with month as the smallest period. Under theoretical points of view, the *MTM* represents the optimal strategy because the changes in environment during the laying period can be considered directly in the model and there is also the possibility to weigh the economic value to each single breeding value. However, the *MTM* faces a numerical problem in the estimation of variance components with REML when all traits are analysed simultaneously. In this case, the analysis was based on six trait models. Large genetic and environmental (co)variances led to non-positive definite matrix, therefore the matrix must be corrected to positive definite before estimating breeding value using MATDEF (MIELENZ, 1996). There could be more traits such as egg weight, feed intake, etc. considered in the selection, which may lead to more numerical problem in the estimation of genetic and phenotypic parameters with *MTM*.

The *RRM* offers a clear alternative although the estimates of heritability for monthly productions were biased upward in the beginning and the end of laying period. The Convergence problems appeared also in the estimation of variance components with *RRM*. As indicator, the estimates resulting from Simplex Method and AI-REML as algorithms to minimise the likelihood were various. The estimates from AI-REML were finally accepted. How far convergence problems with *RRM* software or specific algorithm still requires a definite clarification. The *RRM* wins in attractiveness if the environment is strongly changeable, the test periods were varied from hen to hen, and the number of traits defined in *MTM* exceeds faster programme capacity.

CONCLUSION

Random Regression Model (*RRM*) is an interesting model for genetic evaluation of laying hens, especially if the environment is changeable during the laying period and the test periods were varied from hen to hen. Selection for an increased total production based only on part record from the first to sixth month production with the *RRM* may not be useful. The integration of full year performance from the parent in a selection on the first six month production with the *RRM* increased the correlation with the full performance considerably. In addition, genetic evaluation of total production based on odd month production is sufficient for an efficiency of recording system.

REFERENCES

ALI, T.E. and L.R. SCHAEFFER (1987). Accounting for covariances among test day milk yield in dairy cows. *Canadian Journal of Animal Science*. 67:637-644.

ANANG, A., N. MIELENZ and L. SCHÜLER (2000a). Genetic and phenotypic parameters for monthly egg production on laying hens. *Journal of Animal Breeding Genetics*: 117**:** 407-415.

ANANG, A., N. MIELENZ and L. SCHÜLER (2000b). The use of monthly production for genetic evaluation of laying hens. Presented in novel approaches to commercial poultry breeding. *World Poultry Congress*, Montreal, Canada. 21-24 August 2000.

ANANG, A., N. MIELENZ and L. SCHÜLER (2001a). Monthly models for genetic evaluation of laying hens. I. Fixed regression. *British Poultry Science*. 42:191-196.

ANANG, A., N. MIELENZ and L. SCHÜLER (2001b). Monthly models for genetic evaluation of laying hens. II. Random Regression. *Submitted to British Poultry Science*.

GROENEVELD, E. (1990). PEST user's manual. Institute of Animal Husbandry and Animal Behaviour, Federal Agricultural Research Centre.

GROENEVELD, E. (1998). VCE4 user's guide and reference manual version 1.1.

MEYER, K. (1998). DXMRR, A programme to estimate covariance functions for longitudinal data using random regression model. 6th WCGALP, Armidalle Australian, 27:465-466.

MIELENZ, N. (1996). MATDEF, a PC Programme to determine a positive definite matrix with minimal distance to a given non-positive definite matrix. Institute of Animal Breeding and Husbandry, Martin-Luther University, Halle, Germany.

PREISINGER, R. and SAVAS, T. (1997). Vergleich zweier Methoden zur Schätzung der Varianzkomponenten für Leistungsmerkmale bei Legehennen. *Züchtungskunde*, 69(2):142-152.

SAS INSTITUTE INC. (1990). User'guide. Version 603. Cary, NC, USA.

SAVAS, T., R. PREISINGER, R. RÖHE, and E. KALM (1998). Genetische Parameter und optimale Prüfdauer für Legeleistung anhand von Taillegeleistungen bei Legehennen. *Arch. Tierz.*, 41(5): 421-432.