

GENETIC EVALUATION OF LAYING PERFORMANCE DATA – COMPARISON OF MODELS BASED ON MONTHLY RECORDS

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INTRODUCTION

The generation interval can be reduced if selection is based on part records resulting from the early periods (up to about 40 weeks of age) of egg production. A reduction of the generation interval has a major effect on of genetic progress per year. The genetic correlations between part records and cumulative egg production ranged from 0.65 to 0.70 (Preisinger and Savas, 1997). In conclusion, effective genetic evaluation has to include performance data of parental generation of the completed laying cycle. If number of part-periods is different in the generations or if the experimental conditions changes over part-periods, models based on monthly egg production records become of interest. Monthly records can be treated as different traits or repeated measurements of the same trait by accounting for a egg production curve as covariate function in mixed model analyses. The shape of the egg production curve can be considered in two different ways. Fixed Regression Model (FRM): estimation of one regression function for each group of animals (Ptak and Schaeffer, 1993); Random Regression Model (RRM): the regression fitted to each animal separately (Schaeffer and Dekkers, 1994).

MATERIAL AND METHODS

Data structure. For the analysis egg production data from two commercial purebreed lines (A and D) were used. The period of data collection was extended from the 20th to 64th weeks of age. Data from hens of two generations with pedigree information of three generations were analysed. Only data of hens with complete information (11 periods) was used. In total, of line A records from 4781 hens, offspring of 119 sires and 843 dams, were analysed. For genetic evaluation of line D records from 9735 hens, offspring of 220 sire and 1879 dams, were available. Four different animal models were studied: cumulative model (CM) with summarizing the egg production for all periods, multiple trait model (MTM) with monthly egg productions as separate traits, fixed regression model (FRM) with the covariate function of Ali and Schaeffer (1987) and random regression model (RRM) with the same covariates used by fixed regression. All models contain fixed year, hatch and tier effects. The RRM can be summarised as follow:

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

Whereby YHT_i is the fixed effect of the i 'th year-hatch and tier block, α_{jm} are the coefficients of regression of the j 'th animal, pe_{jm} are the coefficients of the regression for the permanent environmental effects of the j 'th animal and $z_{jk} = (z_{jk0}, \dots, z_{jk4})'$ is the Vector of five covariates. Because the shape of lactation curves and egg production curves are highly similar the model

of Ali and Schaeffer (1987) was used as covariate function. Thus the covariates are given by: $z_{ijk}=(1,c,c^2,d,d^2)'$ with $c=(t_{jk}/11)$ and $d=\ln(1/c)$. Where the t_{jk} are equal 1 to 11. A more detailed description of the models can be found by Anang (2001).

Statistical analyses. Phenotypic and genetic parameters estimated with an animal model using the REML-method are shown in table 1. The heritabilities are highest for month 1 to 2, reach a low estimate of 0.10 for line A and 0.11 for line D at peak production and increase again slowly during the second half of the laying cycle for both lines.

Table 1. Population parameters of laying performances

periods	Line A (n=4781)			Line D (n=9735)		
	\bar{x}	s	h^2	\bar{x}	s	h^2
M1-2	35.4	9.2	0.34±0.02	41.7	8.5	0.31±0.01
M3-4	52.3	2.5	0.10±0.01	53.1	2.0	0.11±0.01
M5-6	52.1	2.1	0.09±0.01	52.6	2.1	0.13±0.02
M7-11	118.0	3.9	0.21±0.02	122.9	3.9	0.15±0.01

Genetic and phenotypic parameters for CM, MTM and FRM were estimated by REML with VCE4 (Groeneveld, 1998) and for the estimation of breeding values PEST (Groeneveld, 1990) was used. Genetic parameters of RRM were calculated with the program package DXMRR by Meyer (1998) based on the REML method. MTM faces numerical problems if all 11 monthly egg productions are analysed simultaneously. For this reason variants of MTM were investigated with 2, 3 and 4 part-periods of the total egg production. The included data sets and the fitted models are presented in table 2.

Table 2. Data sets and models used in genetic evaluation

Data	Models	Remarks
M1-6	CM, MTM, FRM, RRM	Cumulative, monthly record, month 1 to 6
M1-11	CM, MTM, FRM, RRM	Cumulative, monthly record, month 1 to 11
M1-6,7-11	MTM2	Cumulative record, month 1 to 6 and 7 to 11
M1-2,3-6,7-11	MTM3	Month 1 to 2, 3 to 6 and 7 to 11
M1-2,3-4,5-6,7-11	MTM4	Month 1 to 2, 3 to 4, 5 to 6 and 7 to 11

RESULTS AND DISCUSSION

The correlations of estimated breeding values among the four evaluated models for the cumulative egg production from month 1 to 11 are given in table 3. The rank correlations among CM, MTM and FRM for both lines were generally high, ranging from 0.93 to 0.96 for line A and 0.95 to 0.97 for line D, respectively.

Table 3. Rank correlations of breeding values among the models for cumulative egg production in month 1 to 11

Model	Line A			Line D		
	FRM	MTM	CM	FRM	MTM	CM
RRM	0.84	0.91	0.88	0.81	0.83	0.81
FRM	x	0.93	0.96	x	0.95	0.97
MTM	0.93	x	0.96	0.95	x	0.97

The correlations among RRM and the other models were lower, ranking from 0.84 to 0.91 for line A and 0.81 to 0.83 for line D, respectively. The conclusion is that in all models, the trait cumulative egg production has an other definition. Especially the RRM gives other ranking of the candidates for selection. Spearman rank correlations of animal breeding values within four models estimated with part records from month 1 to 6 and with total records (month 1 to 11) with data only from one generation are given in table 4.

Table 4. Correlation of breeding values estimated with part records (M1-6) and total records (M1-11) excluding parental data

Models	CM	MTM	FRM	RRM
Line A	0.71	0.70	0.66	0.59
Line D	0.74	0.76	0.71	0.60

The correlation between total and part records ranged from 0.59 to 0.71 for line A and from 0.60 to 0.76 for line D. The RRM showed the lowest correlations. As result of genetic evaluation with RRM there are five additive genetic effects corresponding to each animal. Fitting individual egg production curves is not a efficient breeding value estimation strategy if only data from the first six months is available. The selection based on part records can be improved by including parental performance data from the completed cycle of egg production. In order to test the ability of the models of including parental information the genetic evaluation was carried out with two data sets. The first data set contained data from 2 generations but only data from period 1 to 6 of the offspring generation (that means until to the point of selection). The second set included all monthly data from period 1 to 11 of parent and offspring generation. Table 5 contains the rank correlations between the breeding values estimated with the two data sets. A comparison of the results from table 4 and 5 shows that including parental information improves the accuracy of breeding value estimation considerably. In the MTM, for example, the correlation increased from 0.70 to 0.89 for line A and from 0.76 to 0.91 for line D. For the RRM the highest increase of the correlations were observed. Thus the correlation increased from 0.59 to 0.91 for line A and from 0.60 to 0.93 for line D, if all animals were included. The model MTM4 based on four part records from period 1 to 2, 3 to 4, 5 to 6 and 7 to 11 yielded the highest correlation also in the case if only selected hens were used.

Table 5. Correlation of breeding values estimated with part records (M1-6) and total records (M1-11) by including parental performance data

Model	All animals		Selected hens only	
	Line A	Line D	Line A	Line D
MTM2	0.84	0.91	0.80	0.87
MTM3	0.91	0.93	0.89	0.89
MTM4	0.91	0.93	0.90	0.90
MTM	0.89	0.91	0.82	0.85
FRM	0.79	0.84	0.70	0.71
RRM	0.91	0.93	0.89	0.89

CONCLUSION

Genetic evaluation of laying hens based on monthly production may be better than using total cumulative production. The RRM gains in attractiveness if the environment is strongly changeable and the test periods varied from hen to hen. Because in RRM the regression coefficients are interpreted as inheritable genetic effects, this model has the ability of fitting egg production curves for all animals also in the situation if only of the parent from period 1 to 11 data are available. RRM and the multiple trait models with 3 or 4 traits showed the same high level of accuracy and should be the most favourable models.

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