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EFFECT OF INBREEDING ON LOIN AND FAT DEPTH IN HUNGARIAN LANDRACE PIGS

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Preliminary communication

SUMMARY

Pedigree and field test data - collected between 1997-2005 - were analyzed in a group of 68062 Hungarian Landrace pigs. The analysed traits were loin depth (LD), fat depth1 (FD1) and fat depth2 (FD2). In the present study inbreeding coefficients, pedigree completeness (complete generation equivalents) and inbreeding depression for LD, FD1 and FD2 were estimated. Increasing number of generations that were considered in the pedigree the estimated inbreeding coefficients did not change after the 5th generation, but pedigree completeness was continuously increasing. The estimated inbreeding depression for LD, FD1 and FD2 were different applying 5 different models but the magnitude of the differences was small. Increasing inbreeding coefficient by 10% caused LD decrease by 0.084 mm, the FD1 by 0.062 mm and did not affect FD2. It can be concluded that the estimated inbreeding depression was low and substantial depression can not be expected in the near future. However, the low level of inbreeding of the studied population can partly be explained by the short pedigrees. This suggests that Hungarian pig breeders may often import breeding animals or carry out herd replacements rather than apply within group selection.

Key-words: pig, inbreeding coefficients, pedigree completeness, inbreeding depression

INTRODUCTION

One of the disadvantageous effects of inbreeding is the reduction of the mean phenotypic value of a trait known as inbreeding depression. Numerous authors experienced inbreeding depression in different domesticated (Miglior et al., 1995; Wiener et al., 1992; Horn and Meleg, 2000; Curik et al., 2003), wild, (Hedrick and Kalinowski, 2000), captive (non-domesticated) (Cassinello, 2005) and experimental (White, 1972) populations. Inbreeding depression is mainly apparent in traits closely related to fitness (Falconer and Mackay, 1996), but the reduction is not confined to reproductive traits. The negative effects of inbreeding are magnified by the fact that they often affect several traits (such as litter size at birth, mortality during the suckling period, litter weight at 21 days of age) simultaneously and are operating through litters and through dams. The inbreeding depression in domesticated species is mainly important because it affects production efficiency. The National Institute for Agricultural Quality Control has been collected pedigree and field test data of the Hungarian Pig populations for many years which is evaluated routinely with linear (animal) models. However, extensive study on the pedigree based inbreeding level and the inbreeding depression for the collected traits has not yet been accomplished. The objective of this study was, therefore, to estimate the level of inbreeding of the Hungarian Landrace population and inbreeding depression for the collected field test traits, namely loin depth (LD), fat depth1 (FD1) and fat depth2 (FD2).

MATERIAL AND METHODS

(1) Zsófia Vígh, Ph.D. student; Petra Gyovai, gradual student; Ph.D. László Csató, Associate Professor; István Nagy, researcher - Department of Pig and Small Animal Production; (2) Árpád Bokor, assistant researcher - Department of Production and Breeding of Ruminants and Horse; (3) Ph.D. János Farkas, Assistant Professor - Department of Informatics, University of Kaposvár, Faculty of Animal Sciences, Kaposvár, 7400, Guba S. u. 40. Hungary

Data recording

The analysis was conducted on the data collected by the National Institute for Agricultural Quality Control of Hungary between 1997 and 2005, in the course of field test. Data of 68062 Hungarian Landrace pigs reared in 26229 litters were analyzed, originated from 63 herds. In the field test ultrasonic measurements were taken from boars and gilts between 80 and 110kg. The measured traits were the loin muscle depth between the 3rd and 4th ribs 6cm laterally from the spinal chord (LD), the fat depth between the 3rd and 4th lumbar vertebrae 8cm laterally from the spinal chord (FD1), and the fat depth between the 3rd and 4th ribs 6cm laterally from the spinal chord (FD2). Gilts were kept in groups up to 25 pigs while boars were raised in smaller groups up to 15 using ad libitum feeding regime (OMMI, 2004). Basic statistics of the field test data are presented in Table 1.

Table 1. Mean and standard deviation of the loin depth, fat depth1 and fat depth2

Traits	No. of records	Mean	St. dev.
LD[a]	68062	45.74	6.05
FD1[b]	68062	12.90	3.23
FD2[c]	68062	11.22	2.78

[a]LD, loin depth; [b]FD1, fat depth1; [c]FD2, fat depth2

Pedigree analysis

The total number of animals in the pedigree was 74914. Data analysis was started with pedigree analysis using the PEDUTIL, NGEN and VANRAD softwares. The first step was accommodating the pedigree data according to the animals with field test records using the PEDUTIL program. Pedigree completeness for every individual was assessed by formula of Boichard et al. (1997):

$$\frac{1}{N}\sum_{j=1}^{N}\sum_{i=1}^{n_j}\frac{1}{2^{g_{ij}}}$$

where **N** is the number of animals in the reference population, $\mathbf{n_j}$ is the total number of ancestors of animal **j** and $\mathbf{g_{ij}}$ is the number of generations between **j** and its ancestor **i**.

Pedigree completeness was assessed by tracing back the pedigree for three, four, five, six and seven generations. (pc_3-pc_7). Inbreeding coefficient (F) (Wright, 1922) was calculated of each individual using VANRAD program.

Inbreeding coefficient was assessed by tracking back the pedigree of three, four, five, six and seven generations. (F_3-F_7). The applied programmes are all a part of the PEDIG software package (Boichard, 2002). After these calculations the results from pedigree analysis were joined with the field test records (PROC MERGE, SAS Institute Inc., 2004).

The differences between the number of generations (pedigree completeness and inbreeding coefficients) were tested with PROC ANOVA (SAS Institute Inc., 2004) using repeated measurements.

Genetic parameters estimation

Genetic parameters and breeding values were estimated using the VCE-5 (Kovac and Groeneveld, 2003) and PEST (Groeneveld, 1990) softwares based on the REML and BLUP methods. Five bivariate animal models were used for all traits. The model variations are presented in Table 2.

Table 2. Model variations applied for loin depth, fat depth1 and fat depth2

Model	F_3+pc_3	F_4+pc_4	F_5+pc_5	F_6+pc_6	F_7+pc_7	Weight	Year-month/month	Sex	Herd/herd-year	Animal	Litter
1	X					X	X	X	X	X	X
2		X				X	X	X	X	X	X
3			X			X	X	X	X	X	X

4		-		X		X	X	X	X	X	X
5					X	X	X	X	X	X	X

The basic linear model was as follows:
y = Xb + Za + Wc + e
where y = vector of observations, b = vector of fixed effects, a = vector of random animal effects, c = vector of random litter effects, e = vector of random residual effects,
X, Z, W, are incidence matrices relating records to fixed effects, random animal and random litter effects, respectively. Body weight measurements, inbreeding coefficients (F) and pedigree completeness (pc) were defined as covariates, herd or herd-year, sex and year-month or month effects were defined as fixed effects, litter and animal effects were defined as random effects in the model. Inbreeding depression (the BLUE estimate of F) referring to the analyzed period was determined for LD, FD1 and FD2. Five models applied were compared by their mean squared error (MSE) using the PREDICT option of the PEST software.

RESULTS AND DISCUSSION

The results of the pedigree analysis can be seen in Figure 1 and 2.

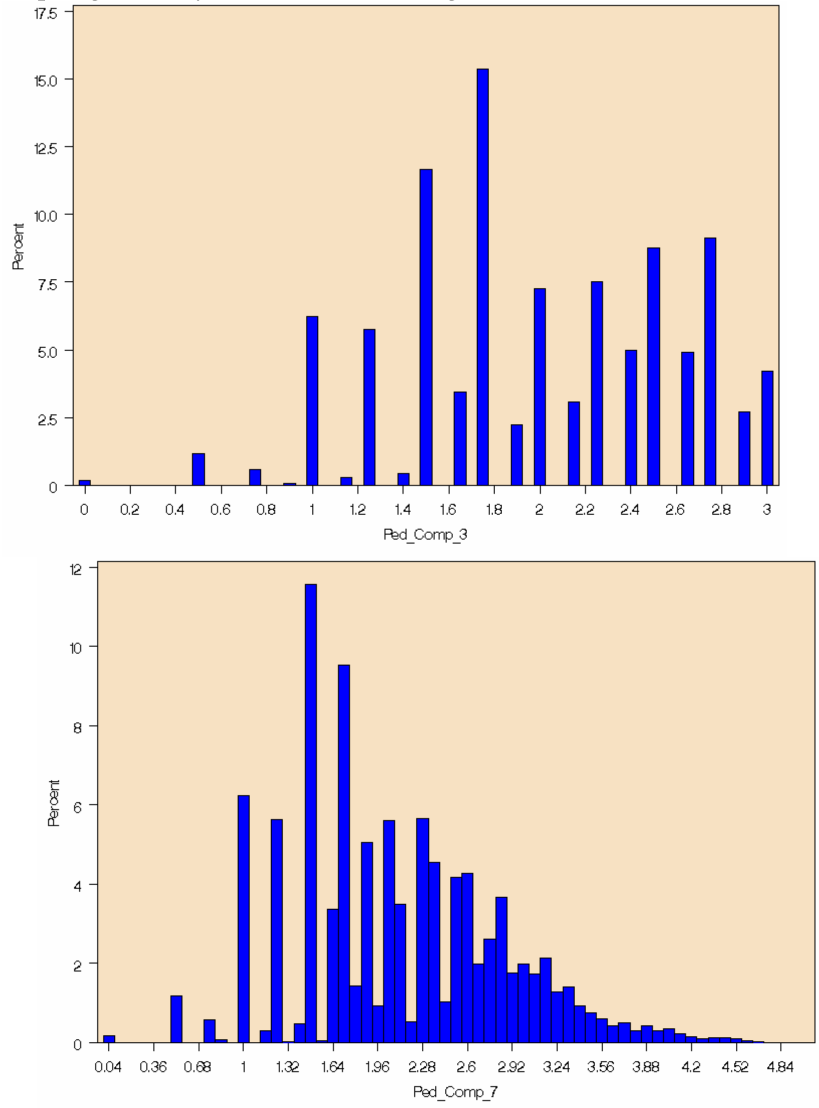

Figure 1. Distribution of pedigree completeness tracking back 3 and 7 generations

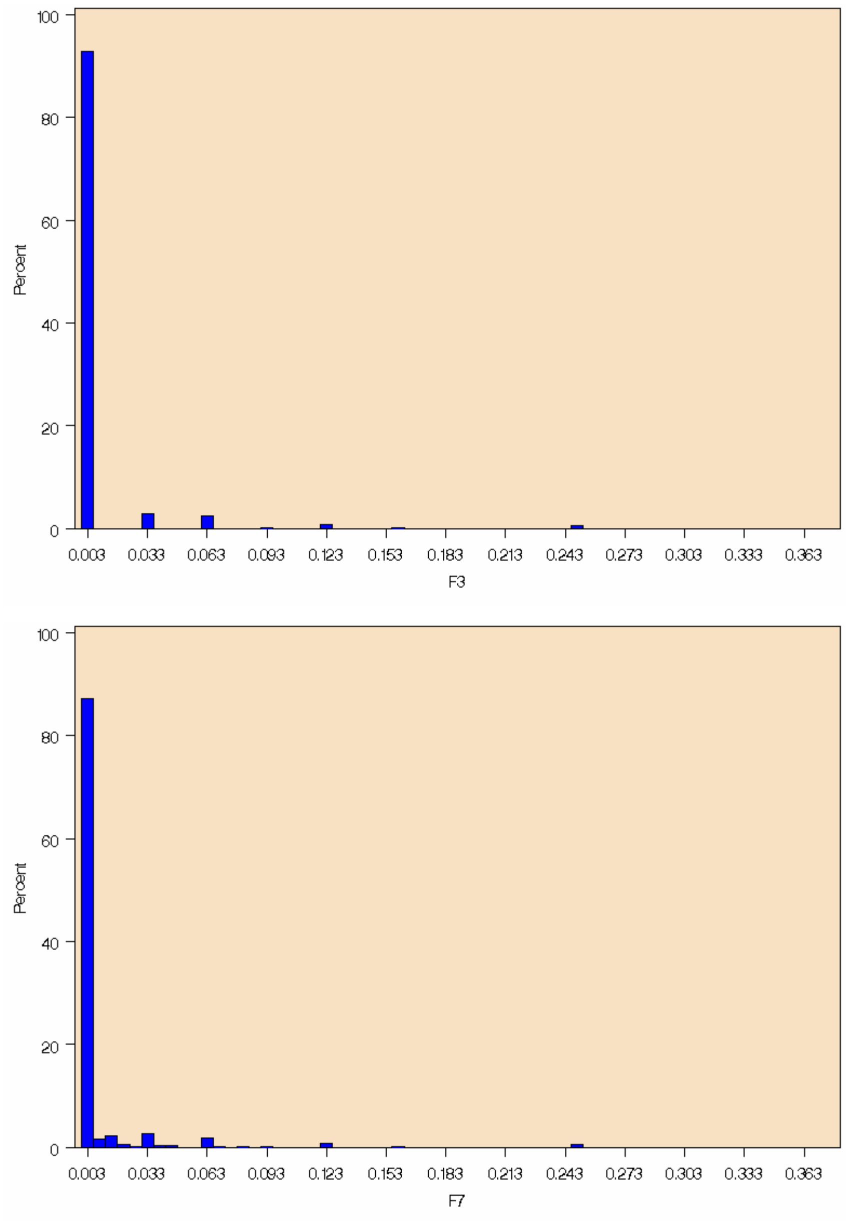

Figure 2. Distribution of inbreeding coefficients tracking back 3 and 7 generations

When tracing more generations in the pedigree the estimated inbreeding coefficients and the pedigree completeness were significantly different ($p<0.01$) among all generations. The estimated inbreeding depressions for LD and FD1 showed small differences applying 5 different models (Fig. 3 and 4) and no inbreeding depression was found for FD2.

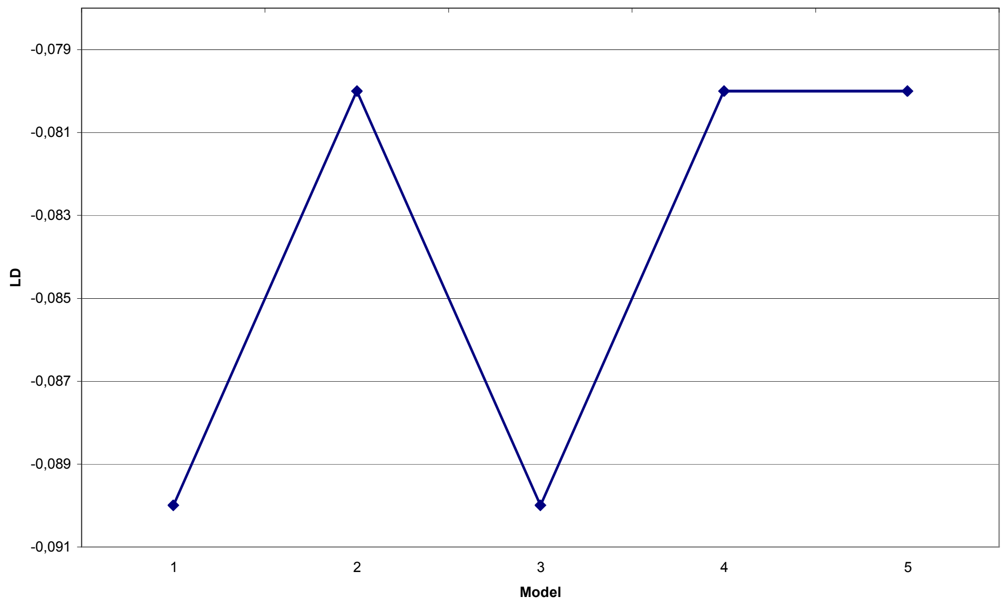

Figure 3. The estimated inbreeding depression for LD

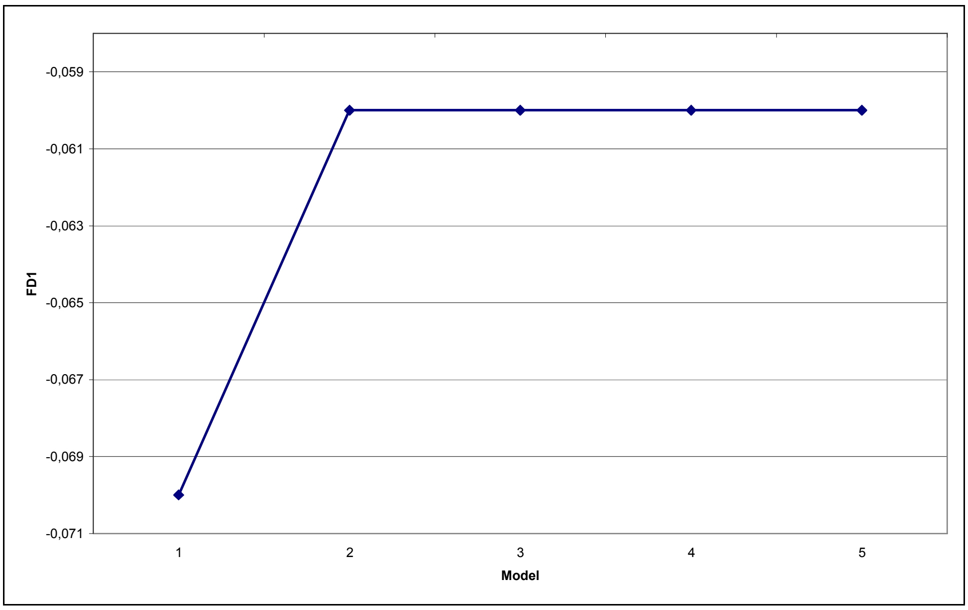

Figure 4. The estimated inbreeding depression for FD1

Increasing inbreeding coefficients by 10% had to LD by decrease 0,084 mm, the FD1 by 0,062 mm. These results were in agreement with Hitoshi Mikami et al. (1977), who examined post-natal performance of progeny on inbreeding for a population of replicated lines subjected to mass selection over a period of nine generations. Inbreeding rate varied between 2.0-2.3% per generation. Regression coefficients per 10% increase in inbreeding was -3.4 mm for backfat. King and Roberts (1959) reported significant changes in mid-backfat (-0.3 mm) for each 10% increase in inbreeding.
Contrary to these results Culbertson et al. (1998) did not find significant inbreeding depression for fat at 104,5 kg in Purebred Yorkshire Swine.
According to Curik et al. (2001) the inbreeding depression is determined by:

$-F\sum 2pqd$

where d depends on the degree of dominance, p and q = allele frequencies affecting the character. Thus the lack of inbreeding depression suggests that the related pig population did not exhibit directional dominance for fat depth.
The comparison of the 5 animal model's fit can be seen in Figure 5, Figure 6 and Figure7.

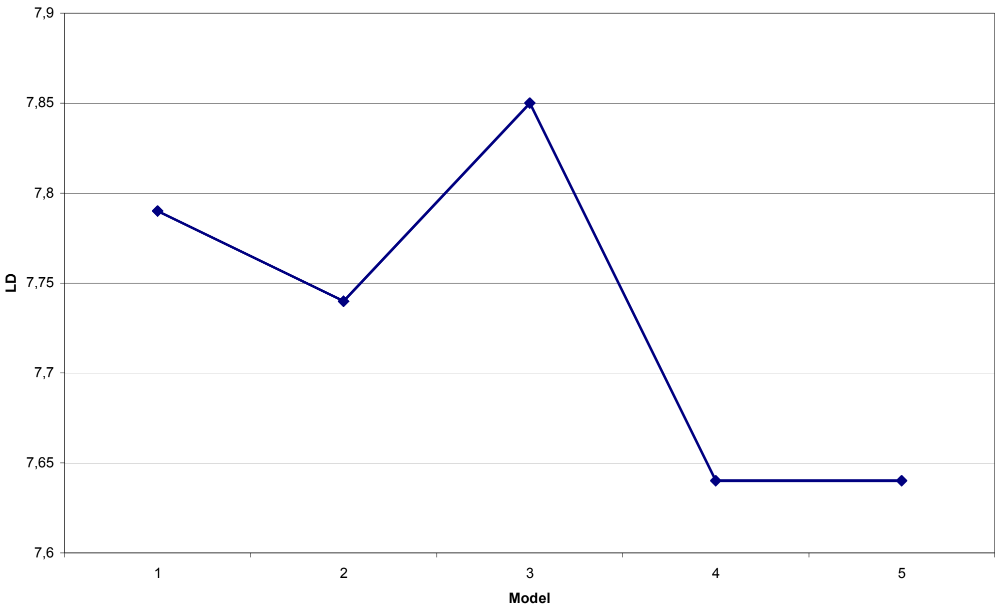

Figure 5. Mean square errors of the applied models for loin dept

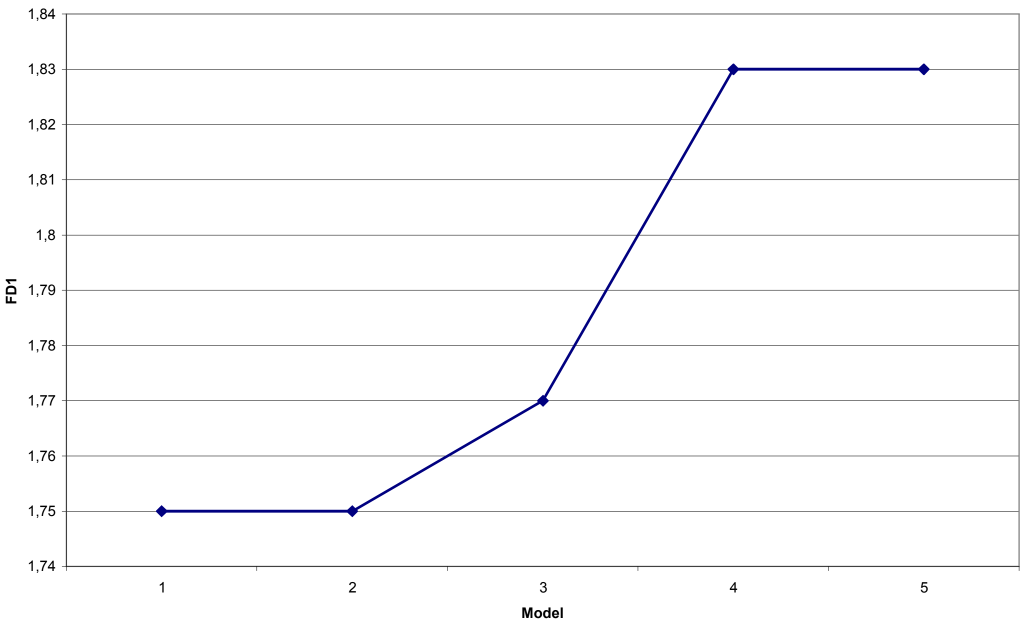

Figure 6. Mean square errors of the applied models for fat depth1

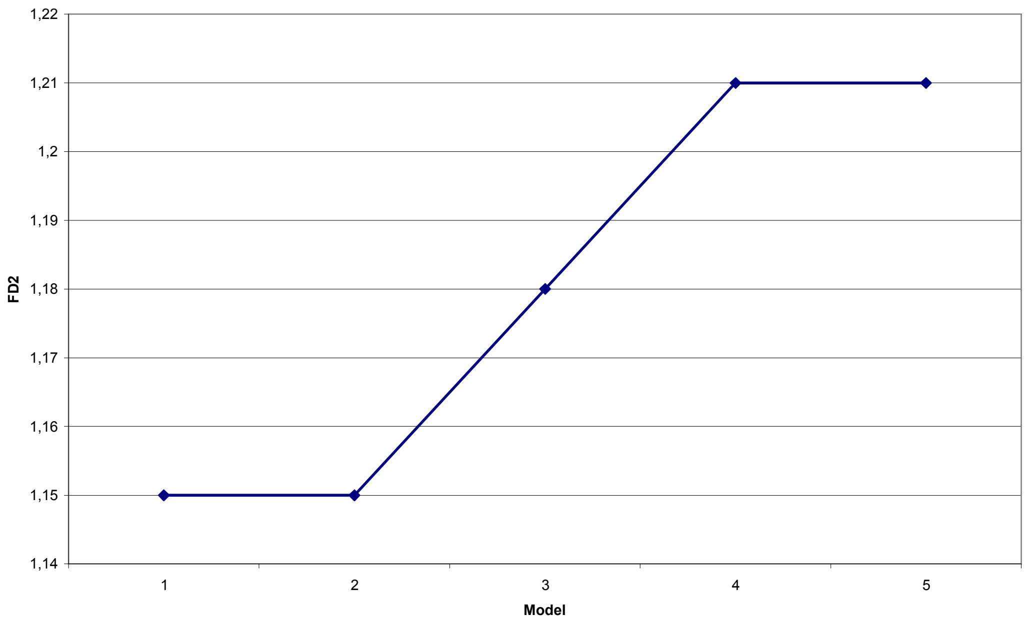

Figure 7. Mean square errors of the applied models for fat depth2

Involving the continuous generations the accuracy of the estimation was not improved probably because of the very short pedigrees.

CONCLUSION

It can be concluded that due to the low inbreeding level and small inbreeding depression of LD, FD1 and FD2, substantial depression can not be expected in the Hungarian Landrace in either trait in the near future. Nevertheless because field test data was available for a 12 year period, the estimated pedigree completeness was very low compared to the possible value (3-4) supposing more complete pedigrees. The absolute level of inbreeding of any animal depends on its pedigree length. Animals with long pedigree had higher probability of being inbred. Thus the negligible inbreeding depression was presumably partly the result of the short pedigrees. This suggests that conventional within group selection in the Hungarian Landrace nucleus farms has only secondarily importance. Pig breeders likely often import breeding animals or from time to time accomplish total herd replacements.

ACKNOWLEDGEMENT

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