

THESES OF DOCTORAL (PhD) DISSERTATION

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**EVALUATION OF INBREEDING IN THE HUNGARIAN
PUREBRED PIG BREEDING PROGRAM**

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1. ANTECEDENTS OF RESEARCH, AIMS

Many breeding companies (e.g.: KA-HYB) utilized inbred lines and animals in breeding, in order to accumulate certain favourable genes. This kind of performance improvement might carry certain risks, since, above a certain level, inbreeding may cause depression of fitness and growth performance, however this level can be different by species, breed, population or even by each animal. Although in the recent years a complex analysis was made (FARKAS, 2008), studying the breeding value estimation system of the Hungarian pig population, detailed aspects of inbreeding were not considered.

The main objectives of my research are the following:

- On the base of the present pedigree data, accomplish the pedigree analysis of the Hungarian Large White (HLW) and Hungarian Landrace (HL) breeds, thus estimate the inbreeding levels of these populations.
- Furthermore, to estimate the inbreeding depression in the HLW and HL breeds on the base of the Field test dataset (FTD; average daily gain, lean meat percentage, loin depth, fat depth 1, fat depth 2), and on the Reproductive performance datasets (RPD; number of piglets born alive and the number of piglets born dead).
- To find the model with the best fit and to decide how many generations to include to attain more exact and reliable breeding values for the Hungarian pig populations.

2. MATERIALS AND METHODS

2.1. Databases

I conducted analyses based on the data collected by the Hungarian National Institute for Agricultural Quality Control (MGSZH). The Pig performance testing code (MGSZH, 2009) contains the requirements for conducting different performance tests. I will introduce different databases for my disposal in table 1.

Table 1. Research databases

Breed	Database	Research period	Pedigree	Number of records
HLW (a)	FTD (c)	1999-2005	1998-2004	115813
HL (b)	FTD	1994-2005	1994-2004	132548 (68062)
HLW	RPD(d)	1986-2009	1975-2009	385648 (e)
HL	RPD(d)	1985-2005	1980-2002	103110 (e)

a: Hungarian Large White, b: Hungarian Landrace c: Field tests, d: Reproductive performance test, e: number of piglets born

Research traits in the case of the Field test database (FTD) were the lean meat percentage (LMP), the average daily gain (ADG), loin depth (LD), fat depth 1 (FD1) and fat depth 2 (FD2), the Reproductive performance dataset (RPD) included calculations for the number of piglets born alive (NBA) and the number of piglets born dead (NBD).

Traits of boars and gilts were measured in the Field tests on live animals weighing 80–110 kilograms. The HLW field test traits and basic statistics are presented in table 2, the same dataset pertaining to the HL is presented in table 3.

Table 2. Field test traits and descriptive statistics of the HLW

	No. of records	Mean	Sd	Min.	Max.
LMP (%)	104177	57,02	1,98	45,54	69,87
ADG (grams/day)	104177	530,91	61,67	270,0	924,53
LD (mm)	104177	47,26	6,29	22,0	80,0
FD1 (mm)	104177	14,3	3,44	2,0	36,0
FD2 (mm)	104177	12,45	2,76	2,00	31,00

Table 3. Field test traits and descriptive statistics of the HL

	No. of records	Mean	St. dev.	Min.	Max.
LMP (%)	68062	57,61	2,14	44,59	69,99
ADG (grams/day)	132548	532,38	62,17	295,0	902,0
LD (mm)	68062	45,74	6,05	20,0	80,0
FD1 (mm)	68062	12,90	3,23	2,0	32,0
FD2 (mm)	68062	11,22	2,78	2,0	31,0

Lean meat percentage is measured by an ultrasonic device calibrated by the Hungarian National Institute for Agricultural Quality Control (MGSZH). Average daily gain is calculated on the base of the weight measured at the end of the examination divided by the age. Loin depth is measured between the 3rd and 4th ribs 6 cm laterally from the spinal chord, fat depth 1 is measured on the left side, between the 3rd and 4th lumbar vertebrae, 8 cm laterally from the spinal chord, fat depth 2 is measured from the back, between the 3rd and 4th lumbar vertebrae, 6 cm laterally from the spinal chord, on the side.

The HL reproduction traits are shown in table 4. below.

Table 4. Basic Reproduction traits and descriptive statistics of the HLW and the HL

Trait	No. of items	Mean	St. dev.
NBA - HLW	358648	9,95	2,70
NBD - HLW	358648	0,46	1,04
NBA - HL	103110	9,98	2,26
NBD - HL	103110	0,46	1,04

2.1. Pedigree analysis

In the case of both the Field test and the Reproductive performance data analysis was begun by pedigree analysis for which I used the PEDUTIL, NGEN and the VANRAD programs. All three programs are part of the PEDIG software package (BOICHARD, 2002).

- By running the PEDUTIL program, I selected the pedigree data from the animals with field test records.
- Then I assessed the pedigree completeness (how many generations can the pedigree of any animal be traced back to-whole generation equivalent) with the NGEN program and with the help of BOICHARD et al. (1997) formula.
- Following this, I calculated the inbreeding coefficient (F) for every animal (WRIGHT, 1922) with the help of the VANRAD program.

In table 5. I describe how many generations were included in the course of pedigree completeness and inbreeding coefficient dataset calculation.

Table 5. Generations used in pedigree completeness and inbreeding coefficient calculation

	Pc	F
FTD	3,4,5,6,7	3,4,5,6,7
RPD	3,4,8,9,10	3,4,8,9,10

After completing these calculations I fitted the results from the pedigree analysis and the database containing the calculations. For the descriptive statistical calculations I used the SAS software (SAS Institute Inc., 2004).

2.2. BLUP-models

Following the preparation of databases, with the help of REML and BLUP methods I conducted genetic parameter estimation and breeding value estimation on the data containing inbreeding coefficients and pedigree completeness, for which I used the PEST (GROENEVELD, 1990) and VCE (KOVAC és GROENEVELD, 2003) softwares.

I ran 5 and 40 models per breed and traits respectively, the model variations are presented in table 6.

Table 6. Model variations run by breeds and traits

Breed	Trait	No. of models
HLW	LMP, ADG, LD, FD1,FD2	40
HL	LMP, ADG	40
HL	LD, FD1,FD2	5
HLW, HL	NBA, NBD	40

In the model variants applied, I listed inbreeding coefficients and pedigree completeness back to different generations, I did estimations with both as a covariant in the models, and I did estimations leaving out pedigree completeness as well. In the models the inbreeding coefficient (F), the pedigree completeness (pc) and the weight I took as covariants, the herd, sex, the year and month of examination were taken as environmental (fixed) effects, while the litter-effect was defined as random. Apart from these, at

the fitness traits the order of birth was taken as a fixed trait, the impact of the boar (father) was taken as a random effect in the model.

With the BLUP method, on the base of estimated environmental effects I defined the inbreeding depression of the populations pertaining to the period examined (BLUP value for F as a c-variant) for the traits of LMP, ADG, LD, FD1, FD2, NBA and NBD. The 40 models applied per trait were contrasted on the base of the PEST software's PREDICT option (best fit) the values examined on the base of the mean squared error (MSE). On this base the model with the best fit can be selected.

The inbreeding coefficient measured in the reproduction analysis (RPD) was analysed by parity as well. I selected data belonging to a given parity an inbreeding coefficients with pedigree completeness, then this was put into a different dataset. Afterwards I ran variant-component (VCE) and breeding value estimation (PEST) programmes by parity. With this I also defined the inbreeding depression for the values of NBA and the NBD. In this case I applied two model variants: in the first I calculated the inbreeding depression with pedigree completeness for three generations back, in the second I took 10 generations into account.

3. RESULTS

3.1. Pedigree analysis

The results of the pedigree analysis of animals taking part in the Field test are presented in tables 7 - 8. Statistics pertaining to the inbreeding coefficients were calculated for values bigger than 0.

Table 7. Descriptive statistics of pedigree completeness and inbreeding coefficient of HLW animals tested in field tests

Trait	No. of records	Minimum	Maximum	Mean	St. dev.
pc3	104177	0.5	3.00	1.18	0.5
pc4	104177	0.5	3.31	1.18	0.51
pc5	104177	0.5	3.31	1.18	0.51
pc6	104177	0.5	3.31	1.18	0.51
pc7	104177	0.5	3.31	1.18	0.51
F3 (%)	926	3.1	37.5	13.65 (a)	8.56
F4 (%)	953	1.6	37.5	13.37 (a)	8.6
F5 (%)	953	1.6	37.5	13.37 (a)	8.6
F6 (%)	953	1.6	37.5	13.37 (a)	8.6
F7 (%)	953	1.6	37.5	13.37 (a)	8.6

a: Inbreeding coefficient means pertain only to inbred animals

Inbreeding coefficient does not grow with the inclusion of different generation, there is a small decrease in mean and minimum between the third and fourth generations. Only 0.9% of the animals examined proved to be inbred.

Table 8. Descriptive statistics of pedigree completeness and inbreeding coefficient of the HL in field tests

Trait	No. of records	Minimum	Maximum	Mean	St. dev.
pc3	132548	0.5	3.0	1.64	0.72
pc4	132548	0.5	4.0	1.71	0.81
pc5	132548	0.5	4.75	1.72	0.84
pc6	132548	0.5	4.98	1.72	0.84
pc7	132548	0.5	5.01	1.72	0.84
F3 (%)	5133	3.0	35	8.0 (a)	7.0
F4 (%)	8555	1.0	35	6.0 (a)	6.0
F5 (%)	9381	0.1	38	5.0 (a)	6.0
F6 (%)	9513	0.1	38	5.0 (a)	6.0
F7 (%)	9514	0.1	38	5.0 (a)	6.0

a: Values of the inbreeding coefficient pertain only to inbred animals

Inbreeding coefficients did not change after the fifth generation, while pedigree completeness showed small steady increase with the inclusion of each generation. 7.17 % of the animals examined proved to be inbred.

The results of the pedigree analysis of animals taking part in the Reproductive performance test are presented in tables 9 - 10.

Table 9. Descriptive statistics of pedigree completeness and inbreeding coefficient for HLW during field tests

Trait	No. of records	Minimum	Maximum	Mean	St. dev.
pt ₃	94844	0,50	3,00	2,15	0,69
pt ₄	94844	0,50	4,00	2,44	0,89
pt ₈	94844	0,50	6,15	2,72	1,15
pt ₉	94844	0,50	6,31	2,73	1,16
pt ₁₀	94844	0,50	6,37	2,73	1,16
F ₃ (%)	4826	3,12	37,50	7,44	6,30
F ₄ (%)	12887	7,81	37,50	3,89	4,91
F ₈ (%)	29633	0,003	37,50	1,93	3,69
F ₉ (%)	30035	0,001	37,50	1,90	3,67
F ₁₀ (%)	30154	0,001	37,5	1,90	3,67

a: Values of the inbreeding coefficient pertain only to inbred animals

The number of inbred HLW gilts was 30154, the average inbreeding coefficient was 3,412. The proportion of the inbred animals was 31,79 %.

Table 10. Descriptive statistics of pedigree completeness and inbreeding coefficient for HL during field tests

Trait	No. of records	Minimum	Maximum	Mean	St. dev.
pc ₃	103110	0.50	3.00	2.30	0.65
pc ₄	103110	0.50	4.00	2.66	0.89
pc ₈	103110	0.50	7.00	3.03	1.22
pc ₉	103110	0.50	7.21	3.04	1.23
pc ₁₀	103110	0.50	7.25	3.04	1.23
F ₃ (%)	7652	0.03	31	6.0 (a)	5.0
F ₄ (%)	18443	0.78	31	3.0 (a)	4.0
F ₈ (%)	30451	0.003	32	2.0 (a)	3.0
F ₉ (%)	30587	0.002	32	2.0 (a)	3.0
F ₁₀ (%)	30642	0.002	32	2.0 (a)	3.0

a: Values of the inbreeding coefficient pertain only to inbred animals

The number of inbred gilts was 5817. Table 9 shows that the ancestry of HL can be traced back to more generations, than that of the animals in the field test dataset. For the inbred animals the average inbreeding coefficient decreased by fifty percent for the fourth generation and at the eighth generation the average inbreeding coefficient was 2 and it stayed like this for another two generations. It can be explained by the fact that taking many generations of ancestry into consideration the program finds more distant ancestors, so the average inbreeding coefficient decreases.

3.2. Weight gain and carcass traits

3.2.1. Lean meat percentage and average daily gain

In the HLW and the HL breeds the models of breeding value estimation based on the field tests – featuring pedigree completeness and the inbreeding coefficient – did not show considerable difference with respect to the mean squared error (MSE), only those models estimated more accurately, which contained the effect of litter and the effect of year-month. Fit was worse if the herd and the year were defined jointly in the model.

The first figure depicts the inbreeding depression with respect to the LMP % of HLW breed on the base of the FTD.

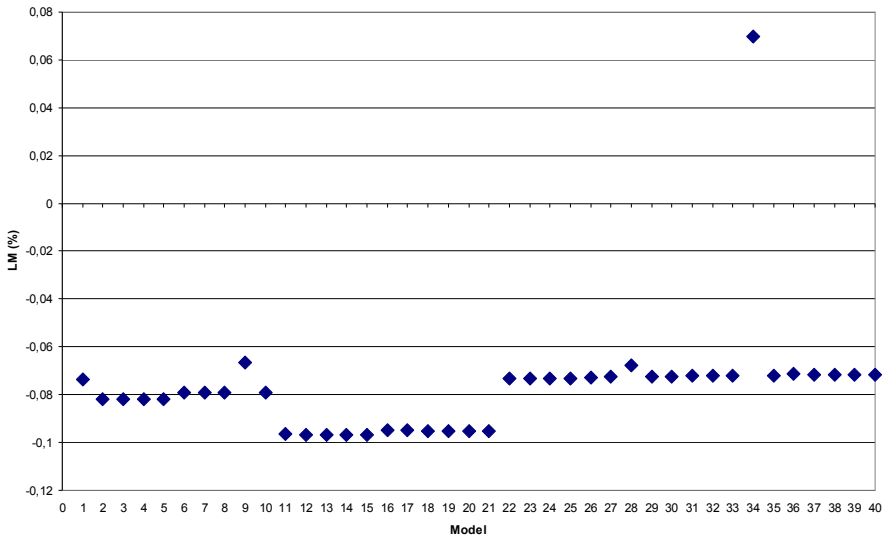


Figure 1. Inbreeding depression (F, 10%) with respect to the LMP of HLW breed on the base of the field tests

In the case of the HLW breed in the LMP % with a 10% increase of the inbreeding depression the expected depression is 0.007 %, on the other

hand, including different generations in the examination did not change the depression considerably.

In the case of the HL in the LMP trait I practically did not find inbreeding depression and including different generations to the examination did not change it considerably.

Figure 2 depicts the estimated inbreeding depression of the HLW's ADG, figure 3 depicts the estimated inbreeding depression of the HL's ADG.

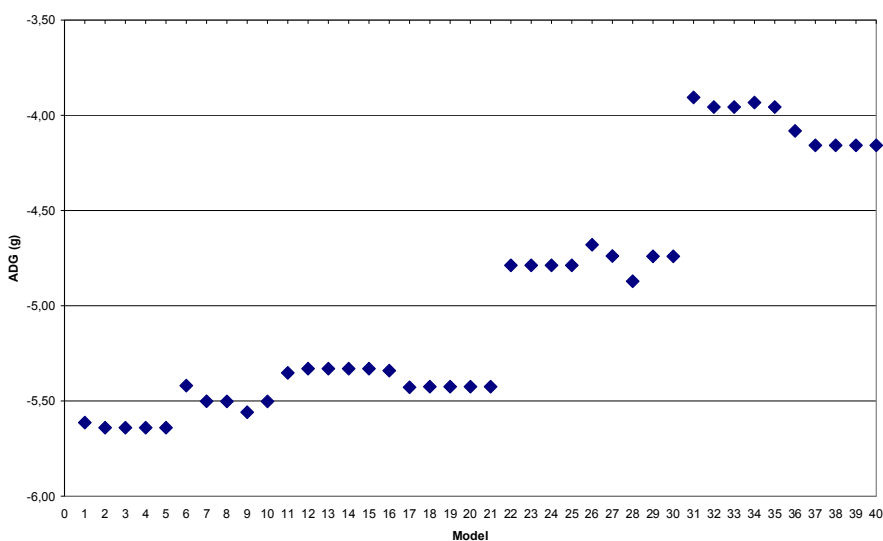


Figure 2. Estimated inbreeding depression(F, 10%) of the HLW's ADG

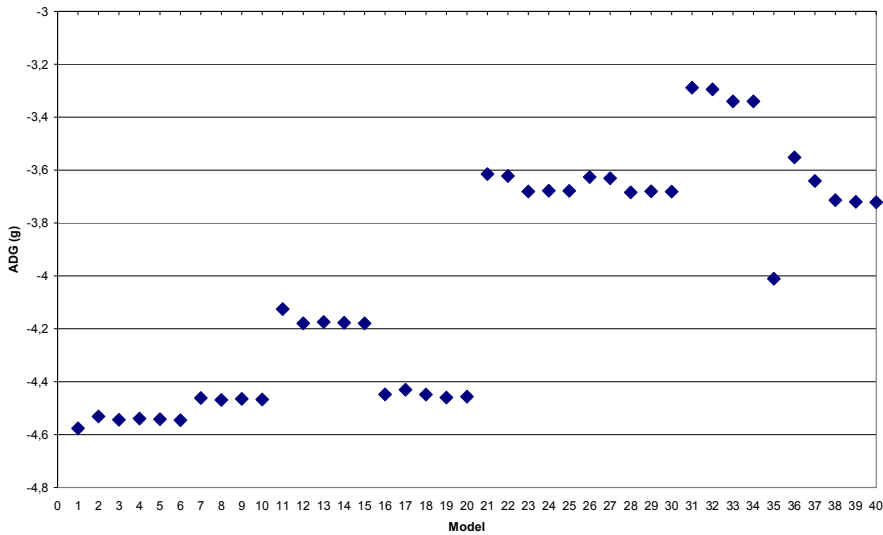


Figure 3. Estimated inbreeding depression (F, 10%) of the HL's ADG

In the case of the ADG of the HLW, 10% increase of inbreeding depression would result in 4.95 g-s of decrease.

Among the depressions estimated for the HL 1,282 g-s of difference can be experienced. A 10 % increase of the inbreeding coefficient causes a depression of 4.01g-s in this trait.

3.2.2. Loin depth, fat depth 1 and fat depth 2

In the case of the HLW the breeding value estimated for LD did not change – that is: did not fit better (MSE) – with the inclusion of several generation data of inbreeding depression and pedigree completeness, while with the HL those models showed better fit which contained pc and F going back to the sixth and seventh generations. This is shown on figure 4.

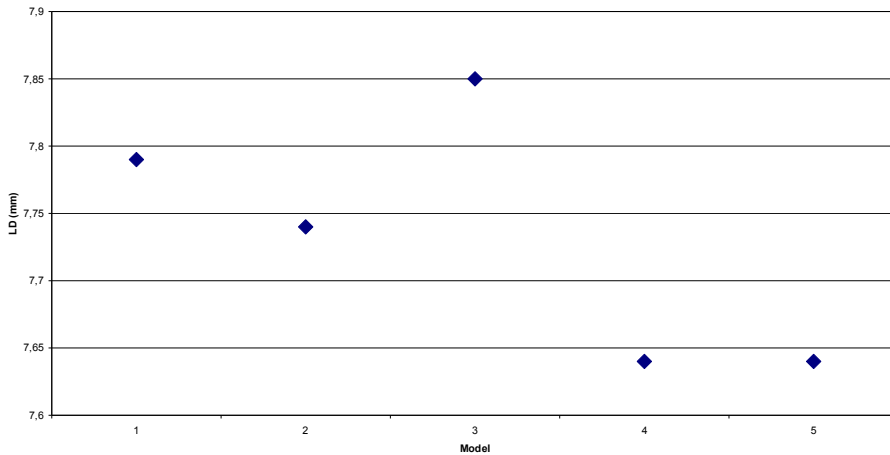


Figure 4. Average mean squares of LD of HL based on FTD

Results of the HLW breed FD1 and FD2 trait model variation are the same as those of the LD. Contrary to this at the HL breed in the cases of FD1 and FD2 models 1 and 2 had the better fit, which suggests that only the 3rd and 4th generations are worth including in the tests, because the inclusion of further generations does not improve the accuracy of the estimation. This is shown on figures 5 and 6.

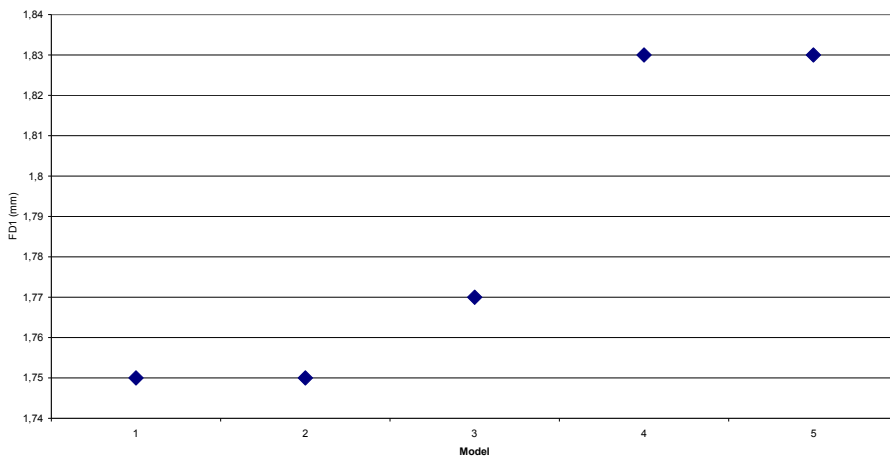


Figure 5. Mean squared errors of FD1 based on the field test data of ML

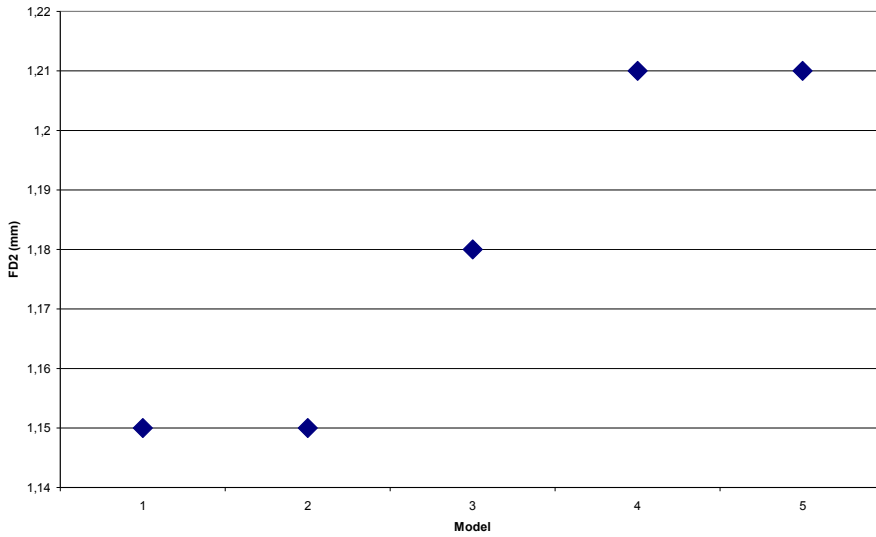


Figure 6. Mean squared errors of FD2 based on the field test data of ML

On the base of 40 models ran for FTD features of HLW the inbreeding depression for LD did not differ from each other, the inclusion of inbreeding coefficient and pedigree completeness for the 5, 6, and 7th generations I estimated slightly higher depression. This is shown on figure 7.

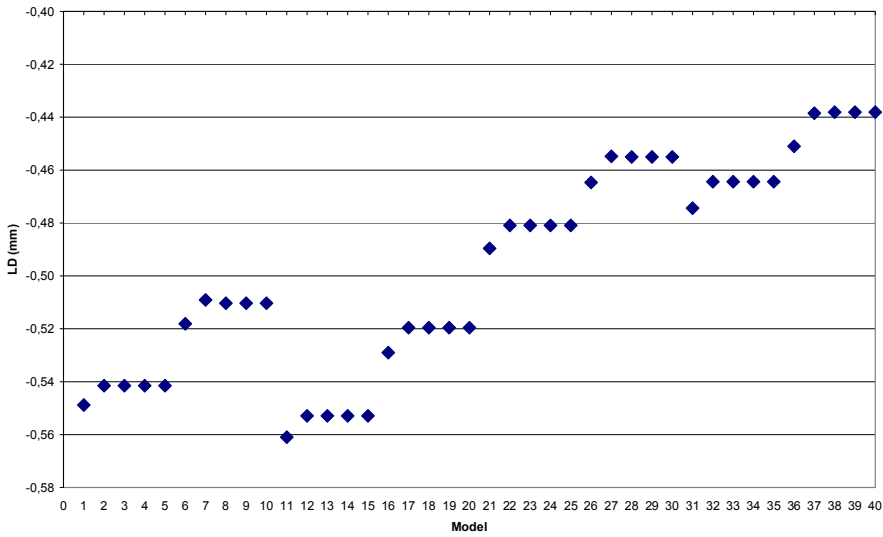


Figure 7. Inbreeding depression (F, 10%) for LD trait of HLW breed based on field tests

10 % growth of the inbreeding coefficient causes 0.49 mm depression in the HLW loin depth trait.

On the base of 5 models ran on field tests of HL inbreeding depression estimated for loin depth did not differ from each other, although I estimated higher depression with those model versions where the inbreeding coefficient and pedigree completeness appeared for the 6 and 7th generations of ancestry, so with the inclusion of more generations inbreeding depression increased. This is shown on figure 8.

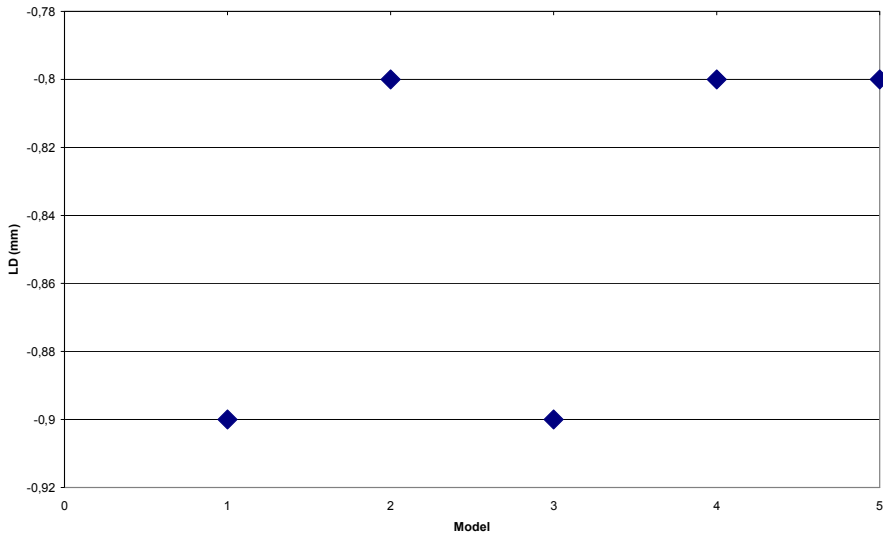


Figure 8. Inbreeding depression (F, 10 %) estimated for LD for HL based on field tests

10 % increase of inbreeding depression would decrease LD by 0.84 mm at the HL breed.

Based on the HLW field test FD1 trait estimated inbreeding depression clearly shows that with the inclusion of more generations (F+pc) the degree of depression is higher, furthermore those models showed depression increase where (F+pc), the two co-variant appear together. These differences are shown on figure 9.

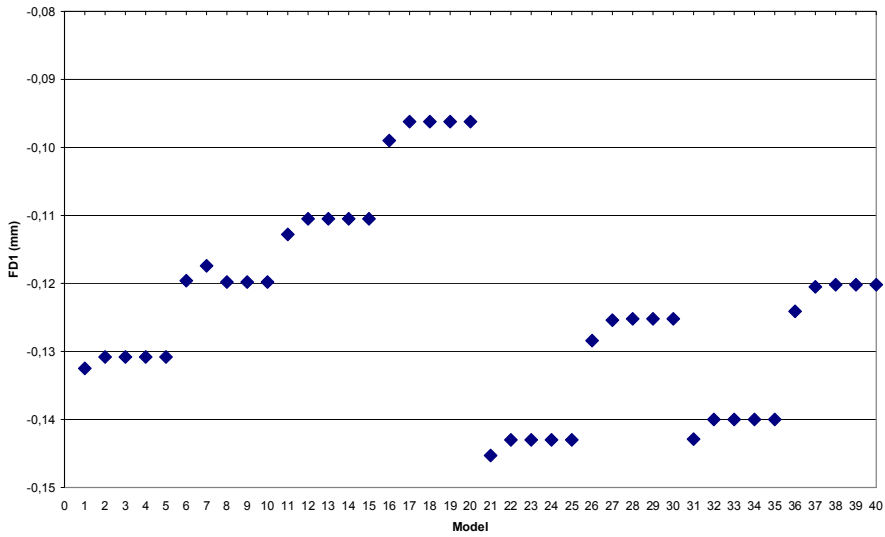


Figure 9. Inbreeding depression (F, 10 %) estimated for FD1 trait based on the HLW breed field tests

With the HLW breed a 10 % increase of the inbreeding depression results in a 0.12 mm decrease in FD1.

It can be seen at the HL field test FD1 trait inbreeding depression, that with the inclusion of more generations (F+pc) the depression increases, the discrepancy between estimated depressions is 0.010g. This is shown on figure 10.

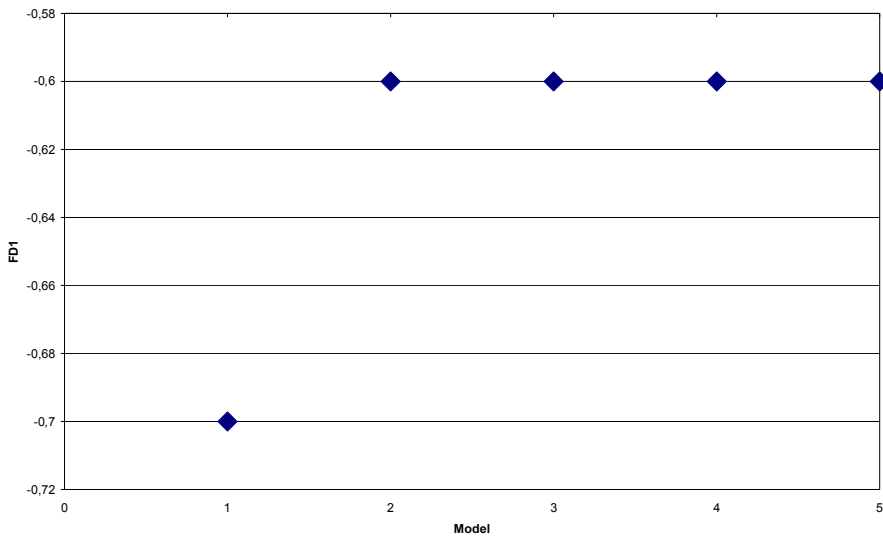


Figure 10. HL field test inbreeding depression (F, 10 %) for FD1 trait

With the HL breed 10 % increase of the inbreeding coefficient decreases FD1 by 0.62 mm.

In the case of the HLW field test FD2 trait among the 40 model variations used for estimation, depression increases with the inclusion of many generations (F+pc), furthermore those models where two covariants appear together showed somewhat higher depression (F+pc). Depression estimated for this trait is shown on figure 11.

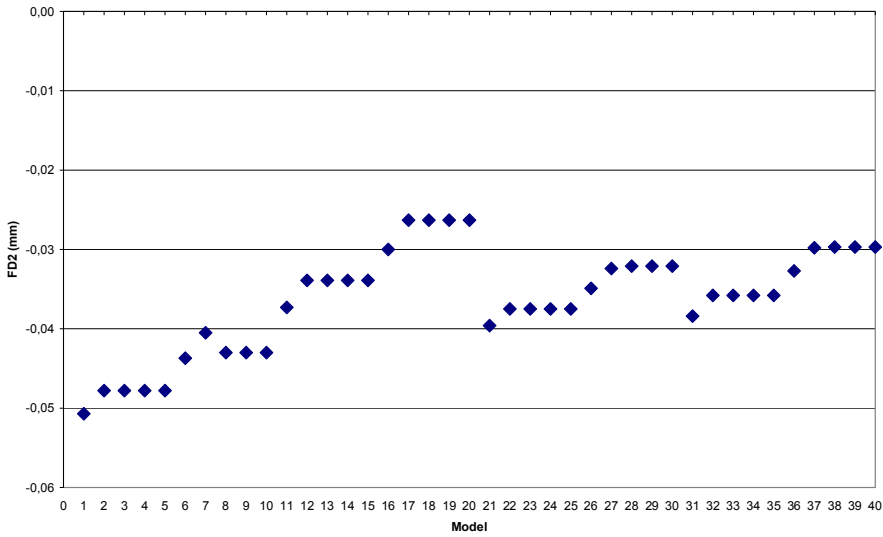


Figure 11. Inbreeding depression (F, 10 %) estimated for FD2 trait at the HLW field tests

At the HLW breed 10 % of the inbreeding coefficient decreased FD2 with 0.03 mm. For the same trait with the HL I did not experience inbreeding depression.

3.3. Reproductive performance traits

Models ran on the RPD the HLW and HL including different generations did not improve fit (MSE).

Figure 12. shows inbreeding depression for NBA from the HLW.

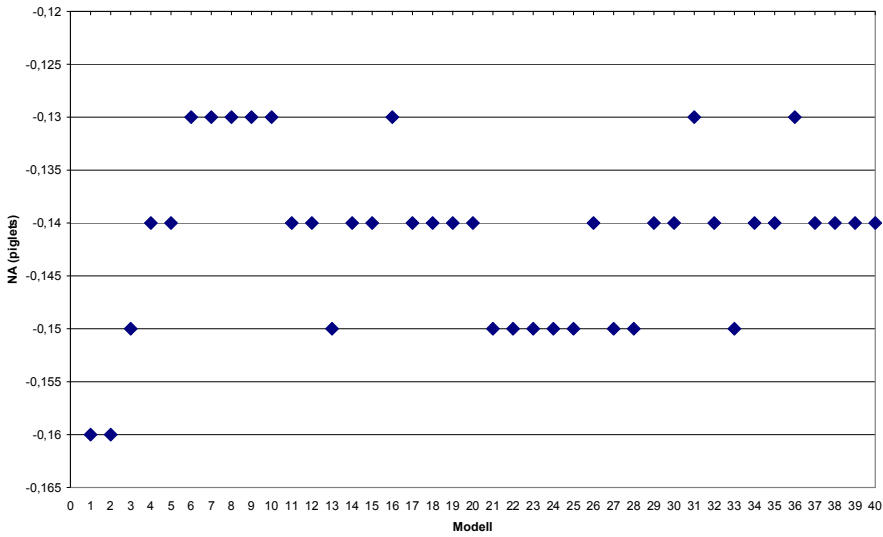


Figure 12. Inbreeding depression (F, 10 %) for piglets born alive from the HLW breed

The biggest difference in the estimated inbreeding depression at the piglets born alive was 0.03 piglets. It is shown on the figure, that taking the inbreeding coefficient and pedigree completeness into account for many generations of ancestry (8, 9 and 10), then the estimated inbreeding depression increased. A 10 % inbreeding coefficient increase decreases the NBA by 0.14 piglets, while increases the NBD by 0.01.

Figure 13. shows inbreeding depression for NBA from the HL

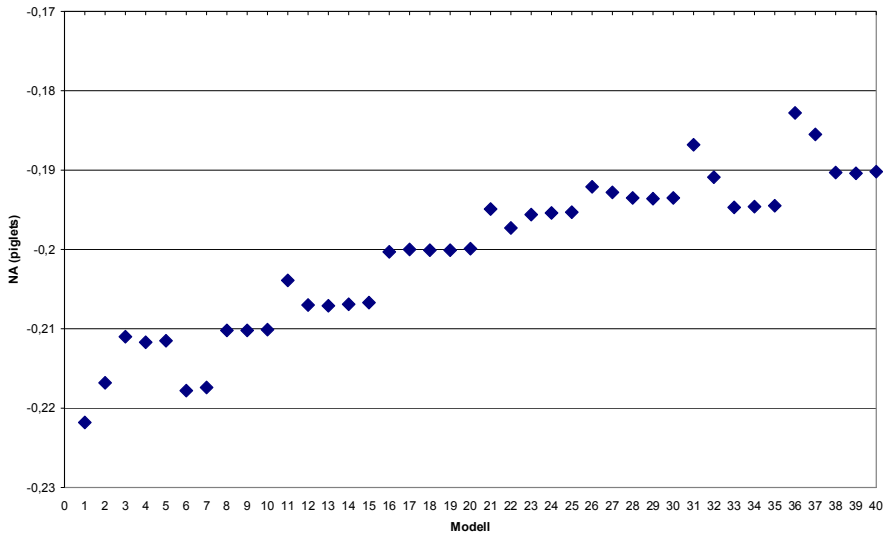


Figure 13. Inbreeding depression (F, 10 %) for piglets born alive from the HL breed

The biggest difference in the estimated inbreeding depression at the piglets born alive was 0.04 piglets. It is shown on the figure, that taking the inbreeding coefficient and pedigree completeness into account for many generations of ancestry (8, 9 and 10), then the estimated inbreeding depression increased. A 10 % inbreeding coefficient increase decreases the number of piglets born alive by 0.20 piglets, while I did not find significant inbreeding depression in the number of piglets born dead (with this trait inbreeding depression would have caused the increase of values).

Figure 14. shows inbreeding depression for NBD from the HLW

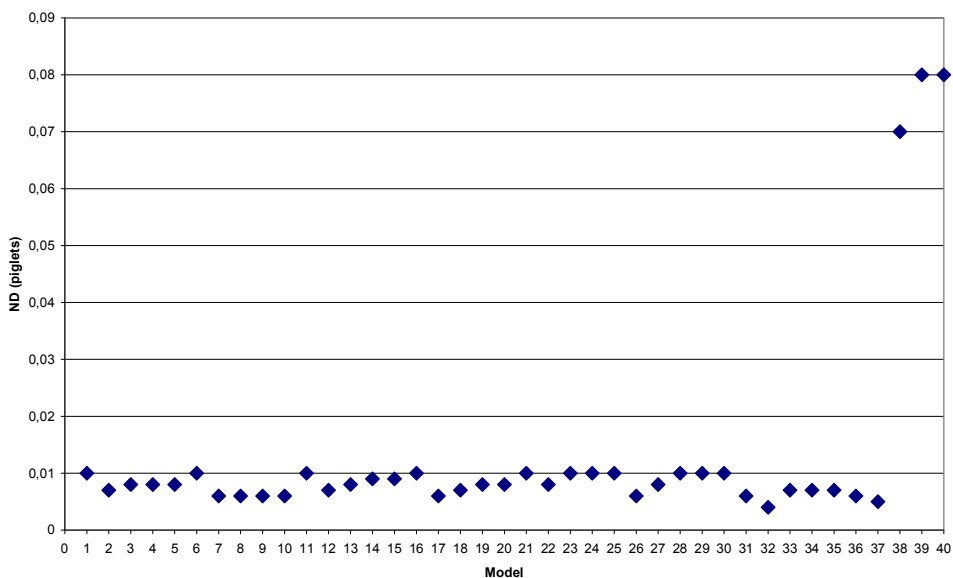


Figure 14. Inbreeding depression (F, 10 %) for piglets born dead from the HLW breed

A 10 % inbreeding coefficient increase increases the NBD by 0.01 piglets.

The estimated inbreeding depression given by the order of births is depicted in table 10.

Table 11. Estimated inbreeding coefficients by parity (HLW breed; F, 10%)

Parity	NBA – f3 and	NBA – f10 and	NBD – f3 and	NBD – f10 and
	pc3	pc10	pc3	pc10
1	-0,2093	-0,2062	0,05071	0,04730
2	-0,1277	-0,1419	0,01235	0,01158
3	-0,0852	-0,0929	-0,04911	-0,04253
4	-0,0727	-0,0279	0,01530	0,00066
5	-0,0964	-0,0653	0,00983	0,00247

Table 11 shows that by the increasing age of the animals examined a decreasing tendency of the inbreeding depression can be observed, which was not in accordance with the relevant literature. (KELLER et al., 2008; CHARLESWORTH and HUGHES, 1996; LILJEDAHL, 1974).

Table 12. Estimated inbreeding coefficients by parity (HL breed; F, 10%)

Parity	NBA – f3 and	NBA – f10 and	NBD – f3 and	NBD – f10 and
	pc3	pc10	pc3	pc10
1	-2,511	-2,238	0,2258	0,1948
2	-1,768	-1,694	-0,3250	-0,3019
3	-2,367	-2,071	0,2285	0,0561
4	-2,175	-2,134	-0,4013	-0,2431
5	-2,746	-2,463	-0,2157	0,2873
6	-2,800	-2,661	0,4300	0,4421
7	-2,547	-2,177	-0,7491	-0,5113
8	-3,553	-2,810	-2,2781	-1,7550

Table 12 shows that by the increasing age of the animals examined we can not see a unified tendency for the two traits with respect to inbreeding depression. At the same time if I compare the average of the inbreeding depression for the first four births with the second four (5-8.) birth averages, then it can be concluded that with the increase of the gilt's age the inbreeding depression increased as well.

4. CONCLUSIONS

Having analysed the pedigrees of the performance test datasets it was concluded that they were very short for the Hungarian Large White and Hungarian Landrace breeds. The pedigree completeness of the Hungarian Large White breed connected to the Field test was 1.18 on average taking into account 7 generations of ancestry. The value of the same parameter was 1.72 for the Hungarian Landrace breed. While monitoring the ancestry of 10 generations the pedigree completeness of the Hungarian Large White breed connected to the Reproductive performance dataset was 3.04 on average.

The inbreeding depression of the evaluated breeds were strongly connected with the length and completeness of the pedigrees. Because of the small pedigree completeness only a small percentage of the populations were inbred for all populations. However, this finding was more the result of the incomplete data recording system rather than the deliberate inbreeding avoidance.

The fit of the model variants were characterised by the MSE values. Thus it could be concluded that for most growth traits the models including the random litter effects gave better fit. For the Hungarian Landrace breed monitoring the ancestry for 7 generations improved the fit of the model of the loin depth. Analysing the number of piglets born alive including the mating boars in the models decreased the precision of the prediction, however the same phenomenon was not found the total number of piglets born alive.

For most of the traits – Hungarian Large White: lean meat percentage, average daily gain, loin depth, fat depth 1, number of piglets born alive – detectable inbreeding depressions were found. However, no inbreeding

depression of the Hungarian Landrace breed was found for lean meat percentage, fat depth 2 and number of piglets born dead, respectively.

5. NEW SCIENTIFIC RESULTS

1. Pedigree analysis connected to the field test dataset going back to 7 generations of ancestry for the HLW showed an average of 1.18 completeness. The same figure for the HL field tests is 1.72, while pedigree completeness belonging to the reproduction and growth dataset going back to 10 generations of ancestry of the HL is 3.04 on average. The pedigree completeness of the Hungarian Large White breed connected to the Reproduction performance dataset was 1.9 on average taking into account 10 generations of ancestry.

2. On the base of the pedigree data belonging to the field test dataset 0.9 % of the HLW proved to be inbred, the average inbreeding coefficient including the 7th generation was 13.37 %. It can be stated that on the base of the HL pedigree examination belonging to the field test dataset, 7.17 % was inbred. Average inbreeding coefficient was 5.0 % (8.0 %) going back to 7 (3) generations of ancestry. On the base of ancestry data belonging to the reproduction dataset, 31.79 % of HLW gilts was inbred, the average inbreeding coefficient was 1.9 % (7.44 %) for 10 (3) generations of ancestry. On the base of ancestry data belonging to the reproduction dataset, 35.59 % of HL gilts was inbred, the average inbreeding coefficient was 2.00 % (6.00 %) for 10 (3) generations of ancestry. Average inbreeding coefficients were calculated taking only the inbred animals into account.

3. For the HLW breed closer fit could be achieved for: loin depth, FD1, FD2, if in the inbreeding coefficient and pedigree completeness included as covariates (considering 7 - 10 for NBA - generations).

4. The estimated inbreeding depressions (per 10% increase of the inbreeding coefficient) of the Hungarian Large White breed were the following:

- 0.07 % (lean meat percentage)
- g (average daily gain)
- 0.49 mm (loin depth)
- 0.12 mm (fat depth 1)
- 0.03 mm (fat depth 2)
- 0.14 piglets (number of piglets born alive)
- 0.01 piglets (number of piglets born dead)

5. The estimated inbreeding depressions (per 10% increase of the inbreeding coefficient) of the Hungarian Landrace breed were the following:

- 4.01 g (average daily gain)
- 0.084 mm (loin depth)
- 0.062 mm (fat depth 1)
- 0.20 piglet (number of piglets born alive)

For the traits of lean meat percentage, fat depth 2 and for the number of piglets born dead no inbreeding depressions were observed.

6. The average of inbreeding depression experienced of the HL gilts during the first four births is lower than that of the latter (5-8.) births, therefore it can be stated that with the increase of gilt age inbreeding depression increased as well.

6. RECOMMENDATIONS

Based on the results the pedigree completeness and inbreeding coefficients should be included in the BLUP models of the Hungarian Large White breed for the following traits: Loin depth, fat depth 1, fat depth 2. The pedigree completeness and inbreeding coefficients should be included in the BLUP models of the Hungarian Landrace breed for the following traits: loin depth and fat depth 1. For predicting the breeding values of the Hungarian Landrace pigs for the number of piglets born alive inclusion of the pedigree completeness and inbreeding coefficients in the models can be suggested taking into account the ancestry of 10 generations.

Increasing the pedigree completeness (requiring the multi-generation pedigree of the possible import individuals) is desirable thus the results related to inbreeding would become more precise.

Avoidance of boars and sows having a common ancestor until the 3-4-5th generation of ancestry can also be suggested.

7. PUBLICATIONS ON THE SUBJECT OF THE DISSERTATION

7.1. Papers published in foreign language peer-reviewed journals

Zsófia Vigh, Petra Gyovai, L. Csató, Á. Bokor, J. Farkas, I. Nagy. (2007): Effect of inbreeding on loin and fat depth in Hungarian Landrace pigs. Agriculture. 13. 1. 41-46.

Vigh, Zs., Gyovai, P., Csató, L., Bokor, Á., Farkas, J., Radnóczy, L., Komlósi, I., Nagy, I. (2008): Effect of inbreeding on lean meat percentage and average daily gain in Hungarian Landrace pigs. Arch. Tierz., Dummerstorf **51**. 541-548.

7.2. Papers published in Hungarian language peer-reviewed journals

Vigh Zs., Csató L., Nagy I. (2008): A pedigréanalízisben alkalmazott mutatószámok és értelmezésük. Szakirodalmi áttekintés. Állattenyésztés és takarmányozás, 2008. 57.4. 549-564.

7.3. Oral presentations at international conferences

Nagy, I., **Vigh, Zs.**, Farkas, J. (2007): Effects of inbreeding on reproductive traits in Hungarian Large White and Landrace. 5th Int. Workshop on Data Management and Genetic Evaluation in Swine, Mariensee, Germany, Oct 18-19.

7.4. Non-scientific publications

Vigh Zs., Gyovai P. (2008). A pedigréanalízis szerepe az állattenyésztési programokban. Agronapló. 114-115. www.agronaplo.hu

8. PUBLICATIONS OTHER THAN THE DISSERTATION TOPIC

8.1. Papers published in foreign language peer-reviewed journals

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8.2. Papers published in Hungarian language peer-reviewed journals

Nagy I., Csató L., Farkas J., Radnóczy L., **Vígh, Zs.** (2002): A magyar nagy fehér húsertés és magyar lapálysértés központi hízekonyságvizsgálatának (HVT) elemzése túlélés becslés (survival analysis) alkalmazásával. *Acta Agr. Debreceniensis*. 9. 37-40.

Nagy I., Gulyás R., Csató L., Farkas J., Radnóczy L., **Vígh Zs.** (2004): Tenyészeteken belüli és tenyészetek közötti genetikai kapcsolat néhány hazánkban tenyésztett sertésfajtánál. Álattenyésztés és Takarmányozás 53. 2. 101-110.

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8.3. Full-length publications in proceedings

Szendrő, Zs., Romvári, R., Nagy, I., Andrassy-Baka, G., Metzger, Sz., Radnai, I., Biró-Németh, E., Szabó, A., **Vígh, Zs.**, Horn P. (2004): Selection of Pannon White rabbits based on computerised tomography. 8th World Rabbit Congress, Puebla, Mexico. 175-180.

Nagy I., Metzger Sz., Gyovai M., **Vígh Zs.**, Romvári R., Petrási Zs., Szendrő Zs. (2005): CT felvételek alapján becsült combizom tömeg genetikai paraméterei pannon fehér nyúlpopulációban. 17. Nyúltenyésztési Tudományos Nap, Kaposvár, 25-58.

Gyovai P., Nagy I., Gerencsér Zs., Metzger Sz., Bíróné N. E., Radnai I., Bokor Á., **Vígh Zs.**, Szendrő Zs. (2007): Szelekció hatása a Pannon fehér nyulak beltenyésztettségére és a szelekciós előrehaladásra. 19. Nyúltenyésztési Tudományos Nap, Kaposvár, 53-59.

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8.4. Hungarian language publications in proceedings/Proceedings-ben megjelent magyar nyelvű közlemények

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Nagy I., Csató L., Farkas J., **Vígh Zs.** (2005): Genotípus és individuális heterózis hatások vizsgálata az átlagos hátszalonna-vastagságra és a vágóértéket kifejező tulajdonságokra nézve egyes hazai sertéspopulációkban. 47. Georgikon Napok. Keszthely. 95.

8.5. Non-scientific publications

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Csató L., **Vígh Zs.**, Gyovai P., Nagy I., Farkas J. (2007). A teljesítményvizsgálat kezdetén mért testsúly és a tenyésztetés kapcsolatának vizsgálata sertéseknél. Agronapló. 10-11. 65-66.

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