

**THESES OF  
DOCTORAL (PhD) DISSERTATION**

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**GENETIC EVALUATION OF THE  
CT-BASED SELECTION PROGRAM  
IN DOMESTICATED RABBITS**

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## **1. ANTECEDENTS OF RESEARCH, AIMS**

The objective of the different domesticated species is to improve the reproductive (eg. litter size) growth (eg. average daily gain) and slaughter (eg. percentage of valuable cuts). Apart from the general conclusions no experimental results can be found in the relevant literature about the slaughter value improvement. This suggests that slaughter traits are not targeted by selection in abroad.

Using the conventional performance tests only progeny test can provide information about the genetic merit of a breeding animal for its slaughter value. Due to Computer tomography (CT) procedure the body composition of an animal can be predicted in vivo. The Institute of Diagnostic Imaging and Radiation Oncology (of the Kaposvár University) makes it possible the apply CT aided selection for the Pannon white rabbit population improving its dressing out percentage. Since 2002 the CT measurements are evaluated using BLUP methodology. Because of the closed population structure of the Pannon white rabbit population the BLUP selection can increase the inbreeding level of the population substantially.

The objectives of my thesis were to evaluate the direct and indirect effects of the CT aided selection on the growth, slaughter and reproductive traits. Additionally my objective was to estimate the genetic parameters and trends of the various growth, slaughter and reproductive traits. Moreover my intention was also to evaluate the stability of breeding values estimated on sub-datasets of different periods. Connected to these objectives I decided to analyse the effects of selection on the population structure and the inbreeding depression of a trait that is not targeted by selection.

## 2. MATERIAL AND METHODS

The experiments were carried out at the rabbit farm of the Kaposvár University using Pannon White rabbits. Growing rabbits after weaning at 35 days of age were kept in a closed rabbit house, in fattening cages (2-3 rabbits per cage). Breeding rabbits were kept in breeding cages individually placed. In the winter the rabbit house was heated to 12-18 °C, during summer the temperature occasionally reached levels as high as 28 °C. Both the growing and breeding rabbits were fed a commercial pelleted diet *ad libitum* and water was available *ad libitum* from nipple drinkers. In the early '90s, namely at the beginning of the development of Pannon White breed, a mating scheme was worked out of, which reduced the matings of relatives in the population. The circular mating scheme used is shown in Figure 1.

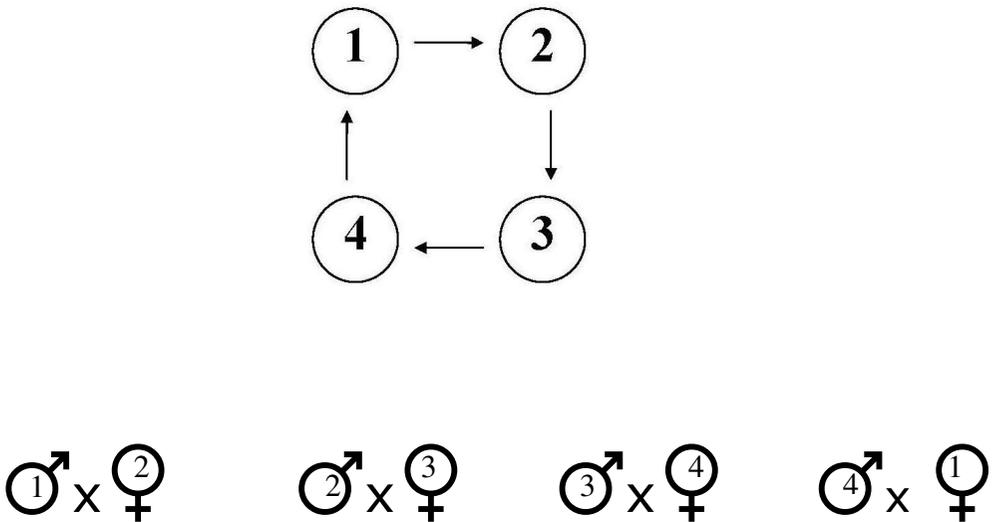


Figure 1. The circular mating scheme used in Pannon white

## **2.1 Pedigree Analysis**

### **Pedigree information and generation interval**

This analysis was performed on those rabbits that were born between January 1992 and December 2007. The pedigree included 4749 individuals. Those individuals that have two unknowns' ancestors ( $n = 363$ ) were considered as founders. In the case of those individuals, where only one parent was known (218), unknown parent was regarded as a founder. Thus the number of individuals in the pedigree increased to 4967. For all the progeny the total pedigree information was assessed, which was the proportion of known ancestors by generations. The complete generation equivalents in the known pedigree is the number of the sum of  $(1/2)^n$ , where "n" the number of generations, in which all ancestors are known.

The generation interval was assessed in all 4 parent-offspring pathes (buck - male progeny; buck - female progeny, doe - male offspring, doe - female progeny).

### **Average relatedness and inbreeding**

In the pedigree all individuals were included to compute the average relatedness (AR). During the investigation two different inbreeding coefficients was calculated. In one case, the coefficient was calculated based on the total pedigree information ( $F_i$ ), while the other cases, only 4 generations of pedigree information ( $F_{i4}$ ) were taken into account.

The partial inbreeding coefficient ( $pF_i$ ) was calculated with the so-called "gene dropping" method ( $10^6$  reps). All 581 founding ancestors were involved in the calculation, which contributed to the level of inbreeding, and allowed to "decompose" the inbreeding coefficient of the 2007 reference population.

## **Effective population size**

Three types of effective population size were calculated: the effective population size from family variance ( $N_{efv}$ ), the inbreeding effective population size ( $N_{eIr}$ ) and the realized effective population size ( $N_e$ ).

## **Probability of gene origin**

Effective number of founders ( $f_e$ ) is the number of equally contributing founders to each descendant generation, which would create the same genetic diversity as found in the investigated population.

In order to be consider the effect of gene loss, which occurs as the result of artificial insemination, the effective number of non-ancestors ( $f_a$ ) was calculated, which is the minimum number of ancestors (not necessarily the founding ancestor) which can be explained by the population's total genetic diversity.

Founder genome equivalent value of the founders ( $f_g$ ) the number of equally contributing founders to each descendant generation, which are the genetic diversity of the studied population if we assume that there is no loss of alleles.

## **Applied software**

Calculation of the genetic variability was done by ENDOG 4.6 software. The Grain 2.0 software was applied for the  $pF_i$  computation. The data manipulation, for descriptive and for the simple statistical analysis the different methods of the SAS program were applied.

## **2.2 Genetic parameters and trends**

### **2.2.1 Average daily gain (ADG), thigh muscle volume (TMV), hind part percentage (HHP) and dressing out percentage (DoP)**

The average daily gain (ADG) was determined based on the measured body weights of rabbits at the age of 5 and 10 weeks. The rabbits showing the best performances were taken to the Institute of Diagnostic Imaging and Radiation Oncology, University of Kaposvár where they were scanned by Computer Tomography (CT). The CT investigation was carried out with Siemens Somatom Plus 40 and Siemens Somatom Emotion 6, without anaesthesia. The rabbits were scanned between the ilium (os ilium) and total knee joint with overlapping, 10-mm slice thickness (11 to 12 scans), in order to determine the pixel frequency of the conducting muscle density. Estimation of  $h^2$ -values of the ADG and the TGV were carried using the data of all the young rabbits which were born in 2003 to 2009. Between February 2004 and January 2010 49 CT examinations were made.

Between December 2007 and December 2009 10 slaughter tests were performed at the slaughterhouse of Olivia Ltd estimate the heritability of the HPP and DoP. The slaughter performance parameters were defined based on the WRSA recommendation. Post-mortem determinations of the mass of hot carcass were carried out (which included the head, liver, kidneys, heart + lungs, kidneys and surrounding fat girdle). After 24-hour cooling (3° C) the chilled carcass weight was measured. The mean and standard deviation values of the examined parameters are shown in Table 1.

**Table 1. Descriptive statistics of the measured traits**

Traits	Number of records	Mean	Standard deviation	Coefficient of variation
ADG (g/d)	29435	43.2	6.68	15.46
TMV (cm <sup>3</sup> )	4434	336	38.9	11.58
HPP (%)	557	31.7	0.97	3.06
DoP (%)	557	60	1.75	2.92
BWCT (g)	4434	2612	238	9.11
BWBS (g)	557	2558	234	9.15
WHC (g)	557	1582	166	10.50
WCC (g)	557	1528	165	10.80
WHPC (g)	557	493	48	9.74

ADG: average daily gain; TMV: thigh muscle volume; HPP: hind part percentage; DoP: dressing out percentage; BWCT: body weight at CT scan; BWBS: body weight before slaughter; WHC: weight of hot carcass; WCC: weight of chilled carcass; WHPC: weight of hind part of carcass

Genetic parameters of ADG, the CT-based thigh muscle volume, proportion of HPP related to the chilled carcass and dressing out percentage were estimated with REML and BLUP methods (applied by PEST and VCE 5 software). The applied linear model was:

$$y = Xb + Za + Wc + e$$

The various factor types included by the model is shown in Table 2.

**Table 2. The considered factors for the examined traits**

Factor	Level	Type of factor	Traits			
			ADG (g/d)	TMV (cm <sup>3</sup> )	HPP (%)	DoP (%)
Year-month	62	F	x	x	x	x
Animal	31402	A	x	x	x	x
Litter	4407	R	x	x	x	x
BWCT	1	C	–	x	–	–
Sex	2	F	x	x	x	x
Pixel	3	F	–	x	–	–

F: fixed effects; A: additive genetic effects; R: random effect; C: covariant; BWCT: body weight at CT-scan

The phenotypic and genetic trends were also estimated in the ADG and TMV. For the estimates of phenotypic trends the animals that were born in the same year were considered, and for the estimation of genetic trends their breeding values averaged, and then mean values were regressed on the years of birth. For the estimation of genetic trend, the breeding values of those rabbits were used that had measurements for the analyzed traits. The trend estimation was carried out using the SAS software.

### **2.2.2 Litter weight at 21 days of age**

The continuous data collection of the litter weight at 21 days of age (LW21) since 1992 made it possible to estimate the heritability of this trait and the impact of selection (for ADG and TMV) on the rearing ability (e.g. litter weight at 21 days of age). In this study the first four parities were evaluated separately. The descriptive statistics of the analyzed traits are represented in Table 3.

**Table 3. Descriptive statistics of the traits**

Parity	Number of records	Mean	Standard deviation	Coefficient of variation
LS21				
1	3143	6.97	1.68	24.10
2	2588	7.59	1.54	20.29
3	2161	7.57	1.57	20.74
4	1746	7.55	1.55	20.53
LW21 (kg)				
1	3143	2.22	0.55	24.77
2	2588	2.69	0.63	23.42
3	2161	2.77	0.66	23.83
4	1746	2.77	0.67	24.19
ADG (g/d)				
1	6462	45.53	6.14	13.49
2	6020	45.79	6.06	13.23
3	5600	45.99	6.04	13.13
4	5251	46.27	5.92	12.79
BWCT (kg)				
1-4	3878	2.62	0.24	9.16
TMV (cm <sup>3</sup> )				
1-4	3878	338	38.67	11.44

LS21: litter size at 21 days of age; BWCT: body weight at CT scan

The estimation of the genetic parameters and breeding values for the litter weight at 21 days of age was completed with the same methods (applied linear model) and the software which were described in Section 2.2.1. The characteristics of the applied model included are presented in Table 4.

The phenotypic and genetic trends calculation also applied the same methods as in Chapter 2.2.1.

**Table 4. The considered factors for the examined traits**

Factor	Type	Parity	Level	Trait		
				LW21 (kg)	TMV (cm <sup>3</sup> )	ADG (g/d)
LS21	C	1-4	1	x	–	–
Year-month	F	1	188	x	–	–
		2	195			
		3	193			
		4	184			
Animal	A	1-4	9772	x	x	x
Litter	R	1	3732	x	x	x
		2	3515			
		3	3240			
		4	2981			
BWCT	C	1-4	1	–	x	–
Sex	F	1-4	2	–	x	x
CT scan year-month	F	1-4	48	–	x	x
Pixel	F	1-4	3	–	x	–

C: covariant; F: Fixed effects; A: additive genetic effects; R: random effect; LS21: litter size at 21 days of age; BWCT: body weight at CT scan

### 2.2.3 Number of kits born alive and dead

The study included 3883 does' 18398 kindling data (they were born between 1992 and 2009). The total number of the pedigree file was 4804. The proportion of kindlings where the number of dead born kits was greater than zero was 24% (4487 records). Descriptive statistics of the data can be found in Table 5.

**Table 5. Descriptive statistics of the traits**

Trait	Number of kindlings	Mean	Standard deviation	Coefficient of variation
Number of kits born alive	18398	8.09	3.34	41.29
Number of kits born dead	18398	0.63	1.58	250.79

The estimation of genetic parameters and determination of breeding values were done by REML and BLUP methods. To define genetic parameters of number of kits born alive and dead the repeatability animal model was used, where each parity were considered as a repeatability trait. Kindling groups formed due to the non-uniform distribution of numbers of parity (1, 2, 3-10, 11 -). The applied linear model was:

$$y = Xb + Za + Wpe + e$$

The various factor types included by the model is shown in Table 6.

**Table 6. The considered factors for the examined traits**

Factor	Type	Level	Trait	
			Number of kits born alive	Number of kits born dead
Parity number <sup>1</sup>	F	4	x	x
Year-month of kindling	F	196	x	x
Inbreeding coefficients of the dam	C	1	x	x
The pedigree completeness of the dam	C	1	x	x
Inbreeding coefficient of the litter	C	1	x	x
The pedigree completeness of the litter	C	1	x	x
Animal	A	4804	x	x
Permanent environmental effect	R	3883	x	x

<sup>1</sup>: 1. parity, 2. parity, 3-10. parity, above 10 parity number;

F: fix effect; C: covariant, A: additive genetic effect; R: random effect

The phenotypic and genetic trends calculation also applied the same methods as in Chapter 2.2.1.

#### **2.2.4 Inbreeding depression**

Because in the Pannon White population no selection is conducted for the number of born alive and dead kits in the herd, this trait has been chosen to estimate the inbreeding depression.

Descriptive statistics of the data is described in Chapter 2.2.3 in Table 5. The applied linear model was:

$$y = Xb + Za + Wc + e$$

The characteristics of the applied model are shown in Chapter 2.2.3. in Table 6. While during the experiment very few parity data were available from does born in 2009, therefore the last two years (2008, 2009) of the study period were evaluated together during the of the inbreeding coefficients and total pedigree completeness calculation.

### **2.3 Stability of genetic parameters and of the breeding values**

In this study data of 47,242 Pannon white rabbits were analyzed, which reared in 7470 litters and were born between 2000 and 2008. The tested animals are originated from 590 bucks and 1849 does. The total number of the pedigree file was 49130. The database was divided into 5-year periods (2000-2004, 2001-2005, 2002-2006, 2003-2007 and 2004-2008), which were analyzed separately. The database and the descriptive statistics are shown in Table 7.

**Table 7. Descriptive statistics of the average daily gain**

Trait	Period	Number of records	Mean	Standard deviation	Coefficient of variation
Body weight at 5 weeks age (kg)	2000-2008	47242	0.88	0.17	19.32
Body weight at 10 weeks age (kg)	2000-2008	47242	2.37	0.29	12.24
ADG (g/d)	2000-2008	47242	42.5	6.35	14.94
	2000-2004	28305	41.7	6.22	14.92
	2001-2005	30585	42.2	6.13	14.53
	2002-2006	29021	42.3	6.26	14.80
	2003-2007	27873	42.8	6.34	14.81
	2004-2008	25132	43.2	6.47	14.98

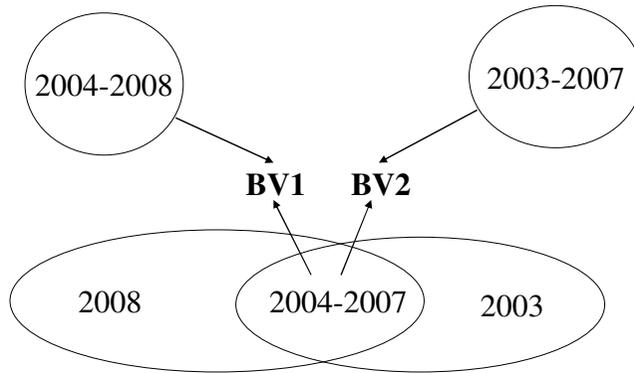
The genetic parameters and breeding values for ADG were estimated by REML and BLUP. The model characteristics are shown Table 8.

**Table 8. The considered factors for the examined traits**

Factor	Type	Period					
		2000-2008	2000-2004	2001-2005	2002-2006	2003-2007	2004-2008
Sex	F	2	2	2	2	2	2
Year-Month	F	102	60	59	58	58	55
Animal	A	49130	30063	32345	30816	29609	27081
Litter	R	7470	4676	4870	4558	4235	3775

After the breeding value estimation the last part database (2004-2008) was merged with the other part database (2003-2007, 2002-2006, 2001-2005 and 2000-2004) (using inner join). In the joint database only those records are left

which were both in the last (2004-2008) and in the other part database. In the joint database every rabbit has two breeding values (BV1, BV2) for the ADG, which was based on two separate 5-year periods. The 2004-2008 and 2003-2007 periods contain the merged database from those rabbits that were born between 2004 and 2007, and they have two breeding values (Figure 2). Based on the last part database (2004-2008) and current part database (per period of 5 years) the Spearman's rank correlation was calculated between the breeding values estimations (BV1, BV2) with the use of the SAS software package.



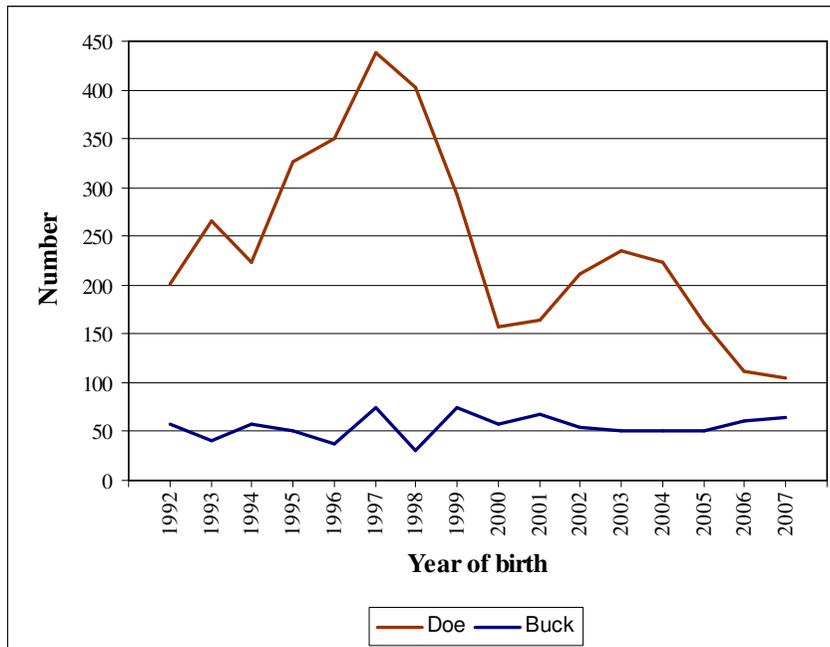
**Figure 2. Breeding values of the rabbits (born between 2004 and 2007) based on breeding value estimations (BV1 and BV2) of different databases**

### 3. RESULTS

#### 3.1 Pedigree analysis

##### Pedigree information and generation interval

Figure 3. shows the numbers of Pannon white does and bucks between 1992 and 2007. The number of does decreased dramatically between 1998 and 2000.



**Figure 3. Pannon white demographic data between 1992 and 2007**

Generation interval calculated across all pathways are presented in Table 9.

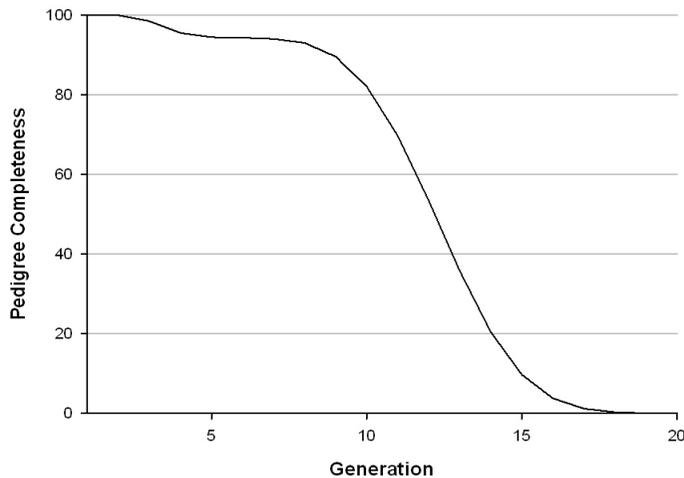
The mean generation interval for the buck pathways was 1.4 year, while mean generation interval for the doe pathways was about a year. The buck-son generation interval was the highest (1.4 years), which was due to stronger

selection pressure on does (110%) than on the bucks, thus the productive life of the does is less than one year.

**Table 9. Descriptive statistics on the generation intervals (in years) in Pannon White rabbits for the evaluated period**

	Number	Mean	Standard deviation
Buck – son	522	1.400	0.739
Buck – daughter	1601	1.399	0.700
Doe – son	535	0.989	0.504
Doe – daughter	1598	1.035	0.530
Overall	4256	1.211	0.652

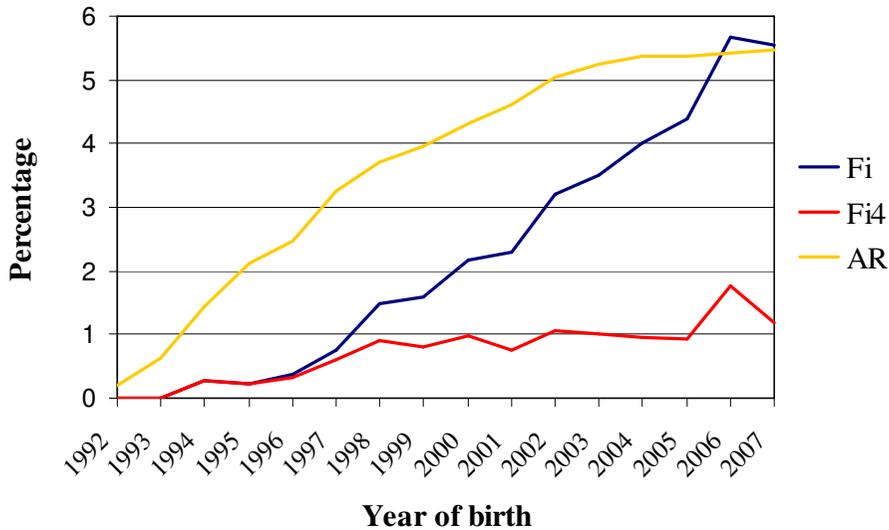
The total pedigree information of the reference population 2007 was above 90% until the ninth generation, which resulted in a large complete generation equivalent of the population (Figure 4).



**Figure 4. Average percentage of known ancestors per generation for Pannon White rabbits born in 2007**

## Average relatedness and inbreeding

Trends for the mean inbreeding ( $F_i$ ) - calculated from the total pedigree information – and average relatedness (AR) for the examined 15-year long period is shown in Figure 5.



**Figure 5. Trends for the inbreeding and average relatedness**

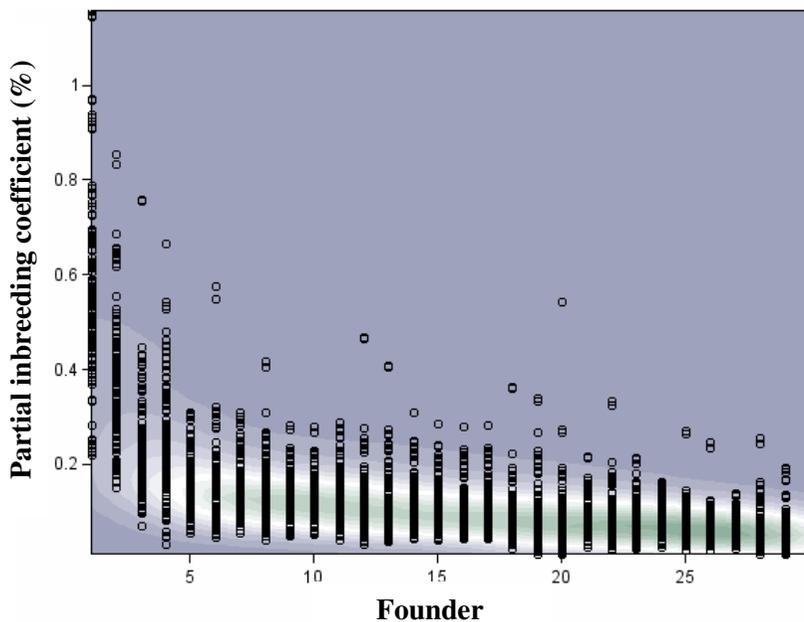
$F_i$ : inbreeding coefficient based on the total pedigree information,  
 $F_{i4}$ : trend for the mean inbreeding related to 4-generation pedigree,  
AR: average relatedness

The average  $F_i$  increased steadily, and showed the maximum growth rate 1.29% between 2005 and 2006. The reason for this finding was the significant reduction in the census size. The value of  $F_i$  exceeded the value of AR in the last two years. AR reached 5.4% but in the last four years the value remains stable (Figure 5).

The inbreeding coefficient estimated from four generations' pedigree information reached 1% and this value remained the same between 1998 and 2005. In 2006 significant increase were observed, but in 2007 it decreased to 1%, which demonstrated the effectiveness of the mating system.

In the 2007 the reference population the individual inbreeding coefficient were studied. Each founders' contribution to inbreeding coefficient was calculated. From 581 founders 148 (i.e. the 25%) contributed to the inbreeding of the reference population. The average of the 146 founders' partial inbreeding coefficient is 0.038%, its variance 0.044%. Figure 6 shows the partial inbreeding coefficients distribution of the 30 founders most contributed to the inbreeding of the 2007 reference population.

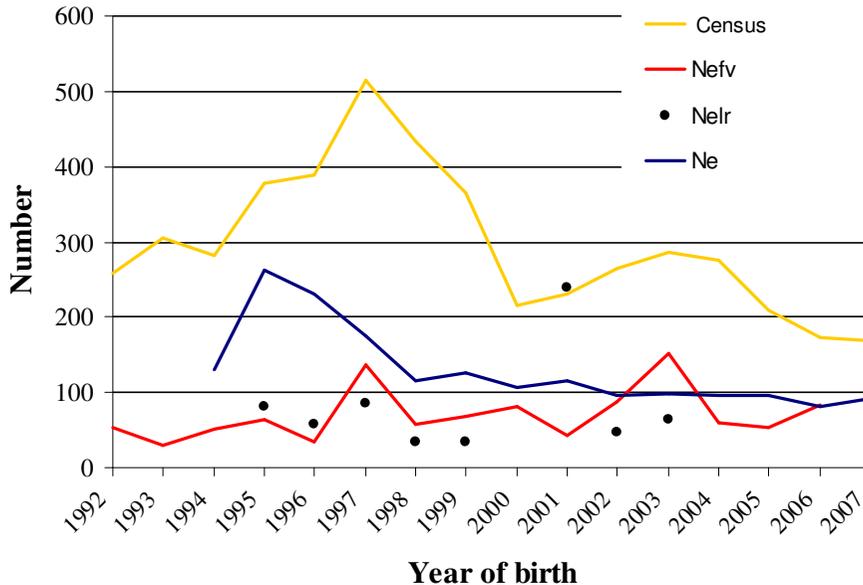
The most contributing 10 and 30 founders gave 42.24 and 73.18% of the total inbreeding of the population. The number of founders contributing the inbreeding of the 2007 reference population fluctuated between 70 and 128, their average was 103.



**Figure 6. Distribution of the partial inbreeding coefficients ( $pF_i$ ) for 30 founders with the greatest inbreeding contribution to Pannon White rabbits born in 2007**

## Census and effective population size

Trends in the census and  $N_e$ , estimated by 3 different approaches, are presented in Figure 7.



**Figure 7. Trends of the census and the effective population size estimated by 3 different ways**

$N_{efv}$ : effective population size calculated on the basis of family variance,  
 $N_{elr}$ : inbreeding effective population size,  
 $\bar{N}_e$ : realized effective population size;

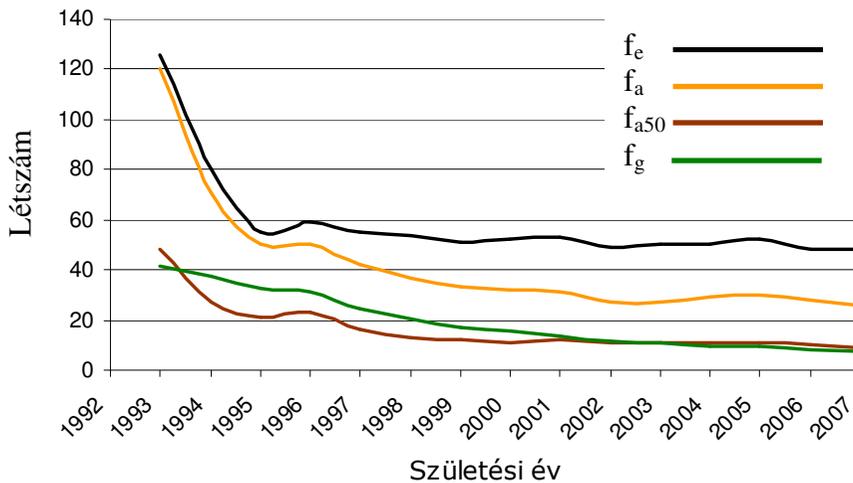
The number of Pannon White breed has grown steadily until 1997, when the census size was over 500. In the next 3 years the number of rabbits halved. Between 2000 and 2005 changed little, but in 2006 greatly reduced and in 2007 it reached the minimum in the reference population ( $n = 169$ ). In the 2007 reference population the effective population size varied between 37.19 and 91.08, depending on the chosen calculation method.  $N_{efv}$  (marked in red) calculation gave no estimates for the last year born individuals (Figure 7). In most cases, the logarithmic regression estimation gives similar results as the family variance calculated effective population size. However, this method

unfavourable characteristic was detected in some years, when deliberately planned matings (to reduce the relatedness between the pair of mated individuals) resulted in interpretable negative effective population size. So in those years when younger individuals were less inbred - such as the 2000-year reference population - it is impossible to give any estimation (Figure 7).

Somewhat higher estimation was observed, when the effective population size calculation based on the individual inbreeding rates. This estimation method was also unreliable in cases where the pedigree was not informative enough, but after the stabilization of the total pedigree information (2002) gives a well understandable result (Figure 7).

### **Probability of gene origin**

Trends of the effective number of founders, the effective number of ancestors and the founder genome equivalents are shown in Figure 8. In the first few years of studied period (1993-1995) a drastic reduction happened in the effective number of the founders ( $f_e$ ) - and non-ancestors ( $f_a$ ), although this was not significant. The only exception was the founder genome equivalent ( $f_g$ ), for all other indicators the value halved between 1993 and 1995 (effective number of founders, ancestors and the ancestors responsible for the 50% of the genetic variance). For the Pannon white breed the applied mating system has been successful in the effective rate of inbreeding and in the scale of the genetic variance loss. These findings are supporting the need for continuous monitoring of the accumulated genetic load and for the genetic variance losses.



**Figure 7. Trends in the probability of gene origin**

$f_e$ : effective number of founders,  $f_a$ : effective number of ancestors,  $f_g$ : effective number of founder genom,  $f_{a50}$ : number of ancestors explaining the 50% of genetic variability

In the Pannon white rabbits the disproportionate use of the ancestors was clear from their genetic contribution. Although in the 2007 population the number of founders was 581, the 10 most influential ancestors' genetic contributions to the genetic variance was very high for the Pannon white rabbits born in 2007 (Table 10).

In the Pannon white breed the applied mating system has been successful in the inbreeding rate and the magnitude of genetic variance loss, although the population size decreased in 2006, which significantly reduced the genetic variability. These findings support the need for continuous monitoring of the accumulated genetic load and genetic variance losses.

**Table 10. The 10 most influential ancestors' genetic contribution (%) to the genetic variability of the Pannon White rabbits born in 2007**

Ancestor identification	Birth Year	Sex	Genetic contribution (%)
200538519	2005	buck	8.80
200109343	2001	buck	7.96
199406850	1994	buck	6.90
200212057	2002	buck	5.63
200506325	2005	doe	5.53
199901085	1999	buck	4.95
200518447	2005	buck	3.95
200506675	2005	doe	3.54
200448283	2004	doe	3.53
200413105	2004	buck	3.19

## 3.2 Genetic parameters and trends

### 3.2.1 Average daily gain (ADG), thigh muscle volume (TMV), hind part percentage (HPP) and dressing out percentage (DoP)

The  $h^2$  values for ADG (Table 11.) are practically identical to the previously estimated heritability estimate for the population (0.25, 0.2, 0.24, 0.27). The  $h^2$  value of TMV (which trait introduced as a selection criterion in 2004) was lower than that of the DoP (0.79) and cross sectional area of the m. Longissimus dorsi (L-value) (0.41). High heritability value was estimated for the HPP, which is very favourable, since the hind part of the rabbit contains the largest share of the valuable cuts. The DoP heritability was low and lower than the earlier estimated 0.47 heritability of the population. Magnitude of the random litter effects on the ADG and on the TMV was small.

**Table 11. The heritability values ( $h^2$ ) (standard errors in parentheses) of average daily gain (ADG), thigh muscle volume (TMV), hind part percentage (HPP) and dressing out percentage (DoP) and the magnitude of random litter effects ( $c^2$ ) (standard errors in parentheses)**

Trait	$h^2$	$c^2$
ADG (g/d)	0.30 (0.01)	0.13 (0.01)
TMV (cm <sup>3</sup> )	0.19 (0.02)	0.12 (0.01)
HPP (%)	0.59 (0.05)	0.07 (0.03)
DoP (%)	0.27 (0.04)	0.17 (0.05)

### The genetic correlations between the investigated traits

Table 12 shows the estimated genetic correlations between the analyzed traits.

**Table 12. The genetic correlations between the average daily gain (ADG), thigh muscle volume (TMV), hind part percentage (HPP) and dressing out percentage (DoP) (standard errors in parentheses)**

Trait	TMV (cm <sup>3</sup> )	HPP (%)	DoP (%)
ADG (g/d)	0.06 (0.06)	-0.08 (0.05)	-0.20 (0.08)
TMV (cm <sup>3</sup> )		0.59 (0.05)	0.01 (0.07)
HPP (%)			-0.16 (0.04)

Moderately strong and positive genetic correlation was found between the TMV and the HPP. It can be concluded that the selection for TMV indirectly increase HPP, which was also demonstrated in a previous study, where the

Pannon genotype showed the best results for HPP. ADG has a weak negative correlation with HPP and DoP. The following table (Table 13) shows the estimated annual genetic and phenotypic trends for the analyzed traits.

**Table 13. The estimated annual phenotypic and genetic progress in average daily gain (ADG), thigh muscle volume (TMV)**

Trait	Genetic progress	Phenotypic progress
ADG (g/d)	0.009 (NS)	0.331 (NS)
TMV (cm <sup>3</sup> /year)	1.909 (***)	1.852 (NS)

NS: not significant, \*\*\*: p <0.001

The estimated annual genetic trend in average daily gain traits is very small. Previously 0.64 g progress was estimated per year. It was not possible to compare to other authors' the results the progress in TMV and HPP. However, it should be mentioned here that in HPP only small amount of data was available which does not allow reliable estimation the genetic trends. The statistically proven genetic progress of TMV confirms the success of CT-aided selection.

### 3.2.2 Litter weight at 21-days of age

The litter weight at 21-days of age (LW21) has shown the highest  $h^2$  values at the fourth parity (Table 14).

**Table 14. The heritability values ( $h^2$ ) of litter weight at the 21-days of age (LW21), the thigh muscle volume (TMV) and average daily gain (ADG), and the magnitude of random litter effects ( $c^2$ ) by parity (standard errors in parentheses)**

Trait	Parity number	$h^2$	$c^2$
LW21 (kg)	1	0.14 (0.02)	0.04 (0.02)
	2	0.10 (0.02)	0.02 (0.02)
	3	0.08 (0.02)	0.07 (0.03)
	4	0.16 (0.03)	0.12 (0.04)
TMV (cm <sup>3</sup> )	1	0.21 (0.02)	0.13 (0.01)
	2	0.21 (0.02)	0.13 (0.01)
	3	0.21 (0.02)	0.14 (0.01)
	4	0.22 (0.02)	0.13 (0.01)
ADG (g/d)	1	0.30 (0.02)	0.33 (0.01)
	2	0.30 (0.02)	0.36 (0.01)
	3	0.31 (0.02)	0.35 (0.01)
	4	0.36 (0.02)	0.30 (0.01)

Random litter effects were very low for LW21 (Table 14), that's why just only a very small part of the maternal effect explain the total phenotypic variance of the litter weight at the age of 21-days.

### The genetic correlations between the investigated traits

Table 15 shows the estimated genetic correlations between the analyzed traits.

**Table 15. The genetic correlations and their standard errors (in parentheses) between the litter weight at the 21-days of age (LW21), the thigh muscle volume (TMV) and average daily gain (ADG) after each parity (standard errors in parentheses)**

Trait	Parity number	TMV (cm <sup>3</sup> )	ADG (g/d)
LW21 (kg)	1	-0.31 (0.14)	-0.02 (0.08)
	2	-0.33 (0.14)	0.23 (0.05)
	3	-0.83 (0.17)	0.15 (0.10)
	4	-0.86 (0.11)	0.10 (0.09)
TMV (cm <sup>3</sup> )	1		0.22 (0.10)
	2		0.10 (0.05)
	3		0.18 (0.10)
	4		0.14 (0.09)

Between the average daily gain and thigh muscle volume and between the average daily gain and the litter weight at the age of 21-days weak positive correlation was found (Table 15). Between the thigh muscle volume and the litter weight at the age of 21-days strong negative correlation was estimated at the third and fourth parity, which indicates that the applied CT selection may decrease LW21.

In the following table (Table 16) the traits' annual genetic and phenotypic trends are shown. The results suggest that the Pannon White breed's litter weight at the age of 21-days (by parity) the estimated genetic trend was significantly greater than the earlier reported values. It should be noted that this trait showed no phenotypic change in recent years, and the estimated

breeding values consistently show a positive residual values in the last few years, which shows the results should be treated with caution.

**Table 16. The estimated annual phenotypic and genetic progress in litter weight at 21-days of age (LW21) by parity and in average daily gain (ADG)**

Trait	Number of parity	Genetic progress	Phenotypic progress
LW21 (kg)	1	0.148 (***)	0.007 (NS)
	2	0.131 (***)	0.027 (***)
	3	0.113 (***)	0.038 (***)
	4	0.121 (***)	0.013 (NS)
ADG (g/d) (1991-2009)		0.304 (***)	0.583 (***)
ADG (g/d) (1991-2001)		0.308 (***)	0.389 (***)
ADG (g/d) (2002-2009)		0.102 (***)	0.336 (***)

NS: not significant, \*\*\*:  $p < 0.001$

### 3.2.3 Number of kits born alive and dead

The  $h^2$  values of the number of live and dead born kits in traits presented in Tables 17. In our study the received heritability values were below 0.1 justifying to the earlier estimates of this breed (0.06 and 0.05).

**Table 17. The heritability values ( $h^2$ ) of the number of kits born alive and dead (standard errors in parentheses)**

Trait	$h^2$
Number of live born kits	0.06 (0.01)
Number of dead born kits	0.02 (0.01)

The following table (Table 18) indicates the estimated annual phenotypic and genetic trends.

**Table 18. The estimated annual phenotypic and genetic trends in the number of born alive and dead kits**

Trait	Genetic progress	Phenotypic progress
Number of born alive kits (kit/year)	0.069 (***)	0.031 (**)
Number of dead born kits (kit/year)	-0.006 (***)	-0.003 (NS)

NS: not significant. \*\*\*:  $p < 0.001$ , \*\*:  $p < 0.01$

Because in this breed no selection was conducted for litter size the observed progress in number of kits born alive was surprising. The found improvement may be explained by the applied selection that increased the adult body weight.

### 3.2.4 Inbreeding depression

In the last two years of the evaluated period (2008, 2009) inbreeding coefficients for the does and litters, and total pedigree completeness for the does and litters are presented in Table 19.

**Table 19. The does' and litters' inbreeding coefficients and pedigree completeness for rabbits born in 2008 and in 2009 (standard errors in parentheses)**

Trait	Number	Mean
Dam inbreeding coefficient	118	6.3 (0.18)
Litter inbreeding coefficient	118	5.9 (0.25)
Dam pedigree completeness	118	12.1 (0.19)
Litter total pedigree information	118	12.6 (0.20)

The expected depressions for the number of kits born alive and dead were separately calculated for the dam and litter inbreeding. Results are shown in Table 20.

**Table 20. Effects of dam and litter inbreeding (per 10%) on the number of of kits born alive and dead**

Trait	Depression (dam)	Depression (litter)
Number of born alive kits	-0.17	-0.40
Number of born dead kits	0.19	0.07

The estimated depression was slight for the number of kits born alive. As expected inbreeding increased the number of born dead kits, but the magnitude of the increase was not substantial.

### 3.3 Stability of genetic parameters and breeding values

The estimated heritability of the average daily gain and the relative importance of random litter effects based on various part databases are shown in Table 21. The estimated  $h^2$  values for five years successive periods were low and stable. The relative importance of random litter effects was also small and stable. Both estimated were in accordance with the values previously estimated for the Pannon White breed.

The slight changes in the heritability estimates of ADG is likely happened due to change of the environmental effects and / or that some ca. 14% of the individuals changed in consecutive part database (per year). Since the Pannon White's pedigree closed in 1992, all individuals had ADG measurements, and pedigree information is also available, so it was expected that the genetic parameters will be accurate.

**Table 21. Based on various part database estimated heritability values ( $h^2$ ) and the magnitude of random litter effects ( $c^2$ ) of the average daily gain (standard errors in parentheses).**

Test period	$h^2$	$c^2$
2004-2008	0.28 (0.02)	0.14 (0.01)
2003-2007	0.28 (0.02)	0.15 (0.01)
2002-2006	0.29 (0.02)	0.15 (0.01)
2001-2005	0.27 (0.02)	0.16 (0.01)
2000-2004	0.28 (0.02)	0.16 (0.01)
2000-2008	0.28 (0.01)	0.15 (0.01)

In different part database the number and part of the common individuals, and the rank correlation between the breeding values based on the part databases are reported in Table 22.

**Table 22. Rank correlation of the breeding values in the average daily gain describing the breeding values' stability**

Joint database (period)	Number of common individuals	Proportion of the common individuals (%)	$r^1$	Significance
2004-2008; 2003-2007	20777	64.5	0.989	***
2004-2008; 2002-2006	16003	41.9	0.979	***
2004-2008; 2001-2005	12562	29.1	0.965	***
2004-2008; 2000-2004	6195	13.1	0.924	***

<sup>1</sup>: Spearman rank correlation coefficient between breeding values based on the most recent sub-dataset and breeding values based on other 5 year long sub-datasets. \*\*\* p <0.001

Rank correlations based on the part databases estimated breeding values' decreased over the years. Nevertheless. the coefficient was still high even in cases when the number of common records in part databases was small.

Next to the breeding value stability. the top hundred and thousand rabbits' breeding values stability was also tested. and the results shown in Table 23 and Table 24.

**Table 23. Breeding value stability of the common individuals in part database**

Joint database (period)	The top breeding value individuals	
	100	1000
2004-2008; 2003-2007	63	846
2004-2008; 2002-2006	67	863
2004-2008; 2001-2005	75	824
2004-2008; 2000-2004	55	761

**Table 24. The average breeding value differences in the common individuals of the part database in the top 100 and 1000 individuals**

Joint databse (period)	The top breeding value individuals	
	100	1000
2004-2008; 2003-2007	0.47	0.14
2004-2008; 2002-2006	0.35	0.10
2004-2008; 2001-2005	0.17	0.12
2004-2008; 2000-2004	0.46	0.24

Table 23 shows that contrary to the great stability of the genetic parameters (Table 21) and breeding values (Table 22) the number of rabbits ranked in the top position in both sub-datasets is relatively low. So the top ranked rabbits evaluated in the different databases showed significant differences in their average genetic value (Table 23).

## **4. CONCLUSIONS**

### **Genetic parameters and trends**

The negative genetic correlation (especially in case of the third and fourth parities) between CT-based selection and litter weight at age of 21 days reveals that the prolific performance of Pannon White breed may decrease significantly in the future.

The estimated phenotypic and genetic trends for the CT based muscle thigh volume parameter have clearly demonstrated the success of the breeding program of Pannon White breed.

### **Inbreeding degradation and pedigree analysis**

Because of the special pairing methods the level of inbreeding is low. it was on average about 6.3% in 2008 and 2009. The inbreeding rate is relatively low. approximately 0.5% per year.

The applied pairing system in the Pannon white breed has been effective for the inbreeding rate and for the scale of genetic variance loss. Although the livestock's population size decrease in 2006 has significantly reduced the genetic variability.

### **Stability of genetic parameters and breeding values**

The genetic parameters of the average daily weight gain were stable for different periods. The different part databases were inserted together and because of the decrease of the common individuals. the stability of the breeding values remains unchanged for the practice. From the various databases' most common individuals the rate of the ones with biggest breeding values is relatively low. This indicates if not entire database is

evaluated because of the limited computing capacity (instead of a defined term. periods. for example: 5 years). preliminary investigations must be done on the stability of breeding values.

## **5. NEW RESEARCH RESULTS**

1. In the Pannon white breed genetic parameters were estimated for the following traits: average daily gain, thigh muscle volume, litter weight at the age of 21 days, number of kits born alive and dead. Genetic trends were estimated for the same traits except for hind part percentage and dressing out percentage. Animal models were used for both procedures.
2. The effectiveness of the CT-based thigh muscle volume selection was justified.
3. The inbreeding depression of number of born alive and dead kits trait was determined related to 10% increase of the does' and litter's inbreeding coefficient.
4. The parameters describing structure and characteristic of the Pannon White population were defined.
5. From test database (5-year periods) based on the genetic parameters and their estimated breeding values for the average daily weight gain trait, their stability were justified.

## **6. SUGGESTIONS**

In order to improve the accuracy of measuring the thigh muscle volume the use of automated software evaluation would be required.

Since in rabbits the prolificacy is related to condition, it would be ideal to carry out the CT examinations on the total body on 10 weeks old rabbits. With this method the condition could be judged and this information could be taken account in the breeding program.

In the case of the growth of the inbreeding rate in the population those methods are recommended which have been recently developed in animal husbandry in order to minimize the inbreeding rate and maximize the selection progress.

In addition to this it is recommended to identify the harmful recessive genes of the ancestors in order to avoid these ancestors' partial inbreeding contribution to the new generations' inbreeding coefficients.

## 7. PUBLISHED IN THE SUBJECT OF THE DISSERTATION

### Papers published in foreign language peer-reviewed journals

**Gyovai, P.**, Nagy, I., Radnai, I., Bíróné-Németh, E., Szendrő, Zs. (2009): Heritability and genetic trends of number of kits born alive in a synthetic maternal rabbit line. *Ital. J. Anim. Sci.* 8: 110-112.

Nagy, I., Curik, I., Radnai, I., Cervantes, I., **Gyovai, P.**, Baumung, R., Farkas, J., Szendrő, Zs. (2010): Genetic diversity and population structure of the synthetic Pannon White rabbit revealed by pedigree analyses. *J. Anim. Sci.* 88: 1267-1275.

Nagy, I., Farkas, J., **Gyovai, P.**, Radnai, I., Szendrő, Zs. (2011): Stability of estimated breeding values for average daily gain in Pannon White rabbits. *Czech J. Anim. Sci.* (in press)

### Papers published in Hungarian language peer-reviewed journals

**Gyovai, P.**, Nagy, I. (2010): Impact of inbreeding for the fitness growth and morphology traits of various species (review). *Hungarian Journal of Animal Production* 59: 157–173.

## **Full-length conference papers in proceedings**

**Gyovai, P.**, Nagy, I., Gerencsér, Zs., Metzger, Sz., Radnai, I., Szendrő, Zs. (2008): Genetic parameters and trends of the thigh muscle volume in Pannon White rabbits. 9th World Rabbit Congress. Verona. 115-119.

**Gyovai, P.**, Vigh, Zs. (2008): Genetic parameters and trends of the thigh muscle volume in Pannon White rabbits. 20<sup>th</sup> Hungarian Conference on Rabbit Production. Kaposvár. 145-149.

Nagy, I., **Gyovai, P.**, Gerencsér, Zs., Matics, Zs., Radnai, I., Bíróné-Németh, E., Szendrő, Zs. (2009): Genetic parameters of carcass traits in Pannon White rabbit population 21<sup>st</sup> Hungarian Conference on Rabbit Production. Kaposvár. 73-77.

Nagy, I., **Gyovai, P.**, Radnai, I., Matics, Zs., Gerencsér, Zs., Donkó, T., Nagyné Kiszlinger, H., Szendrő, Zs: (2010). Genetic parameters of growth in vivo CT based and slaughter traits in Pannon White Rabbits. 22<sup>nd</sup> Hungarian Conference on Rabbit Production. Kaposvár. 115-117.

**Gyovai, P.**, Nagy, I., Gerencsér, Zs., Matics, Zs., Radnai, I., Donkó, T., Szendrő, Zs. (2010): Genetic parameters of growth in vivo Computer Tomography based and reproduction traits in Pannon white rabbits. In Proc. 9th World Congr. Genet. Appl. Livest. Proc.. Germany CD-ROM Commun. No. 343.

Nagy, I., **Gyovai, P.**, Radnai, I., Matics, Zs., Gerencsér, Zs., Donkó, T., Szendrő, Zs. (2010): Genetic parameters of growth in vivo CT based and slaughter traits in Pannon white rabbits. In Proc. 9th World Congr. Genet. Appl. Livest. Proc.. Germany CD-ROM Commun. No. 341.

### **Papers published in non scientific journals**

Vigh, Zs., **Gyovai, P.** (2008): Importance of pedigree analysis in animal breeding programmes. Agro Napló 1. 94-95.