THESES OF DOCTORAL (Ph.D.) DISSERTATION

UNIVERSITY OF KAPOSVÁR
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COMPARATIVE EVALUATION
OF COMPLEX BLUP MODELS
IN THE HUNGARIAN PIG BREEDING

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KAPOSVÁR

2008

1. ANTECEDENTS OF THE RESEARCH, OBJECTIVES

The pig breeding sector – beside cattle and poultry – is one the most important areas of the Hungarian animal breeding, the consumption of pork is traditionally high. However, together with worsening economical conditions the size of the Hungarian pig populations is continuously decreasing while quality requirements are becoming strict.

Under these conditions utilization of performance and quality enhancement has high importance. Improving selection efficiency and selection response can serve as a basic tool for which conducting reliable breeding value prediction is inevitable. Breeding value estimation meant Hazel selection indices in the past that were replaced with BLUP[1] procedure.

Field and station test (and reproduction) data has been collected for several years (which is a prerequisite of BLUP application). The necessary capacity and the appropriate softwares – for relatively simple models – were also available.

The National Institute for Agricultural Quality Control (OMMI) also made efforts for the adaptation of the BLUP procedure. Beside the Hazel selection indices BLUP indices were also provided for the breeders "unofficially" for several years before it was officially recognized from January the first 2008.

Improving the position of the Hungarian pig breeding sector requires domestic research providing information for the public about the breeding value estimation possibilities and utilization. The procedures based on the BLUP procedure help to improve the performances utilizing genetic resources increasing the profitability and competitiveness of the sector.

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[1] BLUP – Best Linear Unbiased Prediction

The main objective of this thesis is to work out complex BLUP-based models for the estimation of breeding values providing useful information for theoretical and practical use.

These tasks include

➢ the creation of simple and complex model variants for production traits (field, station, field+station)

➢ the estimation of the genetic parameters of the examined traits, prediction and analysis of the animals' breeding values, the effect of animals entering and leaving at the turns of years and that of models on genetic parameters and breeding values

➢ the determination of genetic trends

➢ the creation and examination of residuals based on different year groups and models

➢ the comparison of the applied models

➢ the effect of the complex model on genetic parameters and estimated breeding values

➢ the effect of the covariates on genetic parameters and estimated breeding values

The results provide useful information for the Hungarian breeders helping them understanding the main theoretical concepts connected with breeding value estimation and their practical application.

2. MATERIALS AND METHODS

2.1. General information

The objective of the thesis is the analysis of the various BLUP based models evaluating the largest Hungarian pig genotypes: **Hungarian Large White** (HLW), **Hungarian Landrace** (HLR) and Hungarian Large White×Hungarian Landrace **F1** (F1).

The analysis was made using the data of pigs born between 1994–2004. The used 11 year long period was separated to 5 year long periods (based on previous experience) that resulted sub datasets (94_98, 95_99, 96_00, 97_01, 98_02, 99_03, 00_04, 94_04[2]) with appropriate number of records (individuals) and factors, respectively.

2.2. Database

Data were available from the Hungarian Animal Breeding Database containing records for herds defined in the ***Hungarian Pig Performance Testing Code***: animal (**ANIMAL**) (individual identification, genealogy), station test (**ST**) (growth and slaughter performance), field test (**FT**) (self performance test of growing pigs), farrowing (**RP**) (reproduction perform-ance) in Dbase type files. The files were converted to Acces databases using own scripts.

By data conversion data filtering was made erroneous records were de-leted, individual identification codes were recoded by genotypes, additional (calculated) variables were added and structure of the data tables were also modified.

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[2] Joint (11 year long) investigation period

Beside the used variables the data tables contain substantial amount of additional data that can be used for further research. The developed scripts make appending the future records to the dataset possible, continuously updating the dataset. The number of records of the filtered datasets and the flow chart of creating data tables can be viewed in Table 1 and Figure 1, respectively.

Table 1. – Data frequency (number of individuals) between 1994–2004

Genotype	ANIMAL	ST	FT	RP[3]
HLW	323 917	18 048	300 748	360 286
HLR	143 404	7 784	138 860	136 318
F1	318 218	6 943	291 210	362 358
Sum	**785 539**	**32 775**	**730 818**	**858 962**
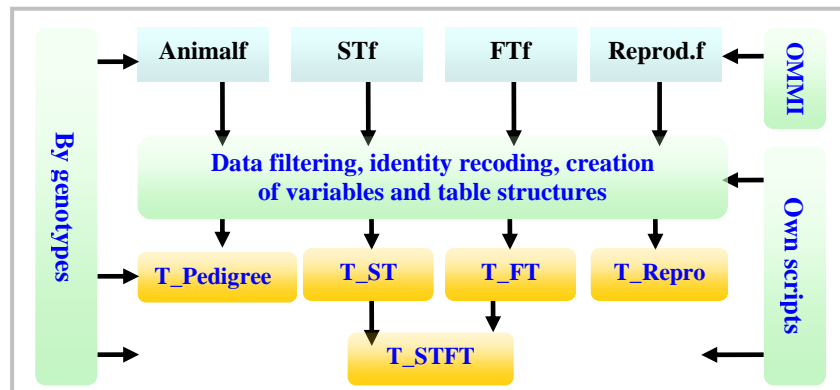
Figure 1. – Flow chart of creating data tables

2.3. Softwares

Evaluations were made using the following softwares:

➢ PEST[4] v2.3 [GROENEVELD (1990)] under Windows, Linux and Solaris for breeding value.

➢ VCE[5] v5.1.2 [KOVAC, GROENEVELD (2002)] under Windows, Linux

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[3] Number of farrowings
[4] PEST – Multivariate Prediction and Estimation
[5] VCE – Variance-Covariance Estimation

and Solaris estimating the (co)variance components necessary for PEST. The software requires substantial computing capacity.

➢ CheckPed used for pedigree and data check (for PEST). The original source code was written by Prof. Groeneveld that was substantially modified by myself using Fortran[6] 90 [LAHEY/FUJITSU FORTRAN 95 LF 95 PRO v5.7, LINUX PRO v6.1 (2002)], for Windows and Linux.

➢ "R" v2.3.1 ["R" v.2.3.1 SOFTWARE (2006)] was used for statistical analyses, evaluation of the various models, graphical presentation of the results, and estimation of genetic trends. Evaluation process was automatized by own written scripts.

➢ Microsoft Access 2000 was used for producing databases and to store the results of PEST and VCE softwares with the help of own written scripts.

2.4. Hardware

Estimation of (co)variance components (required for breeding value estimation) requires substantial computing capacity.

Table 2. – Characteristics of the used computers

Type	CPU	RAM	Operation system	Softwares
PC[7]	Intel Pentium 4 3.6 GHz	4 GB	Windows XP Linux	Pest, VCE, "R", Access, Fortran
PC	Intel Pentium 4 1.6 GHz	4 GB	Windows XP Linux	Pest, VCE, Access, Fortran
Notebook	Intel Centrino 1.6 GHz	512 MB	Windows XP Linux	Access, "R"
SunFire 15000	2x72ps Sun US-III+ 1200 MHz	2x192 GB	Solaris 9	Pest, VCE, Fortran

The size of the memory is critical but from the aspects of running time the processor performance is also important.

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[6] Fortran – a programming language purposely developped for solving problems of large computing capacity
[7] PC – 32 bit, Notebook – 32 bit, SunFire 15000 – 64 bit

Using large databases and complex models application of 32 bit computers is not satisfactory thus using 64 bit computer with dual processor is unavoidable. (The current version of VCE is 32 bit). The main characteristics of the used computers is given is Table 2.

2.5. Methodology of the evaluation process

The evaluation process was made by **genotype** and by **year groups** (within genotype):

➢ Models: the used model types: [ST (basic model), FT (basic model), ST-FT (joint model)] contain model types and variants differing in the use of covariates. Detailed presentation of the various models is given in chapter 3 (Results and Discussion).

➢ Statistical analysis: comprehensive analysis of ST, FT and RP data (descriptive statistics, correlation analysis, regression analysis etc) applying the "R" package. Results are stored both in text and in graphical format. The latter format can be either several PNG or one PostScript[8] file.

➢ Genetic parameter estimation was made for every model using VCE software. From the results the (co)variance components are necessary for predicting breeding values.

➢ Breeding values were predicted for every model and trait using PEST software.

➢ PEST and VCE results were both stored to MS Acces databases helping further process, using own written scripts.

➢ Evaluation of models: genetic parameters and breeding values were evaluated for every models based on statistical methods. The evalua-

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[8] PostScript – standard format that can be visualized by several softwares like Ghostscript under Windows and Linux capable of visualizing and printing PostScript and PDF (Adobe Portable Document Format) files.

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tion were carried out in two directions:

- ♦ According to year groups (94_98 ,…, 00_04) (longitudinal), comparing the results of a certain model across year groups.
- ♦ Within a certain year group comparing the results of the different models or model variations.

Model comparison for the same trait was made according to **Maximum Likelihood Ratio Test**, **MSE**, **Bias**, **correlation coefficient**, **Spearman rang correlation coefficient and normal error variance (of prediction)**.

➢ Genetic trends were estimated for every model. The results were presented graphically using own written scripts for "R" software.

The analysis, processing and evaluation were accomplished for all genotypes (HLW, HLR, and F1). Data presentation (due to its large size) was confined to **HLW**, **97_01** year group and a **predefined** model type.

3.   RESULTS AND DISCUSSION

3.1.   General information

Several models and model variations (within the model) were developed for all data types (**ST**, **FT**, **ST-FT**) differing in the use of covariates (***body weight***). The models were all ***animal*** models treating ***litter effects as random*** and all other effects as ***fixed***. Significance testing of the factors considered in the models was made with the ***GLM*** module of the ***"R"*** software. Evaluation was made by ***year groups*** (vertical) and by ***models*** (longitudinal).

3.2.   FT (Field test)

The objective of the field test is to predict the breeding values of the growing pigs based on performance test data. The traits in the models were: age (***AGE, day***), average backfat depth (***ABF, mm***), average daily gain (***ADG, g/day***), and lean meat percentage (***LMP, %***).

Presentation of the results is confined to model **4a**[9] and for **ADG** and **LMP**.

3.2.1.   Descriptive statistics for the traits and factors

The first step of the analysis was the descriptive statistics calculation of traits and factors considered in the models (Table 3).

It can be concluded that the mean **AGE** and **ADG** substantially decreased and increased, respectively with unchanged coefficient of variation (cv %).

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[9] see Table 4

Table 3. – Descriptive statistics of the traits considered in the models by year groups for HLR

| Trait	Parameter	Year group							
		94_98	95_99	96_00	97_01	98_02	99_03	00_04	94_04
AGE[10]	No records	74 012	71 463	66 642	65 369	59 700	54 253	46 235	132 004
	Mean	187.02	185.16	182.89	180.67	179.20	178.29	177.14	182.96
	Std	24.79	24.15	23.64	23.08	23.17	22.81	22.72	24.27
	CV (%)	13.25	13.04	12.93	12.77	12.93	12.80	12.83	13.27
ABF	No records	67 664	55 037	38 932	24 562	9 240	2 667	980	70 331
	Mean	18.26	18.19	18.08	17.94	17.79	17.42	16.77	18.22
	Std	1.82	1.85	1.86	1.93	1.97	2.00	1.85	1.84
	CV (%)	9.97	10.17	10.29	10.76	11.07	11.48	10.85	10.08
ADG	No records	74 166	71 703	66 973	65 757	60 126	54 683	46 531	132 548
	Mean	519.52	527.10	534.19	540.23	545.66	548.00	549.37	532.39
	Std	58.55	59.68	61.22	61.48	63.12	63.04	63.85	62.17
	CV (%)	11.27	11.32	11.46	11.38	11.57	11.50	11.62	11.68
LMP[11]	No records	10 886	21 730	33 387	46 794	55 486	53 432	46 332	68 062
	Mean	57.30	57.23	57.28	57.44	57.34	57.65	57.80	57.62
	Std	2.26	2.16	2.16	2.17	2.13	2.12	2.11	2.14
	CV (%)	3.94	3.77	3.77	3.78	3.71	3.68	3.65	3.72

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[10] The differences between the **AGE**, **ABF**, **ADG** mean values (adjacent) were significant ($p < 0.01$)

[11] The differences between the **LMP** mean values (except for 95_99 – 96_00) were significant ($p < 0.01$)

This may be explained by the 20% exchange (on average) of individuals between the successive year groups. The mean **ABF** and **LMP** values for the successive groups were practically the same. Correlation and distribution characteristics are depicted in Figures 2-3.
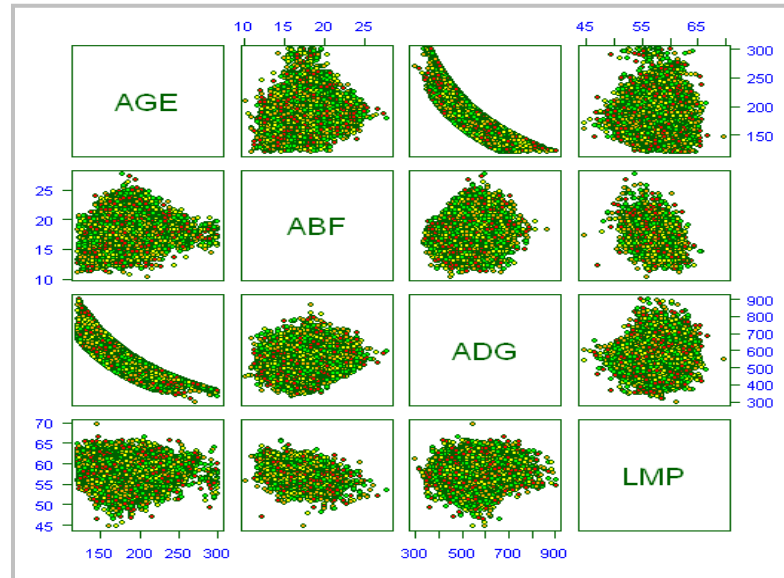
Figure 2. – Association between the model traits (1997–2001) for HLR
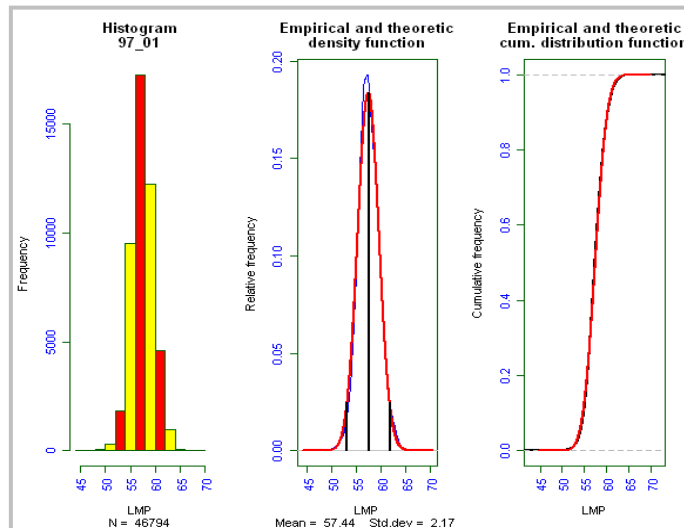
Figure 3. – Distribution characteristics of LMP (1997–2001) for HLR

Comparison of data by **herds** (Figures 4-5.) showed substantial differences between the **ADG** and **LMP** phenotypic values. The origin of these differences (genetics, environment) is unknown. Thus placing the factors into the breeding value estimation models and comparison of the results with the phenotypic values has high importance.
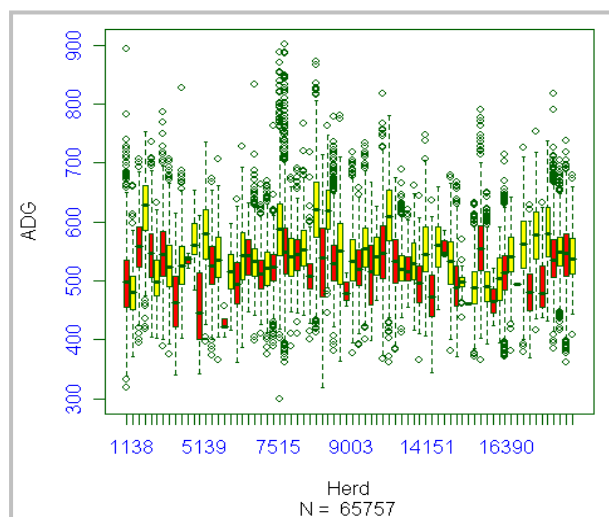

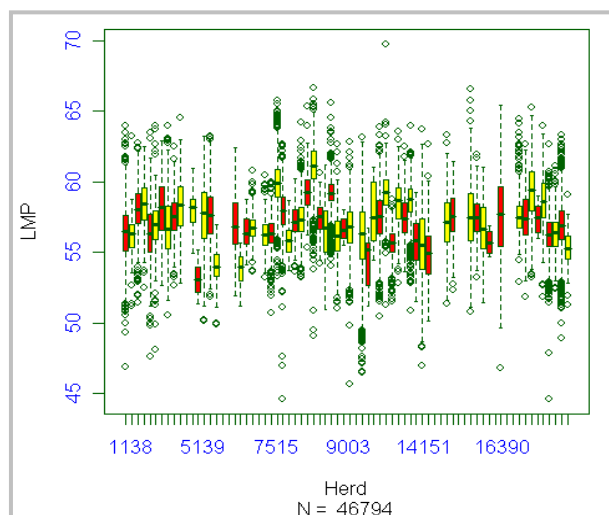**Figure 4. – Phenotypic values of ADG (1997–2001) for HLR by the herds**

Figure 5. – Phenotypic values of LMP (1997–2001) for HLR by the herds

3.2.2. *Applied models*

Based on the 4 examined traits **4** basic models were developed (Table 4), with several model variants.

Table 4. – The applied models

Model types	Trait	Weight	Year-Month	Sex	Herd	Litter	Animal
		C[12]	F[13]	F	F	R[14]	A[15]
1	AGE	x					
	ABF	x					
2a	AGE	x					
	LMP	x					
2b	AGE	x					
	LMP						
3a	ADG	x					
	ABF	x	X	X	X	X	X
3b	ADG						
	ABF	x					
4a	ADG	x					
	LMP	x					
4b	ADG						
	LMP	x					
4c	ADG						
	LMP						

Number of levels for the factors of the model variants is presented in Table 5. The number of additional individuals taken to the analysis from the pedigree (without performance records) for **ADG** [5406, 6660, 7067, 6530, 5917, 5475, 5034], [7 – 12%] for **LMP** [68686, 56633, 40653, 25493, 10557, 6681, 5233], [11 – 630%] for **AGE** [5560, 6900, 7398, 6918, 6343, 5860, 5330], [8 – 12%].

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[12] Covariate
[13] Fixed effect
[14] Random effect
[15] Animal effect

Table 5. – Number of levels for the factors in the examined year groups for HLR

Model type	Trait	Factor		94_98	95_99	96_00	97_01	98_02	99_03	00_04	94_04
		Common	Sex	2	2	2	2	2	2	2	2
			Year-Month	64	64	65	65	65	64	58	130
			Herd	91	91	84	74	70	59	53	97
1	**AGE**	Litter		26 889	26 855	25 468	24 567	22 897	21 232	18 092	49 641
	ABF	Animal		79 572	78 363	74 040	72 287	66 043	60 113	51 565	138 383
2a, 2b	**AGE**	Litter		26 886	26 871	25 498	24 604	22 959	21 299	18 141	49 706
	LMP	Animal		79 572	78 363	74 040	72 287	66 043	60 113	51 565	138 383
3a, 3b	**ADG**	Litter		26 894	26 879	25 509	24 613	22 963	21 302	18 144	49 717
	LMP	Animal		79 572	78 363	74 040	72 287	66 043	60 113	51 565	138 383
4a, 4b, 4c	**ADG**	Litter		26 894	26 879	25 509	24 613	22 963	21 302	18 144	49 717
	LMP	Animal[16]		79 572	78 363	74 040	72 287	66 043	60 113	51 565	138 383

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[16] Number of individuals was based on performance records plus pedigree

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3.2.3. *Genetic parameters of the examined traits*

The software applied for breeding value prediction (PEST) requires the (co)variance component structure of the random, animal and residual effects. Heritability and genetic correlation estimates (using different models) of the examined traits by **year groups** are presented in Table 6.

From the **64** runs **60** and **4** ended without and with warning, respectively but even the latter runs converged and the PEST could be used with the estimated components. Number of equations and CPU time were 194 000 and 22 minutes on average for the year groups and 377 000 and 90 minutes for the whole dataset (**94_04**).

Based on Table 6 it can be seen that the estimated values changed across the year groups regardless of the traits while they were stable within year groups across the models. For **ADG** tendencial differences were found between the model variants (3a, 4a), and (3b, 4b, 4c) because of the covariates considered in the former group. Standard errors of the estimates show the highly reliability of the estimates.

The results suggest that – supposing an unchanged **5 year long** year group structure – **conducting (co)variant component estimation with the successive year groups is advisable**.

The effects of covariates differed by year groups for **AGE**, [0.824 – 1.123] (decreasing values) and **ADG** [2.371 – 3.173] (increasing values); and were the same for **ABF** [0.094 – 0.103] and **LMP**. Within year group the models did not affect **AGE**, **ADG** and **ABF** influenced **LMP** (because of the covariates).

Table 6. – Genetic parameters of the examined traits [h^2 (diagonal elements), genetic correlation coefficient (above diagonal elements)] by year groups for HLR

Model type	Trait	Year group														
		94_98		95_99		96_00		97_01		98_02		99_03		00_04		94_04	
1	AGE	0.17	-0.22	0.16	-0.11	0.20	0.01	0.21	-0.04	0.24	-0.07	0.24	0.05	0.23	0.06	0.22	-0.22
	ABF		0.21		0.19		0.19		0.21		0.32		0.28		0.26		0.21
2a	AGE	0.16	0.09	0.17	0.14	0.20	0.06	0.22	0.10	0.24	0.11	0.23	0.14	0.23	0.06	0.22	0.06
	LMP		0.11		0.20		0.21		0.25		0.28		0.31		0.28		0.31
2b	AGE	0.16	0.09	0.17	0.14	0.20	0.05	0.22	0.10	0.24	0.10	0.23	0.14	0.23	0.05	0.22	0.06
	LMP		0.11		0.20		0.21		0.25		0.28		0.31		0.28		0.31
3a	ADG	0.17	0.23	0.17	0.10	0.19	-0.02	0.18	0.11	0.22	0.07	0.21	-0.06	0.20	-0.09	0.22	0.19
	ABF		0.20		0.19		0.19		0.28		0.32		0.28		0.27		0.21
3b	ADG	0.16	0.24	0.17	0.12	0.18	0.01	0.16	0.13	0.20	0.11	0.19	-0.05	0.19	-0.03	0.19	0.21
	ABF		0.21		0.19		0.19		0.26		0.32		0.27		0.26		0.21
4a	ADG	0.17	-0.06	0.17	-0.14	0.19	-0.04	0.19	-0.08	0.22	-0.08	0.21	-0.10	0.20	-0.02	0.21	-0.03
	LMP		0.11		0.20		0.21		0.25		0.28		0.31		0.28		0.30
4b	ADG	0.16	-0.05	0.16	-0.15	0.18	-0.07	0.18	-0.09	0.19	-0.08	0.19	-0.11	0.19	-0.03	0.19	-0.02
	LMP		0.11		0.20		0.21		0.25		0.28		0.31		0.28		0.31
4c	ADG	0.16	-0.05	0.16	-0.16	0.18	-0.07	0.18	-0.09	0.19	-0.08	0.19	-0.11	0.19	-0.03	0.19	-0.02
	LMP		0.11		0.20		0.21		0.25		0.28		0.31		0.28		0.31

3.2.4. BLUP AND BLUE analyses of traits and factors according to year groups (vertical analyses)

This type of analysis makes the evaluation of breeding values estimated for a certain trait within a year group for all models possible. Analysis consists of **all individuals** having **breeding values**.

For **LMP** (and **ANIMAL**) the histograms (Figure 6) of the models (3a, 4a), and (3b, 4b, 4c) indicate that the models are different.

The same conclusion can also be made for the distribution of breeding values. The characteristics of the linear function describing the association between the models are provided in Table 7 showing that the traits are partly independent from the models. For the (4b, 4c) models – no covariates are included for **ADG** – the predicted breeding values are identical. Slightly larger breeding values were predicted with models with covariates. The results show that although different models result somewhat different breeding values for the same individuals the ranks of the individuals will probably remain the same.

For **LMP** and **ANIMAL** the histograms (Figure 6) are identical although part of the models contains covariate (2a, 4a, 4b) unlike to others (2b, 4c). The same conclusion can be made for the distributions of the breeding values.

The parameters of the linear function: a = [0.99 – 1.00], (straight line with a slope of 45°, the breeding values predicted with the two models are identical), R = 1 (showing the independence of the traits from the models) describing the association between the models are provided in Table 7.

Based on these results **the breeding value of a certain animal for a given trait is the same using different models** thus the position of this animal in the rank remains the same. **AGE** and **ABF** are model independent

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the correlation between the breeding values predicted with the different models are **1**.

<p align="center">Table 7. – Association among the breeding values predicted with different models
for HLR (1997–2001)</p>

ADG – ANIMAL						LMP – ANIMAL				
x	y	y = a x + b		R		x	y	y = a x + b		R
		a	b					a	b	
3a	3b	0.89	-1.33	0.91		2a	2b	0.99	0	1
3b	4a	0.96	1.80	0.91		2b	4a	0.99	-0.01	1
4a	4b	0.90	-1.34	0.91		4a	4b	0.99	0	1
4b	4c	0.99	-0.01	1.00		4b	4c	1.00	0	1

3.2.5. *BLUP and BLUE analyses of traits and factors according to the models (longitudinal analyses)*

This type of analysis makes the evaluation of breeding values estimated for a certain trait and model for all year groups possible. Analysis consists of **all individuals** having **breeding values**.

For **ADG** (and **ANIMAL**) the histograms based on the different year groups are only slightly different. Characteristics of the breeding value distributions are the same (Figure 7).

In the figure the individuals are shown on the horizontal axe according to the increasing birth dates. Within a certain year group the zone of the individuals with positive breeding values became wider with the progressing years and the same tendency was observed for all year groups.

Examining the individuals of high (> 50) and low (< -40) breeding values it can be realized that most of these individuals can be located in few herds having distinct characteristics (compared to other herds).

For **LMP** (and **ANIMAL**) the histograms (Figure 7) based on the different year groups are only substantially different.

With the progressing years breeding value range became wider (to both directions).

Examining the individuals of high (> 2) and low (< -2) breeding values it can be realized that most of these individuals can be located in few herds having distinct characteristics (compared to other herds).

Parameters of the linear function describing the association among the breeding values predicted for different year groups are provided in Table 8.

Table 8. – Association among the breeding values predicted with model 4a for HLR (different year groups)

ADG – ANIMAL					LMP – ANIMAL				
x	y	y = a x + b		R	x	y	y = a x + b		R
		a	b				a	b	
94	95	0.82	-1.61	0.88	94	95	1.24	0	0.75
95	96	0.86	-0.49	0.84	95	96	0.88	0.01	0.88
96	97	0.69	-1.84	0.83	96	97	1.02	0.02	0.88
97	98	0.86	-2.88	0.87	97	98	1.04	-0.04	0.93
98	99	0.77	-1.09	0.90	98	99	0.90	-0.03	0.90
99	00	0.73	-0.07	0.88	99	00	0.70	-0.07	0.91

Viewing the traits through the other models independence of the traits from the models can be seen (**ADG**: 3a, 3b, 4a, 4b, 4c; **LMP**: 2a, 2b, 4a, 4b, 4c; **AGE**: 1, 2a, 2b; **ABF**: 1, 3a, 3b)
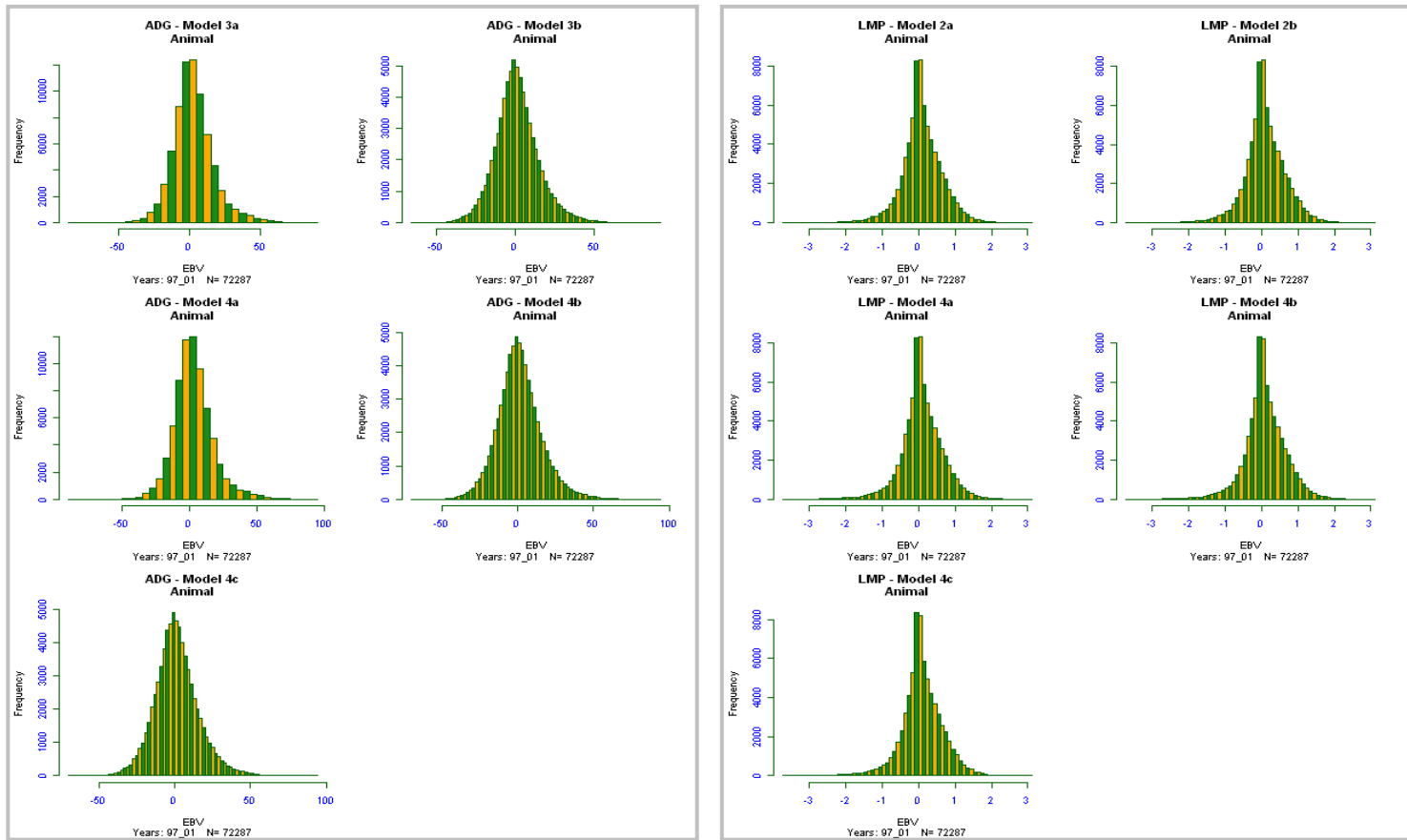
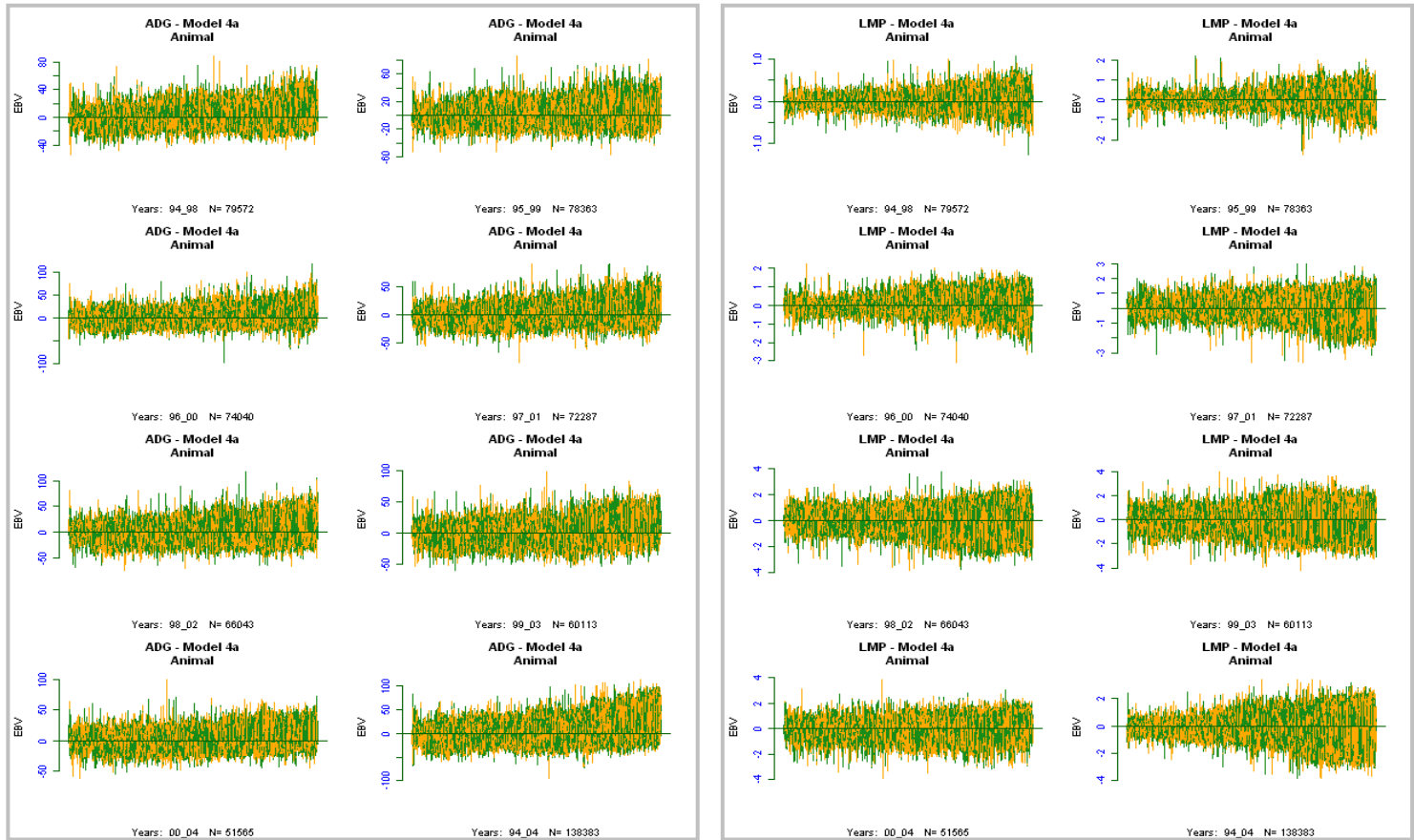**Figure 6. – Histograms of breeding values (predicted by different models) for HLR (1997–2001)**

Figure 7. – Distribution of breeding values (estimated by model 4a) for HLR (different year groups)

3.2.6. *Genetic trends*

The genetic trends (Figure 8) were constructed according to the **breeding values** (performance record or pedigree) of **all animals**.
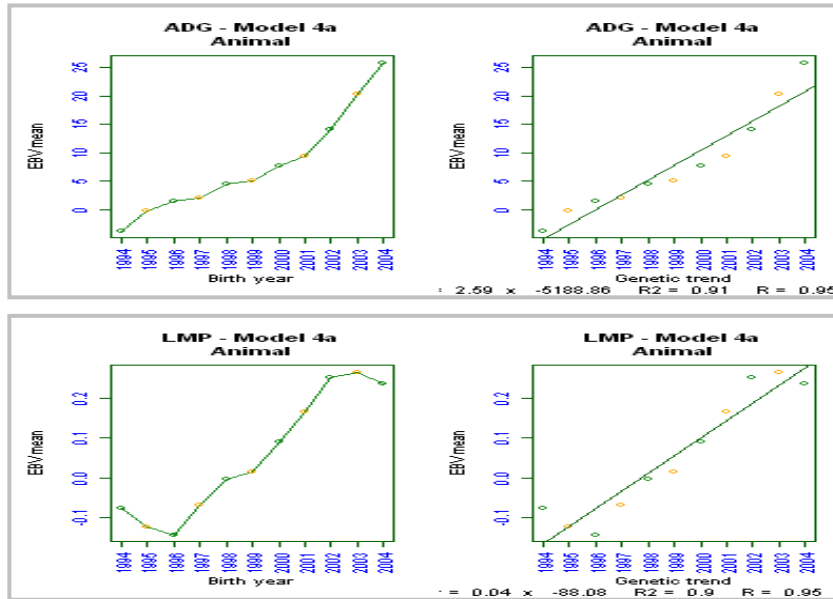

Figure 8. – Genetic trends for HLR (model 4a)

For **ADG** the trends of the models containing covariates (3a, 4a) were identical: $y = 2.59\ x - 5188.86$; $R = 0.95$ different trends were observed for the models that do not contain covariate (the trends were identical within the model group): $y = 1.81\ x - 3680.02$; $R = 0.94$. The average rate of improvement was 2.59 or 1.81 (g/day)/year, respectively. Starting the trend from 1997 or 1998 the following parameters were found: $y = 3.27\ x - 6537.86$; $R = 0.96$; $y = 3.60\ x - 7207.51$; $R = 0.96$, respectively. Substantial increase of the improvement rate is clearly visible justifying more the genetic basis of the phenotypic values.

For **LMP** the genetic trend was identical for all models (model independent): $y = 0.04\ x - 88.08$; $R = 0.95$ the average improvement rate was 0.04 %/year. Starting the trend from 1997 or 1998 the following parameters

were found: y = 0.05 x − 101.39; R = 0.96; y = 0.04 x − 98.53; R = 0.94 thus the rate of improvement was stable.

For **AGE** the genetic trend was identical for all models (model independent): y = -0.86 x + 1714.52; R = 0.96 the same phenomenon was observed for **ABF**: y = -0.03 + 46.54; R = 0.89.

The trends do not change considering the breeding values only of animals with **performance records**.

3.2.7. *Analyses of residuals according to year groups (vertical analyses)*

Residual values $\hat{y} - y$ [17] were estimated (with PEST) for all animals with performance records then they were placed to ACCES databases by **genotypes** and **year groups**.

For **ADG** the histograms (frequency of residuals) of the models (3a, 4a), and (3b, 4b, 4c) show different characteristics that may be caused by the covariates (3a, 4a). The differences between the model groups are clearly visible on Figure 9 (measured and residual values).

Regardless of the two model types negative residuals were found until 400 g/day thus BLUP "under-estimated"; positive and negative residuals were observed between [550 – 700] g/day; mixed "under and over-estimation" while positive residuals were found above 700 g/day which means that BLUP "over-estimated".

The association between the measured and predicted values also describes the differences between the two model groups.

Strong linear association was found for every model but the observed values were the highest for the models (3a, 4a) with covariates: R = 0.94 > R = 0.89, justifying their use.

---

[17] $\hat{y}$ – predicted value, y – observed value

Characteristics of the linear association were different in the model groups (3a, 4a) slope: 0.78 (of the parallel lines), intercept: [115.74; 114.13]; (3b, 4b, 4c) slope: 0.65 (of the parallel lines), intercept: [189.24; 186.22; 186.24]. These parameters indicate the model independence and stability of the traits.

The association between the predicted values of the different model pairs was strong: R = [0.96 – 1], slope of the lines: [0.83; 1.09; 0.84; 0.99]; intercept: [87.12; -50.50; 85.46; 0.02].

For the first 3 model the models of **ADG** contained covariates unlike to the last model (the association between the models can be described with the function of y = x, thus the predicted values were identical).

For **LMP** the histograms show the same characteristics and the same phenomenon was observed for the measured and residual values (Figure 9).

BLUP "under-estimated" until 53% (LMP), mixed "under and over-estimation" of BLUP was observed between 53-57% (LMP) while BLUP "over-estimated" above 63% (LMP).

The identical linear association: R = 0.91, and slope: 0.69 and the almost identical intercepts: [17.64; 17.75; 17.64; 17.71; 17.76] indicate the model independence and stability of the trait.

The association between the predicted values of the different model pairs: R = 1, the slope of the lines: 0.99 (practically 45º), and the intercepts: [0.16; -0.08; 0.10; 0.04] shows the direct proportionally between predicted values of the models, thus for a given trait the predicted values were identical.

3.2.8. *Analyses of residuals according to models (longitudinal analyses)*

The shape of the histograms were practically identical for **ADG** and it was not sensitive to the year group changes (cca 20% of the individuals

were replaced). The previous conclusions for measured and predicted values are valid independently of the year groups.

Identical association were found between the measured and predicted values: R = [0.93 – 0.95] (Figure 10). The type of the linear association was the same in each year group, the slope of the parallel lines were 0.80, the intercepts starting from the year group 94_98 were [121.63; 110.40; 107.90; 114.13; 106.78; 108.59; 109.45]. This means that if any individual occurs in several year groups [2, 3, 4 or 5] than the predicted values of this individual can be different in these year groups. Nevertheless, because of the strong association changing the year groups the rank of the common individuals probably will change only slightly.

The strength of the association between the predicted values of the different year groups was R = 1. The slope of the parallel lines was 1.00 (45°) and starting from the year group 94_98 the intercepts were: [-9.80; -4.56; 1.51; -3.65; 2.44; 1.11].

For **LMP** (Figure 10) indicates strong association for every year group R = [0.86 – 0.92]. The characteristics of the linear association were the same in the different year groups: parallel lines with a slope of 0.70 and with intercepts (starting from 94_98) [19.90; 18.23; 18.81; 17.64; 16.85; 17.13; 17.21].

The strength of association between the predicted values of the different year group was R = 1. The slope of the lines in all year groups was 1.0 (45°) with intercepts (starting from 94_98) [0.12; 0.33; -0.31; -0.01; 0.22; 0.53].

ADG and **LMP** were also evaluated in the models of (3a, 3b, 4b, 4c) and (2a, 2b, 4b, 4c), respectively.

The conclusions made in accordance with model **4a** are also valid for all other models justifying the strong stability and model independence of the trait.
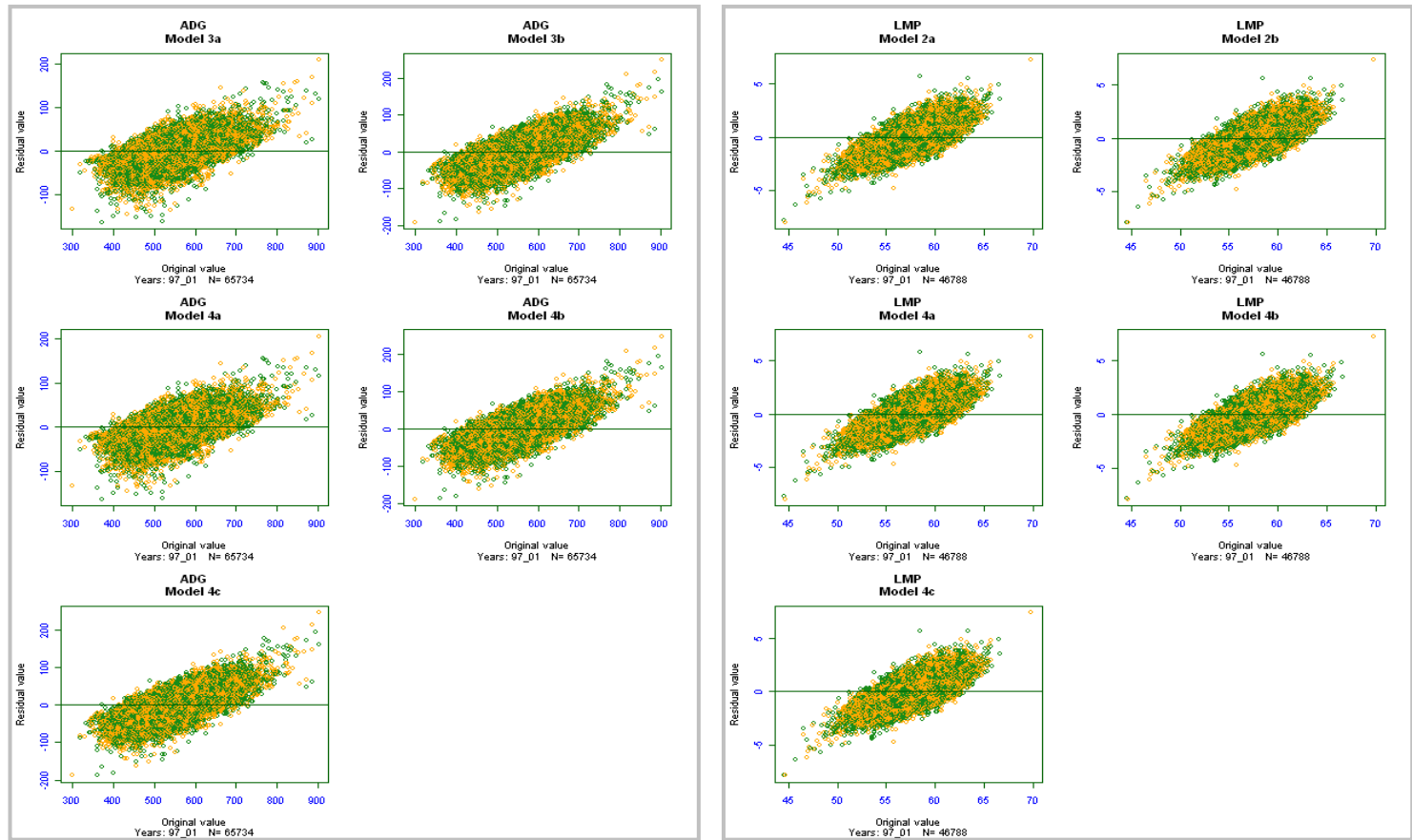
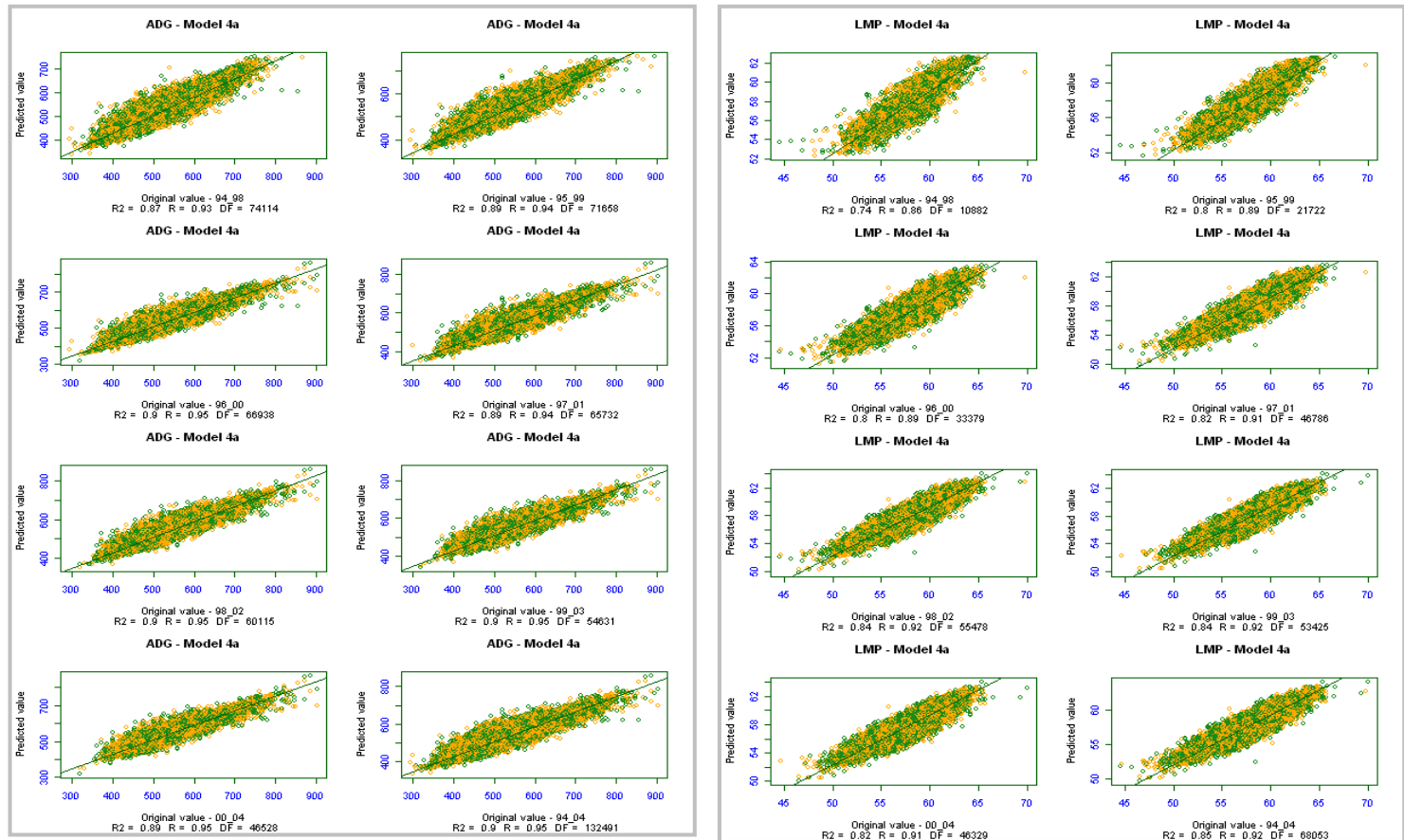**Figure 9. – Association between the measured and residual values of different models for HLR (1997–2001)**

Figure 10. – Association between the measured and predicted values of different models for HLR (1997–2001

3.2.9. Comparison of the applied models

The examined **4** traits were evaluated through several model variants and the results were partly model dependent. This raises the question if there is any model giving the "best result" for a given trait?

According to the most widely used **MSE** method for the trait of **ADG** (**97_01**) significant differences were observed between the models [3a and (3b, 4b, 4c)], [3b and (4a, 4b, 4c)], [4a and (4b, 4c)] ($p < 0.001$); (3a, 4a) ($p < 0.05$) for **LMP** no significant differences were found. The correlations and rang correlations between the breeding values varied between [0.95 – 1].

Table 9. – Model comparison through MSE for HLR (1994–2004)

Year-group	ADG					LMP				
	3a	3b	4a	4b	4c	2a	2b	4a	4b	4c
94_98	482	768	494	769	769	1.38	1.38	1.38	1.38	1.38
95_99	443	775	441	772	772	1.02	1.02	1.02	1.02	1.02
96_00	429	805	426	801	801	1.04	1.04	1.04	1.04	1.05
97_01	474	891	460	863	863	0.93	0.94	0.93	0.93	0.94
98_02	428	850	428	849	849	0.83	0.84	0.83	0.83	0.84
99_03	442	886	443	885	885	0.80	0.81	0.80	0.80	0.81
00_04	470	918	470	919	919	0.88	0.88	0.88	0.88	0.88
94_04	442	778	442	778	778	0.79	0.79	0.79	0.79	0.79

Changing values can be seen with the successive year groups but within a given year groups the tendencies described above for the traits remained the same.

Correlations and rang correlations were [0.93 – 0.95], [0.85 – 0.92] for **ADG** and **LMP**, respectively.

Based on the results the suggested models for practical utilization are those that are defined by **AGE**, **LMP** and **ADG**, **LMP** trait pairs.

3.3. ST (growth and slaughter performance)

The objective of ST is to determine of the parents' breeding values based on the progeny breeding values. Using a sire or dam model the determination of the breeding values is a direct process. The pedigree information is generally ignored in these models thus the relationship information is not used.

In the present study the breeding values of the progenies (and parents) were calculated by evaluating the progenies' performance at ST.

The traits in the models were: days of test (**DOT**, day), total feed consumption (**FEED**, kg), proportion of valuable cuts (**VC%**), weight of valuable cuts (**VC**, kg), brutto daily gain for the fattening period (**BDG**, g), feed conversion ratio (**FCR**, g), meat quality score (**MQ**, score).

3.3.1. Descriptive statistics for the traits and factors

The descriptive statistics calculation of traits and factors given at chapter 3.2.1. was also accomplished for ST. The mean **FEED** and **FCR** continuously decreased with the successive year groups while **VC** and **BDG** increased, with unchanged coefficient of variation (cv %). No observable tendencies were received for **DOT** and **VC%** that could be practically utilized.

Contrary to the favourable increasing mean **MQ** (together with increasing cv %), considering this trait in the model raises several problems.

The histogram and distribution of **MQ** suggest that in its present form the trait is not suitable for placing to the model. (The traits consists of discrete values [0 − 10], values of [8 − 10] totalled up to [85 − 88 %], while [87 − 90%] of the subjective sensory judgement score [0 − 3], was 3).

3.3.2. Applied models

Based on the 7 examined traits **6** basic models were developed (Table 10), with several model variants.

Table 10. – The applied models of ST

Model type	Factor / Trait	Weight	Year-Month	Sex	Herd	Station	Litter	Animal
		C	F	F	F	F	R	A
1a	DOT FEED VC%	x x x	X	X	X	X	X	X
1b	DOT FEED VC%	x x	X	X	X	X	X	X
2a	DOT FEED VC% MQ	x x x x	X	X	X	X	X	X
2b	DOT FEED VC% MQ	x x	X	X	X	X	X	X
3	DOT FEED VC	x x x	X	X	X	X	X	X
4	DOT FEED VC MQ	x x x x	X	X	X	X	X	X
5a	BDG. FCR VC%	x x x	X	X	X	X	X	X
5b	BDG FCR VC%		X	X	X	X	X	X
6a	BDG FCR VC% MQ	x x x x	X	X	X	X	X	X
6b	BDG FCR VC% MQ		X	X	X	X	X	X

Table 11. – Number of levels for the factors (ST) in the examined year groups for HLR

Model type	Trait	Factor		94_98	95_99	96_00	97_01	98_02	99_03	00_04	94_04
		Common	Sex	2	2	2	2	2	2	2	2
			Year-Month	61	63	62	62	62	62	58	129
			Herd	52	53	46	44	42	41	32	60
			Station	7	7	8	7	7	7	8	9
1a, 1b	DOT[18]										
2a, 2b	FEED										
3	VC%	Litter		2 350	2 254	2 029	1 881	1 695	1 446	1 254	3 973
4	VC	Animal[19]		7 870	7 650	7 007	6 571	6 044	5 127	4 375	13 988
5a, 5b	BDG										
6a, 6b	FCR	Animal[20]		(4 444)	(4 318)	(3 910)	(3 643)	(3 285)	(2 802)	(2 398)	(7 571)
	MQ										

[18] Within a given year group **litter** and **animal** values were identical for all models
[19] Number of individuals was based on performance records plus pedigree
[20] Number of individuals was based on performance records

Number of levels for the factors is presented in Table 11. The number of additional individuals taken to the analysis from the pedigree [3 426, 3 332, 3 097, 2 928, 2 755, 2 325, 1 977], that is [77 – 84 %].

3.3.3. *Genetic parameters of the examined traits*

From the **80** VCE runs **73** and **7** ended without and with warning, respectively but even the latter runs converged (number of iterations varied between [39 – 151]. Number of equations and CPU time were 40 000 and 10 minutes on average for the year groups and 70 000 and 30 minutes for the whole dataset (**94_04**). Number of unsuccessful PEST runs was **17** showing that although the (co)variance components could be estimated they were incorrect.

The heritability estimates show no tendency and vary in a given interval, they were **stable** within year groups **across the models**. The estimated values were the following: **DOT** [0.40 – 0.54], **FEED** [0.25 – 0.47], **VC%** [0.64 – 0.71], **VC** [0.56 – 0.63], **BDG** [0.28 – 0.50], **FCR** [0.23 – 0.45], **MQ** [0.06 – 0.21]. Standard errors of the estimates show the high reliability of the estimates.

The effects of covariates differed by year groups without any tendency for **DOT** [-0.007 – 0.268]; **FEED** [1.440 – 1.916], **VC%** [-0.058 – 0.041], **VC** [0.364 – 0.388], **BDG** [7.333 – 9.644], **FCR** [-11.111 – (-6.526)], **MQ** [-0.010 – 0.019]. Within year group the models had no effect the values changed without any tendency.

3.3.4. *BLUP and BLUE analyses of traits and factors according to year groups (vertical analyses)*

The results are presented for year group **97_01** for **ANIMAL**. The histograms and breeding value distributions of **DOT** and **FEED** were slightly different for the models (3, 4) compared to others (1a, 1b, 2a, 2b, 3, 4). This

can probably be explained that the first group used **VC** while the latter group used **VC%**.

Characteristics of the linear association describing the 4 examined traits: y = 0.99 x + 0.00; R = 1. The association can be treated as a function: y = x, breeding values estimated with the two models are identical the traits were model independent. For **BDG**: y = 0.99 x – 0.14; R = 0.99, **FEED**: y = 0.99 x + 0.16; R = 0.99 the traits were model independent, **MQ** was model dependent.

3.3.5. *BLUP and BLUE analyses of traits and factors according to the models (longitudinal analyses)*

The results are presented for model **4** for **ANIMAL**. The histograms show slight changes for the successive year groups, the same phenomenon was observed for the distribution of breeding values.

The association between the breeding values estimated for the different year groups is presented in Figure 11.

The slope of the linear functions describing the association: [1.01; 0.95; 0.89; 0.82; 0.91]; [1.17; 0.99; 0.83; 0.73; 0.89], the intercepts: [0.38; -0.02; 0.18; 0.24; 0.17]; [0.59; -0.17; 0.18; 0.33; 0.24], R = [0.93; 0.91; 0.91; 0.92; 0.92]; [0.90; 0.92; 0.92; 0.89; 0.90] for **DOT**, and **FEED**, respectively.

Based on the results the 25-30% of the population is replaced by the changing year groups (performance records + pedigree), the performance of the outgoing and incoming individuals varied in a small range and the ranks of the common individuals mainly remain the same.
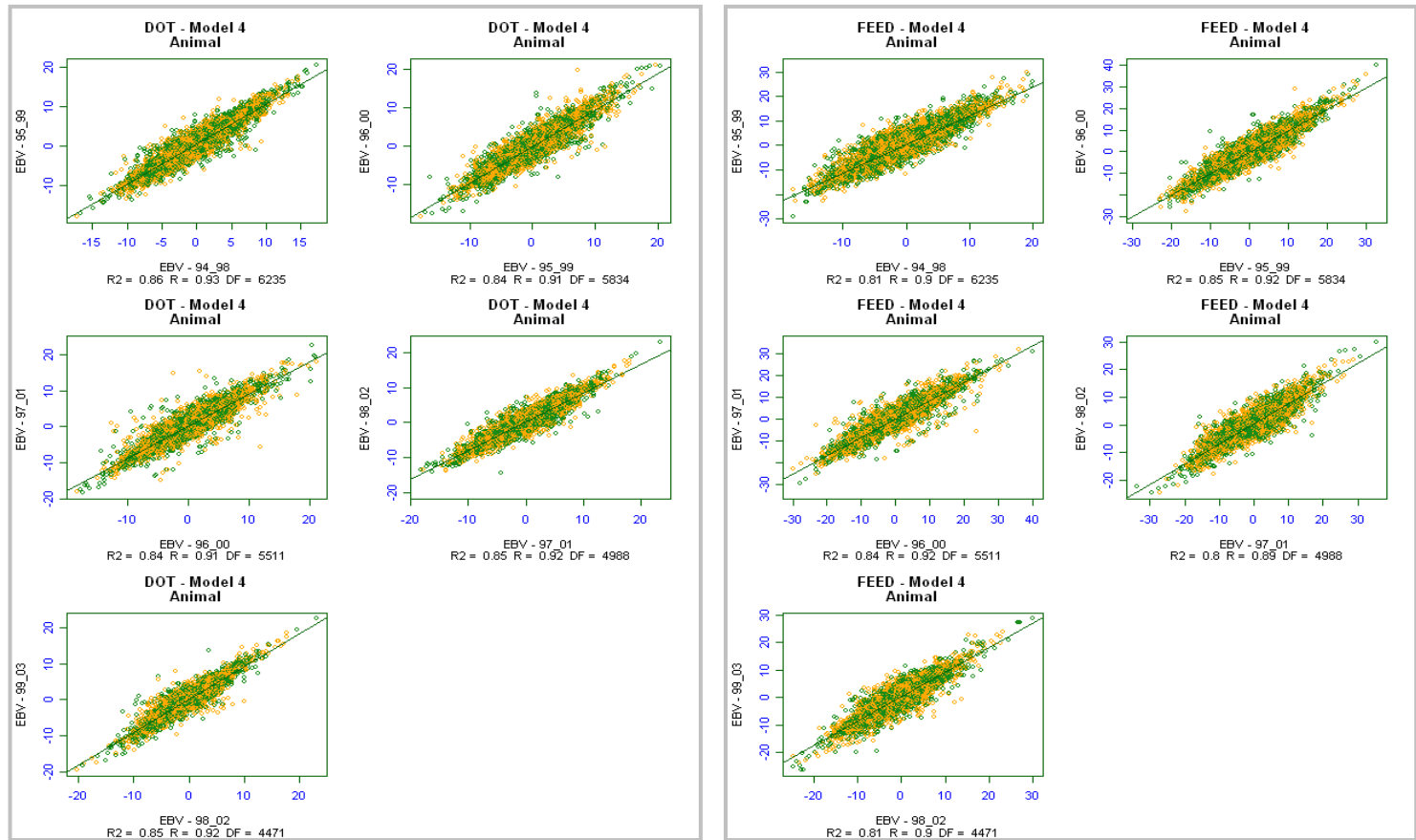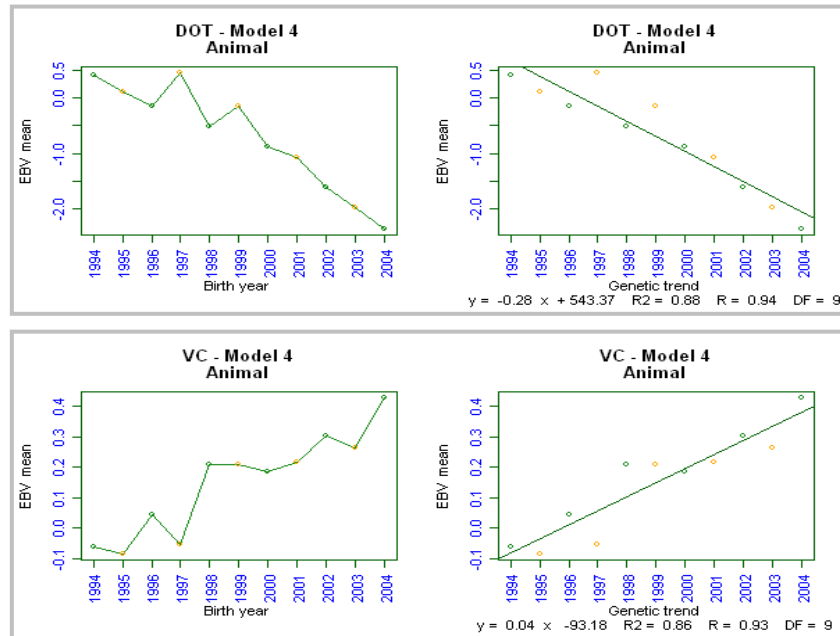
Figure 11. – Association between the breeding values of model 4a for HLR (different year groups)

3.3.6. *Genetic trends*

The genetic trends (Figure 12) were constructed according to the **breeding values** (performance record or pedigree) **all animals**.

Figure 12. – Genetic trends for HLR (model 4 – ST)

For **DOT** (models 1a, 1b, 2a, 2b, 3, 4) the genetic trends were parallel lines (Figure 12), the slope and intercepts were 0.28 and [553.49; 552.68; 552.78; 551.88; 544.02; 543.37], respectively, R = 0.94. The average rate of improvement was -0.28 day/year.

For **VC** (models 3, 4) the genetic trends were also parallel lines, the slope and intercepts were 0.04 and [-92.99; -93.18], respectively, R = 0.93. The average rate of improvement was 0.04 kg/year.

For **FEED** (models 1a, 1b, 2a, 2b, 3, 4) the genetic trends were parallel, the average rate of improvement was -0.48 kg/year, the intercepts were [950.45; 950.82; 925.13; 925.09; 954.19; 928.97], R = 0.90.

For **VC%** (models 1a, 1b, 2a, 2b) – the models contain **DOT** and **FEED** – slope of the trends was 0.05, the intercepts were [-117.02;-116.34;

-116.36; -115.69], R = 0.94 while different trends were received for models containing **BDG** and **FCR** with a slope of 0.07 and intercepts: [-145.62; -145.85; -146.15; -146.15], R = 0.95. In the first case the average rate of improvement was lower (0.04 and 0.07 %/year).

For **MQ** (models 2a, 2b, 4, 6a, 6b) the genetic trends were parallel, the average rate of improvement was 0.01 score/year, the intercepts were [-24.66; -24.64; -24.93; -21.03; -21.92], R = 0.93.

For **BDG** (models 5a, 5b, 6a, 6b) the genetic trends were different [y = 1.66 x − 3317.73; y = 1.73 x − 3455.11; y = 1.60 x − 3197.17; y = 1.68 x − 3370.36], the average rate of improvements were [1.66; 1.73; 1.60; 1.68 g/year], R = 0.89.

For **FCR** (models 5a, 5b, 6a, 6b) the genetic trends were different [y = -3.15 x + 6280.31; y = -3.21 x + 6405.64; y = -2.75 x + 5485.34; y = -2.84 x + 5665.55], the average rate of improvements were [-3.15; -3.21; -2.75; -2.84 g/year], R = 0.89.

3.4. ST–FT (joint model)

Some of the traits and factors evaluated in **ST** and **FT** were chosen and evaluated in a joint model.

The following traits were considered: days of test (**DOT,** day), total consumed feed (**FEED**, kg), weight of valuable cuts (**VC**, kg), meat quality score (**MQ**, score), age (**AGE**, day), average daily gain (**ADG**, g/day), and lean meat percentage (**LMP**, %).

3.4.1. Applied models

Using the 7 examined traits **4** basic models were developed (Table 12) with several model variants.

The level of factors is presented in Table 13, extended with **LITTER** and **ANIMAL**. The table demonstrates the expanding characteristics of

animal and **litter** effects as a result of the increased relationship matrix. Number of records of **ST** is approximately 8-10% (for animal and litter effects) that of the **ST–FT**.

This indicates that depending on the year group cca 50-76 thousand individuals receive breeding values for **ST** traits that were not included in the **ST** evaluation.

This number is only 3-5 thousand for **FT**. Therefore for a given trait evaluating the association of the genetic parameters and predicted breeding values by the **ST**, **FT** and **ST–FT** runs has high importance.

3.4.2. *Genetic parameters of the examined traits*

From the **56** VCE runs **50** and **6** ended without and with warning, respectively but even the latter runs converged (number of iterations varied between [27 − 37]. The PEST converged. Number of equations and CPU time were 610 000 and 4 hours on average for the year groups and 1 184 000 and 20 hours for the whole dataset (**94_04**).

The standard errors of the estimated heritabilities for **FT** traits were the same as those observed at **FT** runs, while the same order of magnitude but lower values standard errors were received for **ST** traits compared to **ST** runs (due to the increased relationships). The estimated heritabilities for **FT** traits were the same as those observed at **FT** runs, while lower but more precise heritabilities (with lower standard errors) were received for **ST** traits compared to **ST**.

The effects of covariates (values and characteristics) for **FT** traits were the same as described for **FT**. For **ST** traits the values changed but the characteristics remained the same as described for **ST**. The effects differed by year groups (they were more stable because of the increased relationships) while they were stable within year.

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Table 12. – The applied models of ST-FT

Model type	Trait	Weight	Year-month ST	Year-month FT	Sex	Herd	Station	Litter	Animal
		C	F	F	F	F	F	R	A
1	DOT	X	X				x		
	FEED	X	X				x		
	VC	X	X		X	X	x	X	X
	AGE	X		x					
	LMP	X		x					
2a	DOT	X	X				x		
	FEED	X	X				x		
	VC	X	X		X	X	x	X	X
	MQ	X	X				x		
	AGE	X		x					
	LMP	X		x					
2b	DOT	X	X				x		
	FEED	X	X				x		
	VC	X	X		X	X	x	X	X
	MQ		X				x		
	AGE	X		x					
	LMP	X		x					
3a	DOT	X	X				x		
	FEED	X	X				x		
	VC	X	X		X	X	x	X	X
	MQ	X	X				x		
	ADG	X		x					
	LMP	X		x					
3b	DOT	X	X				x		
	FEED	X	X				x		
	VC	X	X		X	X	x	X	X
	MQ		X				x		
	ADG			x					
	LMP			x					
4a	DOT	X	X				x		
	FEED	X	X				x		
	VC	X	X		X	X	x	X	X
	ADG	X		x					
	LMP	X		x					
4b	DOT	X	X				x		
	FEED	X	X				x		
	VC	X	X		X	X	x	X	X
	AGE			x					
	LMP	X		x					

Table 13. – Number of levels for the factors (ST–FT) in the examined year groups for HLR

Model type	Trait	Faktor		94_98	95_99	96_00	97_01	98_02	99_03	00_04	94_04
			Sex	3	3	3	3	3	3	3	3
		Common	Year-Month ST	61	63	62	62	62	62	58	129
			Herd	94	92	84	74	70	59	53	99
			Station	7	7	8	7	7	7	8	9
			Year-Month FT	64	64	65	65	65	64	58	130
1a	DOT[21]	FT[22]		26 894	26 879	25 509	24 613	22 963	21 302	18 144	49 717
2a	FEED	(ST)		(2 350)	(2 254)	(2 029)	(1 881)	(1 695)	(1 446)	(1 254)	(3 973)
2b	VC	Litter		27 496	27 225	26 099	25 100	23 424	21 728	18 547	50 847
3a	MQ	Animal[23]		84 052	82 737	78 017	75 996	69 391	62 978	54 002	146 001
3b	AGE	(ST)		(7 870)	(7 650)	(7 007)	(6 571)	(6 044)	(5 127)	(4 375)	(13 988)
4a	LMP	FT		79 572	78 363	74 040	72 287	66 043	60 113	51 565	138 383
4b	ADG										

The "Year group" spans columns 94_98 through 94_04.

[21] Within a given year group **litter** and **animal** values were identical for all models
[22] Values received at the FT and ST evaluations (Tables 5, 11).
[23] Number of individuals was based on performance or pedigree records

3.4.3. BLUP analyses of common traits of ST–FT and ST, FT

Based on the joint (**ST–FT**) model traits, association of breeding values predicted through separate and joint performance tests can be analyzed.

The comparison was made using **4** models: **M01**[1–3–2a], **M02**[2a–4–2a], **M04**[3a–4–4a], **M06**[4a–3–4a] (**ST-FT**, **ST**, **FT** Tables 12, 10, 4).

The common traits were: **DOT**, **FEED**, **VC**, **MQ** (ST), **AGE**, **ADG**, **LMP** (FT).

Using own scripts a database was created containing the breeding values of the common traits predicted by the different models.

The figures consist of two columns: in the first column the trait of the joint model is presented (**ST** – *number of the model*) while in the second column the trait of the separate **ST** or **FT** is given (**ST** – *number of the model* or **FT** – *number of the model*).

3.4.4. BLUP analyses of common traits according to year groups (vertical analyses)

For **DOT** (Figure 13) the **ST–FT**, **ST** histogram pairs show slight differences for every model, probably because of the increased relationships of the **ST–FT** model. These differences were also observed for the breeding value distributions. The association of breeding values for **ST–FT** and **ST** model groups: [M01, M02]: y = 0.91 x + 0.50; R = 0.94, [M04, M06]: y = 0.92 x + 0.46; R = 0.94. Due to the high **R** values having the breeding values predicted with the **ST** model the breeding value can be estimated for the **ST–FT** model with **high probability**. This means the ranks of the individuals in the two separate ranks is the same (or almost the same).

For **ADG** (Figure 13) the **ST–FT**, **FT** histogram pairs were the same for every model, probably because the relationships of the **ST–FT** and **FT** models were the same.

The same phenomenon was observed for the breeding value distributions, with the successive years the breeding value range – at the positive side – became wider.

The association of breeding values for **ST–FT** and **FT** model groups: [M04, M06]: y = 0.99 x – 0.01; R = 1.

The above mentioned tendencies are also valid for **AGE** and **LMP**: y = 0.98 x + 0.01; R = 0.99, and y = 0.99 x – 0.01; R = 1. The association of the 3 **FT** traits practically mean a line with a zero intercept and 45º slope, **the breeding values predicted with the two methods are identical**.

All of the **7** traits are included in several models. This raises the question if there is any model where the **ST–FT** and **ST** or **FT** trait pairs provide the "best results".

It is advisable to calculate the difference between the predicted breeding values $(y_{ST-FT} - y_{ST})$ *and* $(y_{ST-FT} - y_{FT})$ by models and traits. For the **97_01** year group, the **M04** model gave the best **MSE** and **Bias** values for **DOT** and **FEED**, while the models did not differ for the other traits.

According to the most widely used **MSE**, significant differences (p < 0.05) were found between the models [M01, M04], [M01, M06], [M02, M04] for **FEED**, while **no differences** were found for the **other traits**.

Evaluation of the **Bias** values gave the same results as **MSE**. Based on the correlation and rang correlation coefficients no differences were found among the models.

3.4.5. *BLUP analyses of common traits according to the models (longitudinal analyses)*

The results are presented through the **M04** model for **DOT** (**ST–FT**– 3a, **ST**– 4) and **ADG** (**ST–FT**– 3a, **ST**– 4a).

For **DOT** the **ST–FT**, **ST** histogram pairs show slight differences for every year group, probably because of the increased relationships of the **ST–FT** model. These differences were also observed for the breeding value distributions. The association of breeding values for **ST–FT** and **FT** model groups for the trait is provided in Figure 14.

Characteristics of functions describing the linear association starting from 94_98 are: a = [0.94; 0.94; 0.91; 0.92; 0.87; 0.89; ---]; intercepts: [0.36; 0.40; 0.57; 0.46; 0.32; 0.28; ---]; R = [0.95; 0.95; 0.92; 0.94; 0.92; 0.93; ---].

For **ADG** the **ST–FT**, **FT** histogram pairs were the same for every year group, probably because the relationships of the **ST–FT** and **FT** models were very similar. The same phenomenon was observed for the distribution of the breeding values.

The associations between the breeding values predicted by the **ST–FT** and **FT** model groups are presented in Figure 14. The linear associations are shown by the lines with a slope of 0.99, where the intercepts were [-0.08 – 0.05]; R = 1, independently of the year group. Taking the R value as 1 the resulting function (y = x) indicate the identity of the breeding values predicted by the **ST–FT** and **FT** models.
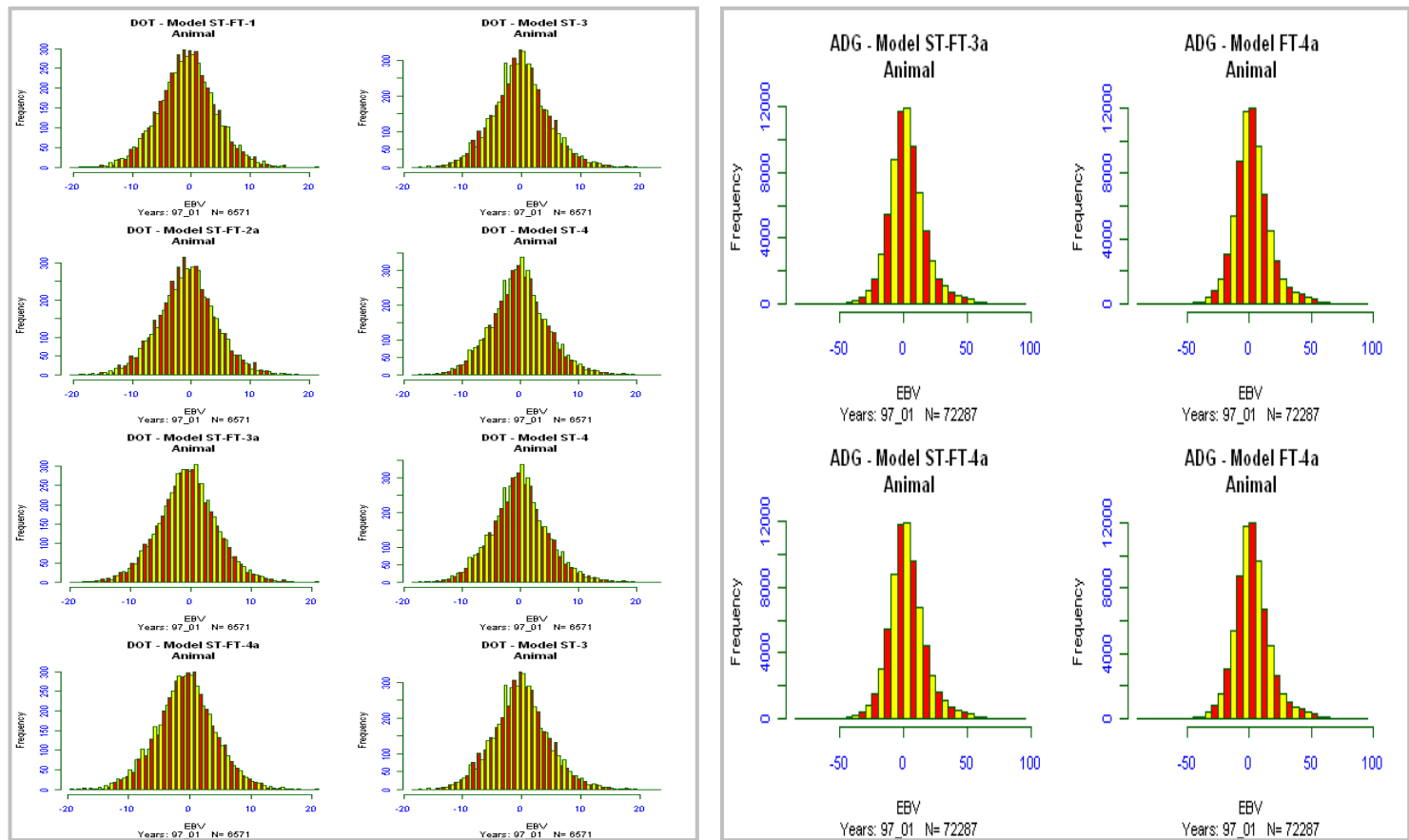
Figure 13. – Histograms of breeding values (predicted by different ST–FT models) for HLR (1997–2001)
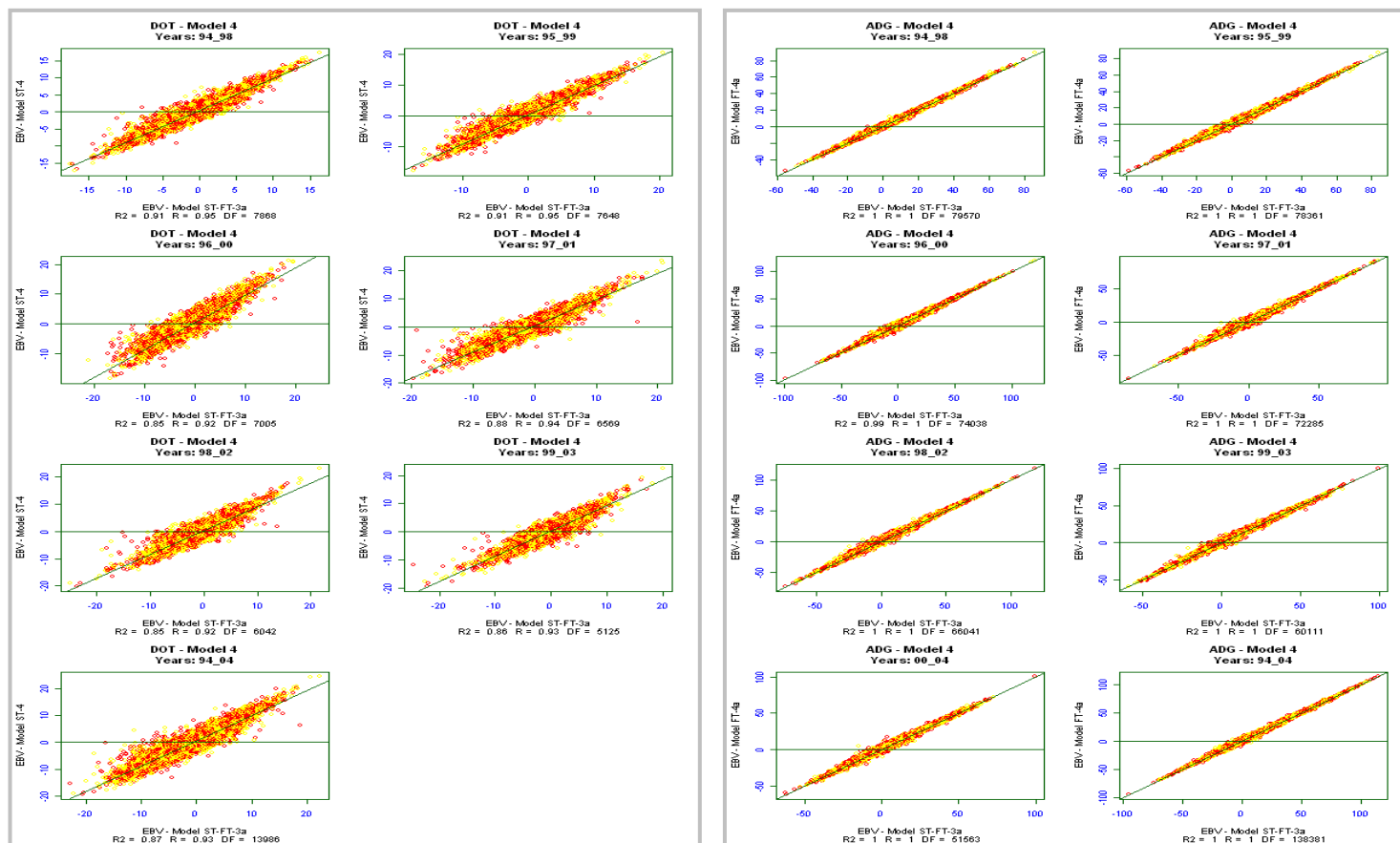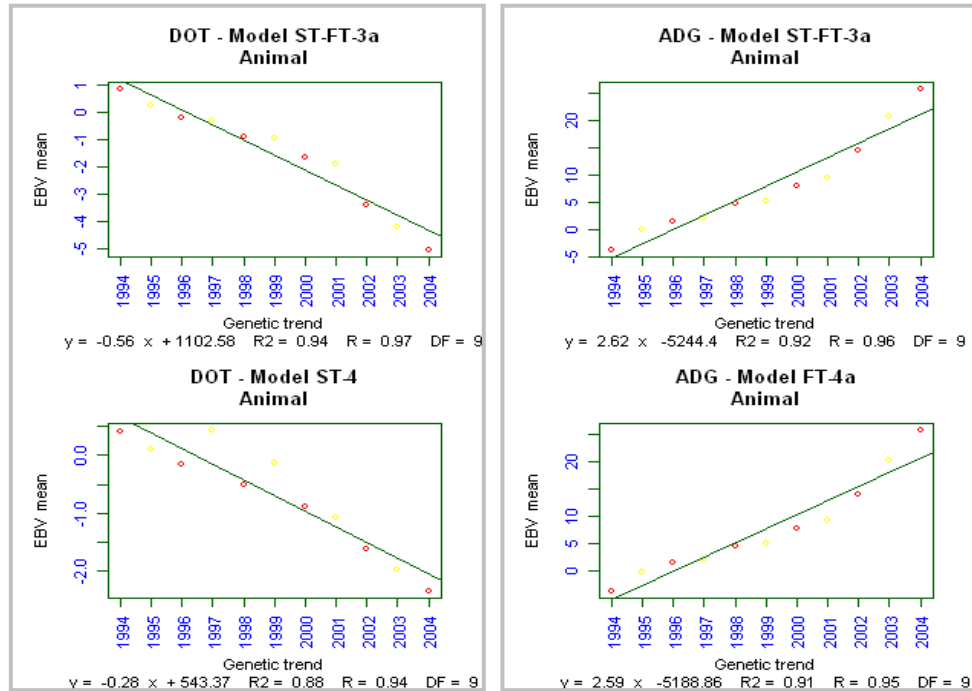
42

Figure 14. – Association between the breeding values of ST–FT models M04[3a–4–4a] for HLR (different year groups)

3.4.6. *Genetic trends*

Based on Figure 15 genetic trends obtained through the joint (**ST–FT**) or separate (**ST** or **FT**) models can be compared.

Figure 15. – Genetic trends of the common ST–FT traits for HLR (M04[3a-4-4a] model)

The genetic trends of **DOT** are substantially different for **ST–FT**: y = -0.56 x + 1102.58; R = 0.97 or **ST**: y = -0.28 x + 543.37; R = 0.94. This is caused by the different mean breeding values induced by the different number of individuals in the various models (**ST-FT**: 146 001; **ST**: 13 988).

For **ADG** the predicted breeding values were also identical with the two model types: y = 2.62 x – 5244.4; R = 0.96 (**ST–FT**); y = 2.59 x – 5188.86; R = 0.95 (**FT**). The same tendency was found for **LMP**: y = 0.04 x – 79.98; R = 0.95 (**ST–FT**); y = 0.04 x – 88.08; R = 0.95 (**FT**). The results may be explained by the almost identical number of individuals evaluated in the two model types (**ST–FT**: 146 001; **FT**: 138 383).

4. CONCLUSIONS AND SUGGESTIONS

Existence of the models, technical background and scientific knowledge are indispensable for the routine application of BLUP.

Based on the knowledge and associations revealed by the accomplishment of the thesis the following conclusions can be made:

➢ The available sofwares computing capacity are not satisfactory for complex model and large databases (several genotypes) thus the depth of the analysis is partly limited.

➢ Based on the statistical analysis it can be concluded the available database is appropriate (except for meat quality) from the aspects of breeding value prediction.

➢ The chosen 5 year long evaluation period is appropriate

➢ The improving pedigree structure will probably result more precise predictions

➢ The number of records are satisfactory for FT but cannot be reduced for ST

➢ Irregular changes of heritability estimates were found with the changing year groups for the different traits thus re-estimation of (co)variance components is advisable at these times

➢ Examination of the model independence of the traits is necessary (several models) as the predicted values are different if the trait is model dependent

➢ Genetic potential of the incoming and outgoing individuals show proportionality

➢ Genetic trends are sensitive to the length of the investigation period thus they comparison requires identical circumstances

➢ Genetic parameters of the ST–FT models are more precise compared

to the ST values (the structure of the pedigree improves substantially), the same tendency was not found for FT (the structure of the pedigree only slightly improved)

➢ The results of the HLW and F1 genotypes showed the same tendency as the HLR.

➢ The conclusions are general (independent of the genotypes), detailed description is provided in the "Results and Discussions" chapter

Suggestions:

➢ In the thesis several models were evaluated with substantial CPU time. Reanalysis of the selected models can be recommended.

➢ Part of the complex (ST–FT) models could not be evaluated for HLR and F1 due to the restricted computing capacity. These models can be run and the results could be compared with that of the HLR breed.

➢ The predicted breeding values are summed in the aggregate genotype. The effect of the changing breeding values on the aggregate genotype could be evaluated.

➢ Detailed evaluation of the BLUE values of herd, station, year-month and litter is necessary (can provide answers for the questions raised by the breeders).

Accomplishment of the suggestions can contribute to the better understanding of the BLUP procedure.

5. NEW EXPERIMENTAL RESULTS

After the data evaluation and literature review the following new experimental results were obtained:

1. Based and the genetic parameter estimation and evaluation using the 5 year long year groups estimation of the (co)variance components is advisable with the successive years.

2. For a given trait the individuals' breeding values were determined by genotypes, year groups and models, the associations between breeding values predicted in changing environments were established.

3. The most appropriate models – independently of the genotype – for **FT** were: **AGE**, **LMP** or **ADG**, **LMP** containing weight as a covariate (for **AGE** and **ADG**).

4. Selection responses were estimated by genotypes and traits (genetic trends were determined).

5. Associations between the predicted breeding values of the common traits for **ST–FT** and **ST** or **FT** were determined by genotypes.

6. In Hungary the effects of year groups on the traits used in the breeding value estimation were analysed for the first time.

6. PUBLICATIONS ON THE SUBJECT OF THE DISSERTATION

6.1. Papers published in foreign language peer-reviewed journals

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