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„THESIS OF DOCTORAL (PHD) DISSERTATION”

TITLE OF DISSERTATION:

Breeding value evaluation of Hungarian Sport horses

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I INTRODUCTION

The role of the horse has been changed that followed by the change in the breeding goals. After the 2nd World War, mainly in the early seventies, number of horses decreased worldwide, especially in the industrialized countries. There were two opposite trends. Despite of the decreasing number of draught horses, number of warmblood horses continuously increased connected with the development of leisure activities. A considerable demand for horses suitable for sport purposes emerged as new breeding goal.

There is a continuously increasing demand for sport horses for show-jumping and dressage worldwide. Most interested fields in Hungary, similar to other European countries, are show-jumping, dressage and eventing in a smaller volume.

Sport horse breeding started in the 1970's in Hungary with mares of traditional Hungarian breeds and imported stallions. Nowadays, the Hungarian sport horse population has the same genetic merit as the European population, mainly based on Dutch Warmblood and Holsteiner.

There are direct and indirect selection criteria in the selection of sport horses. The direct estimates estimating the ability of the animal in practice and the indirect ones measure a character in correlation to the previous ones. Direct estimates in the case of sport horses generally based on the performance of the animals in the various disciplines.

The aims of my thesis are finding new alternatives for the successful selection of Hungarian Sport horses with proper statistical methods based on the available dataset.

II AIMS OF THE RESEARCH

The aims of my thesis were:

1. Pedigree analysis of Hungarian Sport horses

- Estimation of genetic variability
- Analysis of the relationship between breeding stocks

2. Principal component analysis of Hungarian Sport horse mare self performance tests

- Identification of background variables of the evaluated traits

3. Parameter estimation of Hungarian Sport horse self performance tests

- Determination of heritabilities of the evaluated traits
- Estimate correlations between conformational traits
- Estimate correlations between free jumping and movement analysis traits

4. Analysis of genetic progress based on Hungarian Sport horse mare performance tests

- Breeding value estimation for traits evaluated in the Hungarian Sport horse self performance tests
- Estimate selection intensity for traits evaluated in the Hungarian Sport horse self performance tests

5. Analysis of Hungarian Sport horse show-jumping results with different repeatability animal models

- Comparison of various repeatability animal models based on sport performance results

6. Analysis of Hungarian Sport horse show-jumping results with random regression models

- Finding the best fitting random regression model based on sport performance results

III MATERIALS AND METHODS

Hungarian Sport horse self performance test

Traits evaluated on each mare in the national performance recording system are meant to evaluate conformation, free jumping and movement analysis as follows:

Conformation traits: type, head, neck, saddle region, frame, forelimbs, hindlimbs, regulation of movement, impulsion and elasticity of movement, overall impression.

Free jumping: jumping style, jumping ability–sense of distance; observation during training.

Movement analysis: walk, trot, canter, overall impression, test rider's score.

Scores for free jumping and movement analysis traits are on a 0–10 scale. Conformation traits are judged on different scales since 1. January 2000. Weighted traits are neck, forelimbs, hindlimbs and impulsion and elasticity of movement with scores between 0 and 12. Type (0–6), head (0–8) and frame (0–8) are judged with less weight. Before 2000, the conformation traits were scored in the range of 0 and 10. Observation during training, a free jumping trait, is scored by the trainer based upon cumulative impressions throughout training. The test rider's score is given by the test rider based upon subjective judgment of the rideability of the horse. Other traits are scored by an invited judge. The final score for the mare test is the sum of the mean of the conformation score, the mean of free jumping performance scores and the mean of movement analysis scores multiplied by 1, 1.5 and 2, respectively (MSLT, 2000).

Principal component analysis

Data from a mare were utilized only if she completed all exercises successfully. There were 396 records from 3-year-old and 233 records from 4-year-old mares, respectively.

Relationships among traits were examined using principal component analysis. This method was used to determine the relative contribution of factors to total variation of the traits and which traits belong to each identified factor. Eigenvalues of factors show the contribution of each component to total variation. During the evaluation, factors were rotated with Varimax rotation of H. F. Kaiser. The aim of the Varimax method is to maximize the sum of variances of quadratic weights (SVÁB, 1979). The rotation method identifies what is thought to be a valid and biologically reasonable solution, because it accounts for the correlation among background variables. In this case, background variables are not independent from one another. The 'eigenvalue 1.0

criterion', whereby only components with eigenvalues exceeding unity were considered significant and hence retained in the analysis, was used (SZELÉNYI, 1993). Cluster analysis was used for visual representation of the grouping of traits (PODNAI, 1997). Data were analysed using the SAS (SAS INSTITUT, 1999) software package.

Pedigree analysis

Information from all the individuals registered in the Hungarian Sport horse studbook from its foundation (contains ancestors at least 3 generations back), comprising a total of 11.286 (7.517 females) animals. The pedigree data came from The Association of Hungarian Sport horse Breeders (MSLT).

Generation interval was computed in four pathways (stallion- son, stallion - daughter, mare – son and mare - daughter) based on the birth dates of the registered animals and their parents. These values show the average age of parents at the birth of their offspring.

Hungarian Sport horse population was described with the contribution of founders in the total genetic variability and with the inbreeding coefficients.

All parameters were estimated with ENDOG software package (GUTIÉRREZ and GOYACHE, 2005).

Analysis of mare self performance tests

Test records of 3 and 4 year old mares from 1993 to 2004 were analyzed. There were 435 records from 3-year-old and 240 records from 4-year-old mares, respectively. Seventy-nine mares were tested at both ages.

Before estimating the correlation between test results, all phenotypic values were analysed by least-square analysis using the SAS GLM-procedure (SAS, 1999).

A linear model was applied for the analysis of data from STP of mares. The year of the performance test, age of the mare and the owner were included as fixed effects in the model.

Variance and covariance components were estimated by the use of VCE-5 (KOVAC and GROENEVELD, 2003) for each trait. Pedigree used for the analysis contains ancestors of participating mares 2 generations back, containing data of 1368 horses.

Estimation of breeding values and genetic progress

Estimation of genetic progress based on the dataset described in Section “Analysis of mare self performance tests”. Pedigree data of the tested mares and pedigree of their relatives from Hungarian Sport horse Studbook (contains pedigree data three generations back) were used in the analysis. Variance components and the used model was taken from Section “Analysis of mare self performance tests”. Breeding values were estimated for each trait with best linear unbiased prediction animal model (BLUP AM) with PEST software package (GROENEVELD et al, 1990).

Breeding values were presented with the mean 100 and standard deviation of 20 as Koenen (2005) suggested using the formula: $BTE_p = 100 + ((BTE_u - \acute{a}tlag_u) / \sigma_a) * 20$, where BTE_p estimated breeding value in the transformed scale, BTE_u estimated breeding value in the original scale, $\acute{a}tlag_u$ mean of the breeding values in the scale of the reference population, σ_a genetic standard deviation of the observed trait.

Reliability was computed based on the estimated error variance for every trait in the case of each animal. Calculation was done with the formula: $r = \sqrt{1 - PEV / \sigma_a^2}$, where r is the correlation between estimated and the true breeding value, PEV error variance of the estimated breeding value, σ_a^2 genetic variance of the observed trait.

For the determination of the genetic progress, breeding values were sorted into groups based on the animal's birth year and data were evaluated with analysis of variance and regression analysis with SAS PROC MEANS and SAS PROC REG (1999). Selection intensity was calculated as $i = SE / h * \sigma_g$, where i is the selection intensity, SE is the selection progress, h is the square-root of the heritability and σ_g genetic variance of the observed trait.

Analysis of sport competition results

The data used for the analysis based on the show-jumping results from the period 1996 and 2004 in Hungary. Records of the horse were taken into account only if its pedigree is known in the Hungarian Sporthorse Studbook at least 2 generations back. After filtering 22.860 records were left for the analysis.

Ranking of sport races are not normally distributed, but near to exponential distribution. So ranking can be used for genetic evaluation and breeding value estimation only after some mathematical transformation.

For the evaluation of show jumping we created some scores and analyzed these scores with different models. As TAVERNIER (1990) reported, square root, cubic root and fourth root should be considered as normally distributed scales and may be appropriate scales for evaluation. As a fourth measure, we used normalized ranks with Blom-method (BLOM, 1958) as FORAN et al. (1995) showed in the case of Irish Sport horse population. This transformation is taken into account number of starters and creates a normally distributed variable from ranks. With this method the winner of the competition receives positive score, the average performance in the competition receive a score of zero and the horses with poor performance ranked at the bottom of the competition receive negative scores. Further models were investigated. In the fifth measure cotangent function was used to transform ranking. After the transformation of rankings the scale had higher deviation than in the case of Blom-method, which can show better the differences between performances.

Besides scales based on rankings we used other measurements to evaluate the performance. The height of the obstacle was used as further scale. The sixth measure was created as the difference between the height of the obstacle and the fault points. This made easier the comparison of the results of the horses participating in various competitions.

Each case was evaluated with a repeatability animal model. Gender, breeder, age of the horse, year and place of the competition and height of the obstacle were taken into account as fixed effects. Effect of rider and permanent environment effect were taken into account as random effects.

Before the evaluation each fixed effect were analyzed for level of significance using SAS PROC GLM (SAS INSTITUTE 1999).

Variance components and standard errors were estimated with an animal model and a repeatability animal model using REML with VCE-5 (KOVAC and GROENEVELD, 2003) software package.

The goodness-of-fit of these models was assessed by using the log-likelihood value and Akaike's information criterion (AIC) (AKAIKE, 1973). AIC was calculated as follows:

$$AIC = -2 * \log(\text{maximum likelihood}) + 2 * (\text{number of model parameters})$$

The model with the highest log-likelihood value and the lowest AIC was considered as best fitting model for show jumping performance.

Random regression analysis of sport competition results

Results were taken into account during the development of the random regression model from the ages between four and eleven years old and had at least five starts. Because of these conditions 21210 records were left.

Random regression models were fitted to the most favourable measurement of the repeatability animal model.

Residuals should not be assumed to be homogeneous over the observed time (SCHAEFFER, 2004), so consider residual as heterogeneous creation of age classes were necessary. Within age classes residuals assumed to be homogeneous. Age was divided into eight age classes.

Legendre polynomial was used for the random regression fitting. The general form of the Legendre polynomial:

$$\phi_n(t) = \frac{1}{2^n} \sqrt{\frac{2n+1}{2}} \sum_{k=0}^{\left[\frac{n}{2}\right]} (-1)^k \binom{n}{k} \binom{2n-2k}{n} q_t^{n-2k},$$

where q_t is the standardized time t converted between -1 and 1 using the following formula: $q_t = -1 + 2 * (t - t_{min}) / (t_{max} - t_{min})$.

Gender, breeder, year and place of the competition and height of the obstacle were included as fixed effects in the random regression animal model. Effect of rider was taken into account as random effect. The random regression (co)variance components were estimated via REML and were computed by using of VCE-5 (KOVAC and GROENEVELD, 2003). The eigenfunctions and eigenvalues were calculated from the (co)variance components of the random regression coefficients with SAS PROC IML (SAS INSTITUTE, 1999). Eigenvalues represent the amount of variation explained by the corresponding eigenfunction.

IV MAIN RESULTS OF THE THESIS

Principal component analysis

After Varimax rotation, 9 factors with the ratio of variance equal to 80.9 were identified based on test results of 3-year-old mares. Factor pattern coefficients of the rotated factors show the proportion of variation that they account for. These coefficients show the relative contribution of traits to the particular factor.

Factor I. was determined by some conformation trait, a *type, head, saddle region, frame* and *overall impression* (eigenvalue: 3.269, variance of eigenvalue: 18.2%). So the difference among mares was higher in these traits. **Factor II.** (eigenvalue: 2.527, variance of eigenvalue: 14%) is related to movement analysis traits, determined by *trot, canter, overall impression* and *test rider's score*. This means that mares least different in movement than overall conformation. **Factor III.** (eigenvalue: 1.897, variance of eigenvalue: 10.5%) was determined by free jumping performance traits *jumping style* and *jumping ability–sense of distance*. **Factor IV.** was a single trait, *impulsion and elasticity of movement* (eigenvalue: 1.429, variance of eigenvalue: 7.9%). **Factor V.** was *walk* from movement analysis (eigenvalue: 1.199, variance of eigenvalue: 6.7%). **Factor VI.** Were determined as *forelimbs* trait from conformation (eigenvalue: 1.096, variance of eigenvalue: 6.1%). **Factor VII.** was *hindlimbs* (eigenvalue: 1.080, variance of eigenvalue: 6%). **Factor VIII.** was determined as *neck* trait from conformation analysis (eigenvalue: 1.048, variance of eigenvalue: 5.8%). **Factor IX.** was *observation during training* trait from free jumping performance (eigenvalue: 1.022, variance of eigenvalue: 5.7%).

Regularity of movement is in correlation with none of the above factors of the variance of the population in this traits is very small.

After Varimax rotation, 7 factors were determined based on 4-year-old test results, with ratio of variance=74.1. Factor pattern coefficients of the rotated factors shows the relative contribution of traits to the particular factor, similarly as written in the case of 3-year-old test results. **Factor I.** was determined by some conformation trait, a *type, head, saddle region, frame, regularity of movement* and *overall impression* (eigenvalue: 3.631, variance of eigenvalue: 20.2%). So regularity of movement is more important trait in the case of 4-year-old mares than in the case of 3-year-old horses. It is in correlation with the factor covers the most variance. **Factor II.** (eigenvalue: 2.426, variance of eigenvalue: 13.5%) is related to movement analysis traits, determined by

trot, canter, overall impression and test rider's score. Factor III. (eigenvalue: 2.063, variance of eigenvalue: 11.5%) was determined by free jumping performance traits *jumping style* and *jumping ability–sense of distance*. **Factor IV.** was a single trait, *impulsion and elasticity of movement* (eigenvalue: 1.474, variance of eigenvalue: 8.2%). **Factor V.** was determined as *neck* trait from conformation analysis (eigenvalue: 1.451, variance of eigenvalue: 8.1%). **Factor VI.** was *hindlimbs* (eigenvalue: 1.168, variance of eigenvalue: 6.5%). **Factor VII.** was *walk* from movement analysis (eigenvalue: 1.128, variance of eigenvalue: 6.3%).

As shown above, different trait groups are separated in the case of both age groups, what refers to low relationships among components of trait groups (it is similar to the results of correlation analysis). Different sub-groups can be aggregated from conformation traits depending on age-groups.

Using cluster analysis to classify traits to trait groups separately for each age group helped to clarify the separation of traits. The first step is to create a group from two traits which are in the highest correlation. Creation of groups continuing until only one group remains.

Jumping style and *jumping ability–sense of distance* are most related from traits evaluated as 3-year-old. Among the conformation traits scores of *head* are close to the judgement of *type*. *Neck* has a great impact on trait *overall impression* of conformation traits. *Canter* is in close relation with *overall impression* of movement.

Similarly to the results of 3-year-old mares, also *jumping style* and *jumping ability–sense of distance* are most related in the case of 4-year-old mares. From the conformation traits recognizable relation exist only between *head* and *type*. *Overall impression* of conformation, unlike in the case of 3-year-old mares, are closely related with *impulsion and elasticity of movement*. There are also close relationship between *overall impression* of movement and *test rider's score*.

Figure 1 and 2 illustrate the separation of traits among trait groups by cluster analysis of test results of 3-year-old and 4-year-old mares, respectively. Results show the separation of the traits-groups. The trait, *impulsion and elasticity of movement* from conformation judgement, can be classified as a movement judgement trait based on test results from 3-year-old mares but can be classified to conformation traits, especially to the trait, *overall impression*, based on records of 4-year-old mares. This difference could be attributed to the training of the horse, because *impulsion and elasticity of*

movement is similar to movement analysis traits among 3-year-old mares but is more similar to conformation traits for 4-year-old mares.

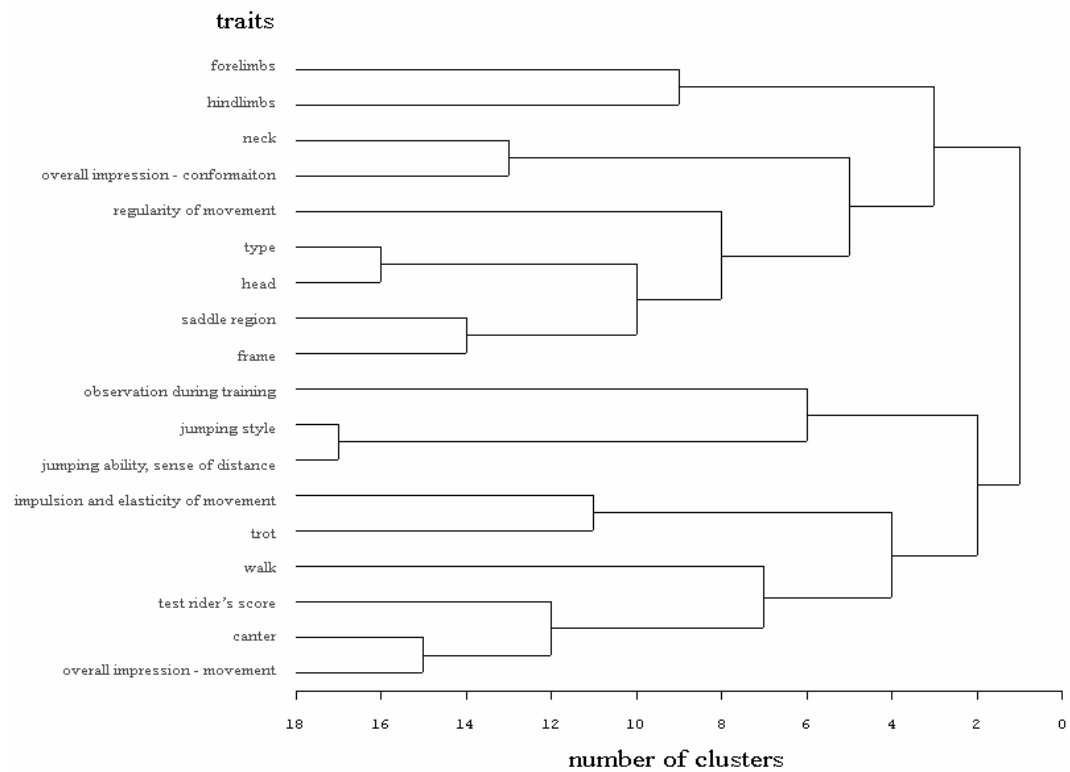


Figure 1.: Dendrogram of traits based on SPT data on mares measured at 3 years of age

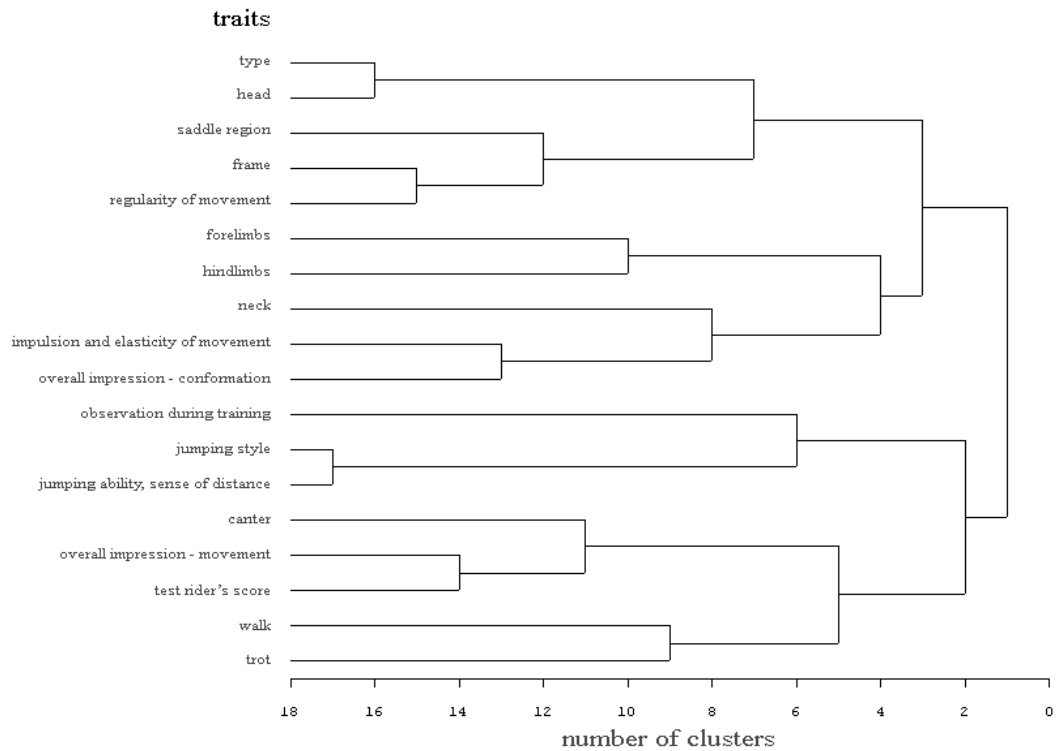


Figure 2.: Dendrogram of traits based on SPT data on mares measured at 4 years of age

Pedigree analysis

Average generation interval is 10.6 years for the Hungarian Sport horse population. *Table 1* shows generation interval through the four pathways. Generation interval of stallions was longer, so they are substituted by their progeny during a longer period.

Generation intervals in the pathways stallion-son and stallion-daughter were compared with independent samples t-test and significant difference was not found. There was significant difference between generation intervals in the pathways mare-son and mare-daughter. Broodmares (above average performance supposed) producing stallions were in breeding stock in average one year longer than broodmares producing mares.

Generation intervals calculated for Hungarian Sport horses similar to the generation intervals of other riding horses (LANGLIOS, 1982; GLAŹEWSKA and JEZIERSKI, 2004).

Table 1.**Generation intervals in the four pathways**

Parent-progeny pathways	Number of horses	Generation interval	Standard deviation of the generation interval
Stallion-son	267	12.12	5.57
Stallion-daughter	2858	11.71	4.93
Mare-son	225	10.56	4.52
Mare-daughter	2758	9.41	4.26
Average	6108	10.64	4.79

Table 2 shows the 10 stallions contributing the most from the genetic variability. Most of them were born in the 1980s and 1990s.

The ancestor contributing the most (2533 *Goliath*) explained 1.72% of the total genetic variability. All of this ancestors were imported, most of them are Holstein and Dutch Warmblood stallions. This indicates the decreasing importance of traditional breeds and the spread of imported stallions and their progeny. The low explained variabilities show the heterogeneity of the population, what can be good for maintaining but prevents the spread of the genetic merit of above average stallions.

Table 2.

Description of 10 ancestors contributing the most to the genetic variability of the Hungarian Sport horse

ID	Name	Sex	Birth year	Breed	Explained variability (%)
IM884830000	2533 Goliath	stallion	1988	Dutch Warmblood	1.723
IM75000To00	1117 Toborzó	stallion	1975	Holstein	1.678
IM912340094	2972 Justboy	stallion	1991	Dutch Warmblood	1.197
IM58000Al00	311 Aldato	stallion	1958	Holstein	1.113
IM79001Mo00	1551 Merano-1	stallion	1979	Holstein	0.974
IM921190095	3001 Koppány	stallion	1992	Dutch Warmblood	0.968
IM885460000	2534 Gringo	stallion	1988	Dutch Warmblood	0.955
HB820010000	1861 Hatalom	stallion	1982	Hannoverian	0.754
IM880022001	3866 Ginus	stallion	1988	Dutch Warmblood	0.746
IM72000Hm00	794 Hullám	stallion	1972	Hannoverian	0.740

Table 3 shows the description of the most inbred horses. Highest inbreeding coefficient was 0.25. There were 42 inbred animals in the population. The most mating between relatives were in 2003 based on annual inbreeding coefficient and average relatedness.

This statement could be confirmed with the inbreeding coefficients of some 2003 born foals as presented in *Table 3*. Inbreeding coefficients and average relatedness of further years suggest avoiding from mating relatives in the examined population. It was surprising that animals responsible most for genetic variability were not inbred in the examined population.

Table 3.

Description of horses with at least 0.125 inbreeding coefficients

ID	Sex	Sire ID	Dam ID	Inbreeding coefficient
MF961000000	mare	SV74003Si00	M 890880000	0.2500
MF032600000	stallion	IM912340094	MF993520000	0.2500
MF013370000	stallion	ZA910500000	ZA920200000	0.1875
MF030960000	stallion	ZA910500000	ZA920200000	0.1875
MF001150000	mare	ZA910500000	SO83081Hm00	0.1250
MF933230000	mare	M 82065Kl00	M 88086Kl00	0.1250
MF013590000	stallion	E 830130000	BA900150000	0.1250
MF944580000	stallion	M 82065Kl00	M 88086Kl00	0.1250
MF981840000	mare	ZA910500000	ZA881020000	0.1250
MF034830000	mare	IM895430000	CD982260000	0.1250
SS87073Ma00	mare	IM71000Ma00	SS82017Mc00	0.1250
MF992160000	mare	M 890890000	SY911820000	0.1250
MF004730000	stallion	MF952150000	IM906120000	0.1250

Table 4.

Nei's genetic distance among the most important studs

Stud	Number of					
	registered	1	2	3	4	5
	horses					
1	Állami Ménesbirtok Rt.	492				
2	Enyingi Agrár Rt.	435	0.012			
3	ORFK Lovasbázis	283	0.023	0.025		
4	Kabala Ménes Kft.	215	0.024	0.026	0.037	
5	Hortobágyi Kht.	195	0.016	0.017	0.030	0.033
6	Bólyi Mg. Rt.	170	0.018	0.025	0.039	0.039
					0.027	

Table 4 shows genetic distances among six studs registered with the most horses in the Hungarian Sport horse Studbook. There are the highest distance between studs named

“Állami Ménesbirtok Rt.” and “Enyingi Agrár Rt.” based on Nei’s genetic distance. Horses from “Kabala Ménes Kft.”, “ORFK Lovasbázis” and “Bólyi Mg. Rt.” are closely related.

Analysis of mare self performance tests

There were moderate phenotypic correlations among conformation traits *type*, *head* and *neck* (Table 5). Scores of *forelimbs*, *hind limbs*, *regularity of movement* and *the impulsion and elasticity of movement* showed low phenotypic correlations with other conformation traits. *Overall impression* – as conformational judgement aspect – with scores of other conformation traits had moderate phenotypic correlations in both ages.

Heritabilities of each trait were low to moderate. Estimated heritabilities are higher than that presented by HARTMANN (1999) and NISSEN (1997). This makes possible more efficient selection in the Hungarian population. Strong genetic correlations were found among *type*, *head* and *saddle region*. *Forelimbs*, *hind limbs*, *regularity of movement* and *the impulsion and elasticity of movement* showed low genetic correlations with other conformation traits. *Overall impression* had moderate and strong genetic correlations with scores of other conformation traits.

Table 5.

Estimated heritability (diagonal), genetic correlations (upper triangle) and phenotypic correlations (lower triangle) of conformation traits.

(Standard errors within brackets)

Trait	1	2	3	4	5	6	7	8	9	10
1 Type	0.45 (0.06)	0.71 (0.10)	0.58 (0.11)	0.74 (0.09)	0.74 (0.07)	0.59 (0.12)	0.29 (0.13)	0.24 (0.15)	0.38 (0.11)	0.80 (0.07)
2 Head	0.54	0.42 (0.07)	0.31 (0.14)	0.55 (0.09)	0.43 (0.12)	0.60 (0.17)	0.12 (0.14)	0.26 (0.18)	-0.02 (0.13)	0.57 (0.10)
3 Neck	0.42	0.34	0.28 (0.07)	0.71 (0.09)	0.66 (0.12)	0.54 (0.14)	0.17 (0.18)	0.55 (0.17)	0.78 (0.16)	0.89 (0.09)
4 Saddle region	0.47	0.33	0.46	0.53 (0.06)	0.84 (0.09)	0.79 (0.09)	0.43 (0.12)	0.24 (0.14)	0.40 (0.11)	0.89 (0.07)
5 Frame	0.61	0.34	0.41	0.47	0.40 (0.07)	0.76 (0.12)	0.27 (0.14)	0.39 (0.15)	0.50 (0.13)	0.91 (0.10)
6 Forelimbs	0.35	0.23	0.24	0.37	0.35	0.30 (0.08)	0.20 (0.17)	0.49 (0.19)	0.23 (0.14)	0.75 (0.09)
7 Hind limbs	0.27	0.17	0.19	0.21	0.27	0.29	0.35 (0.07)	0.29 (0.17)	0.13 (0.13)	0.66 (0.13)
8 Regularity of movement	0.21	0.12	0.22	0.10	0.25	0.28	0.20	0.32 (0.08)	0.77 (0.10)	0.56 (0.13)
9 Impulsion and elasticity of movement	0.32	0.17	0.36	0.18	0.34	0.19	0.23	0.41	0.43 (0.06)	0.73 (0.08)
10 Overall impression	0.63	0.46	0.57	0.51	0.58	0.49	0.42	0.39	0.62	0.43 (0.07)

During the evaluation of free jumping components, we found high, $r=0.82$ phenotypic correlation between *jumping style* and *jumping ability–sense of distance* (Table 6). There was low phenotypic correlation between *observation during training* and other free jumping traits.

Heritabilities of *jumping style* and *observation during training* were low. *Jumping ability–sense of distance* had moderate ($h^2=0.52$) heritability. There were high genetic correlations among free jumping traits.

There were low and moderate phenotypic correlations among movement analysis traits (Table 6). *Canter* showed high phenotypic correlation ($r=0.66$) with *overall impression* component. Gait traits (*walk*, *trot*, and *canter*) showed lower phenotypic correlations than presented by HUIZINGA et al. (1990) for Dutch Warmblood mares and UPHAUS (1993) for German Warmblood mares.

We found low and moderate heritability for movement analysis components. Comparing heritability, there were similar results for *walk* ($h^2=0.22$), but greater values for *trot* and *canter* than estimated by HUIZINGA et al. (1990). The heritability in our

research was similar to the heritability estimates for *walk* and *trot* estimated by LUEHRS-BEHNKE et al. (2002).

There were moderate to close genetic correlations among movement analysis components. Genetic correlations among *walk*, *trot* and *canter* were lower than estimated by HUIZINGA et al (1990) and LUEHRS-BEHNKE et al (2002).

Table 6.

Estimated heritabilities (diagonal), genetic (upper triangle) and phenotypic correlations (lower triangle) of free jumping and movement analysis traits.
(Standard errors within brackets)

Trait	1	2	3	4	5	6	7	8
1 Jumping style	0.29 (0.08)	0.99 (0.05)	0.83 (0.14)	0.87 (0.09)	0.74 (0.05)	0.50 (0.03)	0.42 (0.07)	0.55 (0.04)
2 Jumping ability–sense of distance	0.82	0.52 (0.06)	0.83 (0.09)	0.54 (0.04)	0.63 (0.04)	0.53 (0.03)	0.55 (0.04)	0.83 (0.04)
3 Observation during training	0.36	0.44	0.32 (0.07)	-0.06 (0.06)	0.40 (0.06)	0.37 (0.03)	0.78 (0.08)	0.66 (0.03)
4 Walk	0.26	0.20	0.29	0.22 (0.08)	*	0.41 (0.15)	0.56 (0.15)	0.68 (0.16)
5 Trot	0.27	0.28	0.34	0.36	0.36 (0.06)	0.55 (0.09)	0.84 (0.09)	0.64 (0.12)
6 Canter	0.24	0.13	0.19	0.30	0.50	0.51 (0.06)	0.83 (0.07)	0.78 (0.08)
7 Overall impression	0.30	0.45	0.26	0.46	0.54	0.66	0.33 (0.06)	*
8 Test rider's score	0.49	0.53	0.31	0.26	0.31	0.48	0.57	0.51 (0.06)

Phenotypic correlations among gaits (*walk*, *trot* and *canter*) and free jumping traits were low, within the range of 0.13–0.34.

There were moderate phenotypic correlations between *test rider's score* and *jumping style* ($r=0.49$) and *jumping ability–sense of distance* ($r=0.53$), respectively. Genetic correlations among movement analysis and free jumping components were moderate to high in our analysis. There was high genetic correlation ($r=0.83$) between *jumping ability–sense of distance* and *test rider's score*.

Estimation of breeding values and genetic progress

Breeding values are presented for stallions with the most offspring in mare performance tests.

Figure 3-6 shows the breeding values of some stallions with the most offspring in mare performance tests from the last 10 years. These predicted values show the effect of the stallions compared to the present registered stock. Breeding values near the average shows that progeny of such stallions' are near the average in each judged trait. Reliability of the estimated breeding values was also shown for each trait in the case of every stallion. Breeding values can be only accepted as true breeding values with reliabilities above 0.7.

Breeding values of 2534 *Gringo* are reliable, breeding values of the other stallions are only informative. Low reliability shows that estimated breeding value could change with the increasing number of progenies. 2534 *Gringo* and 2972 *Justboy* (*Figure 3 and 4*) seem to be above average most of the judged traits of the mare self performance tests because their breeding value exceed the average near one standard deviation. As shown in *Figure 5*, 3648 *Laurenz* has negative breeding value for some conformational traits, for *jumping style* and *walk*. This stallion is among the weakest 16% of the Hungarian Sport horse population based on the breeding value of *regularity of movement*. 3114 *Colonado*, showed in *Figure 6.*, seems to have an overall positive effect for each judged trait.

Figure 7 and 8 show the genetic progress of conformation traits. Genetic progress of free jumping performance traits and movement analysis traits are shown in *Figure 9 and 10*, respectively.

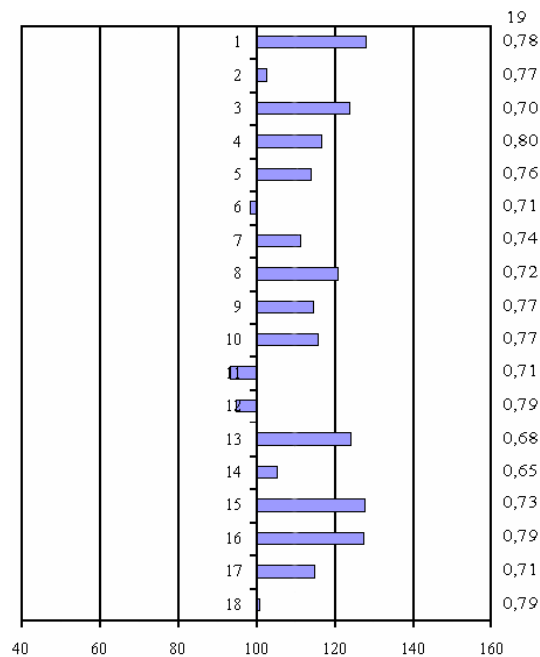
The estimated breeding values were plotted by years to estimate yearly genetic progress. The statistical analysis of data showed significant progress for every trait. *Table 7* shows the estimated coefficient of the regression lines with the level of significance and the selection intensity for each trait. Highest progress can be seen in the case of *type* ($b=0.0082$) and *saddle region* ($b=0.0080$) in conformation traits. In free jumping performance there were high progress for *jumping ability* ($b=0.0075$). The regression coefficient for *canter* ($b=0.0083$) was the highest among the movement analysis traits. Progress was smallest for *forelegs and hind limbs* ($b=0.0063$), *observation during training* ($b=0.0057$) and *walk* ($b=0.0054$) from the three traits groups (conformational traits, free jumping performance and movement analysis), respectively. The regression coefficients showed positive genetic progress in the case of each evaluated

conformation trait. The selection intensity was more accurate for *regularity of movement*, and *neck*. In the case of free jumping performance traits, there was high selection intensity for *observation during training*. Selection intensity was also high for *overall impression* of movement analysis and *walk*. Selection intensity was small for *saddle region*, *jumping ability* and *test rider's score* from the three traits groups, respectively

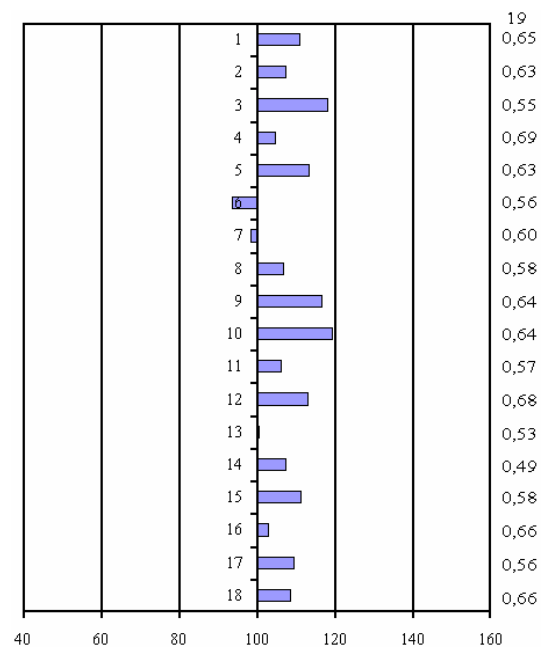
Table 7.

Traits and genetic gain of traits

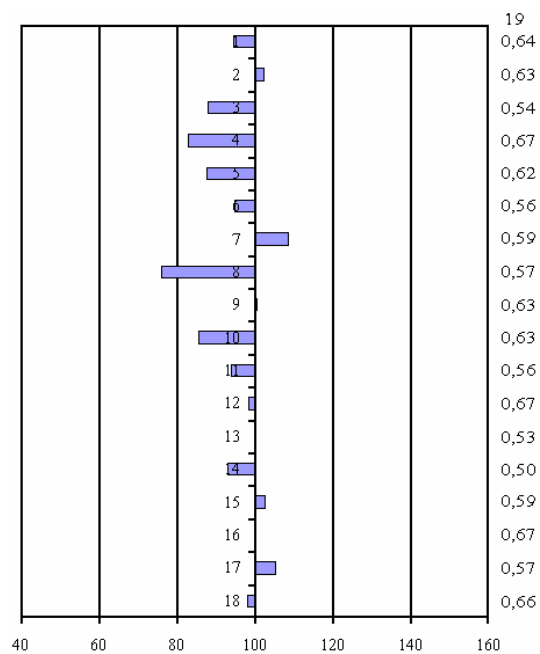
Trait	h^2	σ_g	Selection intensity	Regression coefficient	Level of significance
Type	0.45	0.658	0.019	0.0082	<0.0001
Head	0.42	0.602	0.019	0.0075	<0.0001
Neck	0.28	0.473	0.029	0.0072	<0.0001
Saddle region	0.53	0.749	0.015	0.0080	0.0424
Frame	0.40	0.615	0.019	0.0075	<0.0001
Forelegs	0.30	0.441	0.026	0.0063	0.0024
Hind legs	0.35	0.545	0.020	0.0063	0.0003
Regularity of movement	0.32	0.415	0.031	0.0072	<0.0001
Impulsion and elasticity of movement	0.43	0.661	0.017	0.0075	<0.0001
Overall impression	0.43	0.543	0.021	0.0076	<0.0001
Jumping style	0.29	0.549	0.020	0.0060	<0.0001
Jumping ability	0.52	0.774	0.013	0.0075	<0.0001
Observation during training	0.32	0.356	0.028	0.0057	<0.0001
Walk	0.22	0.420	0.027	0.0054	<0.0001
Trot	0.36	0.463	0.026	0.0072	<0.0001
Canter	0.51	0.645	0.018	0.0083	<0.0001
Overall impression	0.33	0.433	0.029	0.0072	<0.0001
Test rider's score	0.51	0.728	0.016	0.0081	<0.0001



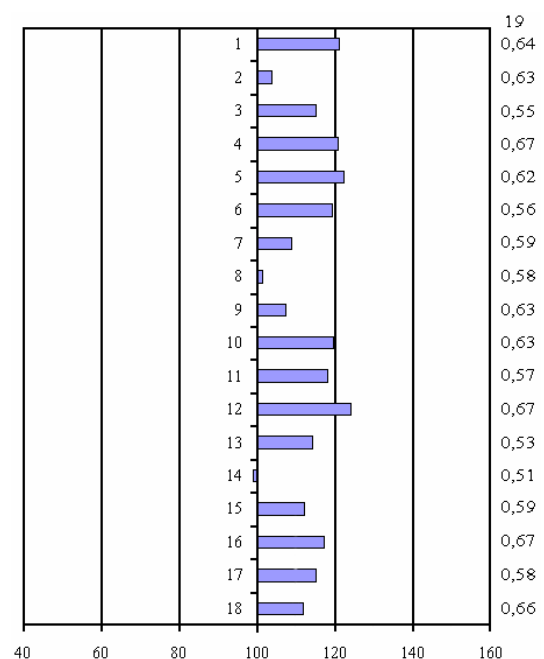
**Figure 3. Breeding values of
2534 Gringo IM885460000**



**Figure 4. Breeding values of
2972 Justboy IM912340094**



**Figure 5. Breeding values of
3648 Laurenz IM890220099**



**Figure 6. Breeding values of
3114 Colonado IM930410096**

Type (1), Head (2), Neck (3), Saddle region (4), Frame (5), Forelimbs (6), Hindlimbs (7), Regularity of movement (8), Impulsion and elasticity of movement (9), Overall impression (10), Jumping style (11), Jumping ability (12), Observation during training (13), Walk (14), Trot (15), Canter (16), Overall impression (17), Test rider's score (18), Reliability (r2) (19).

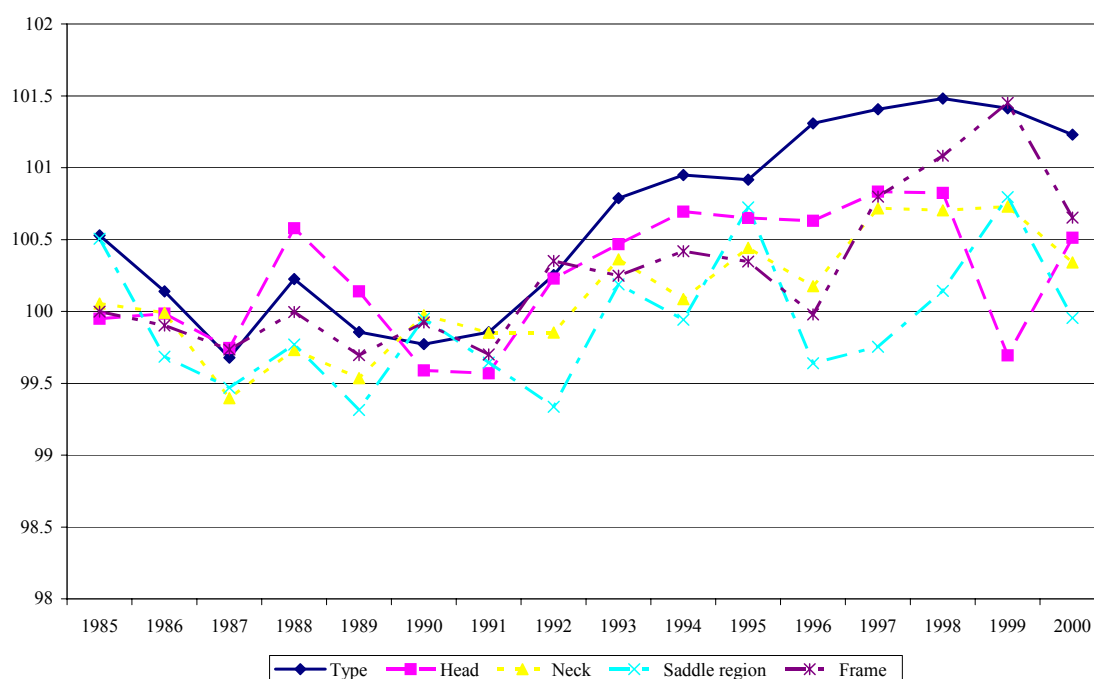


Figure 7. Genetic progress in conformational traits evaluated in mare performance tests

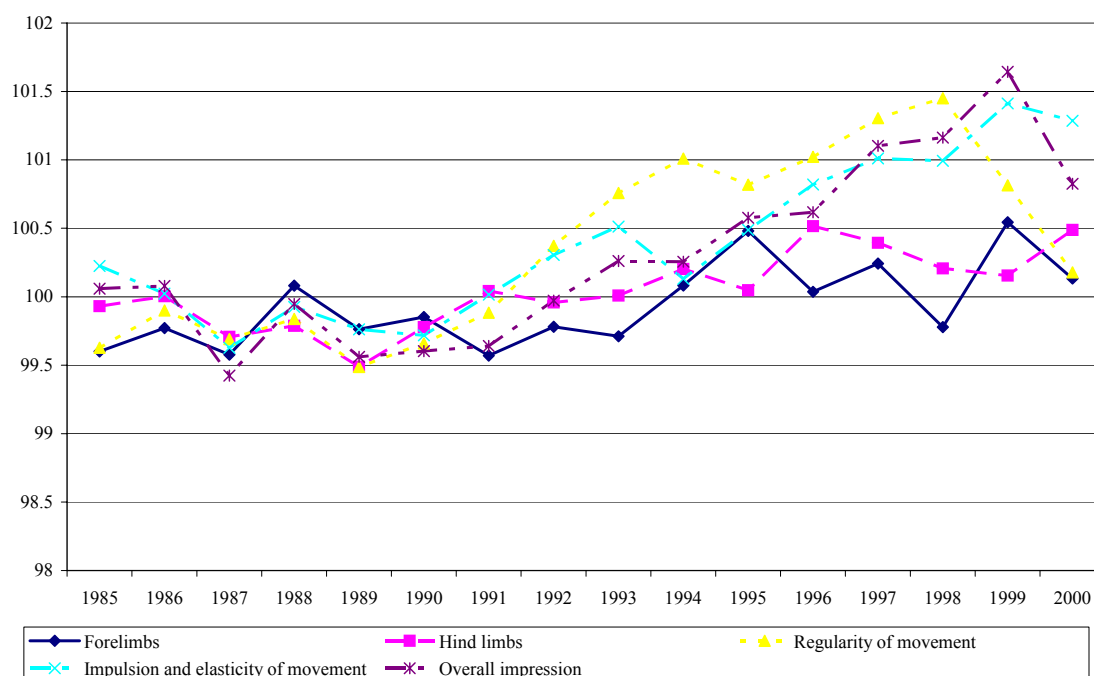


Figure 8. Genetic progress in conformational traits evaluated in mare performance tests

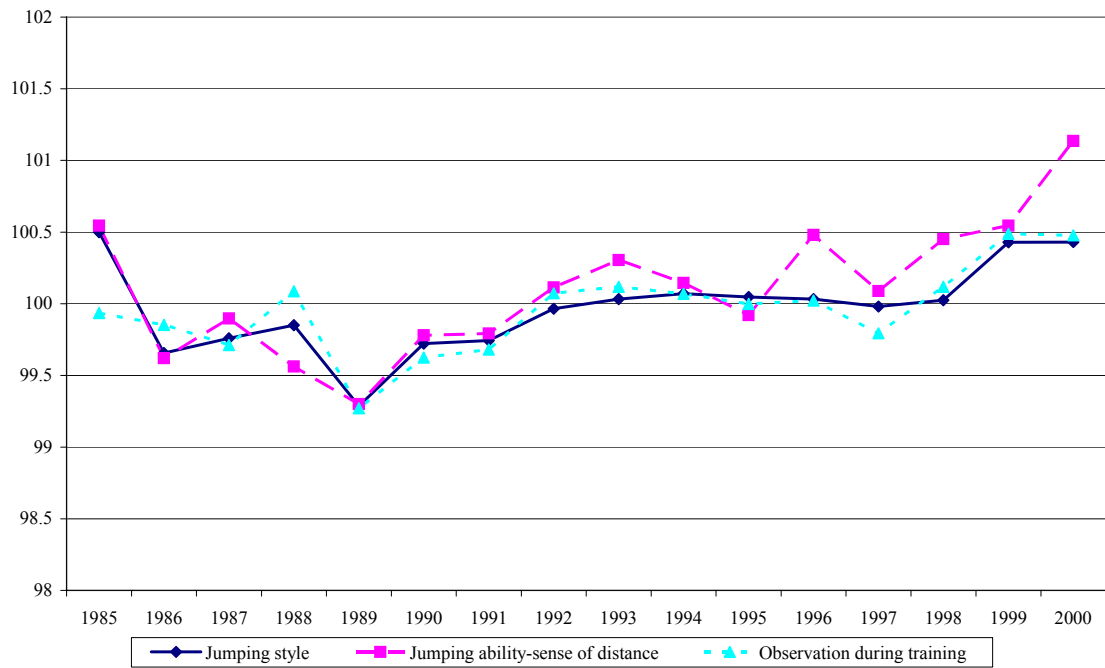


Figure 9. Genetic progress in free jumping performance traits evaluated in mare performance tests

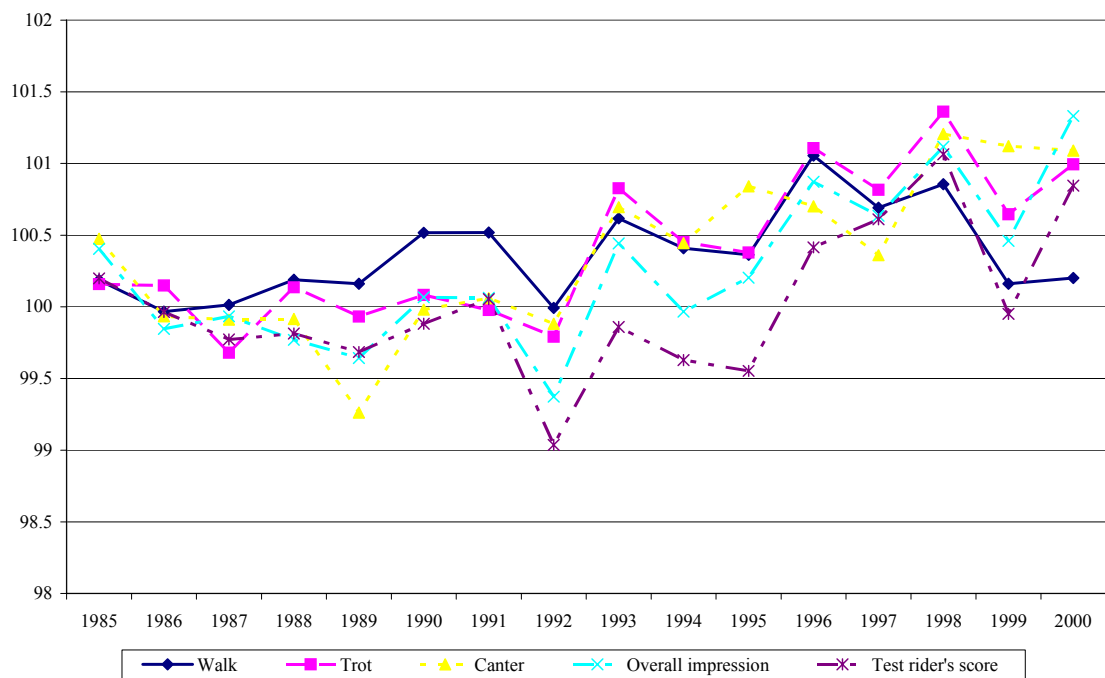


Figure 10. Genetic progress in movement analysis traits evaluated in mare performance tests

Analysis of sport competition results with different measurements with repeatability animal model

Table 8 shows heritabilities estimated with various models. Estimated heritabilities from transformed ranks were below 0.1 for each model. Highest heritability was found in the case of Blom transformed ranks. Our estimated results similar to JANSSENS et al (1997) in the range of 0.02 and 0.09, and FORAN et al (1995) $h^2=0.08$ values. Heritability was computed in each study based on Blom transformed ranks. HASSENSTEIN et al (1998) found heritabilities between 0.07 and 0.13 with repeatability animal model for German Sport horses. These results are higher than in our analysis.

Heritability is as low as HUIZINGA and VAN DER MEIJ (1989) found in the case of Dutch Warmbloods ($h^2=0.20$). Our rank based heritabilities lower than BRUNS (1981) earning and rank based values (from 0.14 to 0.20). WALLIN et al (2003) found heritability 0.27 for Swedish Warmblood based on ranking. This result was also much higher than our results for Hungarian Sport horses. This might show the higher genetic merit of the European population and the better transmitting ability of breeding animals. Smaller heritabilities might be caused for the inclusion of permanent environmental effect in the model.

Table 8.

Heritabilities of the measurements estimated with different models. Standard errors within brackets

Measures	Heritability
Square root of ranks	0.092 (0.024)
Cubic root of ranks	0.092 (0.024)
Quad root of ranks	0.091 (0.024)
Blom score	0.054 (0.024)
Cotangent transformed ranks	0.035 (0.017)
Difference between high of fence and error score	0.041 (0.024)

Table 9 showed the log-likelihood values and the AIC for different models. Smallest log-likelihood value was found for the measure difference between height of fence and error score, so this measure is the least fitting one. Higher log-likelihood values were found for cotangent transformed ranks and Blom score.

Based on AIC criterion, models with cotangent transformed ranks and Blom score were the best fitting ones. Similarly to log-likelihood values, AIC criterion showed also poor fitting of the model with the measure difference between height of fence and error score. Based on these results, cotangent transformed ranks and Blom score were fitted for the show-jumping results. These measures could estimate quite properly the genetic merit of the Hungarian Sport horse population.

Table 9.

Log-likelihood values and Akaike's information criterion (AIC) values using different models

Measures	Log likelihood	AIC	Number of model parameters
Square root of ranks	24710.32	-43202.63	3109
Cubic root of ranks	24810.93	-43403.86	3109
Quad root of ranks	24918.42	-43618.83	3109
Blom score	28059.42	-49900.84	3109
Cotangent transformed ranks	28372.46	-50526.92	3109
Difference between high of fence and error score	8927.40	-11648.80	3103

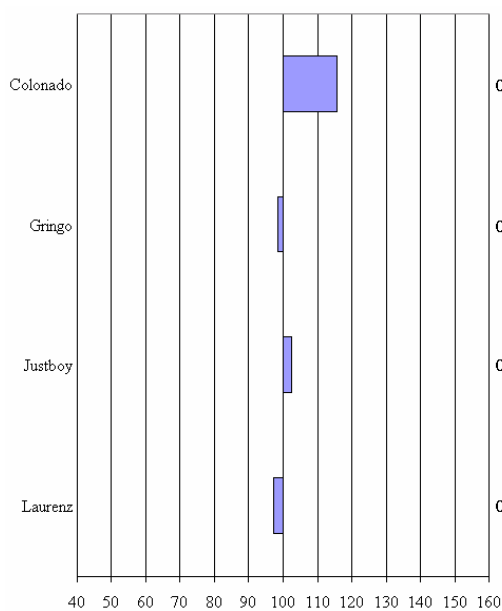


Figure 11. Breeding values based on Blom scores

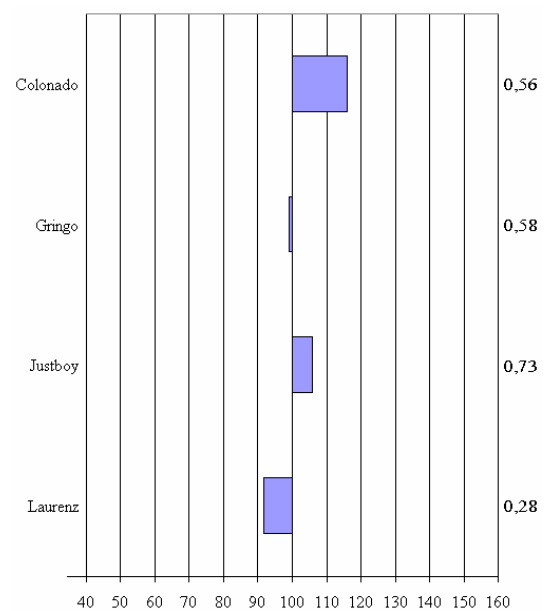


Figure 12. Breeding values based on cotangent transformed ranks

Show-jumping breeding values based on Blom score and cotangent transformed ranks of stallions introduced in the section „ Estimation of breeding values and genetic progress” are shown in *Figure 11. and 12.*

As can be seen, the order of the stallions and reliabilities of the proper breeding values are similar for the two measures.

Random regression analysis of sport competition results

Blom normalized ranks was the most fitted measure with repeatability animal model to the normal distribution, this measure had one of the lowest AIC value.

Various ordered Legendre polynomials were fitted to the Blom scores. Order of polynomials varied in the range of 1 and 5. After examining the estimated variances and variance proportions for each models, the first ordered Legendre polynomial (LP 1) was the best fitting. In the following, only the results of this model are presented.

The variances of random animal effect decreased in the early age (*Figure 13*). Least genetic variance was estimated for in the age of 1930 days. In later age the genetic variance continuously increased. Homogeneous variance was estimated for the random effect of rider, its volume is 0.063. Variance of permanent environmental effect continuously decreased. Variance of residual effect was estimated for age groups. Higher residual variance was found in the group of 10-year-old horses (0.64). Residual variance varied in the range of 0.55 and 0.57 for other age-groups.

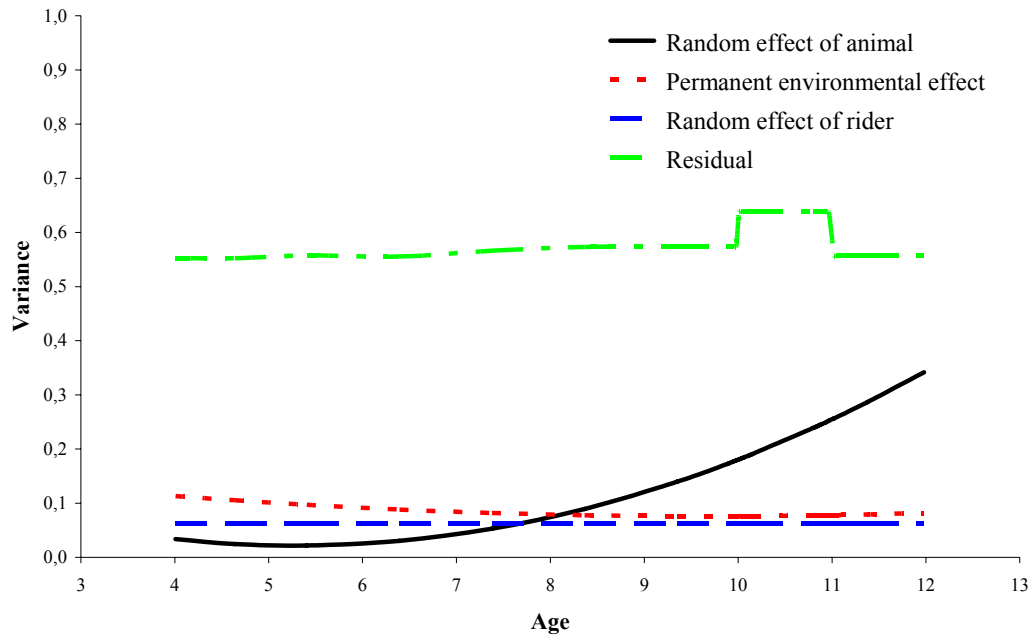


Figure 13. Variances for random and residual effects estimated with random regression model (LP 1)

The heritabilities increased continuously, values were in the range of 0.044 and 0.328 (*Figure 14*). Despite this increasing, proportion of variance for random effect of rider continuously decreased in a little volume. Variance proportion of permanent environmental effect decreased continuously. Proportion of residual variance increased up to 6 years of age and decreased afterwards.

There were both strong genetic and phenotypic correlation between neighbouring age groups (*Figure 15*). The genetic and phenotypic correlations between show-jumping performances in different age classes decreased continuously. There were negative genetic correlation between sport performance in early age and the last third of the age classes. Similarly to the genetic correlations, phenotypic correlations between early and last age classes were low, it was the lowest between the first and the last age in days ($r^2=0.083$).

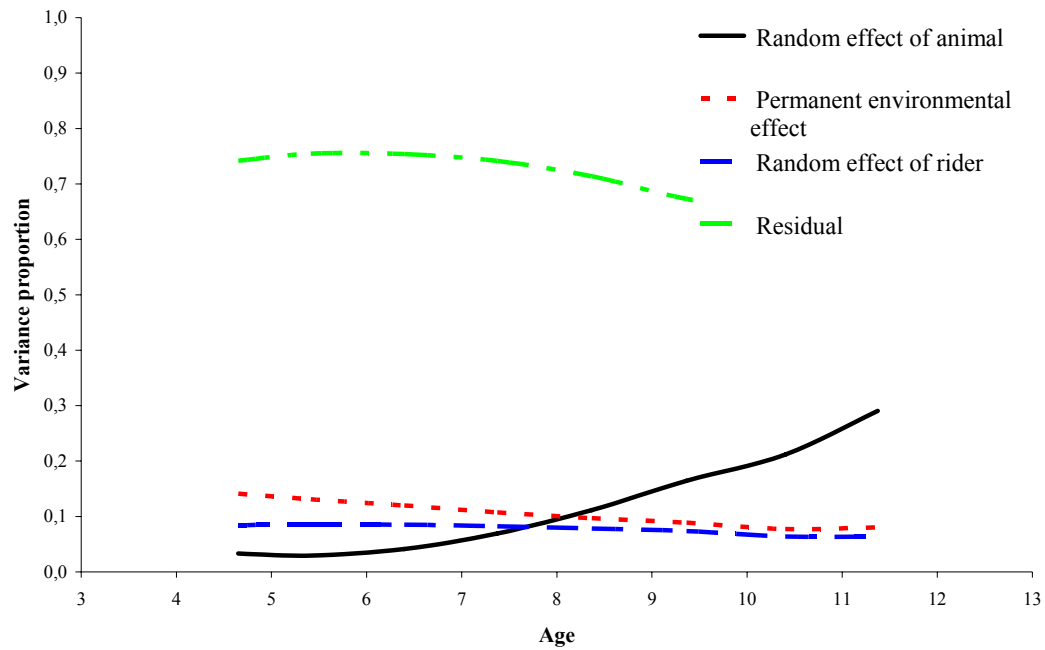


Figure 14. Variance proportions for the random and residual effect estimated with random regression model (LP 1)

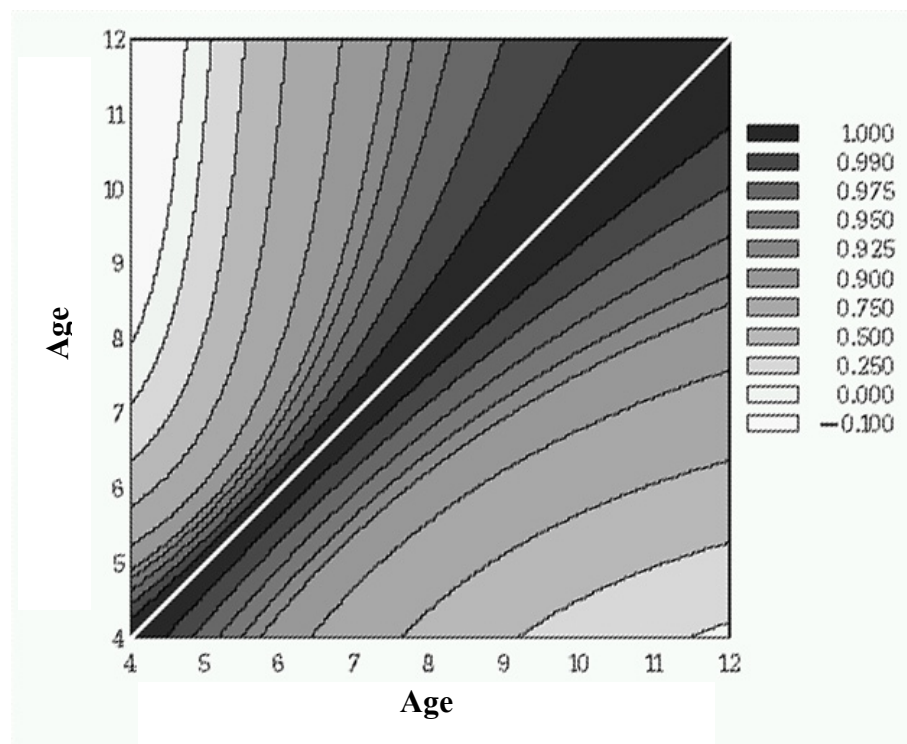


Figure 15. Genetic (above diagonal) and phenotypic (below diagonal) correlations between Blom-scores in different age classes

Breeding values estimated with random regression animal model is shown for previously introduced stallions. Breeding values are presented for five different ages in *Table 10*. and for the whole analysed interval in *Figure 16*. Coefficient of variation shows long time stable performance of the stallions. Performance is stable in the case of 3648 *Laurenz* and 2534 *Gringo*. From the breeding values estimated with random regression models a composite breeding value-index can be computed. The index presented in *Table 10* contains the estimated breeding values of the five ages as equally weighted. With the changes in weights, selection can be modified to prefer early mature or late mature.

The differences between stable and high performance are shown both in *Table 10* and *Figure 16*. 3114 *Colonado* has stable and high breeding values among the presented stallions. Evaluation of 2972 *Justboy* was the most favourable in later age despite its negative effect in early age Breeding values of 3648 *Laurenz* were below average or average for the evaluated age interval. In the order of the stallions based on breeding values only effect of 2972 *Justboy* has been changed, the order of remaining three stallions was continuous.

Table 10.

Breeding values estimated with random regression model in different ages				
	2534 Gringo IM885460000	3648 Laurenz IM890220099	2972 Justboy IM912340094	3114Colonado IM930410096
Four-year-old (X_4)	98	96	83	105
Six-year-old (X_6)	103	97	106	120
Eight-year-old (X_8)	104	99	119	120
Ten-year-old (X_{10})	104	100	121	119
Twelve-year-old (X_{12})	105	100	122	118
Mean of breeding values	102.90	98.32	110.47	116.30
Standard deviation of breeding values	2.62	1.87	16.37	6.60
CV% of breeding values	2.55	1.90	14.82	5.68
Breeding values index	102.90	98.32	110.47	116.30

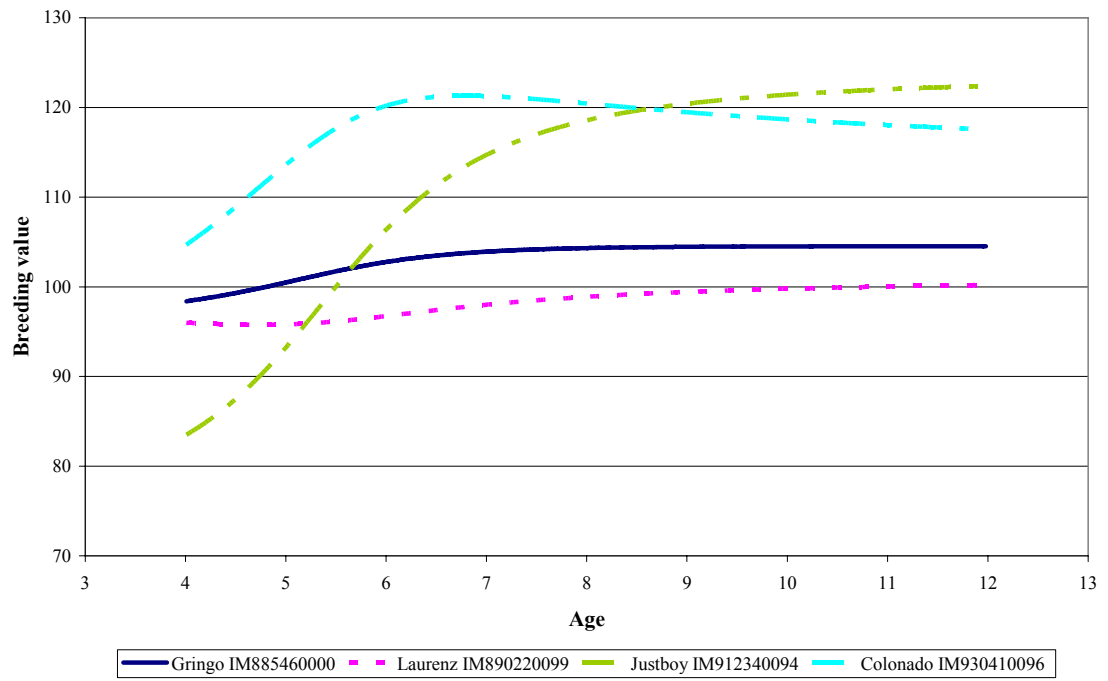


Figure 16. Breeding values estimated with random regression model

V NEW SCIENTIFIC RESULTS

The following scientific results can be established from my dissertation:

1. In the import stallion based Hungarian Sport horse breeding Nei-based genetic distance is between 0.012–0.039 for the most important studs. Generation interval of Hungarian Sport horse is 10.6.
2. Judgement of type, saddle region and head traits from the conformational traits of Hungarian Sport horse self performance tests were closely related.
3. Selection for a single trait from free jumping traits and movement analysis traits has a positive influence for the traits of the other trait group.
4. We found $h^2=0.28-0.53$ for conformational traits, $h^2=0.29-0.52$ for free jumping traits, and $h^2=0.22-0.51$ for movement analysis traits of Hungarian Sport horse self performance tests.
5. Hungarian Sport horse population judged in the period of 1993 to 2004 showed low genetic progress in the traits of self performance tests ($b=0.0054-0.0083$).
6. Blom transformed ranks were suggestible among models evaluating show-jumping results ($h^2=0.054$).
7. The first ordered Legendre polynomial was found as the best for the random regression evaluation of show-jumping results. Heritability continuously increased and variance proportion of permanent environment effect continuously decreased with the increase of age. Breeding value can be estimated in different ages; from these values a composite breeding value index can be computed.

VI PRACTICAL UTILITY OF THE RESULTS

Known heritabilities of the traits judged in Hungarian Sport horse mare self performance tests and show-jumping performance make easier the successful work of specialist working in the Hungarian Sport horse industry. Efficient selection can be done with the knowledge of the genetic correlation between different traits.

Some results of my dissertation show the positive genetic correlation between free jumping performance and movement analysis traits. This means, that separate selection for gaits and jumping performance is not necessary, selection based on the traits with the highest heritability will be positive for the other traits also.

Breeding values based on the transformed ranks makes easier the selection on the show-jumping performance. Consistent selection will give genetic progress and increase the genetic merit of the Hungarian Sport horse population.

Breeding values estimated with random regression model help to find animals with long time good performance.

VII PUBLICATION LIST

Reviewed scientific publications

POSTA J. – KOMLÓSI I. (2006): Fenotípusos korrelációk használata a magyar sportlókancák tenyészérték-bebecsléséhez; Agrártudományi Közlemények, 2006/21. Különszám 38-43. p.

POSTA J. – KOMLÓSI I. – MIHÓK S. (2006): Pedigree analysis of Hungarian Sport horses. Animal welfare, etológia és tartástechnológia, II. évfolyam 3. szám 182-188 <http://www.animalwelfare.szie.hu>

J. POSTA – I. KOMLÓSI – S. MIHÓK (2007): Principal component analysis of performance test traits in Hungarian Sporthorse mares; Archiv für Tierzucht 50, 2007 125-135 p.

POSTA J. – KOMLÓSI I. (2007): Magyar sportló kancák néhány testméretének genetikai elemzése; Agrártudományi Közlemények, Acta Agraria Debreceniensis, 2007/26. Különszám 40-43 p.

POSTA J. – KOMLÓSI I. (2007): Magyar sportló kancák sajátjeljesítmény vizsgájának paraméterbecslései; Állattenyésztés és Takarmányozás, 56. 3. 253-261.

POSTA J. – KOMLÓSI I. – MIHÓK S. (2007): Genetikai előrehaladás vizsgálata a magyar sportló populációban; Állattenyésztés és Takarmányozás, 56. 4. 313–323.

Book, part of book

POSTA J. – KOMLÓSI I. – PRUTKAY Z. – MISLEY B. – MIHÓK S. (ed.: Mihók S.) (2007): A magyar sportlóállományra alapozott tenyészértékbecslési kutatások eredményei; Debrecen, ISBN 978-963-9732-13-1

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POSTA J. (2005): Tenyészértékbecslési alternatívák a sportlótenyésztésben; XI. Ifjúsági Tudományos Fórum, Keszthely, 2005. 03. 24

POSTA J. (2005): Magyar sportló kancák STV paraméterei közötti korrelációk vizsgálata, XLVII. Georgikon Napok Keszthely, 2005. szeptember 29-30.

POSTA J. – KOMLÓSI I. – MIHÓK S. (2006): A magyar sportló fajta kancavizsgálata értékelése főkomponens analízissel. Lótenyésztési Tudományos Napok, Debrecen 2006. 10. 27-28.

POSTA J. – KOMLÓSI I. – MIHÓK S. (2007): Magyar sportló populáció genetikai szerkezetének vizsgálata. XLIX. Georgikon Napok, Keszthely, 2007. 09. 20-21.

Conference proceedings in foreign language

POSTA, J. (2005): Alternatives of breeding value estimation in sport horse breeding; Sustainable Agriculture Across Borders in Europe, Debrecen 2005. 05. 6. 256-258. p

J. POSTA – I. KOMLÓSI – S. MIHÓK (2006): Genetic Parameters of Hungarian Sporthorse mares. 57th Annual Meeting of the European Association for Animal Production (EAAP) Antalya, Turkey H.25.3.

J. POSTA – I. KOMLÓSI – S. MIHÓK (2006): Analysis of Hungarian Sporthorse Studbook; The 4th International Symposium „Natural resources and sustainable development” Oradea, 2006 október 10-11. pp.497-503

J. POSTA – I. KOMLÓSI – S. MIHÓK (2007): Analysis of genetic progress in the Hungarian Sport Horse population. 58th Annual Meeting of the European Association for Animal Production (EAAP) Dublin, Ireland H.17.8.

Other publication

POSTA J. (2006): Tenyésztértébecslési eljárások az európai sportlótenyésztésben 1. rész; Lovasfutár, XV. évfolyam, 2. szám, 2006. 2. 23-24. p

POSTA J. (2006): Tenyésztértébecslési eljárások az európai sportlótenyésztésben 2. rész; Lovasfutár, XV. évfolyam, 3. szám, 2006. 3. 19. p

POSTA J. (2006): Tenyésztértébecslési eljárások az európai sportlótenyésztésben 3. rész; Lovasfutár, XV. évfolyam, 4. szám, 2006. 4. 24. p

POSTA J. (2006): Tenyésztértébecslési eljárások az európai sportlótenyésztésben 4. rész; Lovasfutár, XV. évfolyam, 5. szám, 2006. 5. 23. p

POSTA J. (2006): Tenyésztértébecslési eljárások az európai sportlótenyésztésben 5. rész; Lovasfutár, XV. évfolyam, 6. szám, 2006. 6. 29. p

POSTA J. (2006): A magyar sportló populáció kialakításában jelentősebb ménnek tenyésztértékei; Lovasfutár, XV. évfolyam, 9. szám, 2006. 9. 30-32. p