60th ANNUAL MEETING OF THE EUROPEAN ASSOCIATION FOR ANIMAL PRODUCTION (EAAP)
BARCELONA, SPAIN, AUGUST, 24th - 27th, 2009
Session 14: Free communications in genetics of meat animals

SELECTION OF IMPORTANT TRAITS FOR BREEDING VALUES ESTIMATION OF THE LINEAR DESCRIBED TYPE TRAITS OF THE OLD KLADRUBER HORSES

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OBJECTIVES

Selection of important conformation traits and a reduction in the number of described characteristics from the present 36 to 24 traits and select a suitable model for the estimation of genetic parameters for linear type description in Old Kladruber horses.

MATERIAL AND METHODS

Estimation of the genetic parameters and breeding values for 36 conformation linear described traits was evaluated in 977 Old Kladruber horses with repeated description within the period of 16 years (1990-2006). The reduction of traits (from primary 36 to eventual 24) was carried out using combinatorics *n*-tuple of traits according to:

1) The criterion of genetic similarity (cluster analysis)

2) Measure of uncertainty of multidimensional values

$$f(G) = \sqrt{tr(G)^2 - \sum_{i,j} g_{i,j}^2},$$

3) Values of the variance of aggregate genotype

$$\sigma_H^2 = a'G$$

4) Variance of selection index at a reduction in traits in the selection goal

$$\sigma_{I1}^2 = a'GP^{-1}Ga$$

5) Variance of selection index while maintaining the selection goal

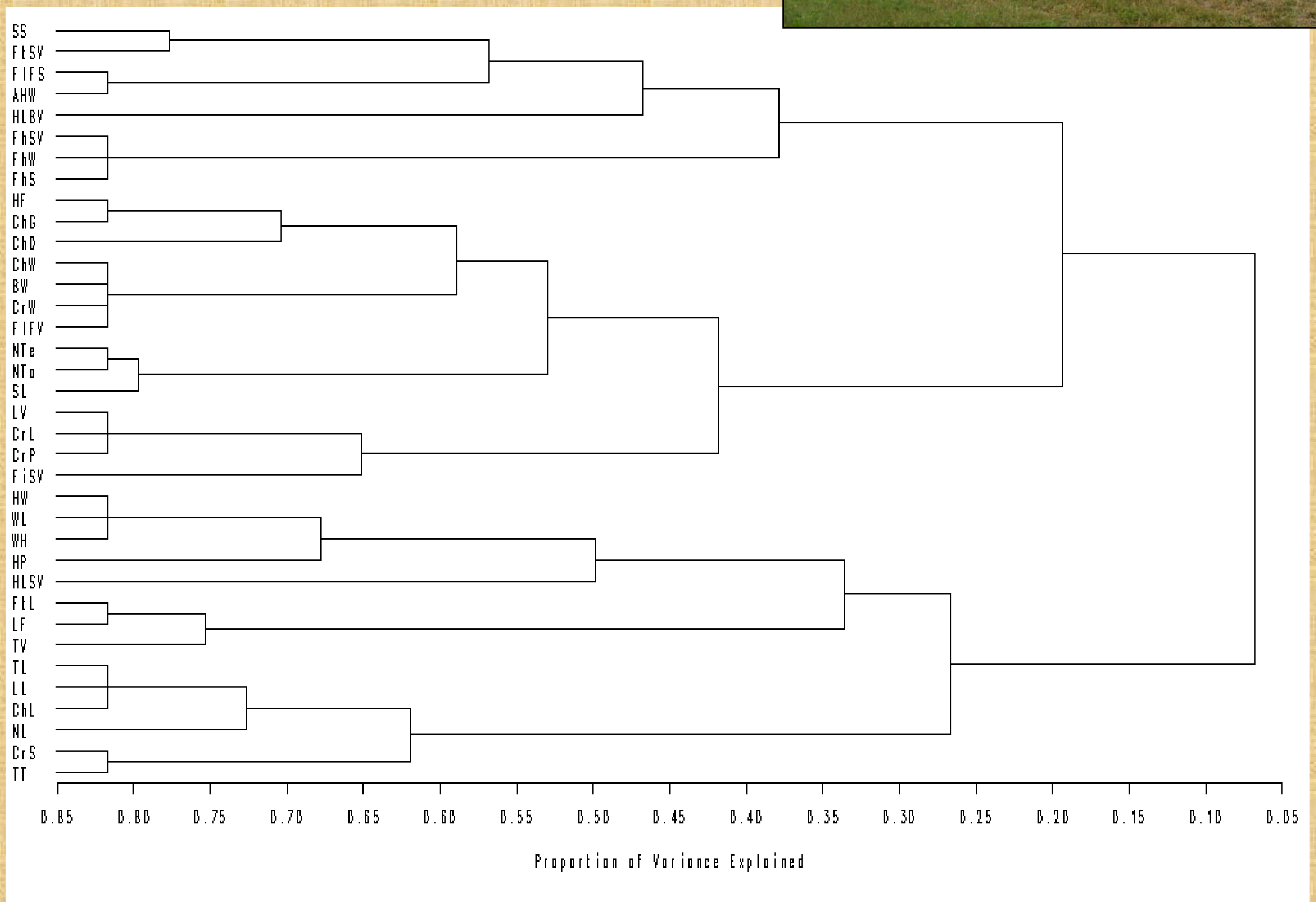
$$\sigma_{I2}^2 = a'CP^{-1}Ca$$

6) The value of correlation of a trait with the first principal component

$$r_{G,x} = \frac{a'G_{,i}}{\sqrt{\sigma_H^2 \sigma_x^2}}$$

RESULTS

Cluster analysis



CONCLUSION

- ❑**The value of the selection index variance was the most appropriate parameter for the selection of important traits out of 36 described.**
- ❑**In this method the highest value of reliability with the selection goal was estimated.**
- ❑**This method rejects the traits with low heritability and low genetic correlation with other traits.**

Comparison of the methods of selection

Trait	Methods					
	1	2	3	4	5	6
AHW				✓		✓
BW			✓			
CrL	✓	✓	✓		✓	
CrP			✓			
CrS				✓		
CrW			✓	✓		
FhS	✓	✓			✓	✓
FhSV	✓	✓			✓	✓
FlFS	✓	✓	✓	✓	✓	
FlFV	✓	✓		✓		
FtL			✓	✓	✓	✓
FtSV		✓			✓	✓
HLBV		✓				✓
HLSV		✓			✓	✓
HP						✓
HW						✓
ChD					✓	
ChL				✓		✓
ChW			✓		✓	
LF				✓		
LL	✓		✓		✓	
LV	✓					
NL		✓				✓
NTe	✓	✓			✓	
SL	✓	✓	✓	✓		
SS	✓	✓				✓
TL					✓	
TT	✓		✓			
TV				✓		✓
WH			✓	✓		
WL	✓		✓	✓		
$r^2_{I2,H}$	0.507	0.506	0.413	0.448	0.532	0.484

The values of uncertainty, aggregate genotype variance and selection index variance with a reduction in the number of traits

Number of traits	$f(v)$	σ^2_H	σ^2_{I1}	$r^2_{I1,H}$	σ^2_{I2}	$r^2_{I2,H}$
36	16.23	2.48	1.37	0.538	1.3361	0.538
35	16.16	2.71	1.51	0.557	1.3360	0.538
34	16.09	2.89	1.63	0.563	1.3357	0.538
33	16.01	2.99	1.80	0.601	1.3351	0.538
32	15.94	3.08	1.83	0.593	1.3346	0.537
31	15.85	3.17	1.93	0.610	1.3339	0.537
30	15.76	3.28	1.98	0.605	1.3331	0.537
29	15.67	3.38	2.05	0.606	1.3317	0.536
28	15.55	3.45	2.12	0.614	1.3304	0.536
27	15.39	3.53	2.16	0.613	1.3286	0.535
26	15.22	3.60	2.19	0.609	1.3267	0.534
25	15.04	3.63	2.23	0.616	1.3240	0.533
24	14.84	3.63	2.23	0.615	1.3211	0.532

Supported by the Ministry of Education, Youth and Sports of the Czech Republic (Project No. MSM 6046070901) and by the Ministry of Agriculture of the Czech Republic (Project No. MZE 0002701404)