Prediction of genotype probabilities at eight coat colour loci in the Icelandic horse

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Objective

- Develope Java Servlet which will add prediction of coat color genotypes and phenotypes of the potential foal into a mate selection program
- The mate selection program also computes EBVs for 17 traits and F% in the potential progenies
- www.worldfengur.com

Data for coat colour genotype analysis

- > 233498 horses in the data base (Worldfengur)
- 60% (142077) horses with a 4 digit colour code

Distribution of basic coat colours

Chestnut	43266	30,45%
Black	41949	29,53%
Bay	23185	16,32%
Palomino	4416	3,11%
Buckskin	1876	1,32%
Red-Dun	8407	5,92%
Blue-Dun	5283	3,72%
Silverdapple	3014	2,12%
”Albino”	167	0,12%

Distribution of additional coat colours

Grey	10514	7,40%
Tobiano	12965	9,13%
Roan	687	0,48%

Locus	Effect	Coat colour
E- (extension)	Eumelanin/phaeomelanin	Black/chestnut
A- (agouti)	Restricts eumel.	Bay
C- (colour)	Dilution	Cream
D- (dilution)	Dilution	Dun
G- (grey)	Greying	Grey
Z- (silverdapple)	Dilutes eumel.	Silverdapple
To- (tobiano)	White spotting	Tobiano, piebald
R- (roan)	Admixture of white hairs	Roan

Genotype frequency

- LL (dominant homozygotes) = p^2
- Ll (heterozygotes)= 2 pq
- ll (recessive homozygotes)= q^2

Gene frequency (H-W eq.)

	E	A	C	D	G	Z	To	R
p	0.39	0.19	0.96	0.05	0.04	0.02	0.05	0.002
q	0.61	0.81	0.04	0.95	0.96	0.98	0.95	0.998

Analysis I

- ”Genotype Elimination Algorithm” (Lange, 1997)
- For every horse: List all possible genotypes in all loci which are compatible with phenotype and pedigree information
- Write out a list with ”errors” where code or pedigree is not according to the Mendelian laws of transmission

Errors detected by GE

E	457	0,3%
A	583	0,4%
C	180	0,1%
D	554	0,4%
G	230	0,2%
Z	102	0,1%
To	479	0,3%
R	130	0,1%

New phenotypic code after GE

Code	Genotype (*e.g.* A locus)
1	ll (aa)
2	Ll (Aa)
3	LL (AA)
4	L- (A-)
5	l- (a-)
9	-- (--)

Analysis II genotype probabilities

- Iterative method and computer program of Kerr & Kinghorn (1996)
- Computes for any horse and any loci the conditional probability of possible genotypes given all data
- Bayesian statistics for combining information sources (Fernando *et al.*1993)

Results

- Results were loaded into MySQL tables which can be accessed with Java Servlet
- www.ihbc.se/app/servlet/IsPedigreeBLUPF
- The servlet displays EBVs for 17 traits, F%, genotype probabilities in 8 loci and possible coat colours of the potential progeny from the selected mating. Picture of each possible colour and probability of that colour.
- Will be moved to www.worldfengur.com

Conclusions

- The Genetic Elimination algortihm of Lange is useful for preparing large data for genotype probabilities estimation
- The method of Kerr & Kinghorn for computing genotype probabilities works (numerical stable) in large data!
- Inclusion of predictions of coat colour genotypes in mate selection program stimulate interest in genetics among breeders!

Thanks !