55th Annual Meeting of the EAAP, Bled, Slovenia, September 5th-9th, 2004. Commission on Animal Genetics (G) and Commission on Horse Production (H), Session V. Paper HG5.3

International genetic evaluations of the Icelandic horse

T. Arnason[1], A. Sigurdsson[2], [1]International Horse Breeding Consultant AB, Knubbo, S-74494 Morgongava, Sweden, [2]Farmers Association of Iceland, Baendaholl v/Hagatorg, IS-107 Reykjavik, Iceland*

Abstract

The International Federation of Icelandic Horse Associations (FEIF) has harmonized a common breeding goal and a standard form of evaluating the conformation and riding ability traits of Icelandic breeding horses on a scale of linear scores. An important step towards global genetic evaluation of the Icelandic horse has been initiated. A global pedigree database has been established containing 190,000 horses with unique identification numbers, whereof 20,000 horses have records from FEIF breeding tests were breeding horses have been evaluated by authorized judges. The material has been used for estimation of genetic parameters and for studying genetic connectedness across country. The genetic correlations between traits evaluated in different time periods and countries have been studied. The genetic model was validated by regressions of solutions from the complete data on solutions from randomly sub sampled data (method R). An animal model MT-BLUP using records from Iceland, Denmark, Sweden, Norway and Finland has been implemented for genetic evaluations of all horses included in the data base. In total 30 traits were included. The information on pedigree, colour, owner, test-results and EBVs is stored in a SQL database and can be accessed on the Web by Java Server Pages for subscribers on URL: http://www.worldfengur.com

Introduction

The Icelandic horse is the only horse breed in Iceland and has existed since the country was settled late in the 9th century. As far as known no importation of genetic material has occurred during the last centuries (Adalsteinsson, 1981). On the other hand many Icelandic horses were exported to several European countries in the latter part of the 19th century and in the former half of the 20th century for work in coal mines and in small farming. Since 1950 about 50,000 horses have been exported to Europe and North-America solely for use as riding horses (and for breeding of Icelandic riding horses). The Icelandic horse has become recognized as an important factor in the Icelandic cultural heritage and image. It is of great importance for the Icelandic tourist industry and is an invaluable advertisement for Iceland and Icelandic products in other countries. This has been acknowledged by Icelandic authorities and therefore the Icelandic horse breeding and horse industry receives considerable support from the government.

Since 1950 the official breeding goal in Iceland has been breeding of horses suited for riding by adult persons as well as youngsters where emphasis is put on the special multi-gaiting ability which is characteristic for the Icelandic horse. A scoring index for registration of individual traits on a linear ordered categorical scale was developed as early as 1950 for assessing the breeding horses and the complete material since 1961 is available in a data base. The material has several times been subject for genetic analyses and since 1982 *EBV*s (estimated breeding values) have been regularly computed for the individual traits by MT-BLUP AM (multiple trait BLUP animal model) (Arnason, 1984). (For historical reviews see Arnason, *et al.* (1994) and Hugason (1994)).

The International Federation of Icelandic Horse Associations (FEIF, www.feif.org) was founded in 1969 with the major goals of co-operation and exchange of experience between the member organizations, preserve the breed and standardize the breeding goal and the evaluation methods for breeding and sport. In general only one organisation from each country can be a member of the Federation. At present 19 countries are members of FEIF. Within FEIF there is a special committee for breeding with the main objective of harmonizing the breeding goals, standardizing the measurements of the traits which are to large extent dependent on subjective scoring, and to accomplish international genetic evaluation of Icelandic horses for the traits included in the breeding objectives.

A major effort towards defining and standardizing the scoring scale was done in 1990-1992 , which resulted in a publication in Icelandic, with complete English and German translations (Ed. Hugason, 1992). Judges have to pass a strict examination in order to get a licence from FEIF for becoming international judges and have to practice regularly, judging many horses annually in order to maintain their licence.

In year 2000 FEIF and the Farmers Association of Iceland (FAIC) assigned an agreement on establishing a data base containing a global register for the Icelandic Horse which can be accessed over the Internet. The web application has been termed ”WorldFengur” with the domain name www.worldfengur.com. The data base is in Structured Query Language (Oracle 8i base) and the information from the database is accessed with use of Java Server Pages which have been developed using the JDeveloper tools from Oracle. The ”WorldFengur” project has received considerable funds from the Icelandic government but is otherwise financed by fee from the member countries and by read-only subscriptions of individuals. The countries with most horses registered into the WorldFengur database March 19, 2004 are listed in Table 1.

Table 1. The 10 countries with most horses registered in WorldFengur March 19, 2004

Country	Number of horses born in the country and registered into WorldFengur
Iceland	163,571
Denmark	18,163
Sweden	4,760
Netherlands	3,329
Norway	907
Switzerland	743
Belgium	666
Austria	582
Finland	532
Germany	508

The database of ”WorldFengur” contains a complete pedigree file where each horse is identified by its standard FEIF-ID number which consists of 12 letters: [Country of birth, 2][Year of birth, 4][Sex, 1][Area, 2][Permanent number, 3]. Information is registered about the breeder, owner, colour of the horse (4-digit code) and identification mark (microchip and/or freeze mark). The results from the scoring tests on conformation and riding ability are directly registered (online) into the database. The tests take place in the spring and in the summer. The results from the genetic evaluation by the MT-BLUP AM are annually loaded into the data base in the autumn. The web application is located in Iceland where also is the central of the administration. The data from the other member countries were initially imported into the central Icelandic data base (Fengur). Subsequently the main rule is that each country register data for the country online directly into WorldFengur.

Queries to the SQL database concerning pedigree trees, test results , EBV (BLUP), progeny information, *etc*, are easily requested through the form menu of the Java Server Pages. The Java platform for ”WorldFengur” makes it very flexible and adoptable to the rapid technical development, as it is made up of portable components which are robust, dynamic and architecture-neutral. Addition of new functions, advanced graphics and future adaptation to dynamic multimedia content and WAP-enabled mobile devices for the database accesses is facilitated.

Creation of a global database which contains all pedigree information and recorded scores on the traits obtained in different countries provides good possibilities to compute EBVs which are comparable across country, in a common analysis. The main objective of this paper is to present some aspects of the validation the data and models for the international genetic evaluations based on this data. The data from the Nordic countries were most homogeneous with respect to the composition of judges’ teams and form of scoring of the traits and these countries have for a long time accepted a common breeding goal. Therefore only records from Iceland, Denmark, Sweden, Norway and Finland were used throughout this pilot-study and all validation was concentrated on data related to these countries.

Material and Methods

Validation of pedigree file

The pedigree file used in this study was loaded from WorldFengur in March 2004. It contained 196,031 horses. The birth year was unknown for 18% of the horses, most of them appearing rather remote in the pedigree and without records. The validation of the pedigree depth and pedigree completeness was based on the 172,569 animals born before year 2000. Younger animals were without records since Icelandic horses are scored as 4-year-olds at youngest.

The pedigree depth in generations from horses born in 1997 to the base animals was counted for the direct paternal and maternal paths, respectively. The pedigree completeness in the pedigree file was quantified by computing the pedigree completeness index (PEC) of MacCluer *et al.* (1983) for animals born in the years 1980 to 1999. Pedigree depth and pedigree completeness was compared between the Nordic countries.

Measures of genetic connectedness between sub-populations

Kennedy and Trus (1993) suggested three methods which can be used in practice for measuring genetic connectedness between populations. The first method was simply a measure of gene flow from the base animals into the different management units (or countries). Since all the foundation animals were born in Iceland the flow of genes was solely in one direction and therefore this measure was of limited value in this material. The second method was computation of the "genetic drift variance" as $\mathbf{X'ZAZ'X}$, where $\mathbf{X}$ and $\mathbf{Z}$ are the incidence matrices for management units and animals in an animal model, respectively, and $\mathbf{A}$ is the numerator relationship matrix. This method was used by Árnason and Ricard (2001) for measuring the genetic drift variance between Icelandic horses born in Iceland, Denmark and Sweden in 1995. The relationship between animals across these countries was found to be almost as high as the relationship within countries and high degree of connectedness or genetic ties was indicated.

The third method of Kennedy and Trus (1993) provides a measurement of the variance of estimated differences between management units effects. This method is considered to be the best practical measure of genetic connectedness in mixed linear models for genetic evaluations since it is a close approximation of the average prediction error variance (PEV) of differences in EBV between animals in different management units. As generally recognized the PEV matrix is prohibitively difficult to compute for animal models involving large populations. The variance-covariance matrix of management unit estimates is as follows:

$$[\mathbf{X'X} - \mathbf{X'Z}(\mathbf{Z'Z} + \mathbf{A}^{-1}\lambda)^{-1}\mathbf{Z'X}]^{-1}\,\sigma^2_e$$

As long as the management units are not too numerous the matrix: $[\mathbf{X'X} - \mathbf{X'Z}(\mathbf{Z'Z} + \mathbf{A}^{-1}\lambda)^{-1}\mathbf{Z'X}]$ is easily invertible. The difficult part is to obtain $(\mathbf{Z'Z} + \mathbf{A}^{-1}\lambda)^{-1}$. The $\mathbf{A}$ inverse is of course easily computed from a pedigree list by the Henderson-Ouaas algorithm (Quuas, 1976). Afterwards selected elements of $(\mathbf{Z'Z} + \mathbf{A}^{-1}\lambda)^{-1}$ can be extracted by sparse matrix technique (Misztal and Perez-Enciso, 1994, Thompson *et al.*,1994).

Árnason and Ricard (2001) showed the use of this method for measuring genetic connectedness between Icelandic horses scored in Iceland, Denmark and Sweden in year 2000. This procedure was now repeated for horses scored in Iceland (n=885), Denmark (215), Sweden (184), Norway (82) and Finland (16) in year 2003. The necessary elements of the inverse of the sparse matrix $(\mathbf{Z'Z} + \mathbf{A}^{-1}\lambda)$, of dimension 7164 x 7164, were computed by the program provided by Misztal and Perez-Enciso (1993) for sparse matrix inversion by the method developed by Takahashi *et al.* (1975).

Validation of traits included in genetic evaluations

The breeding goal is the same for all the member countries according to the FEIF standard. The traits were scored on a ordered categorical scale from 5.0 to 10.0. The distribution of the scores was plotted, the moments were estimated and the consequences of treating the categorical scores as linear in the statistical analysis were evaluated.

A multivariate complex of 14 traits is currently included in the genetic evaluations. The genetic parameters are based on REML analysis from 1997 (Sigurdsson, Hugason and Árnason, 1997). In addition single trait evaluations are performed for mane and tail hairiness and for height at withers. The traits are listed in Table 2 together with phenotypic variation, heritability and relative weights in the total score, ***a*** (reflecting the breeding goal).

Table 2. Traits included in current genetic evaluation of Icelandic horses

	Trait	σ_P	h^2	***a* (rel. weight)**
1.	Head	0.52	0.38	0.030
2.	Neck, shoulders	0.42	0.46	0.100
3.	Back, croup	0.53	0.32	0.030
4.	Proportions	0.49	0.40	0.075
5.	Legs	0.53	0.38	0.060
6.	Correctness of legs	0.50	0.28	0.030
7.	Hoofs	0.55	0.46	0.060
8.	Toelt	0.69	0.43	0.150
9.	Trot	0.73	0.34	0.075
10.	Pace	1.26	0.63	0.090
11.	Gallop	0.62	0.32	0.045
12.	Willingness	0.49	0.34	0.078
13.	Character	0.38	0.19	0.047
14.	Expression	0.51	0.42	0.100
15.	Mane & tail	0.69	0.40	0.015
16.	Height at withers	3.01	0.60	0.000

In Table 3 the genetic and phenotypic correlations between the 14 traits in the multivariate complex are revealed.

Table 3. Genetic correlations below the diagonal and phenotypic correlations above the diagonal

-	0.30	0.10	0.21	0.04	0.07	0.03	0.11	0.04	0.04	0.09	0.09	0.08	0.17
0.51	-	0.16	0.45	0.05	0.05	0.12	0.25	0.16	0.06	0.26	0.20	0.14	0.46
0.12	0.33	-	0.27	0.05	0.04	0.05	0.17	0.13	0.09	0.14	0.10	0.11	0.18
0.34	0.65	0.49	-	0.01	0.01	0.12	0.16	0.11	0.08	0.17	0.09	0.10	0.25
0.06	0.09	-0.01	-0.01	-	0.05	0.12	0.09	0.08	0.02	0.10	0.03	0.04	0.09
0.15	0.21	0.00	0.05	0.08	-	0.03	0.06	0.07	-0.00	0.06	0.06	0.06	0.07
-0.02	0.22	0.08	0.16	0.11	-0.01	-	0.17	0.13	0.08	0.17	0.14	0.07	0.18
0.22	0.33	0.30	0.34	0.07	0.11	0.38	-	0.52	0.10	0.46	0.52	0.38	0.72
0.10	0.11	0.18	0.22	0.09	0.07	0.23	0.71	-	-0.03	0.36	0.30	0.32	0.48
0.08	0.11	0.17	0.14	0.06	-0.07	0.18	0.18	-0.20	-	0.15	0.27	0.18	0.12
0.19	0.40	0.21	0.31	0.17	0.21	0.41	0.79	0.56	0.27	-	0.56	0.24	0.52
0.14	0.21	0.09	0.12	-0.10	0.12	0.29	0.72	0.41	0.42	0.81	-	0.16	0.57
0.39	0.25	0.36	0.33	-0.21	0.20	0.17	0.68	0.44	0.36	0.54	0.43	-	0.41
0.32	0.56	0.33	0.41	0.07	0.14	0.34	0.88	0.60	0.15	0.82	0.72	0.64	-

The variance/covariance matrices were confirmed positive definite and canonical transformation has been applied in order to facilitate the computations of *EBV*s by use of animal model BLUP (Árnason, 1982, 1984). The mixed linear animal model includes the fixed effects of country/year and 8 sex/age effects (male, female; 4-year, 5-year, 6-year and ≥7-year). The correlation structure is generally positive amongst the traits in the multivariate complex and the first principal components (explaining about 50% of the variance) are generally discriminating between "good" and "bad" horses in terms of both conformation and riding ability (Árnason, 1984). The overall heritability in the form of the linear function **a'Ga/a'Pa** is in the order of 0.55.

Validation of the genetic model

The method of Reverter *et al.* (1994 *a,b,c)* was used for testing the predictive ability of the statistical model used for computing the genetic evaluations. The method requires the following statistics to be calculated:

$$R_i = (\mathbf{\hat{a}'}_{\mathbf{0}k}\mathbf{A}^{-1}\mathbf{\hat{a}}_{\mathbf{1}\mathrm{k}})/(\mathbf{\hat{a}'}_{\mathbf{0}k}\mathbf{A}^{-1}\mathbf{\hat{a}}_{\mathbf{0}\mathrm{k}}) ,$$

where $\mathbf{A}^{-1}$ is the inverse of the numerator additive genetic relationship matrix, $\mathbf{\hat{a}_1}$ is the vector of *EBV*s for trait *k* from the analysis of the complete data, $\mathbf{\hat{a}_0}$ is the vector of *EBV*s for trait *k* from the analysis of the data after 50% random sub-sampling of records and $i = 1, \ldots, k^2$. For a correct model $E\,(\mathrm{R_i}) = 1$. Deviations from 1 indicate deficiencies in the fit of the statistical model, possibly due to use of a wrong set of genetic parameters. The procedure was replicated five times and averages and standard errors were computed.

Comparison of genetic levels and environmental effects between countries

Average *EBV*s within countries and years were used for comparing genetic levels across country and for computing genetic trends. Fixed effects of country/year were included in the statistical mixed linear model so trends and levels in environmental factors could be inspected.

Estimation of new genetic parameters

The Icelandic material was split in two data sets for the genetic analyses. The first dataset included records from 1979 to 1989. The latter data was from 1990 to 2003. The variance/covariance components which were used for construction of genetic parameters were estimated by the ASReml software (Gilmour *et al.* 2002).

Results and discussion

Validation of pedigree file

The pedigree file including animals born before the year 2000 consisted of 172,569 animals. Animals were one and/or both parents were missing (base animals) were 39,331 (22.8%). Thereof 30,129 had both parents missing (17.5%), 2,321 had only the sire missing (1.3%) and 6,881 had only the dam missing (4.0%). All base animals were born in Iceland. In the other countries the requirement of pure breed means that only animals, where all pedigree paths can be traced to Icelandic ancestors, are registered. Animals belonging to the youngest generation in the material (years 1990-1999) had one or both parents missing in 3-4% of cases. This figure must be considered too high and effort should be made to fill these gaps in the Icelandic pedigree file.

The results of counting generations from animals born 1997 to the base is revealed in Figure 1 . The direct paternal path could be traced on average little more than 10 generations with little difference between countries. The direct maternal path was about 4 generations long and a bit shorter for animal born in Iceland and Sweden.

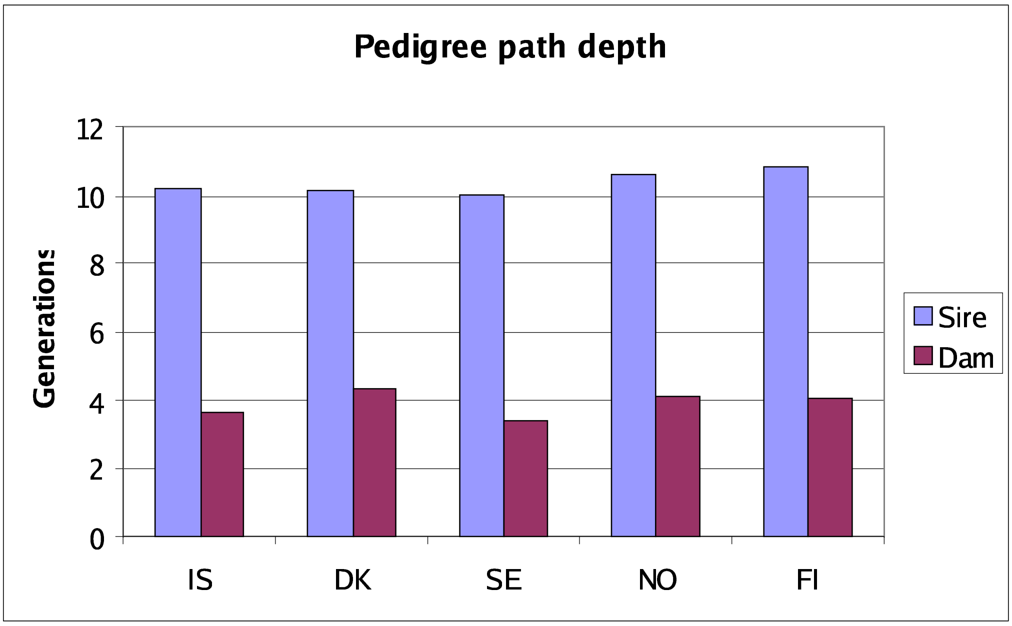

Figure 1. Generations traced from animals born 1997 to the base animals in the pedigree file.

The pedigree completeness index was computed for all animals in the pedigree file. The average PEC values within countries for birth years 1980 to 1999 were plotted in Figure 2. Corresponding values for horses with records are shown in Figure 3. The pedigree completeness was significantly higher for horses with records than for animals without records, especially in the Icelandic data. The pedigree completeness was considerably higher in Denmark, Norway and Finland than was the case for Iceland and Sweden.

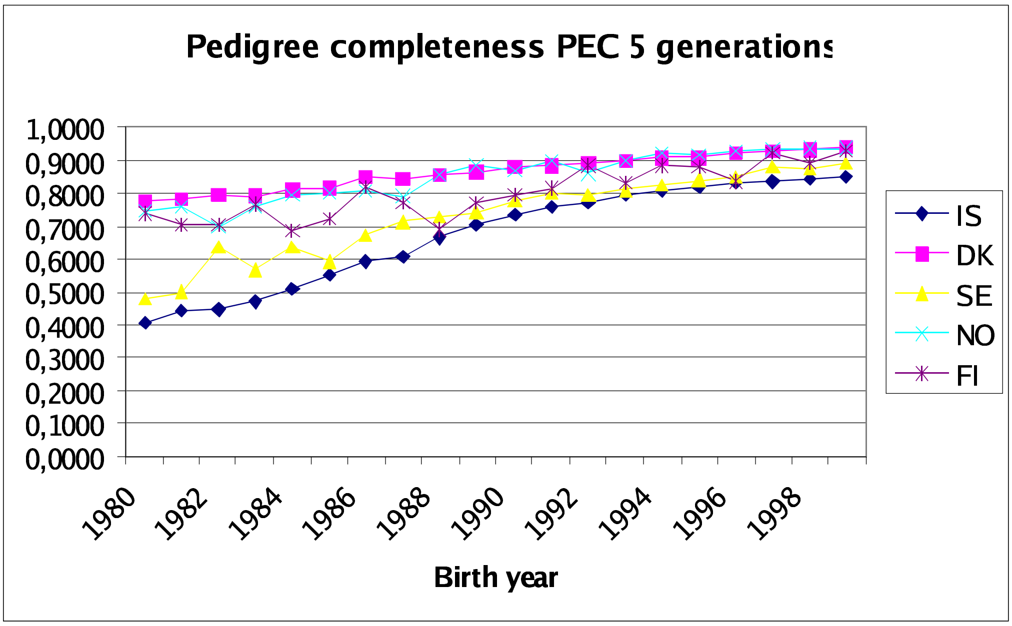

Figure 2. Mean pedigree completeness index (PEC) for all animals born 1980-1999

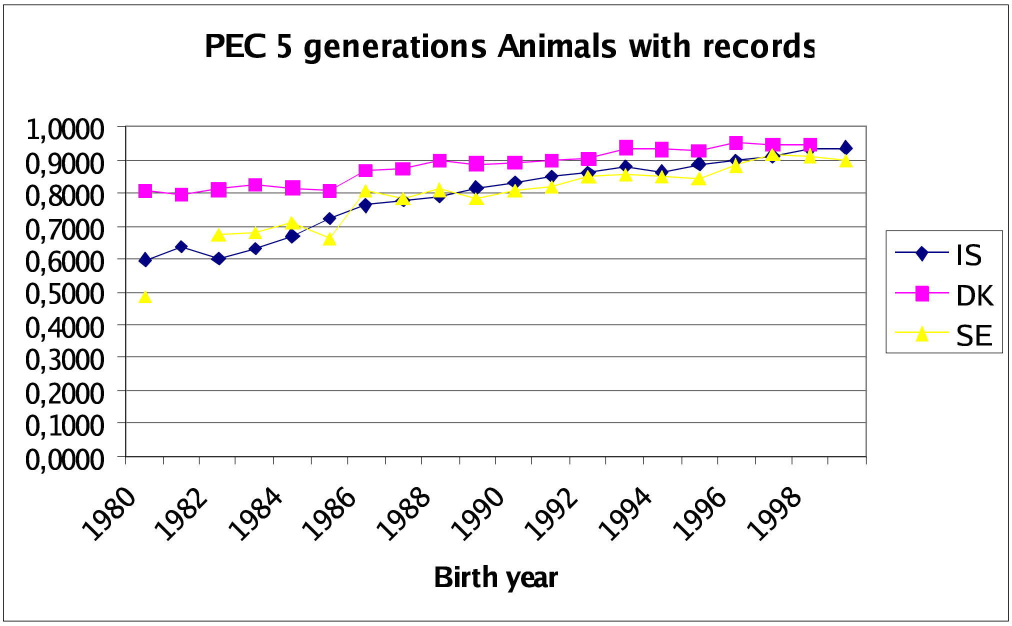

Figure 3. Mean pedigree completeness index (PEC) for animals born 1980-1999 having own records

Genetic connectedness

The following measurements of the variance of estimates of year 2003/country effects were obtained:

$$\mathbf{[X'X - X'Z(Z'Z + A^{-1}}\lambda)^{-1}\mathbf{Z'X]^{-1}}\ \sigma^2_e =$$

$$\begin{bmatrix} \mathbf{0.0113} & 0.0087 & 0.0087 & 0.0084 & 0.0069 \\ 0.0087 & \mathbf{0.0184} & 0.0081 & 0.0081 & 0.0069 \\ 0.0084 & 0.0081 & \mathbf{0.0167} & 0.0078 & 0.0069 \\ 0.0084 & 0.0081 & 0.0078 & \mathbf{0.0298} & 0.0070 \\ 0.0069 & 0.0069 & 0.0069 & 0.0070 & \mathbf{0.1065} \end{bmatrix} \sigma^2_e$$

The diagonal elements reflect the precision in the estimation of genetic level within country. The variance of estimated effects is inversely proportional to the records within country/year effects (IS=885, DK=184, SE=215, NO=82, FI=16, respectively). The positive off-diagonal elements are the results of genetic relationship between animals in the different management units, or genetic connectedness, and these contribute to a reduction in variance of estimates of differences between the country/year effects (Kennedy and Trus (1993).

The measures of the variances of the estimated effects of comparisons between countries i and j become $\mathrm{Var}_i + \mathrm{Var}_j - 2\,\mathrm{Cov}_{ij}$ and is shown in the following matrix:

$$\begin{bmatrix} - & 0.0123 & 0.0112 & 0.0243 & 0.1040 \\ 0.0123 & - & 0.0189 & 0.0320 & 0.1111 \\ 0.0112 & 0.0189 & - & 0.0309 & 0.1094 \\ 0.0243 & 0.0320 & 0.0309 & - & 0.1223 \\ 0.1040 & 0.1111 & 0.1094 & 0.1223 & - \end{bmatrix} \sigma^2_e \quad \begin{array}{c} \text{IS} \\ \text{DK} \\ \text{SE} \\ \text{NO} \\ \text{FI} \end{array}$$

Obviously the estimated effects of small management units are deemed to have high variance. Thus the variance of estimated country/year effects in Finland is more than nine times as high as in Iceland. On the other hand the results show good genetic connections between the countries, so that breeding values of individual horses can be compared across the countries with at least as high accuracy as within the country having the higher prediction error variance (*PEV*). As shown by Kennedy and Trus (1993) this measure of genetic connectedness between management units is highly correlated with *PEV*. The general recommendation is to avoid small fixed subclasses in the statistical genetic model since they are not regressed according to the amount of information in the data. This method is a tool which can generally be used as a practical approximation of the *PEV* of comparisons across the fixed sub-classes of the mixed model and can therefore be used as an aid in the design and testing of suitable genetic models.

Distributional validation of traits

The distribution of scored traits in the Icelandic material from 1990 to 2003 are revealed in Figures 4 and 5. The ordered categorical scores of body conformation are well approximated by the normal distribution as they show little skewness and kurtosis. The scores for the riding ability traits generally show some negative skewness. The departure from normality does not seem serious though and should not hinder the use of the scores in a linear mixed animal model. The only exception is the distribution of the scores for pace. The distribution of pace scores is obviously far from normal. Use of Snell's score transformation (Snell, 1964) was attempted but provided no improvement. Basically scores for pace in the population reflect the nature of a quantitative threshold trait with truncated normally distributed records above the threshold. A part of the population does not naturally exhibit the lateral movement of pace unless the sum of genetic and environmental factors surpass a certain threshold. Horses not showing any pace in the test automatically receive the score of 5,0. As shown in Figure 5 almost 30% of the horses scored received the score of 5,0 for pace. Icelandic horses not showing capacity in pace are said to by 4-gaited (walk, trot, toelt and gallop) while those who have the additional gait pace are said to by 5-gaited. Toelt is a lateral gait with four-beat rhythm and is intermediate between trot and pace. Four-gaited horse are often considered easier to ride, especially for inexperienced riders and often they are more impressive in the toelt. Much training in pace may also impair the toelt. Since toelt is such a valuable trait for the marketing prize of the horse, as reflected in the high relative weight in the aggregate vector $\boldsymbol{a}$, many horses are ridden as 4-gaiters and the pace is not trained at all even if they could perform pace up to a certain level, but at the risk of deteriorated toelt. This means that the category of horses receiving 5 (or very low scores *e.g.* up to 6.0) can be looked upon as a mixture of true 4-gaiters and 5-gaited horses with some capacity in pace, but where the pace is not trained nor shown in the test. This practice seems particularly clear in the more recent part of the data. This nature of the data clearly impairs the validity of genetic analysis including the pace scores of 5,0 and makes the results susceptible to serious bias. In such data the heritability of pace will be overestimated and genetic correlations with other traits will be biased downwards so that negative estimates can easily be created where positive correlations would biologically be expected.

This situation is parallel to the distinction between jumpers and dressage riding horses which causes false negative genetic correlations between jumping traits and dressage traits in analysis of competition material since individual horses usually only get the chance in one of the event. Which event is often subjectively based on an expectation according to pedigree.

This problem is probably best solved by use of Bayesian methods (Sorensen and Gianola, 2002). *A priori* the horses with scores 5,0 would be assumed to belong to two different sub-populations (categories) of animals. One made up of horses which are scored below the phenotypic threshold value because of the insufficient sum of independent, randomly distributed genetic and environmental factors (true 4-gaiters). The other category is made up of horses which would have some potential for showing pace (5-gaiters) but the pace is not trained nor shown in the test, mainly in order to preserve the maximum quality of the toelt. Any horse can partly belong to each category with certain probability, which could be simultaneously estimated from the data by Bayesian procedures when estimating genetic parameters and computing *EBV*s. Such approach is planned in the future.

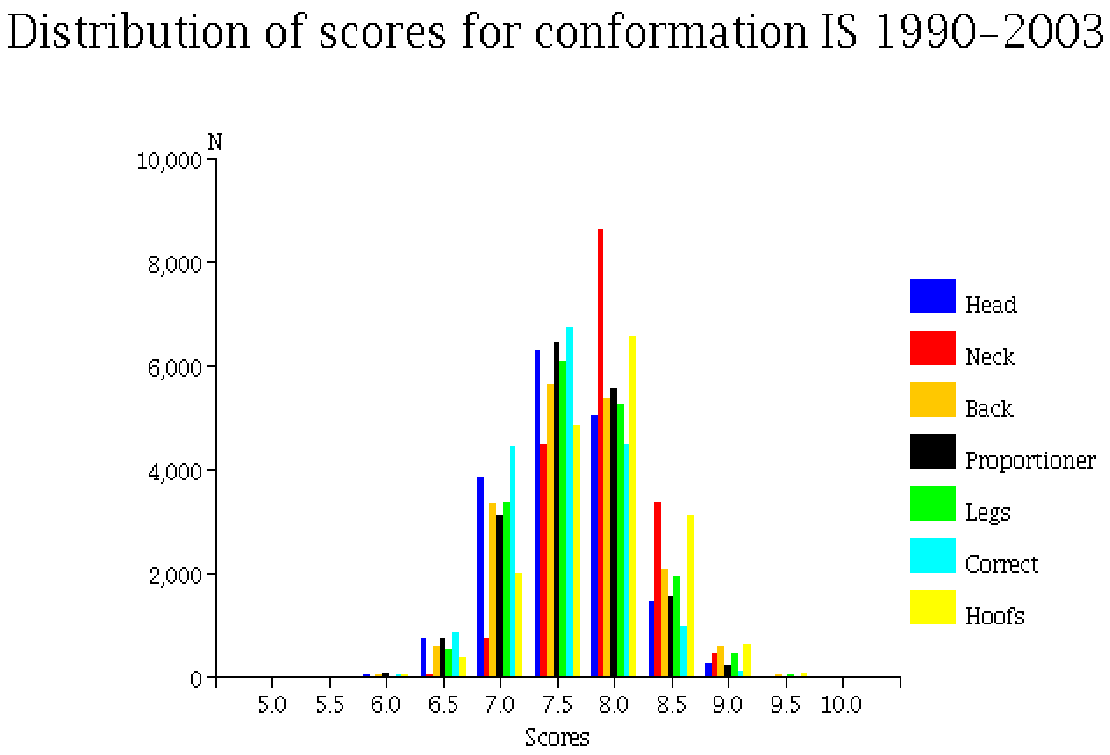

Figure 4 Distribution of conformation traits

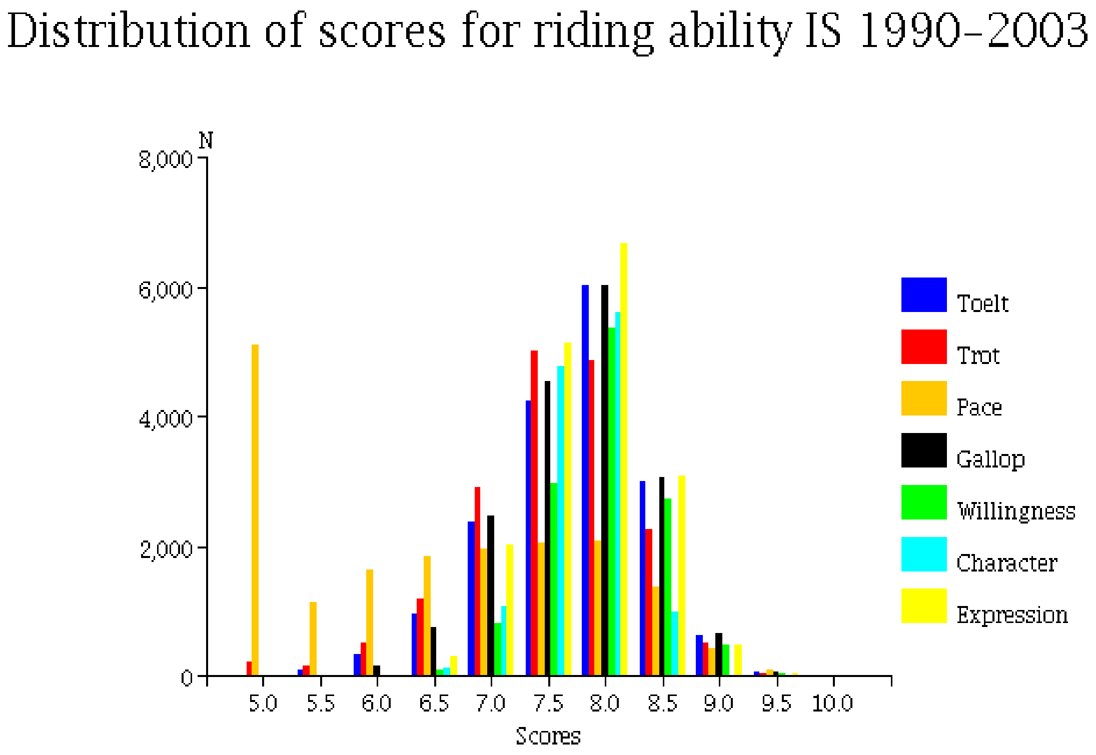

Figure 5. Distribution of riding ability traits.

Validation of the genetic model

The regression coefficients R_i corresponding to the diagonal elements (variances) for respective 14 trait in the multivariate complex are shown in Table 4.

Table 4. Regression of BLUP on sub-sampled BLUP (method R). Diagonal elements.

Trait: *k*	All records 1961-2003		All records 1990-2003		IS records 1990-2003	
	R_i	*s.e.*	R_i	*s.e.*	R_i	*s.e.*
1. Head	0.9876	0.0007	0.9936	0.0006	0.9945	0.0010
2. Neck	0.9866	0.0011	0.9949	0.0005	0.9933	0.0006
3. Back	0.9898	0.0008	0.9989	0.0005	0.9986	0.0010
4. Prop.	0.9882	0.0006	0.9962	0.0006	0.9957	0.0014
5. Legs	0.9859	0.0011	0.9971	0.0013	0.9976	0.0006
6. Correct.	0.9899	0.0006	0.9944	0.0006	0.9935	0.0009
7. Hoofs	0.9846	0.0005	0.9959	0.0007	0.9954	0.0011
8. Toelt	0.9885	0.0004	0.9968	0.0008	0.9959	0.0012
9. Trot	0.9955	0.0007	0.9968	0.0008	1.0029	0.0008
10. Pace	1.0005	0.0007	1.0027	0.0004	1.0028	0.0009
11. Gallop	0.9895	0.0009	1.0015	0.0023	0.9980	0.0009
12. Willing.	0.9918	0.0007	0.9964	0.0006	0.9983	0.0008
13. Charact.	0.9880	0.0006	0.9961	0.0004	0.9950	0.0005
14. Express.	0.9908	0.0007	0.9987	0.0006	0.9973	0.0008

The R_i coefficients are generally lower than one indicating too high heritabilities and genetic correlations resulting in insufficient regression of *EBV*s towards the base means. This seems especially the case when the older material (1961-1989) is included. In the material 1990-2003 the regression coefficients are much closer to one although they still indicate some overestimation of the genetic parameter complex. The inclusion of the records from the Nordic countries did not affect the fit of the genetic model. The R_i coefficients corresponding to the off-diagonals (genetic covariances between traits) were also inspected even though they are not listed in the paper due to want of space. Generally the R_i coefficients corresponding to the covariances were of similar magnitude as for the variances, *i.e.* indicating some general overestimation of genetic correlations. Exceptions were covariances between the conformation traits, where "legs" and "correctness of legs" were involved. There some strong deviations from one were detected.

Comparison of genetic levels and environmental effects between countries

The trend in average *EBV*s within countries and years for all registered horses born 1978-2003 from the five countries is shown in Figure 6. Since the number of horses is limited in Norway and Finland the genetic levels in those countries are subject to large sampling errors. The genetic trend in Iceland during this period of about two generations corresponds to little more than one phenotypic standard deviation. In Figure 7 the genetic trend for horses born in Iceland, Denmark and Sweden in 1978 to 1998 with own recorded scores is revealed. This trend is based on horses with *EBV*s evaluated by higher precision and is representing the active breeding pool as it includes all the stallions and most of the brood mares which will significantly contribute genetic material to future generations. The rate of gain in this group is higher than when all registered animals are included and at the same time the level is higher indicating that these *EBV*s belong to animals which are more selected. Generally the rate of progress seems to be the same in the different countries. The level of *EBV*s of horses born in other countries may be somewhat lower than in Iceland but that seems just to be a matter of few years delay. This does not come as a surprise since there is a constant flow of genetic material from Iceland to the continental part of Europe.

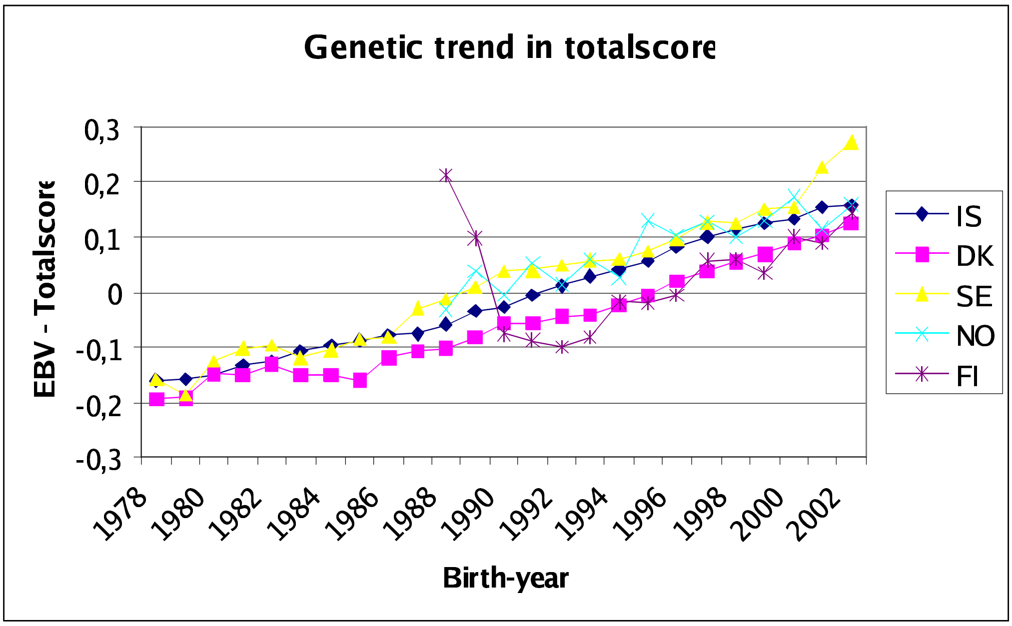

Figure 6. Genetic trends in Total-scores within country.

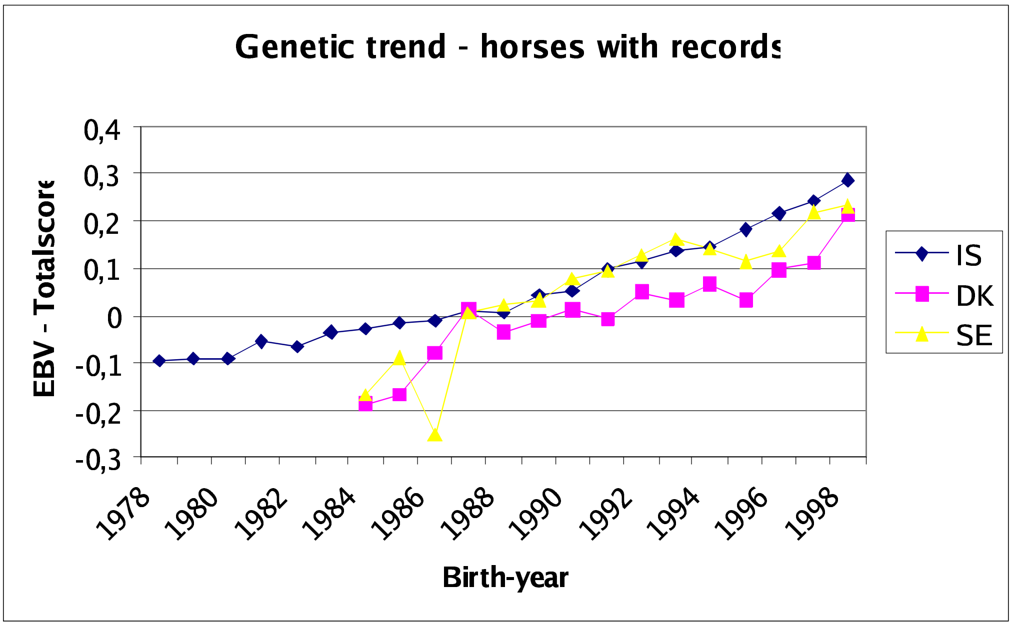

Figure 7. Genetic trends in Total-scores within country. Only horses with records included.

The average BLUEs of the fixed effects of country/year included in the statistical mixed linear model used for computing *EBV*s are shown in Figure 8. Difference in BLUE may reflect difference in the level of the judges' scores and/or the level of riding and training of the horses. Inspection of genetic trend and environmental levels of individual traits within countries is of great value for the leaders of the breeding organisations but is not further presented here.

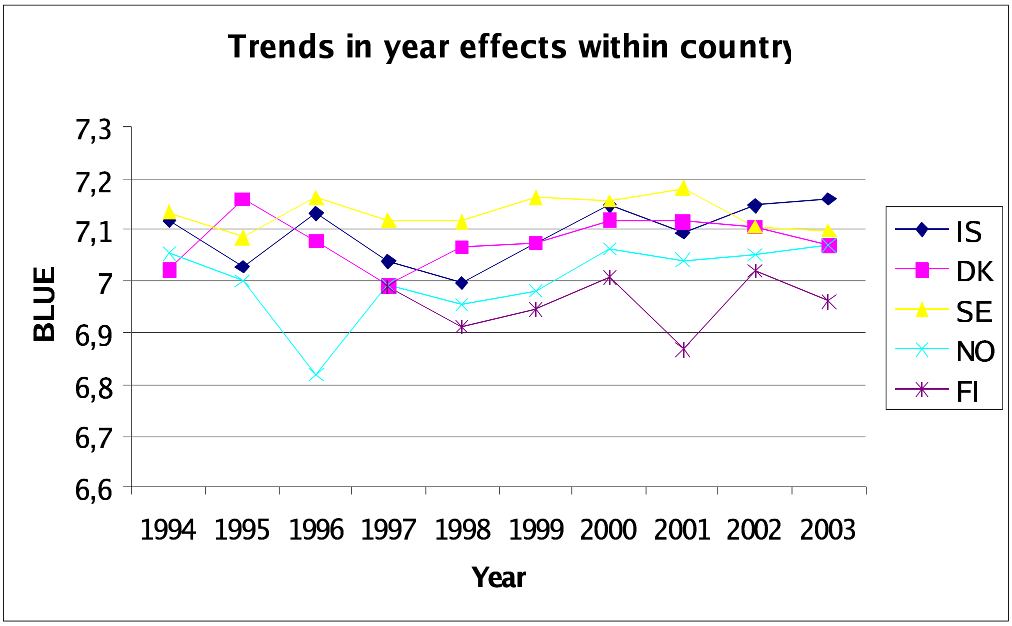

Figure 8. Levels of environmental effects of year of scoring on total-scores within country.

New estimates of genetic parameters

The resulting REML estimates of phenotypic variances and heritabilities when the material was divided into two periods (1979-1989 and 1990-2003, respectively) are shown in Table 5 together with the estimated genetic correlations between the same traits in the different periods.

Table 5. New REML estimates of phenotypic standard deviations, heritabilities and genetic correlations for 14 traits when the data was divided into two periods (1979-1989 and 1990-2003)

Periods:	1979-1989		1990-2003		
Trait	σ_P	**h^2**	σ_P	**h^2**	**r$_A$**
Head	0.37	0.25	0.52	0.29	0.86
Neck	0.35	0.22	0.41	0.36	0.94
Back	0.37	0.20	0.53	0.28	0.88
Prop.	0.33	0.24	0.49	0.35	0.89
Legs	0.36	0.16	0.54	0.38	0.90
Correct.	0.43	0.21	0.50	0.20	0.91
Hoofs	0.40	0.22	0.54	0.38	0.76
Toelt	0.60	0.30	0.64	0.34	0.80
Trot	0.48	0.26	0.72	0.37	0.84
Pace	0.85	0.34	0.90	0.31	0.94
Gallop	0.46	0.25	0.61	0.32	0.68
Willing.	0.44	0.26	0.47	0.34	0.85
Character	0.39	0.16	0.38	0.14	0.85
Express.	0.40	0.32	0.49	0.38	0.75

By comparing the results in Tables 2 and 5 it is clear that too high parameter values are generally used in the current genetic evaluations. Especially for the older part of the material. This observation is also strongly supported by the results of Reverter´s evaluation method above. The difference in variation and heritabilites between the same traits scored in the two different periods is not very surprising as a revision and to some extent a redefinition of the standard basis for the scores was made around year 1990. In the new analysis the genetic parameters involving pace were only based on records where pace score was >5.0. Even for the genetic correlations between the same traits scored in the different periods a significant deviation form one for many of the traits was indicated. Presumably the 14 traits complex should be divided into 28 different traits for this two periods.

New model for the genetic evaluations

Recently some changes have occurred concerning scored traits. Three additional traits are now included namely “walk”, “slow toelt” and “slow gallop”. On the other hand “willingness” and “character” have been combined into one trait. The results above suggest that the traits also have to be redefined according to two different time periods. The traits “height at withers” and “hairiness of mane and tail” will still be evaluated as single traits uncorrelated with other traits. The remaining k=31 traits then build a multivariate complex. There are obviously some computational difficulties associated with such a large covariance structure: The variance/covariance matrices could not be estimated in a single run on ASReml for such a large material and had to be divided into smaller subsets of traits in the estimation procedure. Afterwards the matrices had to be modified (bended) to become positive definite. The number of coefficients in each half-stored covariance matrix is of course $k(k+1)/2=496$. There are 6 different missing patterns in the material. Further complication rises because different models have to be applied to the different missing patterns (different range of country/year effects). The use of canonical transformation of records becomes complicated. However Ducrocq and Besbes (1993) introduced an EM algorithm (Dempster, *et al.*, 1997) for generating and updating missing records based on expected values of missing records through an iterative procedure. For 6 different missing patterns 12 different transformation matrices (**Q**) have to be computed based on the **G** and **R** covariance matrices. As the model differs for different missing patterns the requirement of identical incidence matrices has to be circumvented. In line with a suggestion of Ducrocq and Besbes (1993) the adjusted RHS values $\mathbf{y} - \mathbf{Xb}$ and $\mathbf{y} - \mathbf{Za}$ could be updated given the current estimates of **a** and **b** using the EM philosophy. They suggested that **b** could be computed using a multivariate fixed effect model and **a** obtained after canonical transformation. Then the iterations performed to solve the resulting systems and the EM iterations can be interlaced. A procedure for genetic evaluations of animals in this material using these features is currently under development.

Conclusions

Some necessary prerequisites for the international genetic evaluations are unique identification code for the animals, harmonized data and a common definition of traits across country. These requirements have been fulfilled in the establishment of the WorldFengur database due to an international cooperation within FEIF. There are good genetic ties between animals across country. The pedigree depth and completeness in the pedigree files are reasonably good. Due to the homogeneity of the data across country within the same time periods the data from the different countries can be pooled and the genetic evaluations can by computed in a single run using a common genetic model including fixed effects of country/year. The results of this study show that some revision of the genetic model including estimates of the genetic parameters is necessary, however.

A web based platform preferable based on Java Servlets or Java Server Pages providing dynamic and interactive access to SQL database is probably the optimal way of presenting *EBV*s, precision of estimates, inbreeding coefficients and all other relevant information on the pedigree and the traits involved.

Acknowledgements

A financial support from the Farmer´s Association of Iceland and The Foundation for Preservation of the Icelandic Horse Breed is greatly acknowledged. Ignacy Misztal and Miguel Perez-Enciso are acknowledged for free use of the Fspak sparse matrix subroutines.

References

Adalsteinsson, S. 1981. Origin and conservation of farm animal populations in Iceland. *J. Anim. Breed. Genet.* 98, 258-264.

Árnason, T. 1982. Prediction of breeding values for multiple traits in small non-random mating (horse) populations. *Acta Agric. Scand.* 32, 171-176.

Árnason, T. 1984. Genetic studies on conformation and performance of Icelandic toelter horses. *Acta Agric. Scand.* 34, 409-462.

Árnason, T., Jensen, P., Klemetsdal, G., Ojala, M., Philipsson, J. 1994. Experience from application of animal breeding theory in Nordic horse breeding. *Livest. Prod. Sci.* 40, 9-19.

Árnason, T., Sigurdsson, Á. 1997. Genetic analysis of performance test traits in

Icelandic toelter horses in Iceland and Sweden. 48th Meeting of the EAAP, Vienna, Austria, August 25-28, 1997. Paper H4.7.

Árnason, T., Ricard, A. 2001. Methods for international genetic evaluations of sport horses. 52nd Meeting of the EAAP, Budapest, Hungary, August 26-29, 2001. Paper H5:4.

Dempster, A.P., Laird, N.M., Rubin, D.B. 1977. Maximum likelihood from incomplete data via the EM algorithm. *J. Roy. Statist. Soc.*B. 39, 1-38.

Ducrocq, V., Besbes, B. 1993. Solution of multiple trait animal models with missing data on some traits. *J. Anim. Breed. Genet.* 110, 81-92.

Gilmour, A.R., Gogel, B.J., Cullis, B.R., Welham, S.J., Thompson, R. 2002. *ASReml User Guide Release 1.0.* VSN International Ltd, Hemel Hempstead, UK.

Hugason, K. (Ed.) 1992. *Kynbótadómar og sýningar.* The Agricultural Society of Iceland. Reykjavík, Iceland.

Hugason, K. 1994. Breeding of Icelandic toelter horses: an overview. *Livest. Prod. Sci.* 40, 21-29.

Kennedy, B.W., Trus, D. 1993. Considerations on genetic connectedness between management units under an animal model. *J. Anim. Sci.* 71, 2341-2352.

MacCluer, J.W., Boyce, A.J., Dyke, B., Weitkamp, L.R., Pfennig, D.W., Parson, C.J. Inbreeding and pedigree structure in Standardbred horses. *The Journal of Heredity* 74, 394-399.

Misztal, I., Perez-Enciso, M. 1993. Sparse matrix inversion for restricted maximum likelihood estimation of variance components by expectation-maximization. *J. Dairy Sci.* 76, 1479-1483.

Quaas, R.L. 1976. Computing the diagonal elements and inverse of a large numerator reationship matrix. *Biometrics* 32, 949-953.

Reverter, A., Golden, B.L., Bourdon, R.M., Brinks, J.S. 1994 *a*. Technical note: detection of bias in genetic predictions. *J. Anim. Sci.* 72, 34-37.

Reverter, A., Golden, B.L., Bourdon, R.M., Brinks, J.S. 1994 *b*. Method R variance components procedure: application on the simple breeding value model. *J. Anim. Sci.* 72, 2247-2253.

Reverter, A., Golden, B.L., Bourdon, R.M., Brinks, J.S. 1994 *c*. Multiple-trait method R estimation of (co) variance components. In: Proceedings of the 6th World Congress on Genetics Applied to Livestock Production, Guelph, Canada, August 7-12, 1994. 18, 406-409.

Sigurdsson, Á., Hugason, K., Árnason, T 1997. Breeding strategies and genetic progress in the Icelandic toelter population. 48th Meeting of the EAAP, Vienna, Austria, August 25-28, 1997. Paper H4.6.

Sorensen, D., Gianola, D. 2002. Likelihood, Bayesian, and MCMC Methods in Quantitative Genetics. Springer-Verlag, New York, USA.

Snell, E.J. 1964. A scaling procedure for ordered categorical data. *Biometrics* 20, 592-607.

Thompson, R., Wray, N.R., Crump, R.E. 1994. Calculation of prediction error variances using sparse matrix methods. *J. Anim. Breed. Genet.* 111, 102-109.

Takahashi, K., Fagan, J., Chen, M.S. 1975. Formation of sparse impedance matrix and its application to short circuit study. Proc. 8th Int. PICA Conf. Minneapolis, USA.