Session 36 H36.5 - Connectedness between 7 European countries for horse jumping competition, the Interstallion pilot project II.

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ABSTRACT

Data on jumping breeding values of stallions and pedigree up to 3 generations was provided by 7 countries, including 6317 stallions and 22324 different horses. Identification of horses between countries was done as there was no unique identification number. About 1000 stallions and 5000 ancestors were provided by each country. Common stallions between countries varied from 0 to 308 and common horses from 130 to 1166. "Genetic Similarities" were not the correct measurement of connectedness as size of progeny by country by stallion was not in equilibrium. Correlation between standard errors of country effects was computed in a model including also the genetic value of horses (h^2=0.20, all relationship included). For Germany, Belgium, France and The Netherlands, these correlations were 0.32 to 0.51 corresponding to a balanced schema with 11 to 19 progeny per stallion per country. Other correlations reached 0.08 to 0.27. These results allow continuing the project with calculation of genetic correlations.

Keywords: show jumping horses, connectedness

1 INTRODUCTION

In seven European countries routine genetic evaluations for the performance of jumping horses have been implemented (Koenen & Aldridge, 2002). The estimated breeding values (EBV) are based on national information, with a particular measurement of performance and rules of standardisation for publication, whereas the market of breeding stallions is international. For these reasons, INTERSTALLION was founded as a working group of the European Association for Animal Production (EAAP), supported by the World Breeding Federation for Sport Horses (WBFSH) and the International Committee for Animal Recording (ICAR) in 1998. The main objectives of INTERSTALLION are (1) to describe and discuss current breeding objectives, testing schemes and genetic evaluation procedures, and (2) to explore ways of harmonising and comparing EBVs across countries. INTERSTALLION supports two pilot projects on international comparison of EBVs based on data analyses. The first pilot project makes use of field day test results for dressage and jumping traits of five studbooks (Thorén et al., 2005). The second project, on which we report here, is based on competition results in jumping of seven countries.

An adequate, across country comparison is only feasible if the populations are well connected. Koenen et al. (2004) indicated that European breeding organisations have actively used breeding stallions from other breeding organisations. To evaluate the feasibility of an international comparison of EBV, more detailed and quantitative information on the genetic connectedness is essential. Hence, the aim of this study is the estimation of this connectedness between the participating countries.

2 MATERIAL AND METHODS

2.1 Data

22 breeding organisations from seven countries (Belgium (2), Denmark (1), France (2), Germany (14), Ireland (1), Sweden (1) and the Netherlands (1), contributed information to the project (see on Acknowledgments for the detailed list). Information was collected only on stallions with an EBV during the period 2000-2004. Data included the identification number (ID) of the stallion, his name, the reliability of the EBV, the number of own performances and the number of tested progeny. Also the ID and name of ancestors up to three generations was supplied. Optionally alternative ID numbers recorded (for example for imported horses), with the breed of origin and the birth year of these horses. National EBV'S or results of competition were not included in the request in this step of the project. There were (Table 1) about 1000 stallions per country (except for Sweden, 67), with a maximum of 2025 (The Netherlands). Including pedigree horses there were about 5000 horses per country (except for Sweden 685). The total number of horses was 29057 including 7234 stallions.

2.2 Data editing

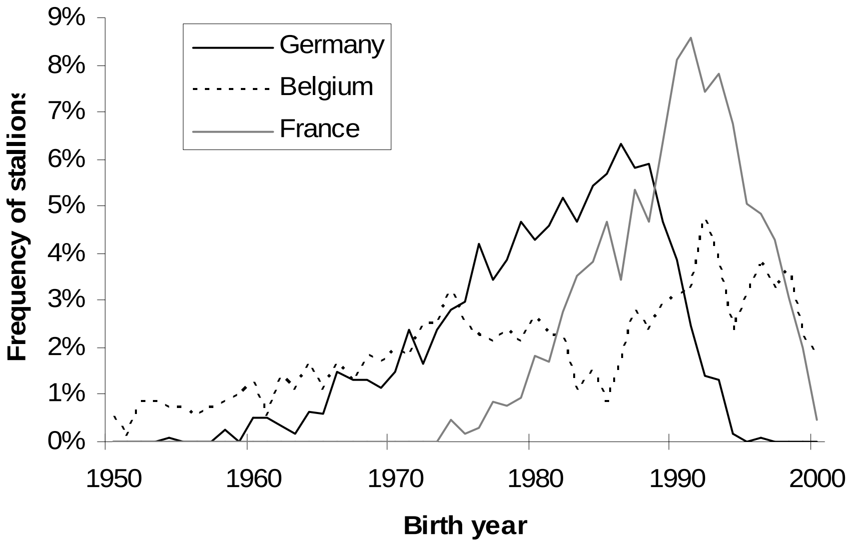
The first task was to identify identical horses (stallions and mares) among all files as the same horse could have different ID numbers in different countries. A first automatic check was based on a part of the name (without number, affix or suffix). Then all horses were checked manually to decide which ID numbers belonged to the same horse in the different countries. Decisions were based on second ID number (if provided), name of parents, breed and birth year. The same was done for horses with the same ID number but this situation was not frequent. A second check was based on the information generated in the first check. If a horse was identified as the same among countries, all ancestors' ID and all progenies' ID's could be matched. An iterative program was written to perform this task.

In the following paragraphs, "stallions" will refer to the sample asked, with a breeding value evaluated at least once during the period 2000-2004 whereas "horses" will refer to all horses present in the final file, i.e. stallions and their ancestors.

After data editing only 22,324 different horses and 6317 stallions remained in the file for further analyses.

There were differences between sampled stallions with respect to range of birth years, reliability and pedigree information. Germany and Sweden have provided only old stallions (born between 1971 and 1991); France has provided a list of reproducing stallions and these were born between 1982-1999; Belgium has provided all stallions born between 1970 and 2000. Stallions of the other countries were from intermediate periods (Figure 1).

Figure 1 – Distribution of birth year of stallions provided by tree different countries.



According to reliability, Germany provided only progeny tested stallions with reliability above 0.75 (mean 0.85). Stallions from France have rather high reliabilities (about 0.66) corresponding to EBV's based on own performances. For Ireland and the Netherlands, the reliability is lower because the list refers to young stallions with a low number of tested progeny (mean 0.25 and 0.35 respectively). In Denmark and Sweden, reliability was not yet calculated as genetic evaluations on jumping results are not yet published. The average number of progeny was 13 in Denmark and 75 in Sweden.

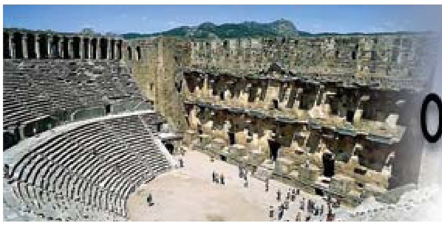
Belgium, France and Sweden provided complete pedigrees up to three generations. Information from Denmark was complete up to two generations. The Netherlands and Germany provided 100% of parents but only about 50% of ancestors in the third generation. Ireland provided pedigrees with 80% of the parents and 35% of the grandparents known.

2.3 Measurements of connectedness.

In this study three measurements of connectedness were used.

The first measurement of connectedness was the number of common stallions and common ancestors between countries.

Secondly, based on the number of common stallions and number of tested progeny, the Genetic Similarity (GS) between countries was calculated, according to the formula introduced by Rekaya et al. (2003). Compared to the number of common stallions between countries, GS is a relative measure (expressed in %) that takes into account the number of tested progenies in each country. GS is calculated as the proportion of tested progenies by stallions having progenies in two countries, in relation to the total number of tested progenies over both countries:



$$GS_{ij} = \frac{\sum_{k=1}^{N_{ij}} \left(n_{ik} + n_{jk} \right)}{\sum_{k=1}^{N_i} n_{ik} + \sum_{k=1}^{N_j} n_{jk}}$$

with N_{ij} number of stallions with progenies in countries i and j, N_i and N_j the number of stallions in the country i and j, n_{ik} and n_{jk} the number of progenies of stallion k in country i and j, respectively.

As the distribution of progenies of individual stallions may be quite skewed, the contribution of each country to the GS was calculated.

Thirdly, connectedness was quantified from correlation between estimates of country effects. These correlations were calculated from the number of own performances of stallions and the number of tested progeny in each countries. The supposed underlying model was:

$$y=Xb+Zu+e$$

with *y* the vector of performances realized by all horses in all countries, *b* the vector of fixed effects of countries, *u* the vector of additive genetic values of all horses and e the vector of residual. In this model we supposed that the same trait was measured in all countries and the difference between performances comes only from differences of level between countries. We supposed that one horse had only one performance. The population was divided in two categories: stallions and ancestors (1), progeny (2). The equations became:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 \\ X_2 \end{bmatrix} b + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

The matrix of variance-covariance of standard errors of parameters was the inverse of the following matrix that did no longer need the knowledge of performances *y*:

$$\begin{bmatrix} X_1^{'}X_1 + X_2^{'}X_2 & X_1^{'}Z_1 & X_2^{'}Z_2 \\ Z_1^{'}X_1 & Z_1^{'}Z_1 + \alpha A_{11}^{-1} & \alpha A_{12}^{-1} \\ Z_2^{'}X_2 & \alpha A_{21}^{-1} & Z_2^{'}Z_2 + \alpha A_{22}^{-1} \end{bmatrix}$$

with A the relationship matrix partitioned according to (1) and (2), and $\alpha = \frac{\sigma_e^2}{\sigma_u^2} = \frac{1-h^2}{h^2}$. Heritability ($h^2$) was assumed 0.20.

The matrices corresponding to progeny (2) were absorbed and we supposed no relationships between mares of progenies (as in a sire model). The final matrix was:

$$\begin{bmatrix} F & C \\ C' & D + \alpha A_{11}^{-1} \end{bmatrix}$$

with

$$f_{ii} = \frac{4\alpha}{3+4\alpha}\sum_{k=1}^{N} n_{ik} + \sum_{k=1}^{N} m_{ik},\ f_{ij} = 0 \text{ for } i \neq j,$$

$$c_{ij} = \frac{2\alpha}{3+4\alpha} n_{ij} + m_{ij}$$

$$d_{ij} = \frac{\alpha}{3+4\alpha} n_{ij} + m_{ij}$$

with n_{ij} the number of tested progenies of the stallion j in the country i, m_{ij} the number of own performance of stallion j in country i (0 or 1). N is the total number of stallions with tested progenies.

The matrix of variance-covariance of estimates of countries effects was:

$$\left[F - C(D + \alpha A_{11}^{-1})^{-1} C'\right]^{-1}$$

from which correlations were computed.

3 RESULTS

In the following tables various measures of connectedness are presented. Table 1 reports the number of stallions and pedigree horses common between different countries. Genetic similarities (GS) are given in table 2 and correlations between estimates of country effects in table 3.

Table 1. Number of common stallions and pedigree horses in genetic evaluations for show jumping in seven European countries. *On the diagonal*: number of pedigree horses (above) and of stallions (below) per country - *Above the diagonal:* number of common pedigree horses - *Below the diagonal*: number of common stallions

	Germany	**Belgium**	**Denmark**	**France**	**Netherlands**	**Ireland**	**Sweden**
Germany	*4274* *1232*	811	1017	518	997	286	177
Belgium	23	*5622* *874*	886	1166	992	456	184
Denmark	129	8	*3497* *587*	613	757	400	296
France	48	41	44	*5591* *1179*	706	457	157
Netherlands	308	130	114	102	*4843* *2025*	394	180
Ireland	67	24	44	60	108	*4545* *1270*	130
Sweden	6	0	14	2	13	8	*685* *67*

Table 2 – Genetic similarities between the seven countries for jumping competition (in %, above diagonal) and the contribution to GS by country in column (in %, below diagonal)

	Germany	Belgium	Denmark	France	Netherlands	Ireland	Sweden
Germany	100	3	20	7	32	12	1
Belgium	63	100	5	5	18	11	0
Denmark	94	93	100	8	13	3	16
France	84	69	13	100	18	17	1
Netherlands	80	80	19	56	100	19	2
Ireland	99	98	83	95	94	100	5
Sweden	48	0	17	2	43	2	100

Table 3 – Correlations between estimates of country effects in mixed model for breeding values in jumping competition.

	Germany	Belgium	Denmark	France	Netherlands	Ireland	Sweden
Germany		0.40	0.40	0.32	0.51	0.13	0.21
Belgium			0.21	0.39	0.38	0.11	0.12
Denmark				0.18	0.27	0.08	0.14
France					0.35	0.12	0.10
Netherlands						0.13	0.17
Ireland							0.05
Sweden							

4 DISCUSSION

We encountered huge problems with the identification of the older horses. At present, the UELN (Unique Equine Life Number) is not available for the horses, born before the UELN introduction (2000). Problems arise because new numbers have been assigned by breeding organisations to imported horses without saving the original ID. This created a huge problem in identification, mainly because both ID is not the same but also because the name is not exactly identical either. This makes automatic checking infeasible. This problem underlines the importance of the use of unique ID-numbers for all horses, the UELN, and the updating of UELN of older horses.

Data provided by the different countries were not completely comparable, probably because requirements were not sufficiently clear. “Stallions with EBV” was interpreted either as tested stallions on progeny (Germany), stallions in reproductive activity (France), or all stallions since beginning of evaluation (Belgium). These differences may lead to underestimation of the connectedness because we compared populations that were slightly different. Especially for Sweden, connectedness should have been underestimated due to the low number of stallions provided. For Germany, connectedness should also have been higher than estimates if younger stallions have been included like in France, Belgium and The Netherlands because commercial exchanges between countries increased recently.

The measurements of genetic similarity were not as expected and maybe GS is not the ideal measurement of connectedness in horse populations. For example, Ireland appears well connected to Germany, Belgium, France and the Netherlands (GS>0.11), better than the connectedness between Belgium and France or Belgium and Germany (GS<0.05). The reason is that some stallions, with high number of progenies have also 1 or 2 offspring in Ireland. In this case all progenies appear in the numerator of GS, even with a huge disequilibrium between countries. That is why the percentage of progenies, provided by each country in the GS calculation was added to the results in Table 2. The GS criterion should therefore be restricted to populations with rather equal number of progeny in each country.

Correlation between estimates of countries effects defined a group of 4 countries well connected: Germany, Belgium, France and The Netherlands (from 0.30 to 0.50). Lower results were obtained for Ireland and Sweden with intermediate position for Denmark but all correlations reached about 0.10 to 0.20. The lower values for Sweden may be due to the rather small sample of generally older stallions included in the study. These correlations can be compared to balanced design with equal number of progenies in each country. A correlation of 0.40 corresponded in this case to 13 progeny per stallions and per country. So present connectedness is equivalent for the group of 4 to a balanced design of progeny test with 11 to 19 progeny in each country, which in horse breeding is a convenient situation (30 offspring gave a reliability (r) equal to 0.78 for the sire with h^2=0.20).

Results on connectedness for the first pilot project supported by Interstallion on field day test results in five studbook and four countries were reported in Thorén et al. (2005). The number of stallions in Thorén et al. was 2457 with 5868 pedigree horses. Lower number of stallions was provided in our study from Sweden, higher from The Netherlands and similar from Germany and Denmark. Belgium, France, Ireland were not involved in that first project. Information requested in our study was on a lower scale of time than in Thoren et al., so stallions were a younger sample: 43% of stallions were born after 1985 in Thoren et al., 54% in the present study. This larger scale of time allowed Thorén et al. to study evolution of connectedness with time that was not possible here. Reliability of EBV of stallions provided from Germany, Denmark and The Netherlands was similar between the two studies but higher for Sweden in the present study. The number of common stallions was largely lower between Sweden and all other countries and higher between The Netherlands and Germany or Denmark. Genetic similarities were not discussed according to the number of progenies in each country so it is difficult to compare with our results which were not very relevant. However, GS were similar in the two studies between the German stud Book of Holsteiner and Denmark (20%-20%) or The Netherlands (31%-32%) but lower with the other German stud Book: the Hannoveraner (respectively 17% and 11%). GS between Denmark and The Netherlands was lower in Thoren et al. (9% versus 13%). Major differences were found with Sweden. So these results were in good agreement in the two studies for the countries involved in both, except for Sweden.

5 CONCLUSION

The various measurements of connectedness indicate that there are enough genetic links to allow estimates of genetic correlations among the populations in question. However, the differences in sampling data from the participating countries may seriously affect the estimates obtained. For more accurate estimates stallions should represent the same time period of birth and include those that have an agreed minimum reliability, equal for all countries, of their EBVs based on jumping competition results of their progenies and own performances. A further improvement might also be made in the choice of methods. The generalized coefficient of determination (Laloë et al., 1996), which compares variance of contrasts between stallions instead of countries might better. We also will test another method developed by the same team. This method simulates differences of genetic level between countries and measures the estimable differences. In any cases, these first results are encouraging and allow the calculation of genetic correlations, which constitute the next point of the Interstallion Pilot project II. Besides, connectedness is expected to increase in the future due to the increasing exchange of genetic material. .

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