

# Crossbreed genetic performance study in the eventing horse competition

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**Abstract.** Eventing is an equestrian discipline combining dressage, show jumping and cross-country exercises. The Spanish Sport Horse (SSH) was used in this study as an example to develop a method to ascertain the influence of parental breeds on particular performances by linking their parental genetic contribution with the individual phenotype value computing the optimal breed contribution for each trait evaluated in eventing. Data included 1220 eventing records from 210 SSH animals. The genetic contribution of six main founder populations were computed for each SSH: the Spanish Purebred (SPB), Arab Horse (A), Thoroughbred (TB), Selle Français (SF), German breeds (G) and North(-west) European (N) breeds. For this analysis we used BLUP (best linear unbiased predictor) animal models for five defined traits and for the total score. The genetic contribution as linear and quadratic adjustment and the interaction between genetic contributions were included as covariates in the genetic model to separate the possible combining ability from the breeding values. The optimal breed genetic contribution for each trait was maximised by using a simplex method. The best combination for conformation was 51% SPB and 49% N, for cross-country aptitude 23% SPB and 77% N, for dressage 48% SF and 52% N, and for show jumping 64% A and 36% N. For cross-country the best performance was predicted using 100% N genetic contribution and for the total score of 24% SF and 76% N. The combination of two breeds (group of breeds) seemed to be the best option for most of the traits. Although the results should be interpreted with caution, the importance of this paper is that it can be considered as a starting point of the analysis. The methodology applied here performed nicely in searching for the best contribution of several breeds to find the best combination for particular interests and could, therefore, be useful for other species/populations.

**Additional keywords:** complementarity, composite breeds, equine, sport competition.

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## Introduction

Composite breeds are originated to benefit from the combinatory aptitude of the performance in the progeny (Goot 1986; Núñez-Dominguez *et al.* 1992; Zhang *et al.* 2000; Tang *et al.* 2014). In these crossbreed populations the genetic contribution of parental breeds varies in number and magnitude. Thus, many horse breeds are formed using two or more different breeds (Hamann and Distl 2008; Cervantes *et al.* 2009; Thorén Hellsten *et al.* 2009; Bartolomé *et al.* 2011) to achieve the desired characteristics in the offspring. The Spanish Sport Horse (SSH) is a recent composite breed, created in 2002 in the search for a multi-purpose breed with a first-rate performance at any of the Olympic equestrian disciplines: dressage, show jumping and/or eventing. As individuals from other breeds are accepted as parents of an SSH animal, immigration (introducing outside breeds into the SSH) is part of the breeding concept (Cervantes *et al.* 2009; Bartolomé *et al.* 2011).

Spanish Sport Horse animals are competing in eventing, which is a heterogeneous equestrian sport combining dressage,

show jumping and cross-country exercises. But selecting individuals for dressage can produce the opposite performance in show jumping (Viklund *et al.* 2010). Moreover, the cross-country activity could also imply selecting for an endurance aptitude, which may not be compatible with other disciplines. A proper combination of different breeds to perform optimally for each trait is demanded by owners who want animals to win this combined competition. The aim of this study was to develop a method to ascertain the influence of parental breeds on particular performances by linking their parental genetic contribution with the individual phenotype value by computing the optimal breed contribution for each trait.

## Materials and methods

### Data

We analysed performance from Young Horse Selection Tests Eventing (4–6 years old) held in Spain between 2004 and 2009. This selection test is based on eventing that includes exercises

of dressage, cross-country and show jumping. These tests were developed to collect data specifically for the breeding program, and a conformation and a 'cross-country aptitude' subjective evaluation are also included in these young competitions in Spain. Finally, five traits and the total score were of interest for our study:

- The conformation is one score for the morphological aptitude of the animal for the eventing competition given by two or three judges on a 1–10 scale. The scores given by each judge were included as different records.
- The cross-country aptitude is a subjective score given by two or three judges (same judges as for the previous trait) during the cross-country exercise. A total of five variables, related to the general aptitude of the horse movements during the cross-country, are recorded by each judge on a scale from 1 to 10. These variables are: balance, cadence, straightness, stride and attitude. The scores for the different variables are averaged and the resulting scores given by each judge are included in the analysis as different records.
- The dressage exercise is an exercise, where different variables (from 12 to 14 depending on the level of the competition) are evaluated by two or three judges in a score range from 1 to 10. The scores for the different variables are afterwards averaged and rescaled to a 1–150 scale. The resulting scores given by each judge are included in the analysis as different records.
- The show jumping exercise is an obstacle race inside a track. The score is registered as penalty points; so the lower the score, the better the performance. For the present analysis, all the scores were converted to positive points, by assigning the lower score (0) to the animals that failed the exercise and higher score (125 points) to the animals with the best performance (0 penalties). The maximum was chosen to guarantee that the maximum penalty was converted to 0 points.
- The cross-country exercise was an obstacle race in a countryside track. Similar to show jumping, the score for the cross-country exercise is registered as penalty points transformed for the analysis in the same way as above, but assigning 200 points to the best performance according to their range of penalties. The maximum was chosen to guaranty that the maximum penalty was converted to 0.
- Total score was the sum of the different traits. Conformation and cross-country aptitude were averaged before being added. The weight for each variable in the total score is 2% for conformation and cross-country aptitude, 31% for dressage, 26% for show jumping and 41% for cross-country.

We worked with each exercise separately using the maximum available amount of data per exercise, and with the total score to test the methodology.

Animals with missing records in each exercise were between 2% and 9% of data depending on the trait. Animals eliminated in the conformation exercise were also included in those missing records. However, animals eliminated in the rest of the exercises were scored with the lowest scores; in any case, very few entries satisfied these criteria, ~0% to 7% depending on the trait. Table 1 includes a statistical description of the data. The data from 210 SSH animals born between 1998 and 2005 included 2660 records for conformation, 2524 for cross-country aptitude, 2768 for dressage, 1299 for show jumping, 1272 for cross-country

**Table 1. Phenotypic data description for conformation, cross-country aptitude, dressage, show jumping and cross-country exercise**

A total of 1220 records for the total score. *n*, number of records; *s.d.*, standard deviation

	<i>n</i>	Average	<i>s.d.</i>	Minimum	Maximum
Conformation	2660	7.26	0.82	4.00	9.75
Cross-country aptitude	2524	7.07	1.45	0.00	9.32
Dressage	2768	96.93	11.12	0.00	128.57
Show jumping	1299	119.65	12.22	0.00	125.00
Cross-country	1272	174.96	52.93	0.00	200
Total score	1220	404.3	49.68	102.33	457.10

exercise, and 1220 for the total score. The difference of records across traits is because not all individuals finished all the exercises. For the total score we used the records from animals that finished all the exercises. The averages across judges were used to compute the total score. When we worked separately for conformation, cross-country aptitude and dressage we increased the number of records because we used the score given by each judge.

## Methods

The genetic contribution of the following populations (breeds or group of breeds) were computed for each SSH: Spanish Purebred (SPB), Arab Horse (A), Thoroughbred (TB), Selle Français (SF), German breeds (G) that included Holsteiner, Hanoverian, Westphalian, Oldenburger and Trakehner breeds, and North(-west) European breeds (N) that included Dutch Warmblood, Belgian Warmblood, Danish Warmblood and Zangersheide breeds. We decided to include several breeds in the same group, by following geographic criteria, because of the number of breeds with low number of founders. We will refer to these populations as 'breeds' across the paper despite some of these groups having several breeds. The genetic contribution of each breed for each animal was computed as the sum over all known founders of the different breeds of the terms computed as the sum of  $(1/2)^n$ , where *n* is the number of generations separating the individual to each of its known founders. Founders were individuals ending pedigrees without parents in the SSH studbook. All the available pedigrees were used to compute the genetic contribution (Bartolomé *et al.* 2011). The average of equivalent complete generation of the horses included in this study was 3.7. As this is a composite breed, many of the animals from other populations appear as founders in the pedigree of SSH leading to a rather global shallow pedigree. Therefore, some animals were assigned to a group that could have been changed if there was a deeper knowledge of their genealogy. This will be taken into account when discussing the results. Bartolomé *et al.* (2011) found that for all SSH animals born between 2000 and 2004, the ancestor genetic contributions for each breed/group of breeds were: 14% SPB, 6% A, 12% TB, 9% SF, 13% G and 6% N. The rest of the genetic contribution was explained by SSH ancestors (20%) and other minority or unknown breeds (20%). These results obtained by Bartolomé *et al.* (2011) illustrate the composition of all animals born during that period in which

our sample is included. Note that although the Official Studbook was founded in 2002, animals born before could still be registered. Table 2 shows the average, minimum, maximum genetic contribution and number of founders giving those contributions of different breed/group of breeds in our sample. The highest averages of genetic contributions were TB (29.9%), G (19.0%) and SF (14.1%) breeds. In general, breeds with a high number of founders had more genetic contributions. Regarding breeds with minority contributions (A, SPB and N), the case of N breeds is noticeable because it has a half number of founders of SPB and its genetic contribution is higher than that for SPB.

Univariate BLUP (best linear unbiased predictor) animal models were applied for five defined traits (conformation, cross-country aptitude, dressage, show jumping and cross-country exercises) and for the total score. Given the artificial nature of the scores, their distribution was not Gaussian. However, restricted maximum likelihood methodology has been shown to perform ideally in such circumstances (Goyache *et al.* 2003; Gutiérrez *et al.* 2007). The models included as fixed effects: age (4, 5 and 6 years), sex (male, female and geldings), judge-event interaction (but not in cross-country, show jumping exercises and total score) with 165 levels for dressage, 148 levels for cross-country aptitude and 145 levels for conformation, event (only in show jumping, cross-country and total score) with 68 levels, training (with 36 levels for show jumping, cross-country and total score, 38 levels for conformation and cross-country aptitude and 42 levels for dressage), and stress (with 43 for show jumping, cross-country exercise and total score, and 44 levels for conformation, cross-country aptitude and dressage). The training level was defined as the combination of the factors 'number of previous events where the animal has participated' (<5 competitions, 5–10, 10–20 and >20), 'daily hours of training' (<3 h, 3–6 h, 6–10 h and >10 h) and 'time since the horse had been training' (<6 months, 6–12, 12–24 and >24 months). The stress level was defined as the combination of the factors 'transport to the event' (walking, lorry or van), 'trip time to the event' (<30 min, 30 min to 2 h, 2–4 h, 4–6 h, 6–8 h and >8 h) and 'time of arriving before the beginning of the event' (<6 h before, 6–12 h before, 12–24 h before and >24 h before). The information for the training level and the stress level was collected from a questionnaire given to the person in charge (rider/breeder) of each horse during each event.

**Table 2. Average, minimum and maximum genetic contribution in percentage and number of founders (% of total founders in brackets) of different breed/group of breeds in our sample**

Breed	Average	Minimum	Maximum	Number of founders
Arab horse	4.60	0	50.00	52 (6.0)
Thoroughbred	29.90	0	87.50	256 (29.3)
Spanish purebred	2.60	0	50.00	67 (7.7)
Selle Français	14.10	0	68.75	86 (9.9)
German breeds	19.00	0	100.00	175 (20.0)
North(-west) European breeds	3.30	0	56.25	38 (4.4)

The genetic contributions of the parental breeds were included as covariates using a linear and quadratic adjustment. The second-order interactions between effects were also included as covariates. We included the covariates to extract the possible combining ability from the breeding values. Under this model the obtained breeding values are strictly additive genetic values, excluding the portion of the genetic values, which should be attributed to combinatory effects between breeds. Note that interactions, grouping more than two breeds, are not fitted but still might be important in some cases.

Additive genetic and residual effects were included as random factors beside the rider-horse interaction effect (in all traits except conformation exercise) with: 377 levels for cross-country aptitude, 410 for dressage, 408 for show jumping, 402 for cross-country exercise and 388 for total score. The rider-horse interaction effect combines the pair rider-horse and tries to measure the different behaviour of a horse with specific riders.

Four generations back of pedigree were used to solve the model with 1395 records.

The values for linear coefficients could lead to an approximation of the best genetic contribution for each trait, but the existence of quadratic covariates and interactions could also provide different solutions for the best performance. Finally, a simplex methodology (Nelder and Mead 1965) using the estimated regression coefficients was applied to compute the optimal breed contribution combination to achieve the maximum performance for each trait using the function ( $F$ ):

$$F = \mathbf{c}'\mathbf{b}_1 + \mathbf{c}'\mathbf{B}_2\mathbf{c}$$

where  $\mathbf{c}$  is the vector of unknown contributions vector for the six breeds/group of breeds,  $\mathbf{b}_1$  is the linear covariates vector and  $\mathbf{B}_2$  is the second-order covariate matrix of order 6 divided by 2, the elements outside diagonals.

The function was applied for each trait separately and for the total score. The statistical analyses were made with SAS 9.2 for Windows (SAS Institute Inc. 2008) and for the breeding value estimation we used VCE 6.0 (Groeneveld *et al.* 2008). The programs used for the simplex methodology were developed by the authors.

## Results and discussion

Performance comparisons among breeds and their crosses are justified because genetic differences among breeds or strains are large relative to genetic variation within breeds. These differences are an important potential source of genetic improvement in performance (FAO 1993). Furthermore, crossbreeding involving different breeds is frequently used for the production of riding horses. Many outstanding show jumpers and eventing horses have resulted from successful crosses (Arnason and Van Vleck 2000). The SSH breed originated mainly from the German Warmblood sport horse breeds such as the Holsteiner, Hanoverian, Westphalian, Oldenburger or Trakehener, thus demonstrating the breeders' preferences for the aptitudes of these foreign breeds (Bartolomé *et al.* 2011). Warmblood horses are used worldwide for the Olympic equestrian disciplines (dressage, show jumping and eventing) and countries such as Germany and France, who have a long tradition of breeding, act as

exporters, whereas other countries import the bred horses as stock (Koenen *et al.* 2004).

Most of the Warmblood horses are bred to perform the three types of competitions (Koenen *et al.* 2004). In general, the disadvantage of considering a multiple trait breeding objective is that the genetic improvement per trait (in absolute biological units) can be considerably lower when compared with single trait breeding goals. Thus, selecting individuals for different disciplines without using a global selection index will lead to a strong subdivision (Cervantes *et al.* 2008) as found in the SSH population by Cervantes *et al.* (2011). Heritabilities and genetic correlations can indicate in individual situations the extent to which the traits of interest can be improved simultaneously. Show jumping and dressage have only a weak genetic correlation (Huizinga and van der Meij 1989; Ducro *et al.* 2007a, 2007b; Viklund *et al.* 2010). Ricard and Chanu (2001) reported moderate genetic correlations between eventing and other equestrian disciplines like show jumping (0.45) or dressage (0.58). Regarding the exercises within the eventing competition, the genetic correlation between show jumping and cross-country exercise is close to 1 and dressage has a better correlation with cross-country (0.38) than with show jumping (0.27) (Cervantes *et al.* 2007). Therefore, an improvement in the dressage exercise will not establish a sufficient response in cross-country or show jumping exercises.

Table 3 shows the estimated heritabilities for the different analysed traits using univariate models. As the breed contribution effect is fitted in the model, these values are assumed to be within breed or combination of breeds, and all have the same heritability value. The values ranged between 0.09 for cross-country exercise and 0.45 for conformation. The values for cross-country aptitude (0.17), dressage exercise (0.19), show jumping (0.26) and total score (0.16) were moderate. The heritabilities were in agreement with other authors (Ricard and Chanu 2001; Kearsley *et al.* 2008), but any comparison should be made with caution because these authors did not include the breed in the model. The rider-horse ratio (variance of rider-horse interaction effect over phenotypic variance) ranged between <0.01 for cross-country exercise, and 0.41 for the show jumping trait. For dressage, cross-country aptitude and show jumping exercises, the rider-horse ratio was higher than the heritability, thus highlighting the importance of this rider-horse pair. Very few authors investigating the influence of the rider, Kearsley *et al.* (2008) showed an important influence for the rider effect in their analysed trait models, and Bartolomé *et al.* (2013), concluded that by excluding the rider-horse interaction could produce less fitted genetic models.

The significant regression coefficient genetic contributions for each trait are shown in Table 4. Despite only a few of them were significant – SF\*A for cross-country aptitude, SPB and G\*TB for dressage, and SF, G\*G, N\*SPB and N\*N for cross-country exercise, A\*A, N\*SPB and N\*N for total score – all values were used in the function to test the methodology. The genetic contributions were included in the model as covariates in order to separate the additive genetic effect from the possible combining ability effects. If these interactions were not included, the breeding values would be obtained by assuming a Gaussian distribution, which tends to regress all of them to the mean to fit the distribution assumptions. As data was from different

**Table 3. Heritabilities and rider-horse ratios (rh ratios) and the standard errors (s.e.) for the analysed traits**

	$h^2$	s.e	rh ratios	s.e
Conformation	0.45	0.035	–	–
Cross-country aptitude	0.17	0.061	0.20	0.046
Dressage	0.19	0.057	0.26	0.045
Show jumping	0.26	0.079	0.41	0.072
Cross-country	0.09	0.034	0.00	0.028
Total score	0.16	0.047	0.04	0.040

**Table 4. Regression coefficients (×1000) from the covariates in BLUP animal model-method (significant values,  $P < 0.05$ , in bold)**

A, Arab Horse; TB, Thoroughbred; SPB, Spanish Purebred; SF, Selle Français; G, German breeds; N, North(-west) European breeds

Breed	Conformation	Cross-country aptitude	Dressage	Show jumping	Cross-country	Total score
A	24.20	5.00	–363.00	–71.60	–957.30	–2207.90
TB	–2.00	28.40	–25.90	266.80	361.40	589.00
SPB	–32.70	–23.90	<b>–926.80</b>	177.60	1376.40	537.20
SF	6.40	51.00	–45.70	208.60	<b>1433.90</b>	1134.80
G	4.20	15.90	241.10	353.30	223.30	859.90
N	26.80	68.40	513.10	505.70	2421.30	2967.90
A*A	–0.60	–0.50	6.00	6.50	17.70	<b>44.00</b>
TB*A	0.00	–0.30	0.90	–3.10	–3.00	–6.00
TB*TB	0.40	0.60	11.70	3.30	–11.90	0.70
SPB*A	0.00	–0.60	0.50	–0.10	–17.20	–9.70
SPB*TB	0.00	0.00	–2.00	–2.30	2.60	–4.00
SPB*SPB	–0.30	–0.10	–4.60	–3.30	8.40	–5.40
SF*A	0.20	<b>1.20</b>	4.30	–5.00	18.40	15.80
SF*TB	1.30	0.70	5.90	6.20	42.40	39.90
SF*SPB	0.60	0.40	6.30	1.50	5.90	5.00
SF*SF	–0.50	0.50	2.10	9.10	–4.00	–14.60
G*A	0.10	–0.30	–0.70	–2.70	–4.50	–3.50
G*TB	0.30	–0.90	<b>18.30</b>	–15.40	–56.70	–28.10
G*SPB	–0.40	–0.20	–3.80	–8.30	–13.80	–9.40
G*SF	0.00	–0.20	–3.80	–4.00	4.10	–2.90
G*G	0.00	0.00	3.60	–6.80	<b>–39.40</b>	–36.60
N*A	–0.20	–0.40	–2.60	–5.70	–2.40	–12.00
N*TB	–1.40	–0.80	7.60	17.50	3.80	33.20
N*SPB	–0.10	–1.70	–7.50	–8.80	<b>–68.40</b>	<b>–68.50</b>
N*SF	2.40	1.00	–0.10	–11.10	–13.80	–22.70
N*G	0.20	0.00	9.20	8.20	5.30	27.60
N*N	–0.50	–1.10	–12.10	–10.60	<b>–61.80</b>	<b>–81.60</b>

combination of breeds, there were systematic effects underlying the genetic differences. These effects can only be disentangled by including simultaneously linear (and/or quadratic) covariates as systematic effects in the model describing the genetic contribution of parental breeds. However, it must be pointed out that most of the covariates were finally non-significant and any claims should be made with caution.

Few authors have studied the breed contribution influence on sport horse performances. Stewart *et al.* (2010) obtained better results for Warmblood horses than others in Dressage, but the model fitted the breed as a fixed effect making it impossible to

measure the rate of the original breed contribution as well as their interaction. The phenotype explained by the covariates was computed for each participant animal using the coefficient regressions. Table 5 shows the *F* maximum, the real maximum in the SSH animals with records in the dataset and the performance obtained for a hypothetical animal with a balanced genetic composition for each group of breeds and for each trait. The regression coefficient of the covariates was used to develop the equation of the regression surface. The simplex methodology maximised these functions for each trait giving the best combination of breed genetic contribution for each trait (Figs 1–5). The best combination for conformation was 51% SPB and 49% N, for cross-country aptitude 23% SPB and 77% N, for dressage 48% SF and 52% N and for show jumping 64% A and 36% N. For cross-country exercise the best performance was predicted using 100% N genetic contribution, and for total score the best combination was 24% SF and 76% N (Table 5). Moreover, performance surfaces considering two

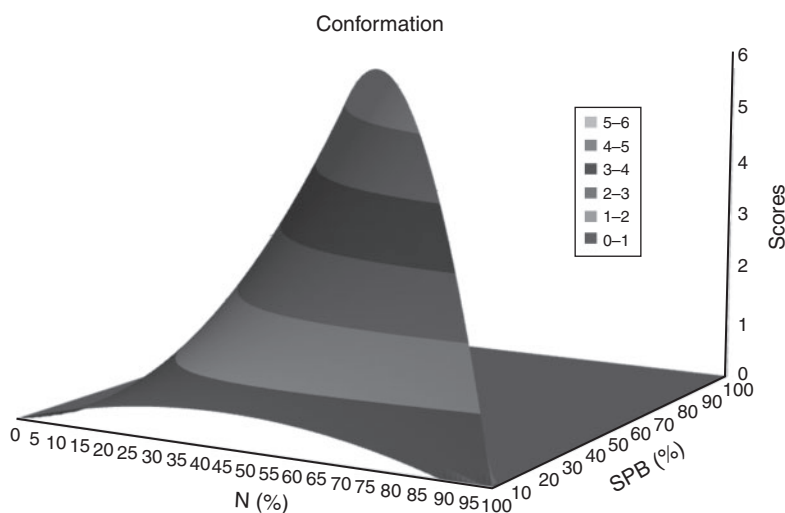
breeds are also interesting for exploring the performance under particular contributions. These are relative values because the rest of the fixed effects included in the model are not included in this expected phenotype.

The use of interactions and quadratic covariates gave different solutions from using only linear covariates to compute the best combination of genetic contribution for each trait. The increase in the performance is ensured when the *F* function is maximised. For example, applying the function using covariates with the highest and positive regression coefficient in conformation (A and N) and combining them in 50% each, the trait gave a score of -3.05, whereas the maximum of the *F* function was 5.80 (51% SPB and 49% N). The *F* function maximum required a combination of genetic contribution breeds that was not found in our database because no animal showed those breed combinations (Table 5). The *F* maximum values are far from the realistic scenario; for conformation, the best animal in the dataset had 7.2 standard

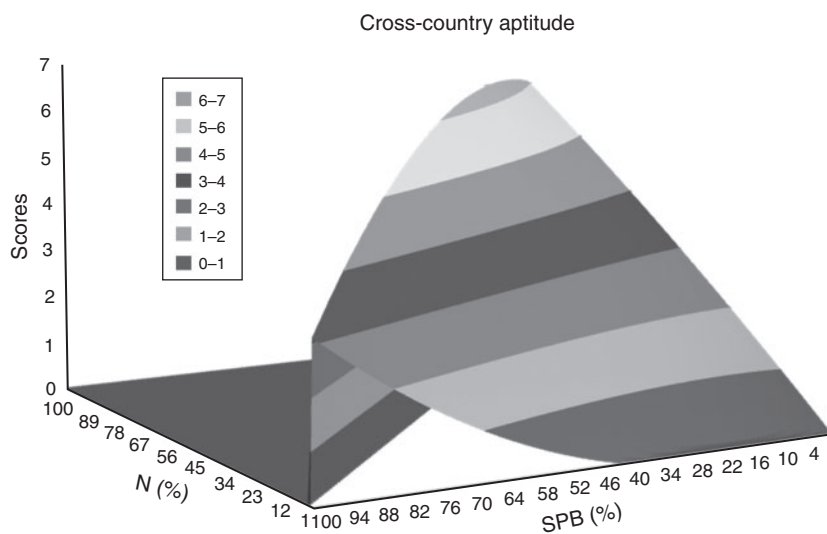
**Table 5. Phenotypic values explained by the genetic contributions computed using the coefficient regressions**

Function maximum, the real maximum in the Spanish Sport Horse animals with records in the dataset and the performance obtained for a hypothetical animal with a balanced genetic composition for each group of breeds. A, Arab Horse; TB, Thoroughbred; SPB, Spanish Purebred; SF, Selle Français; G, German breeds; N, North(-west) European breeds

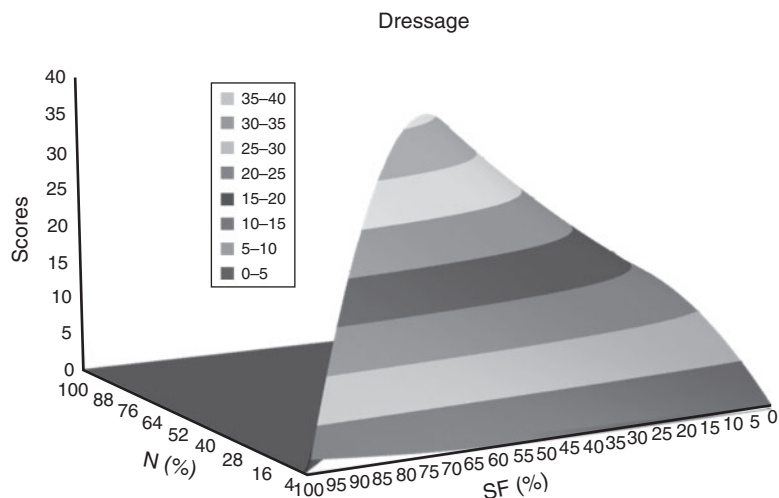
	Function maximum		Value	Maximum in dataset		Value	Balanced genetic contribution	
	Value	Genetic composition		Genetic composition	Genetic composition			
Conformation	5.80	51% SPB, 49% N	0.65	3.125% TB, 25% SPB, 3.125% G, 15.625% N	0.86	16.6% each one		
Cross-country aptitude	6.32	23% SPB, 77% N	2.16	25% A, 25% TB, 25% SF	1.69	16.6% each one		
Dressage	35.92	48% SF, 52% N	9.12	12.5% TB, 25% SF, 18.75% G, 31.25% N	0.80	16.6% each one		
Show jumping	76.30	64% A, 36% N	21.38	37.5% TB, 6.25% SF, 50% SPB	14.33	16.6% each one		
Cross-country	326.53	100% N	67.77	25% TB, 50% N	28.92	16.6% each one		
Total score	266.63	24% SF, 76% N	70.64	12.5% TB, 25% SF, 18.75% G, 31.25%N	26.65	16.6% each one		



**Fig. 1.** Surface response of the best combinations of breed contributions (% in x- and z-axes) for conformation exercise scores (y-axis). SPB, Spanish Pure breed; N, North (-west) European breeds.



**Fig. 2.** Surface response of the best combinations of breed contributions (% in x- and z-axes) for cross-country aptitude scores (y-axis). SPB, Spanish Pure breed; N, North(-west) European breeds.



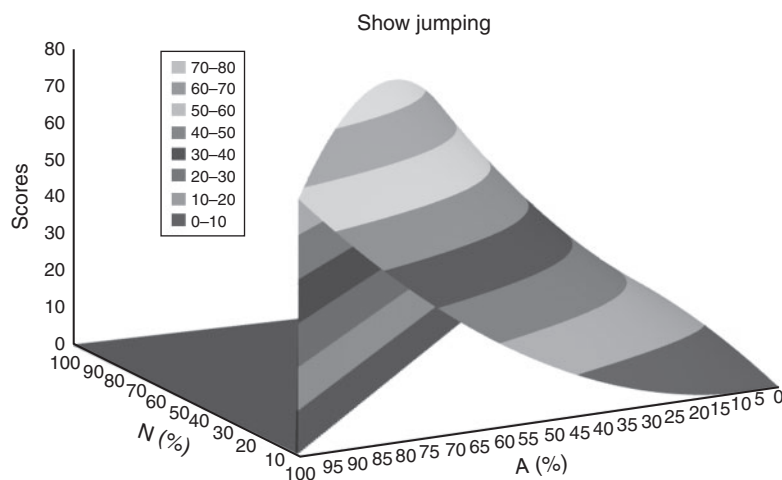
**Fig. 3.** Surface response of the best combinations of breed contributions (% in x- and z-axes) for dressage exercise scores (y-axis). SF, Selle Français; N, North(-west) European breeds.

deviations less than the maximum. And the differences in standard deviations were: for cross-country aptitude 2.9, dressage 2.9, show jumping 3.6, total score 4.2 and cross-country exercise 5.1. Regarding values using balanced genetic contributions, they were smaller to the maximum in the dataset except for the conformation.

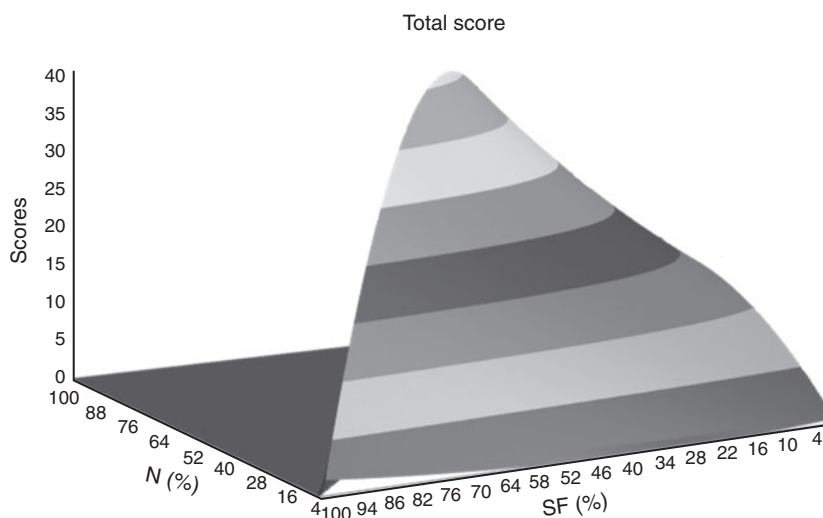
Here we found that the best performance is achieved with the contribution of two breeds (group of breeds) or only using the N group. Note that G and N are a group of breeds, and the contribution is an average of those breeds included in the group. The genetic distance between breeds inside the G group, i.e. between Trakehner and Holstein could be higher than those found between Holstein and SF or Zangersheide. Also the main breeding goal could be different in these grouped breeds and the inside breeds where there are specialised lines. This could, more or less, overlap the important influence of some of

the breeds gathered in the group. It was not possible to split these groups because of the number of breeds with small contributions and they were grouped by geographical criteria. Specifically, Zangersheide has a marginal contribution  $\sim 0\%$  in SSH population. SPB genetic contribution appeared with an important value in the optimum performance for conformation and the evaluation for cross-country aptitude. In the case of conformation we could identify a combinatory ability in which the percentage of SPB is  $\sim 50\%$ . However, this combinatory effect is not specific to one breed, but only the general behaviour by mixing SPB with one of the N breeds. However, better results were obtained for dressage and total score when the optimal contribution came from foreign breeds, such as SF from France and the N breeds.

Regarding show jumping, the best combination included, at 64% presence, the Arab horse, a very old breed and spread



**Fig. 4.** Surface response of the best combinations of breed contributions (% in x- and z-axes) for show jumping exercise scores (y-axis). A, Arab horse; N, North(-west) European breeds.



**Fig. 5.** Surface response of the best combinations of breed contributions (% in x- and z-axes) for total score (y-axis). SF, Selle Français; N, North(-west) European breeds.

worldwide, which has been used to create and improve the performance characteristic from the beginning of Warmblood horses (Schröder *et al.* 2010). Finally, the cross-country performance was better with the N genetic pool that included four different breeds, although it is far from being a unique breed combination. Other studies on Hanoverian Warmblood included the different genetic contributions as fixed effects with different classes depending on the percentage of genes (Schröder *et al.* 2010). Schröder *et al.* (2010) recommend increasing the usage of Thoroughbred and Trakehner stallions for breeding to increase the conformation scores, but no analyses recommending a combination of breeds had been done before.

There is no evidence of introgression of foreign breeds within specific lines of SSH. Nevertheless, SSH is a subdivided population (Bartolomé *et al.* 2011) because animals are selected for three different disciplines: dressage,

show-jumping and eventing performance. Therefore, it could be possible that foreign animals had been introduced within sublines in SSH according to their particular aptitude, as SSH breeders would probably select foreign animals following specialised lines of selected animals. Regarding representation of foreign animals in their original population, probably those founders appearing in our SSH animals are not a random sample of paternal breeds, but our sample is exactly representative of those founders preferably chosen to be used in the formation of SSH population. For example, the N animals appearing as founders of SSH are not a random sample of the N population, but our sample could be representative of those N founders used in the formation of SSH population. Moreover, these results should be interpreted with caution. As the optimum combination was far from the best combination actually present in the dataset, the regression coefficients need to be recomputed

when a different range in the genetic contributions appears in the future, given that linearity approximation was only checked in the range present in the dataset. In fact, this solution can be considered as the starting point. Therefore, breeders can manage matings in the direction of that is defined as the best combination, but optimal percentages being far from those present in the actual dataset, are not really advisable because they have not yet been tested. For example, today the use of Arab genetics can be recommended to improve show jumping, but it could be risky searching directly for a percentage of 64% as required by the optimal solution, i.e. it is certain that increasing the percentage of the Arab breed in the range it is actually present will lead to an increase in the performance for show jumping, but it could also be possible that by increasing that representation a lot would lead to a worsening performance. Another important issue to consider is the representativeness of the essayed animals in their original population and it must be pointed out that these conclusions refer to the Arab animals used as founders and their close relatives, but do not refer to other Arab animals. For example, it could be that the great show jumping 'breeds' (e.g. Holsteiner, SF) used in the creation of those SSH animals have a high percentage of French Anglo-Arabs, which are indirectly providing the Arab blood.

The combination of two breeds (group of breeds) seems to be the best option for most of the traits. This could be partially due to heterosis/dominance effects, but here most cases are not a result of mating two animals from pure breeds but the cumulated effect of contributions of several of them across generations. A combining ability or a genotype–genotype interaction could, therefore, be involved. Breeders might be recommended to try and fit optimal contribution towards the best combination of breeds in future generations. In fact this solution can be considered as the starting point. If a breeder tries to find this combination, it could be possible to assess later how this combination performs. Therefore, we think that the approach has to be carried out periodically trending to better determine the optimal contribution. In the present study we have tried to advantage the complementarity in the mating. However, it is worth pointing out that both additive genetics and complementarity can be used simultaneously to search for a better performance in the progeny.

## Conclusion

We conclude that only one or two group of breeds accounted for optimal performance for each trait. However, we only considered the first- and second-order interactions in the method given that an enormous amount of data would be needed to properly estimate third-order interactions and this could be conditioning the results. The search for an animal with complicated combinations of contributions from more than two breeds seems not to be practical. Although the results should be interpreted with caution, the importance of this paper is that it can be considered as a starting point of the analysis. The methodology applied here performed nicely in searching for the best contribution of several breeds to find the best combination for particular interests and could, therefore, be useful for other species/populations.

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## References

- Arnason T, Van Vleck LD (2000) Genetic improvement of the horse. In 'The genetics of the horse'. (Eds AT Bowling, A Ruvinsky) pp. 473–497. (CABI Publishing: New York)
- Bartolomé E, Cervantes I, Valera M, Gutiérrez JP (2011) Influence of foreign breeds on the genetic structure of the Spanish Sport Horse population. *Livestock Science* **142**, 70–79. doi:10.1016/j.livsci.2011.06.021
- Bartolomé E, Menéndez-Buxadera A, Valera M, Cervantes I, Molina A (2013) Genetic (co)variance components across age for Show Jumping performance as an estimation of phenotypic plasticity ability in Spanish horses. *Journal of Animal Breeding and Genetics* **130**(3), 190–198. doi:10.1111/jbg.12001
- Cervantes I, Bartolomé E, Gómez MD, Medina C, González MA, Valera M (2007) Genetic parameters for young eventing competition in Spain: correlation between dressage, jumping, cross and conformation. 58th Annual Meeting of the European Association for Animal Production, 26–29 August, Dublin, Ireland.
- Cervantes I, Goyache F, Gutiérrez JP (2008) Ratio between inbreeding and coancestry rates as a measure of population subdivision. Preliminary results. *ITEA-Información Técnica Económica Agraria* **104**, 303–307.
- Cervantes I, Gutiérrez JP, Molina A, Goyache F, Valera M (2009) Genealogical analyses in open populations: the case of three Arab-derived Spanish horse breeds. *Journal of Animal Breeding and Genetics* **126**, 335–347. doi:10.1111/j.1439-0388.2008.00797.x
- Cervantes I, Goyache F, Molina A, Valera M, Gutiérrez JP (2011) Estimation of effective population size from the rate of coancestry in pedigreed populations. *Journal of Animal Breeding and Genetics* **128**, 56–63. doi:10.1111/j.1439-0388.2010.00881.x
- Ducro BJ, Koenen EPC, van Tartwijk JFM, van Arendonk JAM (2007a) Genetic relations of First Stallion Inspection traits with dressage and show-jumping performance in competition of Dutch Warmblood horses. *Livestock Science* **107**, 81–85. doi:10.1016/j.livsci.2006.09.019
- Ducro BJ, Koenen EPC, van Tartwijk JFM, Bovenhuis H (2007b) Genetic relations of movement and free-jumping traits with dressage and show-jumping performance in competition of Dutch Warmblood horses. *Livestock Science* **107**, 227–234. doi:10.1016/j.livsci.2006.09.018
- FAO (1993) 'Evaluation of breeds and crosses of domestic animals.' (FAO: Rome, Italy)
- Goot H (1986) Development of Assaf, a synthetic breed of dairy sheep in Israel. In '37th annual meeting of the European Association for Animal Production, 1–4 September, Budapest, Hungary'. pp. 1–29. (European Association for Animal Production: Budapest, Hungary)
- Goyache F, Gutiérrez JP, Álvarez I, Fernández I, Royo LJ, Gomez E (2003) Genetic analysis of calf survival at different preweaning ages in beef cattle. *Livestock Production Science* **83**, 13–20. doi:10.1016/S0301-6226(03)00044-7
- Groeneveld E, Kovac M, Mielenz N (2008) 'User's guide and reference manual version 6.0.' (Neustadt, Germany) Available at ftp://ftp.tzv.fal.de/pub/vce6/doc/vce6-manual-3.1-A4.pdf [Verified 19 March 2015]
- Gutiérrez JP, Goyache F, Fernández I, Álvarez I, Royo LJ (2007) Genetic relationships among calving ease, calving interval, birth weight, and weaning weight in the Asturiana de los Valles beef cattle breed. *Journal of Animal Science* **85**, 69–75. doi:10.2527/jas.2006-168
- Hamann H, Distl O (2008) Genetic variability in Hanoverian warmblood horses using pedigree analysis. *Journal of Animal Science* **86**, 1503–1513. doi:10.2527/jas.2007-0382



- Huizinga HA, van der Meij GJW (1989) Estimated parameters of performance in jumping and dressage competition of the Dutch Warmblood horse. *Livestock Production Science* **21**, 333–345. doi:[10.1016/0301-6226\(89\)90093-6](https://doi.org/10.1016/0301-6226(89)90093-6)
- Kearsley CGS, Woolliams JA, Coffey MP, Brotherstone S (2008) Use of competition data for genetic evaluations of eventing horses in Britain: analysis of the dressage, showjumping and cross country phases of eventing competition. *Livestock Science* **118**, 72–81. doi:[10.1016/j.livsci.2008.01.009](https://doi.org/10.1016/j.livsci.2008.01.009)
- Koenen EPC, Aldridge LI, Philipsson J (2004) An overview of breeding objectives for warmblood sport horse. *Livestock Production Science* **88**, 77–84. doi:[10.1016/j.livprodsci.2003.10.011](https://doi.org/10.1016/j.livprodsci.2003.10.011)
- Nelder JA, Mead R (1965) A simplex method for function minimization. *The Computer Journal* **7**, 308–313. doi:[10.1093/comjnl/7.4.308](https://doi.org/10.1093/comjnl/7.4.308)
- Núñez-Domínguez R, Dickerson GE, Cundiff LV, Gregory KE, Koch RM (1992) Economic evaluation of heterosis and culling policies for lifetime productivity in Hereford, Angus, Shorthorn and crossbred cows. *Journal of Animal Science* **70**, 2328–2337.
- Ricard A, Chanu I (2001) Genetic parameters of eventing horse competition in France. *Genetics, Selection, Evolution*. **33**, 175–190. doi:[10.1186/1297-9686-33-2-175](https://doi.org/10.1186/1297-9686-33-2-175)
- SAS Institute Inc (2008) 'SAS/QC® 9.2 user's guide.' (SAS Institute Inc.: Cary, NC)
- Schröder W, Stock KF, Distl O (2010) Genetic evaluation of Hanoverian warmblood horses for conformation traits considering the proportion of genes of foreign breeds. *Archives Animal Breeding* **53**, 377–387.
- Stewart ID, Woolliams JA, Brotherstone S (2010) Genetic evaluation of horses for performance in dressage competitions in Great Britain. *Livestock Science* **128**, 36–45. doi:[10.1016/j.livsci.2009.10.011](https://doi.org/10.1016/j.livsci.2009.10.011)
- Tang G, Yang R, Xue J, Liu T, Zeng Z, Jiang A, Jiang Y, Li M, Zhu L, Bai L, Shuai S, Li X (2014) Optimising a crossbreeding production system using three specialised imported swine breeds in south-western China. *Animal Production Science* **54**, 999–1007. doi:[10.1071/AN13308](https://doi.org/10.1071/AN13308)
- Thorén Hellsten E, Näsholm A, Jorjani H, Strandberg E, Philipsson J (2009) Influence of foreign stallions on the Swedish Warmblood breed and its genetic evaluation. *Livestock Science* **121**, 207–214. doi:[10.1016/j.livsci.2008.06.014](https://doi.org/10.1016/j.livsci.2008.06.014)
- Viklund Å, Braam Å, Näsholm A, Strandberg E, Philipsson J (2010) Genetic variation in competition traits at different ages and time periods and correlations with traits at field tests of 4-year-old Swedish Warmblood horses. *Animal* **4**, 682–691. doi:[10.1017/S1751731110000017](https://doi.org/10.1017/S1751731110000017)
- Zhang S, Bidanel JP, Burlot T, Legaul C, Naveau J (2000) Genetic parameters and genetic trends in the Chinese x European Tiameslan composite pig line. I. Genetic parameters. *Genetics, Selection, Evolution*. **32**, 41–56. doi:[10.1186/1297-9686-32-1-41](https://doi.org/10.1186/1297-9686-32-1-41)