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## Original article

### Genetic improvement of canine hip dysplasia through sire selection across countries

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## **Abstract**

Breeding against canine hip dysplasia (HD) may benefit from the importation of foreign sires. When foreign sires are evaluated on a different HD scale, this may diminish the efficacy. Using stochastic simulations, we evaluated genetic change and inbreeding levels for different scenarios of importing sires with high genetic merit for HD. Population size and genetic parameters (e.g. heritability, accuracy of selection, genetic correlation) were based on actual data for HD in Golden retrievers and Labrador retrievers in the UK and Sweden.

For countries with different HD scales and an estimated breeding value (EBV) evaluation in place, the importation was useful if imported sires had EBV rankings in the top 50% and if genetic correlations between EBV systems were above 0.85. When importing sires with EBV rankings in the top 10%, moderate accuracies of EBVs ( $> 0.40$ ) and moderately strong genetic correlations ( $> 0.70$ ) were needed. Selection against HD without the importation of sires may increase inbreeding levels, while the importation of sires can decrease inbreeding levels. For national genetic evaluation and selection programmes, importing sires with high genetic merit can be an effective breeding strategy, but care is needed to estimate reliable EBVs.

*Keywords:* Canine; Estimated breeding value; Hip dysplasia; International breeding programme; Stochastic simulation

## **Introduction**

Canine hip dysplasia (HD) is an abnormal development of the coxofemoral joint in dogs, and as it progress can lead to lameness, arthritis and hip pain. HD is one of the most common orthopaedic disorders/diseases in dogs and has been reported in more than 188 dog breeds, with a prevalence varying from 1.0 to 71.2%<sup>1</sup>. Unlike the control of undesirable single-gene traits where genetic testing (where the gene is known) can be used to guide breeding, the control of undesirable complex traits (i.e. those determined by multiple genes and interactions with environment, such as HD), through genetic screening is more difficult. Worldwide, three different scoring schemes for HD are widely used: the BVA/KC (British Veterinary Association/The Kennel Club) scheme in the UK, Australia and New Zealand; the OFA (Orthopedic Foundation for Animals) scheme in the USA; and the FCI (Fédération Cynologique Internationale) scheme in Europe, Asia and Latin America. Furthermore, veterinary training for the measurement of hip joint laxity using other schemes, e.g. PennHIP (The University of Pennsylvania Hip Improvement Program), developed by Smith et al. (1990), are also commercially available.

Selection after the evaluation of estimated breeding values (EBVs) is the most effective way to genetically improve hip joint status (Wilson et al., 2011; Lewis and Windig 2016). Genetic evaluation routines have been implemented in some countries, such as Denmark, Finland, Germany, Norway, Sweden and the UK (Wang et al., 2018). In most countries, however, selection to improve hip joint status is based solely on phenotypic assessments. Meanwhile, in recent years, the exchange of breeding animals and semen

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<sup>1</sup> See: OFA – Orthopedic Foundation for Animal. 2018. (Available at <https://www.ofa.org/diseases/breed-statistics#detail> (Accessed 10 March 2019))

between countries has increased (Wang et al., 2017a). This exchange can increase the risk of importing dogs with unknown or low genetic merit for HD, thereby reducing the efficacy of the breeding programme. However, genetic progress towards improvement in HD may be accelerated by genetic evaluation across countries via an enlarged pool of breeding candidates (Fikse et al., 2013).

The potential for improvement in the genetic progress against HD was demonstrated for the Golden retriever and Labrador retriever subpopulations in the UK and Sweden (Wang et al., 2017b). However, the grading systems used to indicate the severity of hip joint were not the same; the UK uses the BVA/KC scheme with scores ranging from 0 (no HD) to 106 (severe HD), while FCI countries, such as Sweden, follow a specific FCI scheme with five-level grades: A and B are normal, C is mild and D is moderate and E is severe. Imported dogs evaluated using a different scale may not be of expected genetic merit if the (genetic) correlation between traits measured on these different scales is substantially below 1.0, and a further reduction in efficacy may occur if the accuracy of the EBVs are low (Wang et al. 2017b). The consequence may be that a higher selection intensity is needed to allow only the importation of dogs with a (very) high genetic merit.

Evaluating the efficacy of various strategies for importing sires with high genetic merit has not been explored as a breeding strategy, and the influence of genetic correlations across countries and the accuracies of EBVs has also not been examined. Computer simulation can be an effective tool to predict genetic changes and inbreeding levels, especially for complex situations, such as overlapping generations and exchange between different subpopulations. In dogs, computer simulation has been used to study strategies aimed at reducing single-gene defects and high inbreeding rates in pedigree dogs (Leroy and Baumung,

2011; Windig and Oldenbroek, 2015). Based on estimated genetic parameters for the Golden retrievers and Labrador retrievers in the UK and Sweden (Wang et al. 2017b), a computer simulation study was used to study the efficacy of international breeding strategies to import sires with high genetic merit.

## **Materials and methods**

### *Simulation program*

A FORTRAN program 'GenManSim' (Windig and Oldenbroek, 2015) was used and extended with the facility to simulate subpopulations (Windig and Doekes, 2018). The specific functions needed in our study were added to the original simulation workflow of 'GenManSim', including generation of breeding values and phenotypes for individual animals and selection based on EBVs and/or phenotypes of HD. Because genetic evaluation across two countries with different HD scales was to be simulated, all animals had two sets of true breeding values (TBVs) and EBVs simulated:  $TBV_1$  and  $EBV_1$  for the scale used in country 1 (country 1 scale) and  $TBV_2$  and  $EBV_2$  used in country 2 (country 2 scale). The method about how TBVs and EBVs for HD were calculated is shown in Appendix (see Supplementary document 1). The objective of this study was to simulate genetic change as a result of selection across two countries having two HD grading systems, with possible importation from country 1 to country 2. Given the gene flows previously observed from the UK to Sweden (Wang et al. 2017), country 1 therefore corresponds to the UK, and country 2 corresponds to Sweden.

Input values for the simulation parameters are shown in Table 1, including those necessary to run the simulation: population size and structure; phenotypes and genetic parameters; breeding selection and mating restrictions options. In countries using FCI scale,

grade A and B indicate normal status of hip joint in dogs, which corresponds to BVA/KC scores below 26 in the UK (Flückiger, 2007). However, in order to perform the genetic evaluation required, the FCI grades A, B, C, D and E were replaced with 1, 2, 3, 4 and 5, respectively (Wang et al. 2017b), while the BVA/KC scores 0-106 (with an addition of 1) were transformed by natural logarithms (Lewis et al. 2010). In this study, transformed phenotypic mean (SD) of HD measures in country 1 and country 2 were set as 1.67 (0.6) and 2.66 (0.7) as in Wang et al. (2017b). Therefore, to differentiate between dogs being affected (20%) or unaffected (80%) by HD in country 1 and country 2, respectively, 2.259 and 3.165 of transformed phenotypic values were set as threshold assuming a normal distribution (Table 1). Additional details regarding the function of the simulation program and how input values for the simulation parameters were chosen are shown in the Appendix (see Supplementary document 1).

### *Simulation scenarios*

Eight scenarios with varying importation of sires and use of EBVs in selection were studied (Table 2). No selection occurred in the scenario 1, while in all other scenarios, only dogs without HD were allowed to reproduce. Comparison to this strategy allowed us to determine the effect of selection in the other models. In scenarios 1-3, no foreign sires are imported, while in scenarios 4-5, 20% of the sires used in breeding were foreign. This allowed us to determine the effect of the importation of sires.

In the scenarios without importation, selection of sires differed: either (1) no sire selection (random mating), abbreviated as NoSel; (2) sire selection on phenotype only (Pheno<sub>2</sub>); or (3) sire selection on both phenotype and EBV, i.e. sires must have *EBV*<sub>2</sub> in the top 50% (Pheno<sub>2</sub>+DomEBV<sub>2</sub>). Phenotypes and EBVs for scenarios 2 and 3 were evaluated on

the domestic scale (country 2). In all scenarios with importation of sires, all sires were selected based on their phenotype using the scale of their country of birth (e.g. scale 2 for domestic sires, scale 1 for foreign sires). The scenarios differed in the use of EBVs in the selection of sires: (4) No selection on EBV (Pheno+IntAll); (5) selection on EBV for foreign sires only, i.e.  $EBV_1$  in the top 50% (Pheno+Int $EBV_1$ ); (6) selection on EBV for domestic sires only, i.e.,  $EBV_2$  in the top 50% (Pheno+Dom $EBV_2$ +IntAll); (7) selection on EBV for both foreign and domestic sires, both on the scale of their own country of birth (Pheno+Dom $EBV_2$ +Int $EBV_1$ ); (8) was as (7) but foreign sires were evaluated on the scale of the country of importation (Pheno+Dom $EBV_2$ +Int $EBV_2$ ). These scenarios enabled us to evaluate the effect of using EBVs for selection, either on the domestic or on the foreign scale, when importing sires.

Each scenario was run for 10 years with 40 replicates. Four statistics of newborn pups in country 2 were calculated: average  $TBV_2$ , percentage of dogs with HD, average inbreeding and coancestry coefficients. In all scenarios, in country 1 phenotypic selection and selection on EBV (Pheno<sub>1</sub>+Dom $EBV_1$ ) was employed. This strategy enabled us to evaluate the importation of sires from a country with selection based on EBV to countries either with or without selection based on EBV. Restriction on relatedness between mating partners ( $<0.125$ ) was applied for all the scenarios.

Scenario 7 Pheno+Dom $EBV_2$ +Int $EBV_2$  was regarded as the basic standard scenario to evaluate the efficacy of importing sires in this study. This scenario was further explored with various selection intensities of sires, percentages of foreign sires used in breeding, accuracies, and genetic correlations. The selection intensities regarding the EBVs of imported sires were varied from the top 10% to top 50% (with an interval of 10%); the percentages of litters

produced by foreign sires were varied from 0% to 60% (with an interval of 20%); the accuracy of  $EBV_2$  was varied from 0.45 to 0.75 (with an interval of 0.1); and the genetic correlation between the two HD scales was varied from 0.65 to 0.95 (with an interval of 0.1). To evaluate what parameters are worthwhile for imported dogs, the outcomes of the above alternatives were compared with a purely national breeding programme in country 2 (referred to as scenario Pheno<sub>2</sub>+DomEBV<sub>2</sub>).

## **Results**

Because the study focused only on changes in the populations of countries importing foreign sires, and not on countries exporting sires, only results for country 2 are reported, i.e., the TBVs below are actually  $TBV_2$ , unless otherwise indicated. Note that TBV scores describe the severity status of hip joint, with lower scores being better.

### *Breeding strategies*

As expected, neither genetic improvement nor reduction in the prevalence of HD was achieved by random mating in scenario NoSel (Table 3). In contrast, the scenario without the importation of foreign sires but with selection of only healthy dogs within country 2 in scenario Pheno<sub>2</sub>, reduced the average TBVs to -0.23 and the prevalence of HD to 11.2% at year 10. Adding a restriction on domestic dogs' EBVs (use of top 50% only, scenario Pheno<sub>2</sub>+DomEBV<sub>2</sub>) further reduced the average TBVs to -0.62 and the prevalence of HD to 3.0%. In country 1, under the same strategy for each scenario focusing on  $TBV_1$ , an average  $TBV_1$  of -0.62 and an average  $TBV_2$  of -0.46 were achieved at year 10 (see Appendix: Supplementary Table 1).

When 20% of the newborn litters were produced by foreign sires each year, and only healthy dogs within country 2 were used, but with no restriction on imported dogs (Pheno+IntAll), the average TBV decreased to -0.24 and the prevalence of HD decreased to 11.0% (Table 3). When a restriction was added to use only foreign sires from the top 50% (based on the EBV in the exporting country), similar genetic progress was achieved (average TBVs of -0.27 and prevalence of HD of 10.2% (Pheno+IntEBV<sub>1</sub>). Compared with scenario Pheno+IntAll, also including a restriction on the EBVs of domestic dogs, (Pheno+DomEBV<sub>2</sub>+IntAll) resulted in substantial improvement in the genetic progress, from -0.24 to -0.53 in average TBVs and from 11.0% to 4.3% in HD prevalence. However, the addition of a restriction on the EBVs of imported dogs (on either scale) resulted in only a slight improvement in genetic gain; average TBV -0.56 and prevalence of HD 3.8% in scenario Pheno+DomEBV<sub>2</sub>+IntEBV<sub>1</sub>, and average TBV -0.57 and prevalence of HD 3.8% in scenario Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub>. In short, for scenarios Pheno+IntAll and Pheno+DomEBV<sub>2</sub>+IntAll, the importation of sires (regardless of EBV) resulted in genetic progress, however the genetic progress was always lower compared to similar scenarios including selection on EBV using domestic sires only (Pheno<sub>2</sub> + DomEBV<sub>2</sub>). The trends of the genetic progress made in the first 10 years for each breeding strategy are shown in Fig. 1.

Inbreeding reached a level of 0.30% after 10 years without importation or selection (NoSel). Selection on phenotype only slightly increased the inbreeding level (0.37%), while selection on EBV resulted in a notable increase in the inbreeding level to 1.28%. The importation of foreign animals decreased inbreeding levels to 0.22% when there was only phenotypic selection, and to an average of 0.70% with additional selection on EBV in domestic animals. Coancestry levels followed the same pattern but reached values of approximately four times the inbreeding levels. This observed difference between coancestry

and inbreeding levels was probably linked to restrictions on mating partners that were close relatives.

#### *Selection intensity of importing sires*

The average TBVs of newborn pups in year 10 improved from -0.57 to -0.65 when the selection intensity was increased from importing top 50% sires to top 10% under Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub> (Table 4). The prevalence of HD decreased from 3.8% to 2.9%. The increase in the inbreeding level was only slight when the required EBV rankings of sires changed from the top 50% to the top 20% (from 0.70% to 0.74%), while it increased to 0.99% when the required EBV rankings of sires were the top 10%.

#### *Percentages of litters produced by foreign sires*

Increasing the percentage of litters produced by foreign sires from 20% to 60% reduced the rate of improvement in genetic progress in both scenarios Pheno+DomEBV<sub>2</sub>+IntAll and Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub> (Table 5). The absolute difference of average TBVs between scenarios Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub> and Pheno+DomEBV<sub>2</sub>+IntAll was 0.04 in the pups born in year 10 when the percentages of litters was 20%, and the absolute differences were 0.07 and 0.09 when percentages of litters were 40% and 60%, respectively. Additionally, using more foreign sires in breeding also reduced inbreeding.

#### *Accuracy of selection*

The accuracy of selection is the correlation between EBV and TBV and indicated how well the EBV represented the TBV. When the accuracy of selection increased from 0.45 to 0.75, genetic progress improved (Fig. 2): from -0.53 to -0.61 (from -0.55 to -0.69) when the

requirement was set to sires in the top 50% (top 10%). Regardless of which level of accuracy was used for selection, the TBVs achieved by importing sires with EBVs ranking in the top 50% (scenario Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub>) were always lower than the genetic progress made in scenario Pheno<sub>2</sub>+DomEBV<sub>2</sub>. Compared to the genetic progress made in scenario Pheno<sub>2</sub>+DomEBV<sub>2</sub>, the TBVs achieved by importing sires with EBVs ranking in the Top 10% (scenario Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub>) was higher only when the accuracy of selection was over 0.40.

### *Genetic correlations*

When the genetic correlations between  $TBV_1$  and  $TBV_2$  increased from 0.65 to 0.95 in scenario Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub>, the average TBV changed from -0.54 to -0.65 when the required sire rankings were in the top 50%, and the average TBV changed from -0.60 to -0.72 when the required sire rankings were in the top 10% (Fig. 3). Compared to the genetic progress made in scenario Pheno<sub>2</sub>+DomEBV<sub>2</sub> (average TBV was -0.62), the TBV achieved by importing sires with EBVs ranking in the top 50% (top 10%) were higher when the genetic correlation was over 0.85 (0.70).

## **Discussion**

Controlling the prevalence of inherited disorders constitutes an important issue for the health and welfare of pedigree dogs. The use of sires with high genetic merit in an international context has been viewed as a promising breeding strategy to improve the health and welfare of dogs (Wilson and Wade, 2012; Fikse et al. 2013), and the simulation of such a breeding strategy is informative to national kennel clubs and may assist in the genetic management of various breeds. This study underlines how the international exchange of breeding animals may be used to improve the situation for a complex disease such as HD.

A posterior evaluation of HD trends over recent decades, where selection was implemented based solely on phenotypic observations, has shown favourable trends in the long run (Malm et al., 2008; Lewis et al., 2013; Oberbauer et al., 2017). In some cases, the magnitude of the detected improvement for HD has been notable, for example in Swedish Rottweilers and Bernese mountain dogs, genetic progress corresponded to 0.67 and 0.57 genetic SD units, respectively, over the last 10 years by only breeding from dogs without HD (Malm et al. 2008). This observed trend is in agreement with the trend of the simulation results in our study, showing that phenotypic selection can reduce the prevalence of HD when applied for a long period. In our simulation, the genetic change corresponded to 0.61 genetic SD units in the first 10 years of the breeding programme when only considering phenotypic selection (scenario Pheno<sub>2</sub>) (Table 3). In Europe, most countries have phenotypic restrictions for breeding but do not have genetic evaluation routines of HD for domestic selection. Nevertheless, they can make use of foreign stock for breeding which is evaluated by scenario Pheno+IntAll in this study. For countries without EBVs, it can be recommended that breeders import sires from countries that already have EBV evaluation in place, thus choosing sires with good EBVs, as illustrated by comparing scenario Pheno+IntEBV<sub>1</sub> to scenario Pheno+IntAll.

Our simulation study confirmed that implementation of international genetic evaluation can bring further genetic improvement of HD by the importation of sires with higher genetic merit (Table 4). When more litters were born by foreign sires, the difference in the genetic progress between scenarios with and without international evaluations of foreign sires became larger (Table 5), which means that more benefits can be expected using EBV-evaluated foreign sires with an increased exchange of breeding animals. For countries such as

the UK and Sweden, genetic evaluation has been implemented and is publicly available and there is migration of dogs between the two countries, which can be considered similar to scenario Pheno+DomEBV<sub>2</sub>+IntAll (average TBVs of -0.53, Table 3) assuming Swedish breeders importing UK sires do not consider their UK EBVs. Without international evaluation implemented, but considering UK EBVs, more genetic progress (average TBVs of -0.56) could be achieved by scenario Pheno+DomEBV<sub>2</sub>+IntEBV<sub>1</sub>. Once the international evaluation is implemented, as in scenario Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub>, some further genetic progress can be achieved (average TBVs of -0.57). However, the additional genetic gain achieved from scenario Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub> (average TBVs of -0.57) compared to Pheno+DomEBV<sub>2</sub>+IntAll (average TBVs of -0.53) was small, if not negligible. More genetic progress would be achieved by scenario Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub> if either the accuracy of selection or genetic correlation is higher than the default values (0.65 and 0.75, respectively) that were set in the simulation (Figs. 2 and 3). In practice, reducing the average TBVs from -0.53 to -0.57 in the first 10 years corresponded to changing the genetic SD units of HD scores from 1.39 to 1.50 based on the transformed phenotype on the scale of country 2, which was an important genetic improvement and was reflected in the reduced prevalence of HD from 20% to 3.77 – 4.28% (Table 3).

The simulation also demonstrated the benefits of importing sires with very high genetic merit (sires with EBV rankings in the top 10%; average TBVs of -0.65) compared to using sires with EBV rankings just in the top 50% (average TBVs of -0.57). Nevertheless, a moderate level of accuracy of selection was necessary to ensure the efficacy of importing sires based on EBV rankings. When the accuracy of selection was lower than 0.40, the genetic progress achieved by importing sires with EBV rankings in the top 10% (scenario Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub>) was not higher than from a purely national breeding

programme, as in scenario Pheno<sub>2</sub>+DomEBV<sub>2</sub> (Fig. 2). Accuracy depends on the heritability and the number of (close) relatives available. Similar to sire selection based on progeny testing in dairy cattle, sires that have HD screening records and have multiple offspring with HD screening records have higher accuracies in genetic evaluation. For instance, the accuracy of sires with only their own HD records can reach 0.55 when the heritability is 0.30, while at the same heritability the accuracy of sires without their own HD records can reach 0.44 once two offspring are tested. Hence, we highly recommend importing sires with their own HD records that have had several offspring screened.

A strong genetic correlation is also required to make the importation of sires worthwhile. The genetic correlation should be over 0.85 to ensure that more genetic progress is made from importing sires with EBVs in the top 50% (scenario Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub>) compared with the progress that could be achieved from a purely national selection programme, as in scenario Pheno<sub>2</sub>+DomEBV<sub>2</sub> (Fig. 3). This may also be a reason for the small difference in genetic progress between scenarios Pheno+DomEBV<sub>2</sub>+IntAll (average TBVs of -0.53) and Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub> (average TBVs of -0.57) when the genetic correlation was 0.75 (Table 4). This finding is similar to simulation studies carried out by varying genetic correlations in dairy cattle breeding programmes. A genetic correlation as high as 0.80–0.90 was required to obtain an extra 15% improvement in genetic gain (Mulder and Bijma, 2006).

Theoretically, the genetic correlation between HD in the UK and Sweden should be close to 1.0, which has been confirmed by bootstrap simulation (Fikse et al. 2013). However, because the BVA/KC and FCI schemes evaluating the severity of hip joint status used in the UK and Sweden are measured on different scales, genetic correlations >0.90 may not be

reached. Therefore, consensus across countries in screening protocols for HD would be useful to improve genetic correlations. Moreover, the genotype–environment interaction (G x E) in the genetic evaluation of HD may also exist across countries due to differences in veterinary care for HD, which could also prevent genetic correlations from reaching unity.

In all breeding scenarios in our study, the relatedness between mating partners was required to be less than 0.125. This result was because mating between close relatives, e.g. between a father and daughter or between half siblings, is not recommended or allowed in most European countries. Comparing inbreeding levels after 10 years in scenarios Pheno<sub>2</sub> (0.33%) and Pheno<sub>2</sub>+DomEBV<sub>2</sub> (1.28%), which modelled breeding in a closed population, to scenarios Pheno+IntAll (0.22%) and Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub> (0.70%), which modelled the use of foreign sires, shows that the rate of inbreeding can be effectively controlled by importing sires. This finding meets the expectation of Wang et al. (2017a) that the management of inbreeding can benefit from the international exchange of breeding animals. However, if high-EBV ranking foreign sires are heavily used, inbreeding levels will also increase more quickly. This observation is clearly shown when changing the use high-EBV sires from the Top 20% to the Top 10%, increasing the inbreeding level from 0.74 to 0.99 in 10 years (Table 3). This phenomenon has been largely illustrated in Holstein cattle, with a decrease in genetic variability related to the worldwide use of the best bulls through artificial insemination and frozen semen (Brotherstone and Goddard, 2005; Doekes et al. 2018). Therefore, although dog breeders and owners are generally free to choose mating sires, national kennel clubs should develop breeding management strategies to ensure that no sires are used too extensively, especially when importing foreign sires with high genetic merits.

Future research could focus more on the systematic design of breeding programmes. For instance, research may simulate genetic progress by considering the removal of recessive alleles and selection on complex traits at the same time, as well as considering the willingness of breeders to participate. Moreover, a benefit not shown from this study is that the reliability of estimation could be improved after receiving more phenotypic data from joint evaluation. In addition, genomic prediction of HD-related traits was performed in UK Labrador retrievers (Sánchez-Molano et al. 2015), and joint genomic evaluation of HD between UK and US Labrador retrievers has also been reported (Edwards et al. 2018), demonstrating the possibility of performing genomic prediction for HD. This could be the basis for future improvement of HD with faster genetic progress.

## **Conclusions**

Our simulation study demonstrated that, for countries that do not have an EBV evaluation system, it would be beneficial to import dogs with high genetic merit from countries with EBV systems. Additionally, for countries with EBV systems, importing sires with high genetic merit could be an effective breeding strategy to improve the status of hip joints in pedigree dogs, although the outcome depends on the accuracies of EBVs, genetic correlations of HD across countries, selection intensities, and percentage of litter produced by foreign sires. When considering using foreign sires with EBV rankings in the top 50%, which is the selection intensity suggested by the British Kennel Club, strong genetic correlations ( $> 0.85$ ) are necessary to ensure genetic progress equivalent to selection within an individual country. When considering the use of sires with high EBV rankings, e.g. in the top 10%, more moderate EBV accuracy ( $> 0.40$ ) and moderately high levels of genetic correlation ( $> 0.70$ ) are needed to improve on genetic progress achievable using domestic breeding stock alone.

## **Conflict of interests**

None of the authors has any financial or personal relationships that could inappropriately influence or bias the content of the paper.

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## **Appendix: Supplementary material**

Supplementary data associated with this article can be found, in the online version, at doi: ...

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**Table 1.**

Parameters used in breeding strategies simulation.

Scenario	Item	Country 1	Country 2	
			Standard	All alternatives
Population size and structure	# Breeding females	600	600	-
	# Breeding males	150	150	-
	# Litters produced in total by year	300	300	-
	Percentage of litters produced by foreign sires	0.0%	20%	0/20/40/60%
Phenotypes and genetic parameters	Phenotypic mean	1.67	2.66	-
	Phenotypic variance	0.36	0.49	-
	Phenotypic value of dogs affected by HD	> 2.26	> 3.17	-
	Percentage of dogs with HD in base generation	20%	20%	-
	Heritability	0.40	0.30	-
	Genetic SD	0.38	0.38	-
	Accuracy of selection	0.65	0.65	0.45/0.55/0.65/0.75
	Genetic correlation of TBVs between country 1 and 2	0.75	0.65/0.75/0.85/0.95	
	Relatedness between parents	< 0.125		-
Breeding selection and mating restrictions	HD restriction allow to reproduce	Only dogs without HD		-
	EBV ranking of domestic sires	Top 50%		-
	EBV ranking of foreign sires	-	Top 50%	Top 10/20/30/40/50%,

HD, hip dysplasia; EBV, estimated breeding value; SD, standard deviation

**Table 2.**

Illustration of percentages of litters produced by domestic/foreign sires and selection options in eight breeding scenarios for country 2.

Breeding scenarios	Domestic selection			International importation			
	% litters produced by domestic sires	Pheno <sub>2</sub>	EBV <sub>2</sub>	% litters produced by foreign sires	Pheno <sub>1</sub>	EBV <sub>1</sub>	EBV <sub>2</sub>
NoSel	100%	No	No	0%	-	-	-
Pheno <sub>2</sub>	100%	Yes	No	0%	-	-	-
Pheno <sub>2</sub> +DomEBV <sub>2</sub>	100%	Yes	Yes	0%	-	-	-
Pheno+IntAll	80%	Yes	No	20%	Yes	No	No
Pheno+IntEBV <sub>1</sub>	80%	Yes	No	20%	Yes	Yes	No
Pheno+DomEBV <sub>2</sub> +IntAll	80%	Yes	Yes	20%	Yes	No	No
Pheno+DomEBV <sub>2</sub> +IntEBV <sub>1</sub>	80%	Yes	Yes	20%	Yes	Yes	No
Pheno+DomEBV <sub>2</sub> +IntEBV <sub>2</sub>	80%	Yes	Yes	20%	Yes	No	Yes

HD, hip dysplasia; EBV, estimated breeding value

Pheno<sub>1</sub> – Only dogs without HD (country 1 scale) allowed to reproduce

Pheno<sub>2</sub> – Only dogs without HD (country 2 scale) allowed to reproduce

EBV<sub>1</sub> – Using sires in the top 50% based on EBV (country 1 scale)

EBV<sub>2</sub> – Using sires in the top 50% based on EBV (country 2 scale)

**Table 3.**

Average true breeding values (TBVs), percentage of hip dysplasia (HD), coefficients of inbreeding (F) and coancestry (C) of newborn pups at year 10 comparing eight breeding scenarios in country 2 (standard error).

	No importation			With importation				
	NoSel	Pheno <sub>2</sub>	Pheno <sub>2</sub> +DomEBV <sub>2</sub>	Pheno+		Pheno+DomEBV <sub>2</sub> +		
				IntAll	IntEBV <sub>1</sub>	IntAll	IntEBV <sub>1</sub>	IntEBV <sub>2</sub>
TBVs	0.00 (0.01)	-0.23 (0.01)	-0.62 (0.04)	-0.24 (0.03)	-0.27 (0.03)	-0.53 (0.01)	-0.56 (0.02)	-0.57 (0.02)
HD (%)	20.40 (0.38)	11.21 (0.19)	3.04 (0.12)	11.04 (1.10)	10.19 (1.11)	4.28 (0.23)	3.82 (0.17)	3.77 (0.16)
F (%)	0.30 (0.01)	0.37 (0.01)	1.28 (0.03)	0.22 (0.13)	0.26 (0.14)	0.70 (0.09)	0.69 (0.10)	0.70 (0.10)
C (%)	1.37 (0.01)	1.57 (0.01)	4.42 (0.06)	1.11 (0.39)	1.17 (0.42)	2.81 (0.26)	2.72 (0.28)	2.81 (0.25)

NoSel – Random mating,

Pheno<sub>2</sub> – Only dogs without HD (country 2 scale) allowed to reproduce

Pheno – Only domestic dogs without HD (country 2 scale) and foreign dogs without HD (country 1 scale) allowed to reproduce

DomEBV<sub>2</sub> – Using domestic sires in the top 50% based on EBV (country 2 scale)

IntAll – No EBV requirement when using foreign sires

IntEBV<sub>1</sub> – Using foreign sires in the top 50% based on EBV (country 1 scale)

IntEBV<sub>2</sub> – Using foreign sires in the top 50% based on EBV (country 2 scale)

No importation: 100% of litters produced by domestic sires

With importation: 80% and 20% of litters produced by domestic and foreign sires respectively

**Table 4.**

Average true breeding values (TBVs), percentage of hip dysplasia (HD), coefficients of inbreeding (F) and coancestry (C) of new born pups at year 10 comparing different estimated breeding value (EBV) rankings of foreign sires used in breeding in country 2 (standard error).

EBV ranking of foreign sires <sup>a</sup>	Top 50%	Top 40%	Top 30%	Top 20%	Top 10%
TBVs	-0.57 (0.02)	-0.58 (0.02)	-0.61 (0.02)	-0.61 (0.02)	-0.65 (0.02)
HD (%)	3.77 (0.16)	3.52 (0.15)	3.31 (0.18)	3.10 (0.17)	2.91 (0.15)
F (%)	0.70 (0.10)	0.71 (0.10)	0.73 (0.10)	0.74 (0.10)	0.99 (0.09)
C (%)	2.81 (0.25)	2.84 (0.28)	2.90 (0.30)	2.95 (0.30)	3.92 (0.21)

<sup>a</sup> Assuming that 20% of litters are produced by foreign sires, scenario 'Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub>' was used to run the comparison of cases that only allowing healthy dogs to reproduce; using the top 50% domestic dogs and the top 10-50% of foreign dogs based on EBVs (country 2 scale).

**Table 5.**

Average TBVs, percentage of hip dysplasia (HD), coefficients of inbreeding (F) and coancestry (C) of newborn pups at year 10 comparing with and without estimated breeding value (EBV) requirements of using foreign sires by different percentages of litters produced by foreign sires in country 2 (standard errors within brackets).

Percentage of litters produced by foreign sires <sup>a</sup>	0%	20%		40%		60%	
		IntAll	IntEBV <sub>2</sub>	IntAll	IntEBV <sub>2</sub>	IntAll	IntEBV <sub>2</sub>
TBVs	0.00 (0.01)	-0.53 (0.01)	-0.57 (0.02)	-0.48 (0.01)	-0.55 (0.01)	-0.41 (0.01)	-0.50 (0.01)
HD (%)	20.40 (0.38)	4.28 (0.23)	3.77 (0.16)	5.39 (0.40)	4.21 (0.22)	6.74 (0.59)	4.92 (0.35)
F (%)	0.30 (0.01)	0.72 (0.09)	0.70 (0.10)	0.47 (0.12)	0.57 (0.12)	0.41 (0.12)	0.64 (0.10)
C (%)	1.37 (0.01)	2.81 (0.26)	2.81 (0.25)	1.99 (0.36)	2.27 (0.37)	1.76 (0.38)	2.37 (0.34)

<sup>a</sup> Full descriptions of ‘IntAll’ and ‘IntEBV<sub>2</sub>’ herein are ‘Pheno+DomEBV<sub>2</sub>+IntAll’ and ‘Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub>’ and the difference is with and without using top 50% foreign dogs based on EBVs (country 2 scale).

1 **Figure legends**

2

3 Fig. 1. Evolution of average true breeding values (TBVs) of newborn pups in 10 years  
4 comparing eight breeding scenarios in country 2. Indicating specific breeding strategies under  
5 various scenario, 'NoSel' is random mating, 'Pheno2' is only dogs without hip dysplasia  
6 (HD; country 2 scale) that were allowed to reproduce, 'Pheno' is only domestic dogs without  
7 HD (country 2 scale) and foreign dogs without HD (country 1 scale) that were allowed to  
8 reproduce, 'DomEBV2' is domestic sires were used in the top 50% based on EBV (country 2  
9 scale), 'IntAll' is no EBV requirement of using foreign sires, 'IntEBV1' is using foreign sires  
10 in the top 50% based on EBV (country 1 scale), 'IntEBV2' is using foreign sires in the top  
11 50% based on EBV (country 2 scale). Dotted lines indicate scenarios with no importation of  
12 foreign sires and solid lines indicate scenarios where 20% of litters were produced by foreign  
13 sires.

14

15 Fig. 2. Average true breeding values (TBVs) of newborn pups at year 10 as a function of  
16 accuracy of selection in country 2. 'Pheno<sub>2</sub>+DomEBV<sub>2</sub>' is scenario using only healthy dogs  
17 and top 50% domestic sire dogs (no foreign sire dogs used); 'Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub>  
18 (Top 50%)' and 'Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub> (Top 10%)' are scenario  
19 'Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub>' that using only healthy dogs, using top 50% domestic sire dogs  
20 based on estimated breeding value (EBV; country 2 scale) for 80% new born litters, and using  
21 top 50% or top 10% of foreign sire dogs based on EBV (country 2 scale) for 20% newborn  
22 litters in each year. Dotted lines indicate the simple linear trend for each simulation scenario.

23

24 Fig. 3. Average true breeding values (TBVs) of newborn pups at year 10 as a function of  
25 genetic correlation in country 2. 'Pheno+EBV<sub>2</sub>' is scenario using only healthy dogs and top

26 50% domestic sire dogs (no foreign sire dogs used); ‘Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub> (Top 50%)’  
27 and ‘Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub> (Top 10%)’ are scenario ‘Pheno+DomEBV<sub>2</sub>+IntEBV<sub>2</sub>’ that  
28 using only healthy dogs, using the top 50% domestic sire dogs based on estimated breeding  
29 value (EBV; country 2 scale) for 80% newborn litters, and using top 50% or top 10% of  
30 foreign sire dogs based on EBV (country 2 scale) for 20% newborn litters in each year. Dotted  
31 lines indicate the simple linear trend for each simulation scenario.

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33





