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ANÁLISE DE STATUS DE QUADRIL DE GOLDEN RETRIEVERS NO BRASIL- UM ESTUDO DE SAÚDE E MELHORAMENTO GENÉTICO

ANALYSIS OF THE HIP STATUS OF GOLDEN RETRIEVERS IN BRAZIL - A STUDY OF HEALTH AND GENETIC IMPROVEMENT

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Dissertação apresentada como um dos requisitos à obtenção do grau de mestre em Zootecnia

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I'd thank my many sisterdogs here, but they're no longer among us, and being dogs, they couldn't read anyway…except Fiona, who was so smart I'm certain she could have learned.

Análise de status de quadril de Golden Retrievers no Brasil- Um Estudo de Saúde e Melhoramento Genético[1]

Autora: Luiza Pinto Coelho Ribeiro Jardim
Orientador: Jaime Araújo Cobuci
Co-orientadora: Fabiana Michelsen de Andrade

RESUMO A displasia coxofemoral canina (DCC) é uma doença ortopédica debilitante e dolorosa caracterizada pela frouxidão das articulações do quadril, que afeta cães de todos os tamanhos, mas é especialmente prevalente e grave em raças grandes. Seu modo de herança é multifatorial, tornando desafiador reduzir sua prevalência apenas por meio de estratégias de reprodução tradicionais, uma vez que essas estratégias dependem exclusivamente do fenótipo. Os valores genéticos estimados (EBV) têm sido um elemento chave na redução da DCC em muitos países, acelerando o progresso genético ao superar as limitações das práticas de reprodução tradicionais. O objetivo deste estudo é comparar vários modelos estatísticos e identificar o mais eficaz para predizer os EBVs para DCC em uma amostra brasileira. A partir de dados fornecidos por criadores voluntários para este estudo, foi criado um banco de dados composto por 1692 indivíduos, dos quais 955 tínhamos conhecimento dos fenótipos, os escores de quadril. Com a fonte de escore de quadril sendo o efeito fixo do melhor modelo (DIC = -3973.5320), uma análise bayesiana forneceu os EBVs para 1.614 animais, variando de -0,259 a 0,381, com uma precisão de 0,01 a 0,67. A estimativa de herdabilidade no modelo escolhido foi relativamente baixa, com $h^2 = 0,14$. O coeficiente médio de endogamia (F) foi 0,04 e 0,07 entre os endogâmicos, que constituíam 54,78% da amostra. A tendência genética entre os anos de 1975 e 2021 apresentou um padrão relativamente estável (b = -0,0017; $R^2 = 0,026$), o que reflete a ausência de um programa de reprodução no Brasil. Os resultados deste estudo sugerem que a implementação de um programa de reprodução no Brasil, aliado à participação ativa dos criadores, pode desempenhar um papel crucial no aprimoramento da pesquisa genética em cães. O estudo indica que nossas instituições possuem os recursos tecnológicos necessários, capacidades de recuperação de dados e pessoal qualificado para executar um programa de reprodução de alta qualidade. Com aumento da participação dos criadores, temos o potencial de fazer contribuições significativas para mitigar a prevalência de DCC e aprimorar o bem-estar dos cães no Brasil.

Palavras chave: Valores genéticos estimados, genética canina, tendência genética, bem-estar canino, displasia coxofemoral e endogamia.

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Analysis of the hip status of Golden Retrievers in Brazil – A Study of Health and Genetic Improvement[1]

Author: Luiza Pinto Coelho Ribeiro Jardim
Advisor: Jaime Araújo Cobuci
Co-advisor: Fabiana Michelsen de Andrade

ABSTRACT: Canine hip dysplasia (CHD) is a debilitating and painful orthopaedic disease characterized by the laxity of the hip joints, that affects dogs of all sizes, but is particularly prevalent and severe in large breeds. Its mode of inheritance is multifactorial, thus making it challenging to reduce its prevalence through traditional breeding strategies alone, as these strategies rely solely on phenotype. Estimated breeding values (EBV) have been a key element in reducing the CHD in many countries, hasting the genetic progress by overcoming the limitations of traditional breeding practices. The objective of this study is to compare various statistical models and identify the most effective for predicting EBVs for CHD in the Brazilian sample. From data acquired from 326 sires and dams provided by volunteer breeders for this study, a pedigree database was created, consisting of 1692 individuals, 955 of which with reported phenotypes, their hip scores. With source of hip score being the fixed effect of the best model (DIC =-3973.5320), a Bayesian analysis provided the EBVs for 1.614 animals, ranging from -0.259 to 0.381, with an accuracy from 0.01 to 0.67. The estimate for heritability in the chosen model was relatively low with h^2 = 0.14. The average coefficient of inbreeding (F) was 0.04, and 0.07 among the inbreds, which constituted 54.78% of the sample. The genetic trend between the years 1975 and 2021 displayed a relative stable pattern (b = -0.0017; R^2 = 0.026), which reflects the absence of a breeding program in Brazil. The findings of this study suggest that the implementation of a breeding program in Brazil, coupled with active participation from breeders, can play a crucial role in enhancing genetic research on dogs. The study indicates that our institutions possess the necessary technological resources, data retrieval capabilities, and qualified personnel to execute a high-quality breeding program. With increased breeder participation, we have the potential to make significant contributions to mitigating the prevalence of CHD and enhancing the welfare of dogs in Brazil.

Key-words: Estimated breeding values, canine genetics, genetic trendings, dog welfare, hip dysplasia, inbreeding.

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LIST OF ABBREVIATIONS AND SYMBOLS

BVA	British Veterinary Association
CBKC	Confederação Brasileira de Cinofilia
CBRGR	Conselho Brasileiro da Raça Golden Retriever
CBRV	Colégio Brasileiro de Radiologia Veterinária
CHD	Canine hip dysplasia
COI	Coefficient of inbreeding
DI	Distraction Index
EBV	Estimated breeding values
F	Coefficient of inbreeding
FCI	Fédération Cynologique Internationale
GR	Golden Retriever
GSD	German Shepherd Dog
HD	Hip dysplasia
LR	Labrador Retriever
OFA	Orthopedic Foundation for Animals

CHAPTER I

1. INTRODUCTION

1.1. Introduction.

For centuries, dogs have been bred for various purposes, such as the many styles of hunting, herding, and guarding. The selection based on their abilities created the dog breeds as we know them in the modern years. However, as common practice, the birth of a new breed, and the maintenance of it, is based around inbreeding, and as such, has brought up many genetic conditions, previously masked by their recessive alleles. The present days have changed the purpose of a dog, in which their abilities are no longer the main product, but the individuals themselves, thus turning their wellbeing into a matter of concern. The practices of inbreeding and the selection of sires and dams disregard for their health has left many defects, one of which is the instability of their hip joints, known as canine hip dysplasia (CHD), the most common orthopaedic disease in large and giant breeds. It has multifactorial aetiology, but the selection made by private breeders in general is based entirely on the individual’s phenotype, in the form of a hip score, and excluding severely affected dogs from their breeding programs. While it doesn’t worsen the current conditions, this method hasn’t shown much improvement either. However, as shown within different breeds, there is room for improvement in the current schemes through the use of EBVs, which consider a dog’s CHD phenotype together with the CHD phenotypes of relatives.

This study has focused on the Golden Retriever and the prediction of their estimated breeding values for CHD, in a partnership with Brazilian kennels who shared the goal of improving the wellbeing of future litters through a better selection of sires and dams.

1.2. Interest.

The influence of the dog in our society is illustrated by its population of 55,9 million, totalizing 38,7% of all animal companions, the highest in our country

(ABINPET, 2020). The percentage of Brazilian homes with at least one dog reached 33,7% (IBGE, 2019), surpassing the same percentage for children (CRMV-SP, 2015). The turnover for the Brazilian pet industry, which encompasses pet food, pet care, and veterinary products, reached BRL 27,02 billion in 2020, ranking seventh place worldwide (ABINPET, 2020).

Among the hundreds of canine breeds recognized by the FCI (Fédération Cynologique Internationale), the Golden Retriever (GR) stands as one of the most popular worldwide. Known for its smooth golden pelt, gentle temperament, and intelligence, this breed, originated in the United Kingdom, it was recognized by the FCI in 1954, and classified in Section 1 within Group 8, which consists of the group of retrievers, hunting dogs whose initial purpose revolved in retrieving unscathed game (FCI, 2022). Yet, nowadays, it has found more versatile purposes, ranging from simple companions to complex tasks such as detecting cancerous cells, drugs, and explosives (MacLean & Hare, 2018), and is one of the two standard breeds used as guide dogs for the blind, the other being the Labrador Retriever (KNOL *et al*, 2011). The Golden Retriever has been one of the most popular breeds in Brazil in the last decade, occupying the 5th position among the most registered breeds, and the 2nd among the large breeds, with 6.344 registered pups in 2020 (CBKC, 2020). As it unfortunately occurs to most purebreds, the Golden Retriever have a “breed predisposition” to various genetic diseases, such as hypothyroidism, entropion, diabetes mellitus, portosystemic shunt, Von Willebrand’s disease, cataracts, subaortic stenosis, retinal dysplasia, elbow displasia and hip displasia (CIDD, 2011).

1.3.Hip dysplasia.

Canine hip dysplasia (CHD) is a defect caused by the laxity of the hip joint, resulting from a shallow acetabulum and/or a small, misshapen head of the femur (OMIA, 2022), as seen in Figure 1. It is characterized by lameness in the back legs and a bunny-hopping gait (ZHU, 2012) and eventually develops secondary osteoarthritis (OA). It is multifactorial, having multiple genes and environmental factors influencing its susceptibility (OMIA, 2022). It is the most common orthopaedic disease in large and giant breeds (BALDINGER, 2020), and according to OFA's statistics (Orthopaedic Foundantion for Animals), had its highest prevalence found in the Olde English Bulldogge, affecting up to 71,9% of dogs, while the average prevalence for all 202 breeds evaluated reached 14,4%. According to the same statistics, the Golden Retriever has a higher-than-average prevalence, with up to 19,6% of dogs suffering from this disease (OFA, 2022). Its difficulties and expenses concerning treatment, and emotional losses, make it one of the most frustrating diseases in veterinary medicine, due to the aforementioned secondary osteoarthritis as a consequence of malformation, thus being incurable if not relying on the rather expensive and painful surgery (LEWIS, 2010), ending with almost always leading to the lifelong administration of glycosaminoglycan polysulfates (KING, 2017), and as for working dogs, euthanasia, being the most common reason for it (MOORE, 2001).

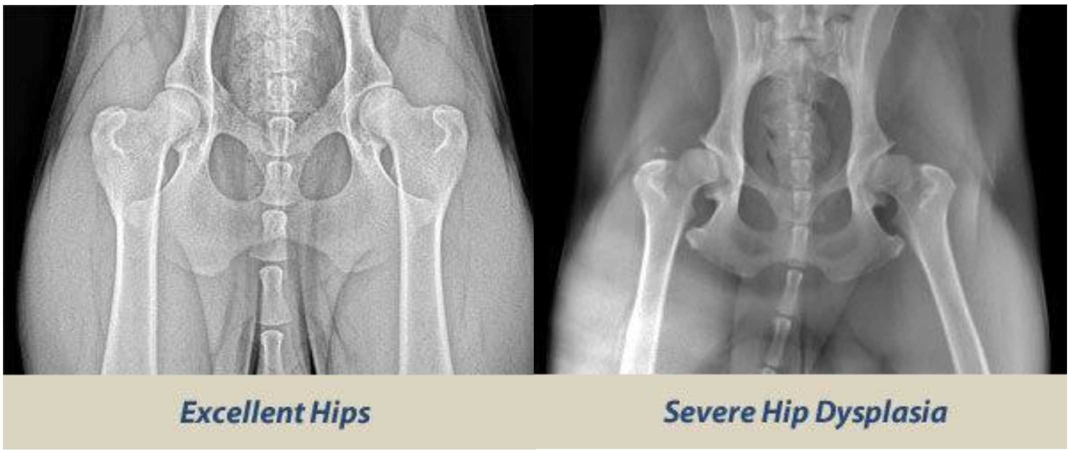

Figure 1. Excellent scored hips compared to severe displasia. Source: OFA, 2022.

Environmental factors do not cause CHD, but rather determine its expression and severity (KING, 2017). The external factors which contribute to the expression of CHD are of either environmental, nutritional or hormonal nature. In the matter of hormonal factors, as shown when giving either relaxin or estrogen to pups, one can conclude that some hormones are contributors to the development of CHD (KING, 2017). In addition to it, an investigation of neutering of male and female pups identified both an increase in the risk of developing CHD at an early age, for pups neutered before 5.5 months old, as well as a higher severity of CHD for the ones neutered at or after it, being three times more likely to be euthanized than their earlier-neutered counterparts (KING, 2107).

Regarding nutritional factors, excessive food consumption can affect the expression of CHD; a cohort of 48 Labrador Retriever dogs has shown that limiting food intake to 75% of that fed to ad libitum-fed pups resulted in a significant reduction in the prevalence of hip dysplasia at two years of age, with five out of the 24 limit-fed dogs being diagnosed with CHD, while the ad-libitum group had 18 affected (KEALY, 1992). Another example of the contribution of dietary imbalance to the development of CHD is the excessive calcium in their diet, by supplements or vitamin D, resulting in decreased osteoclastic activity, delaying normal ossification, thus causing CHD in predisposed puppies (KING, 2017).

Regarding the housing and exercise-related risk factors, those play a more significant role within the first three months of a pup’s life. Increased risks were reported in dogs that used stairs daily during the aforementioned period (KRONTVEIT, 2012), as were in pups up to the age of weaning raised on slippery flooring, being 1.6 times as likely to develop the clinical signs of HD as opposed to those raised on non-slippery floors, such as carpets (WITTE, 2019). Pups who were raised on farms and pups who had access to off-leash exercise in park-like terrains were shown to have a decreased risk of developing radiographic HD (KRONTVEIT, 2012).

Although some clinical signs were previously described, the definite diagnosis of CHD is obtained through radiography evaluation confirming the hip laxity. The most commonly applied diagnostic schemes for CHD use the ventrodorsal, hip-extended (VDHE) pelvic radiograph, from which evidence of radiographic subluxation (laxity) of the coxofemoral joint is scored, either subjectively or objectively (SMITH, 2010). One of the main components of the objective evaluation is the Norberg angle (NA) (GENUÍNO, 2015), which is a quantitative measure of hip congruity (JIANG, 2021). The NA represents the angle between a line connecting the center of the femoral head between the left and right hips and another line connecting the center of the femoral head with the lateral tip of the cranial acetabular rim, with an angle of 105º or higher considered a healthy joint (Figure 2).

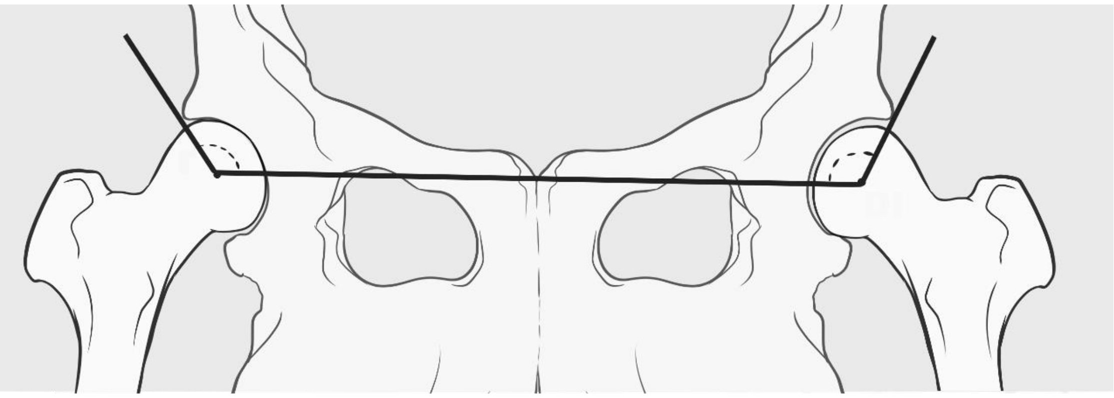

Figure 2. Norberg angle: the angle between the line connecting the centers of the femoral heads and the line connecting the center of each femoral head with the tip of the cranial rim of their respective acetabula. Image drawn by the author.

The FCI (Fédération Cynologique Internationale) and the BVA/KC (British Veterinary Association/Kennel Club) are the main screening schemes used to evaluate the status of canine hip dysplasia (HD) in Europe. The FCI method scores according to a five-class grading scale, in which each joint is assigned to one of five grades (A-E) and the final grade refers to the worst joint. Grade A is considered as normal joints (non-dysplastic), whereas grade B represents an almost normal joint, and C, D and E represent mild, moderate and severe dysplasia, respectively (BALDINGER, 2020). Radiographs taken with VDHE and submitted to the BVA/KC Hip Dysplasia Scheme are scored in a way the hip score is the sum of the points accrued for each of nine radiographic features in each hip joint. The lower the score the less the degree of CHD. The minimum score for each hip is zero and the maximum is 53 (for each joint), thus giving a range for the total score of 0 to 106 (BVA, 2022). In the United States, OFA scores the VDHE radiograph of dogs over 2 years of age, according to a 7-point subjective evaluation scheme, ranging from excellent hips to severe dysplasia (OFA, 2022). Table 1 show these distinct kinds of classification, together the relation among them.

Table 1. Hip International Ratings correspondence.

OFA (North America)	FCI (Europe)	BVA/KC (UK/Australia)	CBRV (Brazil)
Excellent	A	0-4 (no >3/hip)	HD--
Good	A	5-10 (no >6/hip)	HD--
Fair	B	11-18	HD+/-
Borderline	B	19-25	HD+/-
Mild	C	26-35	HD+
Moderate	D	36-50	HD++
Severe	E	51-106	HD+++

Source: OFA, 2022; ABRV, 2022.

Another technique available for HD diagnosis, also used for risk predisposition in young puppies is the PennHIP (Pennsylvania Hip Improvement Program) distraction view (LEIGHTON, 2019). The PennHIP measures the degree of hip joint laxity of three different views of the pelvis under stress, under heavy sedation and anaesthesia: the standard hip-extended view (used by the BVA/KC scheme), the compression view, which forces the femoral heads into the acetabulum and the distraction view, which deviates the femoral heads from the acetabulum with the aid of a distractor, thus the Distraction Index (DI) is obtained, calculated by dividing the distance between the center of the femoral head in compression and the center in distraction by the radius of the femoral head (GUILLIARD, 2014). The addition of DI values to OFA measurements has been shown to improve the hip joint quality in a population of purpose-bred dogs, compared to OFA measurements alone (HANEY, 2020). However, as demonstrated by Leighton *et al.*, the estimated genetic correlations between hip-extended scores and PennHIP DI phenotypes were small within the 3 breeds studied, suggesting that genes controlling the expression of joint laxity have only slight overlap with genes that control the expression of hip joint conformation as seen in the HEV radiograph (LEIGHTON, 2019).

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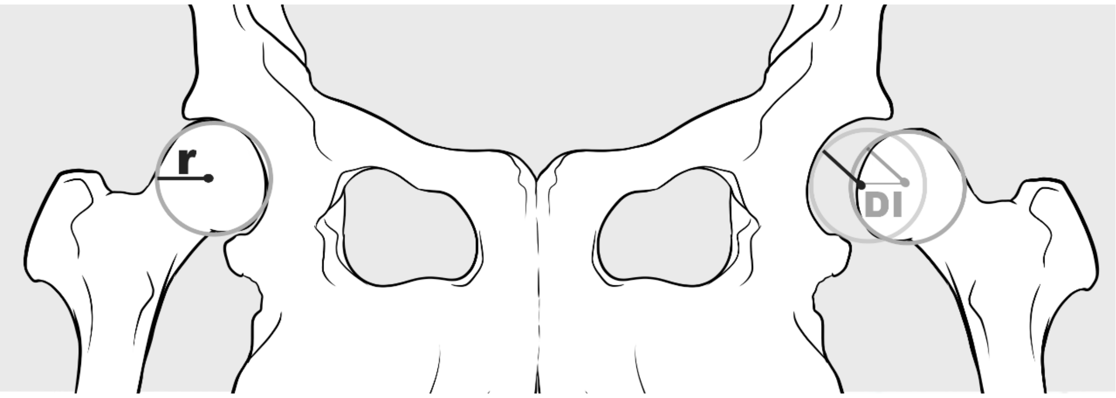

Figure 3- Concept of the Distraction Index. Image drawn by the author.

1.4.Challenges in selection towards CHD.

The reduction of the prevalence of CHD through control programs is not an unfamiliar, avant-garde concept amongst breeders, veterinarians, and zootechnics. It has been a tiresome endeavor over the years, involving the selection of apparently the best sires and dams based on the individuals' phenotypic score. In Brazil, the FCI hip scoring system is widely used for animal selection. Dogs with moderate to severe dysplasia, scoring "D" and "E", respectively, are not allowed to reproduce. Dogs with mild dysplasia, scoring "C", are only bred with the healthiest hips, scoring "A". Dogs with close-to-healthy hips, scoring "B", are only bred with other "B" or "A" scored dogs. Dogs with score A, however, are allowed to be bred with dogs that scored A, B, or C. A retrospective study in France by Baldinger compared the prevalence of CHD in ten breeds over the course of 20 years (1997-2017). During this period, six breeds had shown a significant reduction, with the best improvements found in Cane Corso, going from a prevalence of 72,7% to 49,9%, and in the Gordon Setter, going from 36,9% to 23%. In the meantime, however, the lowest prevalence, found with the Siberian Husky, suffered an increase of 3,1%. As discussed, these results are from the selection based solely on hip radiograph screenings (BALDINGER, 2020).

A study in the USA used the OFA database, researching 60 breeds (each with over 1000 individual hip evaluations) starting from the year of 1970 to 2015. Regarding the hip joint, the genetic trend for the three breeds with most individual evaluations (German Shepherd, Labrador Retriever, and Golden Retriever) indicated slow improvement: within the period between 1980 and 2010, the mean EBV had shown a little decrease of -0,2 for the German Shepherd, an even smaller decrease of -0,1 for the Golden Retriever and hardly any changes at all for the Labrador Retriever (OBERBAUER; KELLER; FAMULA, 2017).

In the same study, it was shown substantial phenotypic progress within the Labrador Retriever, despite the stable trend concerning their EBVs. This phenomenon could be explained, however, by the “migration” of new animals registered within the OFA database, increasing the proportion of founders whose hips scored “Excellent” (OBERBAUER; KELLER; FAMULA, 2017).

Other retrospective studies compared the genetic trendings for CHD through the selection based on the OFA schemes. First, a single breed, the Labrador Retriever, showed a decrease of 0,1 in its mean EBV, the equivalent of a rather modest (17% of the total phenotypic standart deviation) improvement in their hip scores (HOU, 2010), and similar results within the second study (16,4%) as the average of 74 breeds (HOU, 2013). The hip scores of Labrador Retriever in the United Kingdom, where the BVA/KC evaluation is the main, and inarguably the most precise scale of CHD evaluation, have also shown a slow and steady improvement between the years 2000 and 2007, with analyses demonstrating the use of EBVs in this scheme could achieve a 19% greater response compared to phenotypes alone (LEWIS, 2010). While not denying the genetic progress with the selection based on phenotype, a study with the british population of Labrador Retriever estimated a substantial change in the hip scores median would take over 40 years (LEWIS; BLOTT, WOOLIAMS, 2010), hence the need for alternative methods such as EBVs (WOOLIAMS; LEWIS; BLOTT, 2011).

As the concept of Norberg Angle was introduced, the Swedish Hip Dysplasia Program had it implemented in the early 1960s, first with German Shepherds from the Swedish Armed Forces and later on with many other breeds, and its progress was evaluated in 2019. With the selection based solely on their hip scores, the early results were successful in the reduction of all grades of HD (C, D, and E), yet followed by a much slower decrease, due to milder selection pressure from phenotypic selection, with less variation in the population due to a higher proportion of dogs with normal scores. It was noted that the percentage of dogs with hips scored “C” had also increased in the later years (Hedhammar, 2020).

Therefore, in order to decrease the prevalence of HD in places where phenotypic screening is already mandatory, the use of more refined tools is a must. As it happens in Sweden, each dog’s EBV is calculated by linking pedigree information with data from the registrations of hip status, allowing the genetic risk to be calculated for every individual in the pedigree. In this country, EBVs are computerized and updated every week currently for 44 breeds (Hedhammar, 2020). The radiographic hip evaluation of sires and dams is also mandatory for their puppies to be registered in the Dansk Kennel Club. For each parent, an EBV is calculated and recalculated as new hip scores are registered in the breed, and for breeding is recommended that the mean parent EBV is equivalent to or better than the average breed EBV (DANISH KENNEL KLUB, 2022). The common understanding between the aforementioned studies is the application of EBVs would not only improve but hasten these schemes, thus being of utmost importance in the selection of breeding.

1.5.Estimated breeding values (EBV) for CHD in the world.

Estimated breeding values (EBV) are the best linear unbiased predictor of a dog’s breeding value derived from their lineage information used in its calculation thus, a more accurate estimate of the genetic susceptibility of a trait than the individual phenotype alone (LEWIS, 2013). Still, breeding values could also be estimated for dogs with no hip joint trait information available, as pedigree relationships allow EBVs of such dogs to be calculated (ZHANG, 2008). Its implementation should be a priority to substantially increase the effectiveness of selection and to enable genetic trends to be monitored as prospectively and dynamically as possible in all populations under selection. This is the best way to ensure that selection is operating effectively and to provide up-to-date feedback to the end users of the scheme concerned with canine welfare (WILSON, 2011).

The estimation of breeding values for CHD has been the focus of some studies for either comparative analyses of genetic trends and/or to advise both breeders and tutors regarding their dog and future litter's health, thus enhancing the breeding programs. In the work of Zhang et al (2008), four traits were considered to derive the EBVs of 2,716 dogs of various breeds, including Labrador Retriever and Golden Retriever: hip dysplasia (HD), distraction index (DI), dorsolateral subluxation (DS) and extended hip joint radiograph (EHR). DI and DS were highly genetically correlated, as were EHR and Norberg Angle. Over half of the Labrador Retrievers in the study came from the Guiding Eyes for the Blind (NY), where the selection is based on their NA and EHR values, and had better hip conformation overall, indicating their breeding practices were indeed effective in improving hip joint conformation. Their NA and EHR breeding values were also predicted with highest accuracy, indicating a more intensive selection for those traits. Between age, sex, breed, and weight, breed had the largest influence on the hip joint trait, with the others expressing minimal influence (ZHANG, 2008).

A longitudinal study evaluated litters of Boxer dogs born between 1994 and 1995, monitoring them throughout their lives in the Netherlands to illustrate the use of EBVs to predict the risk of developing CHD in the progenies of different sires. The mean EBVs were calculated for the 10 best sires and 10 worst sires, with the best sires scoring an average of -0,32, whereas the worst sires scored 0,42. The predicted risk ratio of the progeny of the 10 best and 10 worst sires to develop CHD with age was 0.725 and 1.526, respectively. At the end of the cohort, at the age of 8 years, the predicted proportion of Boxers free of CHD from sires with the lowest mean EBV (best sires) was decreased by 6%, in contrast to the Boxers sired by the males with the highest mean EBV (worst sires), of which 13% were predicted not to be free of CHD (van HAGEN et al, 2005).

Being one of the richest databases on orthopaedic data in the world, the OFA data for hip ratings of 60 dog breeds was used to derive the genetic and phenotypic improvement from over 30 years of selection by phenotype. The most evaluated breeds regarding hip joints were the GR, LR and German Shepherd dogs (GS), each showing the slow and steady improvement in their breeding values, with the remaining breeds sharing similar results. It was worth noting that their EBV showed a slow decrease, showing small genetic improvement through phenotypic selection. Nevertheless, regarding phenotypic improvement, there was a peak of “Excellent” scored LR, which could be explained by the arrival of new registers and the selection done by breeders to reduce the CHD (OBERBAUER; KELLER; FAMULA, 2017).

A study in Portugal focused on the Estrela Mountain Dog, a popular large breed native to the country. Unlike the aforementioned studies, the data from the 313 animals were obtained through complete clinical evaluations and radiographic screening executed by the authors themselves and their peers. A single radiologist, the author himself, was responsible for the grading of every radiograph, thus allowing an unbiased estimation of the breeding values. From the initial 313 animals, it was possible to obtain the pedigree information of 843 dogs, and estimate the breeding values of 632, born between 1991 and 2005. The mean EBV was shown to be stable between 1991 and 2003 (ranging between 0,2 and 0,4), with improvement starting in 2004, with a drastic decrease from 0,4 to 0, the lowest shown so far. It was also shown the clinical evaluation alone could result in false negatives even among severe-scored hips, reiterating the need for radiographic screening (GINJA *et al*, 2009).

As for the use of EBVs for dogs in Brazil, there has been one published article up til now. Using German Shepherd dogs, researchers of the State University of Maringá used the hip scores and dysplasia status of 1632 dogs born between 1990 and 2013. As shown in the study, there was little phenotypic improvement in the Brazilian population, with a minimal decrease, and a genetic improvement shown in a decrease (0.52% per year) of the EBV for CHD scores. Again, these data show the inefficacy of selection based on phenotype, urging the use of EBVs in breeding schemes in the country (BABÁ et al, 2019).

There have been several studies around the world aiming to decrease the prevalence of CHD in many breeds, either by working with EBVs or by encouraging the use of it (LINGAAS & KLEMETSDAL, 1990; LEIGHTON, 1999; GINJA *et al*, 2009; SOO & WORTH, 2015). Seeing as Brazil shelters the second largest canine population in the world (ABINPET, 2022), the need for more studies concerning the health and welfare of purpose-bred dogs in the country should be acknowledged.

2. HIPOTHESIS

The genetic variability for CHD within a Brazilian sample of Golden Retrievers is sufficient to perform a selection aiming for the reduction of the disease.

3. OBJECTIVES

Evaluate different statistical models through Bayesian analysis to determine which effects yield the best fit for predicting breeding values for CHD.

Estimate the individual breeding values for CHD of Golden Retriever dogs from volunteered kennels within the country, in order to assess the magnitude of genetic merit variability among animals.

CHAPTER II

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[1] Elaborado conforme as normas da Revista Brasileira de Zootecnia

ANALYSIS OF THE HIP STATUS OF GOLDEN RETRIEVERS IN BRAZIL – A STUDY OF HEALTH AND GENETIC IMPROVEMENT

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ABSTRACT

Canine hip dysplasia (CHD) is a challenging orthopaedic condition of the hip joints with a complex mode mode of inheritance that has proven difficult to address through traditional breeding practices. This study aimed to estimate the breeding values (EBVs) of Golden Retrievers from ten Brazilian kennels using Bayesian analysis on a pedigree sample of 1692 dogs, including 955 with known phenotypes. The model with the lowest DIC value (-3973.5320) considered the sources of the hip scores as its only non-genetic effect. Heritabilities estimates for hip score in the chosen model were 0.14 (0.00 – 0.50). The EBVs ranged from -0.259 to 0.381, with an accuracy from 0,1% to 67%. The coefficient of inbreeding of the sample was 0.04 and 0.07 among the inbreds, with a maximum value of 0.33. The genetic trend concerning hip scores have been stable since 1975 ($b = -0.0017$; $R^2 = 0.026$), with subtle fluctuations matching peaks within the phenotypic trend. The study provides breeders with a valuable tool to make informed decisions about selecting sires and dams and accelerate genetic improvement towards the decrease of prevalence of CHD in Golden Retrievers, an optimal outcome in the pursuit of improving the welfare of this breed.

Keywords: Estimated breeding values, canine genetics, genetic trendings, dog welfare, hip dysplasia, inbreeding.

1. Introduction

Canine hip dysplasia (CHD) is one of the most common orthopedic diseases in dogs, characterized by a malformation of the hip that results in laxity of the coxofemoral articulation. This laxity can develop into painful osteoarthritis. It has been an issue for breeders and tutors, especially of large and giant breeds (BALDINGER, 2020), one of which is the Golden Retriever, a very popular breed in Brazil (CBKC, 2022). This breed has a relatively high prevalence, being of 19,6% within the breed's population in North America, according to the Orthopaedic Foundation for Animals (OFA, 2022). Not exclusive to the aforementioned breed, the most commonly employed method for reducing CHD is the selection by phenotype, which is based on the observable physical traits of sires and dams, which in this case consists of their hip scores in the FCI scale, in which animals suffering from moderate to severe dysplasia, with hip scores of "D" and "E" respectively, are cut off from reproduction programs altogether, close-to-healthy hips scored "B", are bred restrictedly to other animals scored "B" or healthier (A), while animals with mild dysplasia, scored "C" are bred only to the healthiest hips, scored "A", those of which have no restrictions among the passable scores (CBRGR, 2020). However, once CHD mode of inheritance is multifactorial (OMIA, 2023), environmental factors also contribute to the variations in the phenotype, for example, a study comprising 60 breeds, with heritabilities for CHD ranging from 46% for English Setters to 75% for Boxers, has shown a heritability around 65% for the Golden Retriever (OBERBAUER; KELLER; FARMULA, 2017).
As such, it's eligible for genetic improvement through the use of estimated breeding

values (EBV), a more accurate estimate of the genetic liability of a trait than the individual phenotype (LEWIS, 2013), a method already in use in several developed countries (HEDHAMMAR, 2020).

The challenges faced by professionals and responsible breeders across the country are often imposed not by their lack of conjoint effort or interest in the welfare of future litters, which is a growing concern, but by the traditional breeder who remains adamant about science's endeavours. This study's objectives are to determine the best way of estimation of the genetic values of the Brazilian population of Golden Retrievers, and as result, to provide a more accurate method for selection by breeders, to reduce the prevalence of the disease in Golden Retrievers and to encourage breeders from across the country to follow the example.

2. Materials and methods

Using information from 326 Golden Retrievers provided by ten Brazilian kennels, we traced four generations of ancestors and compile a database comprising 1692 individuals. The database included 1049 females and 643 males, with birthdates dating back from 1975 to 2021. The data used in this study came from pedigrees and hip reports provided by breeders and an open database of the breed, K9data.com. Traits of the studied sample are shown in table 1.

The database contained each individual's name, pedigree information, sex, year of birth, country of origin, kennel, source of the hip score, and the hip score itself. All hip scores included in this study were conducted with the animals under sedation. The hip scores were standardized accordingly and classified as 1 for healthy hips, 2 for fair hips, and 3 for mild dysplasia (as worse scores were not found within the sample). The fixed effects included in the models were sex, year of birth, the continent of origin, and source of the scores (whether were they presented as a signed report from a veterinarian or from OFA itself, or if they came from indirect sources such as sites or breeders), also weighted the estimation of breeding values. Each veterinarian was also given an individual code, adding up to 45 possible sources of scores.

Fourteen different models were tested, with all the possible combinations of fixed effects. The THRGIBBS1F90 program (Misztal *et al.*, 2014) was used to estimate the variance components and breeding values, with 1.400.000 iterations of the GIBBS Sampler ran with a burn-in period of 600.000 iterations and sampling interval of 100 iterations, following the single-trait model:

$$y = Xb + Za + e,$$

where $\boldsymbol{y}$ is the hip score for the individual, $\boldsymbol{b}$ the vector of fixed effects (sex, year of birth, continent of origin and source of scores, according to the evaluated model), $\boldsymbol{a}$ the vector of random additive genetic effects, $\boldsymbol{e}$ the vector for random residual effect, and X and Z the incidence matrices relating the phenotype to $\boldsymbol{b}$ and $\boldsymbol{a}$, respectively. The study evaluated 14 different models for assessing the influence of various factors (Table 3). Using the final samples generated by the Gibbs sampler, we employed the POSTGIBBSF90 software (Misztal et al., 2014) to derive the posterior means and standard deviations of the EBVs, as well as the posterior distributions of the variance components.

To diagnose convergence and calculate descriptive statistics of variance components, we utilized the BOA package (Smith, 2007) of the R software (R Core Team, 2021). The test of confidence interval half-width was employed to monitor convergence, with a value below 0.01 considered acceptable.

An analysis of the population structure was obtained through CFC software (Coancestry Inbreeding Contribution) and Poprep 2.0 ®. For this analysis, the sample comprised of the 1692 dogs from the initial group, and an additional 429 founders, totaling 2121 dogs. The F was calculated using the formula:

$$F_x = \sum \left(\frac{1}{2}\right)^{n_1+n_2+1} (1 + F_A)$$

where $\boldsymbol{F_x}$ is the coefficient of inbreeding of $\boldsymbol{x}$, $\boldsymbol{n_1}$ is the number of generations from sire to the common ancestor, $\boldsymbol{n_2}$ is the number of generations from dam to the common ancestor, and $\boldsymbol{F_A}$ is the coefficient of inbreeding of the common ancestor.

The effective size (Ne) of the sample was evaluated with the POPREP 2.0 ® software, following the Ne-Ecg method (Gutierrez et al., 2009):

$$\Delta F_i = 1 - {}^{ecgi-1}\sqrt{1 - F_i}$$

where *ecgi* is the sum of all known ancestors with $\left(\frac{1}{2}\right)^n$, and F_i is the individual inbreeding coefficient.

For measuring accuracy, we utilized the formula:

$$\sqrt{}(1-(SE^2)/(1+F)*\sigma^a$$

where **SE** represents standard error, **F** denotes the coefficient of inbreeding of the individual, and σ^a is the estimated additive genetic variance in the population (Lewis *et al.*, 2013).

The statistical analysis was conducted to examine the relationship between the obtained values and the fixed effects. The tests employed in the analysis included Spearman correlation, Kruskal-Wallis, and post-hoc tests. The relationship between F and EBVs, as well as between phenotypes and EBVs, was examined using Spearman correlation. Additionally, a linear regression analysis was performed to assess the relationship between phenotype and EBV. The Kruskal-Wallis test was used to assess differences between sexes, kennels, and origins, with post-hoc tests employed to evaluate differences in origin and EBVs.

3. Results

The pedigree database had a total of 2121 individuals, with 1162 inbred dogs (54,78%). The average coefficient of inbreeding (F) for the total sample was 0.040, and 0.074 between the inbreds, with the maximum F going up to 0.333. The average number of discrete generation equivalents was 4.61, with a maximum of 10.77. The effective population size (Ne) in 2021 was increased to 86, the latest years of 2020, 2019, and 2018 had their Ne of 74, 71, and 64, respectively. The mean age of breeding females between the years 1981 and 2021 was 3.1, while the sires’ average was 4.6 years of age

(Table 2). The mean generation interval was 4 years, with females exhibiting a slightly lower interval of 3.7 years, while males showed an interval of 4.3 years.

To account for the effects of sex, year or birth, origin, and source of hip scores in the estimation of genetic values, a total of 14 different models were evaluated. The models that took the source of scores into consideration (Models 1 to 7) performed superiorly compared to their parallels that did not incorporate this effect, showing a higher adjust with their lower DIC values. The best fitting model was Model 7 (DIC = -3973.5320), and had "source of score" as its only fixed effect. The elected model has shown a rather low to moderate heritability of 14% (0-50%) and a genetic variance of 0.105 (0.000 – 0.429) (Table 4).

The estimated breeding values through the chosen model 7 ranged from -0.259 to 0.381, appointing the best choices of sires and dams to reduce the trait in the breed as the individuals with lowest values. Furthermore, dogs holding positive breeding values were identified as contributors for worst hip scores in the offspring. The individuals with EBVs had an average accuracy of 36%, going up to 67%.

Females had slightly higher EBVs than males ($p = 0.061$). Besides, breeding values varied according to the continent of origin ($p= 0.00163$), with dogs born in South America showing smaller EBVs than dogs with unknown origin ($p=0{,}0013$ in the post hoc test). When Brazilian dogs were analyzed apart, and compared with all the other origins and with dogs with unknown origin, this difference was still present, showing smaller (and better) EBV in dogs born in Brazil.

Figure 1 depicts both genetic and phenotypic trendings from 1975 to 2021. Figure 1a shows some significant peaks of dogs scored "B" (fair hips) in the 1980, as well as a surge of dogs scored “C” (mild dysplasia) in 2015. As possible consequence, there was also a slight peak in the breeding values for those periods. However, despite these fluctuations, the genetic trend displays a relatively stable pattern over the entire period (Figure 1b; $b = -0.0017$; $R^2 = 0.026$).

To assess the potential impact of the “kennel of origin” effect on the study outcomes, a complementary analysis was conducted: in a more limited sample wherein this effect was available, the chosen model 7 had its resulting breeding values compared to its parallel with an added effect of the kennel of origin, showing a statistically significant positive correlation between the breeding values generated by both models ($p < 0,001$). Nevertheless, once the breeding values of the two models are strongly correlated and in order to expand the sample size once this information was lacking in most individuals, the final prediction of breeding values was performed without this effect.

As expected, the relation between the sample’s phenotypes (hip scores) and breeding values suggests an incomplete correspondence. This is demonstrated in Figure 2 where, while a few animals scored “C” had low EBVs, animals with high, undesirable EBVs were not exclusive to this group, but found in all groups including the supposedly superior “A”. Animals without known phenotype were still able to have their breeding values estimated due to information from their relatives. This group has shown two distinct concentrations, one centered around the neutral zone, and another exhibiting higher breeding values.

A linear regression analysis has shown a significant relationship ($P < 0.0001$) between the HD scores (phenotype) and the EBVs, with the first explaining 54.51% of the variance of the latter (Figure 2). However, the remaining 46.49% of the variance is not explained by these scores, meaning other factors could influence the EBVs. These data show the importance of preferring breeding values to phenotype in the breeding choices.

The possible influence of inbreeding on phenotype and also breeding values was evaluated, but hip scores and inbreeding coefficients were not related ($p > 0.05$). Also, a regression between the EBV and F value held a non-significant slope coefficient estimate ($p > 0.05$).

Seven sires were identified as the most influential sires based on the numer of pups sired (Table 5). Among them, three individuals (S.5, S.6 and S.7) were classified as the least favourable sires based on breeding values, while the other were the most favourable ones. Notably, S.5, despite having positive breeding values, was found to be the second most popular sire in the sample with 29 descendants. Alternatively, among the best sires, S.1 and S.2 had the lowest EBVs in the entire sample. Of the seven sires identified, S.2 and S.3 had the greatest impact on lowering the breeding values in the offspring. Sires with best (lower) EBVs had more offsprings with hip score “A”, while sires with worst (higher) EBVs had descendants with scores “B” and “C” (Figure 3).

4. Discussion

Brazil has the world’s second-largest dog population, with 55,9 million dogs, trailing only the United States (Abinpet, 2022). Although there have been some efforts to discourage dog breeding and promote adoption through the popular slogan “Não compre, adote” (don’t buy them, adopt them”), the number of registries in the country has continued to rise in recent years (CBKC, 2022). Despite the significant population of dogs and the growing industry surrounding them, the scientific understanding of canine genetics and its applications to promote their welfare is limited and underdeveloped in the country. Although some breeders understand the importance of controlling the prevalence of CHD for the welfare of purebred dogs, the traditional breeding practice in the country do not consider the genetic information from the extended family of breeding dogs. As result, the focus remains exclusively on the phenotype of the sires and dams. This selection strategy has not resulted in significant genetic progress, and studies regarding genetic values of hip scores associated with genetic diversity of the Brazilian populations are imperative.

While the effective population size (Ne) in this sample remains low, it has risen from 64 in 2018 to 86 in 2021, indicating a growth in genetic diversity within the population. This trend towards a larger Ne suggests a positive impact on the population's genetic health. Interestingly, a previous study with the Golden Retriever population in the UK reported a similar Ne of 61.32 in 2015 (Lewis, Abhayaratne, Blott, 2015), also low despite being one of the most registered breeds in the country.

The average inbreeding level of the total sample of Brazilian Golden Retrievers was 0.040, with a maximum of 0.33. In comparison with Leighton’s study on USA-born Golden Retrievers (Leighton, 2019), our study had a slightly lower average inbreeding coefficient (0.052 vs 0.040), but a higher maximum value (0.27 vs 0.33). Zhang’s study with various breeds showed similar results, with average F of 0.08 for the Golden Retriever, and a maximum of 0.25. The average F and among the inbred dogs in all breeds studied was 0.062, with and a a maximum value of 0.37 (Zhang *et al*, 2008). Therefore, the Brazilian sample's inbreeding levels were found to be within the average range of samples already investigated. Inbreeding has been a topic of discussion among breeders, zootechnics, and veterinarians. While inbreeding was historically used to preserve desired traits in dog breeds, the practice has become less relevant in modern times due to the established lineage within each breed. The author's perspective suggests that inbreeding should be minimized, if not avoided altogether, in order to maintain genetic diversity within dog breeds. The standard technical recommendation is that the coefficient of inbreeding of an individual should be under 0.0625, which is equivalent to the mating between cousins.

The heritability estimates for hip scores were in the low range of 0.14 (with an additive genetic variance of 0.105 and environmental variance of 0.599), which is consistent with the findings of some previous studies such as Lingas & Klemetsdal (1990) and Lavrijsen *et al* (2014), whose heritability estimates were 0.17 and 0.18, respectively, for the Golden Retriever. However, other studies, such as Lewis *et al* (2013) and Oberbauer *et al* (2017), reported higher heritabilities of 0.40 and 0.65, respectively. In Lewis's work, the additive genetic variance was 0.313 and the environmental variance was 0.126. These differences can be explained by the genetic variations in the population studied, environmental factors and inclusion of effects such as the coefficient of inbreeding (as in Lewis's study), and the methods used to measure hip scores, such as in Lavrijsen's work, where a closed trio of radiology and/or orthopaedic surgery experts evaluated anonymous radiographs.

We suspected that the quality of the source of scores could play a role in the breeding value estimation. Unlike other studies in which x-rays were performed and evaluated by the team (Silvestre *et al*., 2007) or had reliable sources, such as OFA's database (Oberbauer *et al*., 2017) and Brazilian Society of German Shepherd Breeders (Babá *et al*., 2019), ours had faced challenges with the origin of the information. Therefore, we included the source of score as an additional effect.

The stability of genetic and phenotypic trends, despite the conscientious efforts from breeders, was unfortunately anticipated due to relying exclusively on phenotype in their breeding practices. This highlights the limitations of solely phenotype-based selection methods in achieving genetic improvements in canine breeding programs. Several studies, both nationally and globally, have produced similar results in this subject, with unanimous conclusions that the implementation of EBVs in their breeding programs would effectively hasten the genetic progress (Hamann; Kirchhoff; Distl, 2003; Wooliams; Lewis; Blott, 2011; Soo & Worth, 2015; Oberbauer *et al*., 2017).

As one of the objectives of this study was to examine the ineffectiveness of the selection based on hip score, the relation between the individual's resulting breeding value and phenotype was found to be consistent with the anticipated outcomes, with many animals scored different breeding values than stipulated from such breeding practice. In a practical perspective, it's evident that selection based solely on X-rays is a limited and ineffective approach. This is true especially when the majority of the population share the same hip phenotype, as discussed by Hedhammar in their study with Swedish dogs of different breeds, where they encourage the usage of EBVs to achieve further decrease in the prevalence (Hedhammar, 2020).

In this study, no significant correlation was found between the F and hip scores or

EBVs ($p > 0.05$), which is consistent with Comhaire's study with Belgium dogs of various breeds. This contrasts with the commonly held belief that inbreeding has a negative impact on hip dysplasia (Comhaire, 2014). A correlation was reported, however, in Leighton's study involving German Shepherd Dogs, Labrador Retrievers, Golden Retrievers, and their crosses, with significant correlation ($p < 0.001$) for all three breeds. For each 1% increase in their F, a decrease of 0.001 units in their distraction index (DI), which is the distance between the center of the femoral head in compression and the center in distraction by the radius of the femoral head, was observed (Leighton, 2019).

The most influential sires were selected among the popular sires based on offspring number, which would have the most significant impact on the population. Some of these popular sires have not had hip scores made available to the public, thereby deviating from the current breeding practices. Among the least favourable males, S.7 had the highest EBV of 0.104, which had a discernible impact on his EBV offspring. Despite this sire being scored "A", his offspring had an average EBV of 0.07, indicating the inefficacy of their selection. However, as the offspring's average EBVs were lower than those of their sire, it also highlights the importance of using a high-quality dam to improve the litter's EBVs. Even without hip score reports, S.5 and S.6 were among the most bred sires in the sample, with 29 and 25 pups, respectively. This highlights the issues associated with the popular sire effect, whereby males are overbred based on their superficial qualities, such as titles and appearance, as is the case with both dogs in question who hold international champion titles (data not shown), despite their detrimental impact on canine health and genetic improvement, which should be the priority in breeding programs. To illustrate the effectiveness of selection by EBVs, Figure 4 shows the average EBV of the sample, as well as the average EBV of the pups from 5% parents with the best values and the 5% parents with the worst values.

While it may seem like a simple solution to remove animals with positive EBVs from the breeding stock, it is important to prioritize maintaining genetic diversity in the population. To achieve this, it is important to retain as many sires and dams as possible to avoid the risk of an increased coefficient of inbreeding and a lower effective population size. Removing too many animals could worsen existing problems and create unintended consequences, so it is crucial to carefully consider the long-term implications of breeding decisions. Not to mention, caution must be exercised in interpreting the results of this study, mainly when our accuracies values are considered. It is important to acknowledge that the subjects under investigation are dogs, which are valuable to the breeders, who have invested on their acquiring, raising and maintanance. Therefore, any recommendations resulting from this research must be presented with sensitivity and consideration for the potential impact on the breeder and their relationship with their animals. Selection intensity should not be as rigid as with production animals, as there is a risk of some breeders disregarding the research or even abandoning their dogs if they feel their priorities are not being respected.

5. Conclusions

Through Bayesian analysis of multiple statistical models, we identified the most most suitable model for predicting breeding values for CHD in our sample. A total of 1614 individual EBVs were obtained, ranging from -0.259 to 0.381, indicating sufficient variability for effective selection. Relying on the proper interpretation of the results, these EBVs can be utilized by breeders to establish successful breeding programs. Additionally, the study provided valuable insights into the genetic structure of the sample through a complementary population analysis. Given the critical role that dogs play in the lives of millions of Brazilians, it is imperative to invest in scientific research to promote their well-being and improve their living conditions on a genetic scale. Enhancing our scientific understanding of dog genetics can help establish more effective policies and regulations to better control the dog breeding industry and ensure the welfare of dogs, right from their conception onwards.

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Table 1. General characteristics of the studied sample

	N	%
Sample size		
Total sample (with founders)	2121	-
Sample with phenotype	955	56.42
Number of males	818	38.56
Phenotype – FCI scores		
Total scores	955	
A (= score 1)	671	70.26
B (= score 2)	249	26.07
C (= score 3)	35	3.66
Birth date distribution		
Before 1990	123	7.27
1990-2000	260	15.36
2001-2010	680	40.18
After 2010	629	37.17
Continent of origin		
South America	569	33.62
North America	450	26.59
Europe	87	5.14
Unknown	586	34.63

FCI - Fédération Cynologique Intenationale.

Table 2. Population parameters of the Golden Retriever sample in Brazil

Parameter	
Average breeding age (years)	
Male	4.6
Female	3.1
Mean generation interval (years)	
Male	4.3
Female	3.7
Mean number of offspring	
Male	2.5
Female	1.6
Inbreeding coefficient (F) (from total sample)	
Total sample (with founders)	2121
F>0 (n - %)	1162 – 54.78
F>0.1 (n - %)	310 – 14.61
Total F mean	0.040
Mean F among inbred dogs	0.074
Max F value	0.333
Effective population size (Ne)	
2016	58
2017	58
2018	64
2019	71
2020	74
2021	86

Table 3 - Fixed effects of each model.

Model	Source of score	Sex	Year of Birth	Origin
Model 1	x	x	x	x
Model 2	x	x	x	
Model 3	x		x	x
Model 4	x	x		
Model 5	x			x
Model 6	x		x	
Model 7	**x**			
Model 8		x	x	x
Model 9		x		x
Model 10		x	x	
Model 11		x		x
Model 12		x		
Model 13				x
Model 14			x	

Table 4. Posterior means and 95%CI of variance and heritability components

	Models	
	Model 1	**Model 8**
σ_a^2	0.139 (0.001 – 0.621)	0.207 (0.000 – 0.698)
σ_e^2	0.817 (0.40 - 1.556)	0.647 (0.285 – 1.161)
h^2	0.14 (0.00 – 0.56)	0.24 (0.00 – 0.62)
DIC	-3108.3118	-2935.2301
	Model 2	**Model 9**
σ_a^2	0.130 (0.001 – 0.708)	0.159 (0.016 – 0.505)
σ_e^2	0.805 (0.382 – 1.509)	0.505 (0.270 – 0.879)
h^2	0.13 (0.00 – 0.50)	0.23 (0.02 – 0.66)
DIC	-3104.1370	-3257.8324
	Model 3	**Model 10**
σ_a^2	0.143 (0.000 – 0.753)	0.213 (0.003 – 0.808)
σ_e^2	0.803 (0.330 – 1.472)	0.626 (0.281 – 1.100)
h^2	0.15 (0.00 – 0.54)	0.25 (0.00 – 0.60)
DIC	-3149.5208	-3095.5954
	Model 4	**Model 11**
σ_a^2	0.097 (0.000 – 0.485)	0.217 (0.006 – 0.793)
σ_e^2	0.608 (0.261 – 1.049)	0.634 (0.288 – 1.133)
h^2	0.13 (0.00 – 0.53)	0.25 (0.00 – 0.65)
DIC	-3875.5571	-3052.0723
	Model 5	**Model 12**
σ_a^2	0.097 (0.001 – 0.428)	0.157 (0.005 – 0.625)
σ_e^2	0.618 (0.267 – 1.021)	0.497 (0.256 – 0.895)
h^2	0.13 (0.00 – 0.51)	0.23 (0.00 – 0.70)
DIC	-3772.2578	-3328.7072
	Model 6	**Model 13**
σ_a^2	0.097 (0.000 – 0.485)	0.164 (0.002 – 0.476)
σ_e^2	0.608 (0.261 – 1.049)	0.500 (0.269 – 0.870)
h^2	0.13 (0.00 – 0.53)	0.24 (0.00 – 0.56)
DIC	-3207.5871	-3323.3320
	Model 7	**Model 14**
σ_a^2	**0.105 (0.000 – 0.429)**	0.613 (0.265 – 1.131)
σ_e^2	**0.599 (0.320 – 0.979)**	0.222 (0.004 – 0.824)
h^2	**0.14 (0.00 – 0.50)**	0.26 (0.00 – 0.65)

DIC	**-3973.5320**	-3205.8235

σ_a^2 - additive genetic variance; σ_e^2 - environmental variance; h^2 - heritability;
DIC - deviance information criterion.
Non-genetic effects used in each respective model:
Model 1 (Source of score, year of birth, country of origin and sex); Model 2 (Source of score, year of birth and sex); Model 3 (Source of score, year of birth and country of origin); Model 4 (Source of score and sex); Model 5 (Source of score and country of origin); Model 6 (Source of score and year of birth); Model 7 (Source of score); Model 8 (Year of birth, country of origin and sex); Model 9 (Country of origin and sex); Model 10 (Year of birth and sex); Model 11 (Year of birth and country of origin); Model 12 (Sex); Model 13 (Country of origin); Model 14 (Year of birth).

Table 5. Influential sires based on breeding values and offspring count

Best males	Number of offsprings	EBV	EBV of offspring	Accuracy	Hip score
S.1	17	-0.2590093	-0.02 ± 0.32	0.35	A
S.2	12	-0.251942	-0.13 ± 0.30	0.39	B
S.3	14	-0.19344	-0.11 ± 0.29	0.42	A
S.4	13	-0.13116	-0.04 ± 0.31	0.32	--
Mean EBV of Offspring			-0.075 ± 0.30		

Worst males	Number of offsprings	EBV	EBV of offspring	Accuracy	
S.5	29	0.045193	0.01 ± 0.30	0.35	--
S.6	25	0.075226	0.02 ± 0.31	0.37	--
S.7	12	0.104665	0.07 ± 0.29	0.33	A
Mean EBV of Offspring			0.03 ± 0.30		

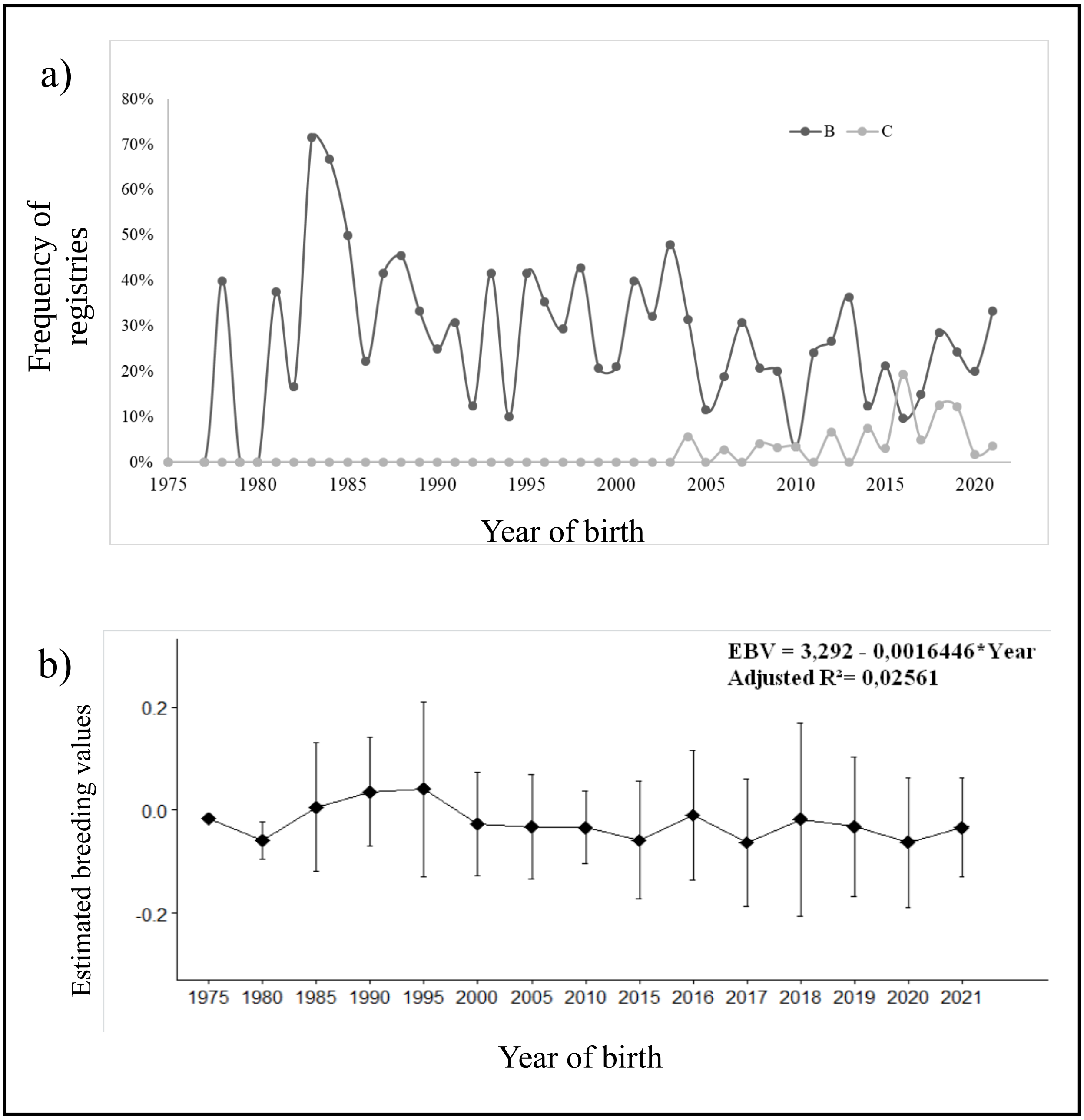

Figure 1. Phenotypic and genetic trends through the years.

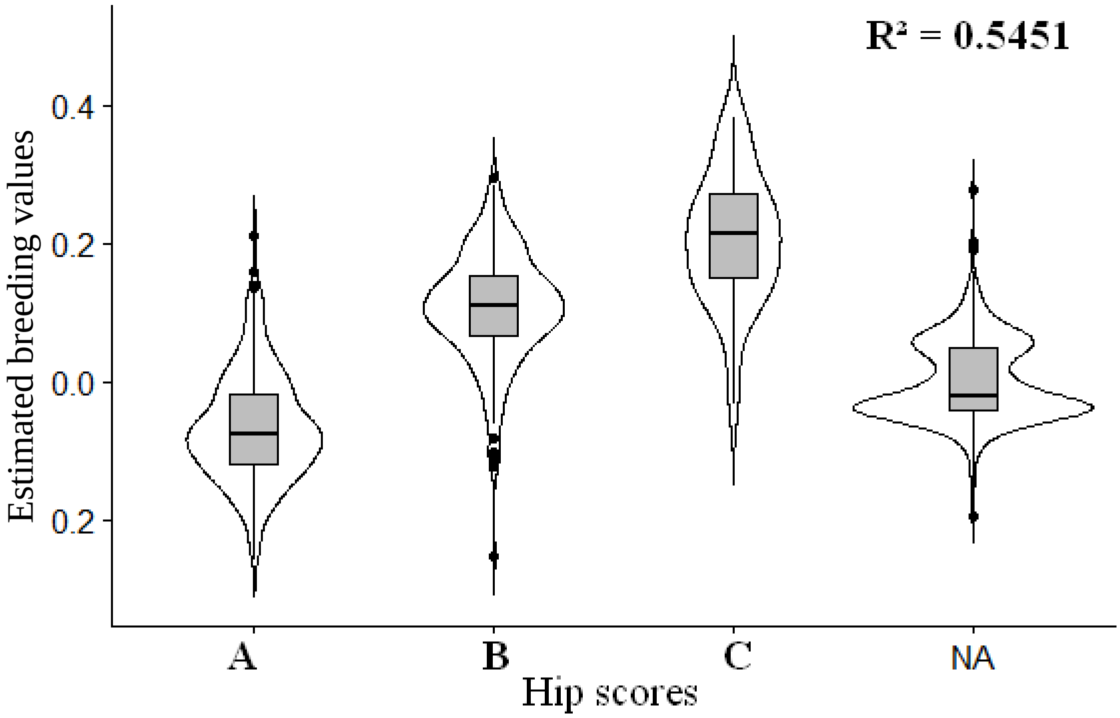

Figure 2. Correspondence between hip score and breeding value (NA = non avaible).

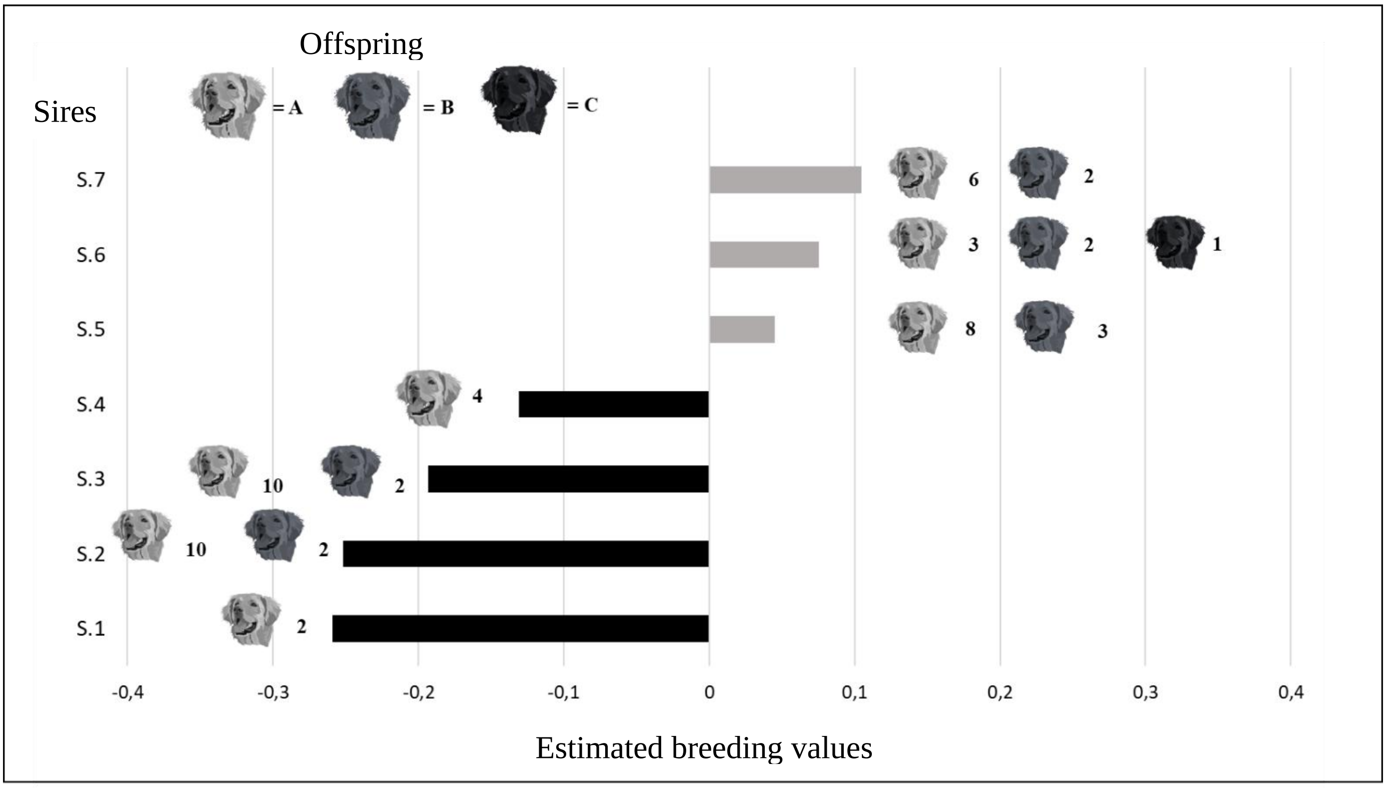

Figure 3. EBVs of the most influential sires and their offspring's known phenotypes. The EBVs of sires 1 to 4 are marked in black, while the EBVs of sires 5 to 7 are marked in gray. Beside each breeding value are the known phenotypes of their offspring. For instance, S.1 had two pups in the sample with known phenotype, and both were scored as "A". On the other hand, S.6 had six pups in the sample with known phenotype, with three being scored as "A", two as "B", and one as "C".

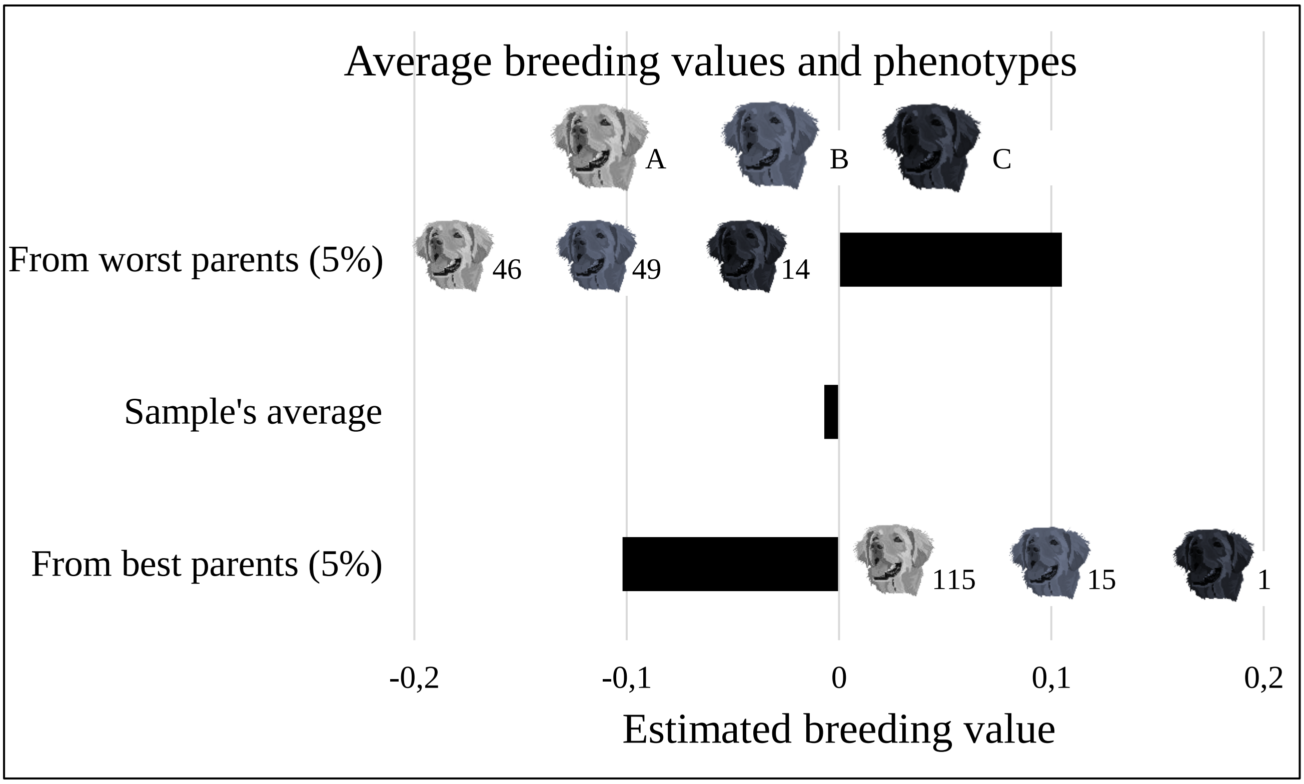

Figure 4. Comparison between the average estimated breeding values (EBVs) of offspring born from the 5% parents with the best (lowest) EBVs, born from the 5% parents with the worst (highest) EBVs, and the average breeding value of the sample. In addition, the sum of the known scores (A, B and C) from both groups.

CHAPTER lll

1. FINAL REMARKS

Given the situation with purebred dogs in the country, it comes to the surprise of no one that many dog breeders in Brazil prioritize factors other than the health and welfare of their litters when pursuing what they'll label "genetic improvement". In some cases, breeders may prioritize maintaining certain breed characteristics, even if they are harmful to the dogs' well-being. This can create a potential conflict with the perspectives of veterinarians, zootechnics and biologists, who prioritize the animals' health and welfare above all else. Unfortunately, the field of genetic improvement for dogs in Brazil often fails to receive the attention it deserves. This can be attributed to factors such as reluctance among these breeders, as well as a perception among some groups that investing in the health of purpose-bred dogs is a trivial matter in light of the significant number of abandoned dogs in need of homes. Furthermore, misconceptions regarding the potential benefits of genetic improvement, coupled with a lack of awareness regarding the role of genetics in animal welfare, contribute to the neglect of this important area of research.

During the course of the study, several open workshops were organized by the research team in an effort to educate breeders about genetic trends in the country and facilitate discussions on related topics. These workshops played an important role in attracting breeders to the project, as well as differentiating between various types of breeders, based on their level of interest and understanding of the subject matter. Furthermore, by analyzing the priorities of the breeders who attended the workshops, we were able to identify trends in their concerns. While serious breeders were interested in the health of their future litters, they were a minority, as most breeders' priorities lied within trivial matters, with some emphasizing the appearance of the pups, such as pelt colour and size, while others were more concerned about legal issues associated with irresponsible breeding. Regardless, we were pleased to work with the small minority, as it allowed us to avoid any potential conflicts with those whose priorities were focused on anything other than the well-being of their dogs.

Initially, the project aimed to involve both the Golden Retriever and the Labrador Retriever. However, there was a lack of interest among the Labrador breeders, as very few provided the required materials despite claiming their willingness to participate. This lack of interest was not limited to Labrador breeders alone, as many Golden Retriever breeders failed to provide the required materials despite several reminders and their earlier promises to do so.

As breeders often have their own beliefs and practices based on personal experience and tradition, introducing scientific evidence proved to be quite challenging, despite the clear and user-friendly nature of the instructions provided in the reports (as seen in the appendix). After receiving reports on their dogs' EBVs, some breeders expressed dissatisfaction with our assessment that their dogs were not as good as breeding candidates as they had anticipated, and chose to ignore our findings.

The challenges in this project, unfortunately, did not only pertain with the breeders. In contrast to studies conducted in other countries, which relied on the full database from registries of their respective Kennel Clubs, this study relied upon data collected from the sires and dams of interest of their breeders, and four generations of their respective ancestors. The Confederação Brasileira de Cinofilia (CBKC) does not maintain any data collection or actions related to health and states that this role has been delegated to breed councils. The Conselho Brasileiro da Raça Golden Retriever (CBRGR) declined to provide support for this project despite several invitations and contacts. It is worth noting that neither organization lists the welfare of purebred dogs as their objective, with CBRGR's primary focus being to promote camaraderie among Golden Retriever breeders. Furthermore, despite being associated with FCI, both organizations support certain breeding practices that are not in line with FCI guidelines, such as the practice of inbreeding under different labels like "line breeding". This includes the mating of individuals who are not as closely related as parents and offspring or siblings, such as between a grandfather and granddaughter or between an aunt and nephew. These differences in breeding practices underscore the need for ongoing education and dialogue within the breeders' community.

The persistence of efforts to create novel dog breeds, juxtaposed with the resistance encountered when seeking to prioritize their health and well-being among groups of self-proclaimed dog enthusiasts, is indeed a remarkable phenomenon. While dogs have been considered man's best friend for centuries, it can be argued that this friendship has been toxic from man's perspective due to irresponsible breeding and exploitation. Providing a loving home and amending past mistakes to ensure a healthy life is the bare minimum of our responsibility towards our beloved companions.

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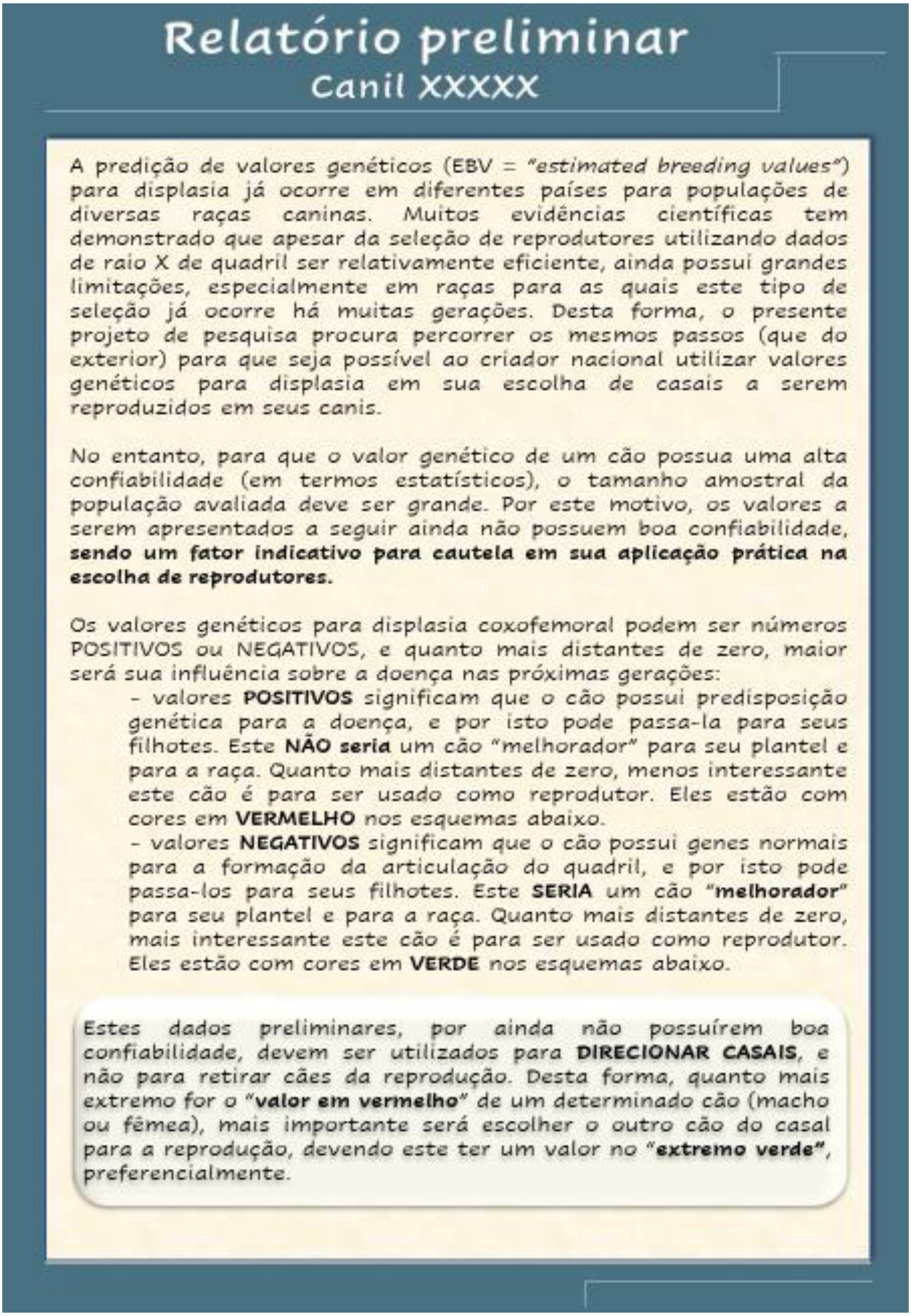
2. APENDIX



Relatório preliminar

Canil XXXXX

A predição de valores genéticos (EBV = *"estimated breeding values"*) para displasia já ocorre em diferentes países para populações de diversas raças caninas. Muitos evidências científicas tem demonstrado que apesar da seleção de reprodutores utilizando dados de raio X de quadril ser relativamente eficiente, ainda possui grandes limitações, especialmente em raças para as quais este tipo de seleção já ocorre há muitas gerações. Desta forma, o presente projeto de pesquisa procura percorrer os mesmos passos (que do exterior) para que seja possível ao criador nacional utilizar valores genéticos para displasia em sua escolha de casais a serem reproduzidos em seus canis.

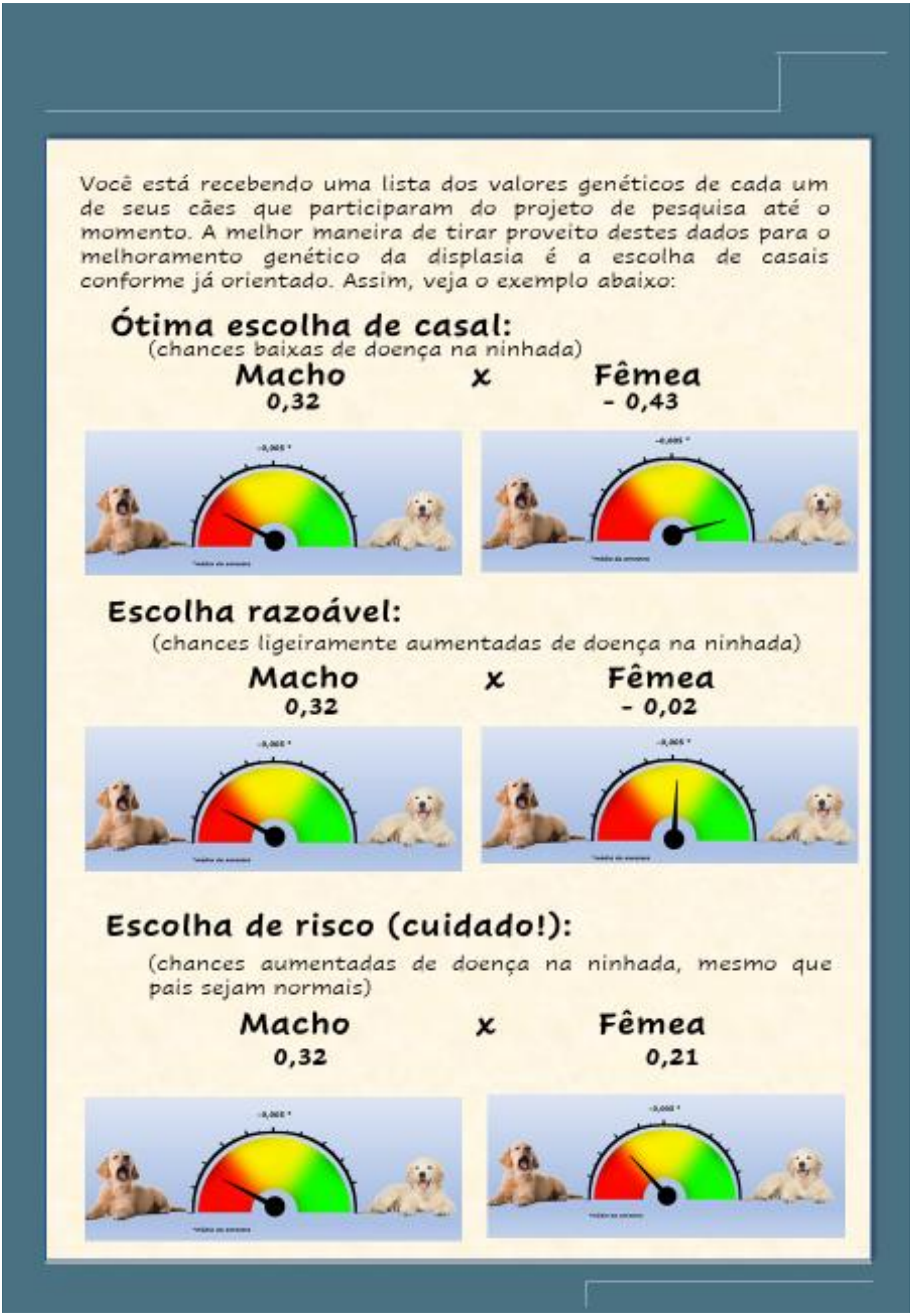
No entanto, para que o valor genético de um cão possua uma alta confiabilidade (em termos estatísticos), o tamanho amostral da população avaliada deve ser grande. Por este motivo, os valores a serem apresentados a seguir ainda não possuem boa confiabilidade, **sendo um fator indicativo para cautela em sua aplicação prática na escolha de reprodutores.**

Os valores genéticos para displasia coxofemoral podem ser números POSITIVOS ou NEGATIVOS, e quanto mais distantes de zero, maior será sua influência sobre a doença nas próximas gerações:

- valores **POSITIVOS** significam que o cão possui predisposição genética para a doença, e por isto pode passa-la para seus filhotes. Este **NÃO seria** um cão "melhorador" para seu plantel e para a raça. Quanto mais distantes de zero, menos interessante este cão é para ser usado como reprodutor. Eles estão com cores em **VERMELHO** nos esquemas abaixo.
- valores **NEGATIVOS** significam que o cão possui genes normais para a formação da articulação do quadril, e por isto pode passa-los para seus filhotes. Este **SERIA** um cão **"melhorador"** para seu plantel e para a raça. Quanto mais distantes de zero, mais interessante este cão é para ser usado como reprodutor. Eles estão com cores em **VERDE** nos esquemas abaixo.

Estes dados preliminares, por ainda não possuírem boa confiabilidade, devem ser utilizados para **DIRECIONAR CASAIS**, e não para retirar cães da reprodução. Desta forma, quanto mais extremo for o **"valor em vermelho"** de um determinado cão (macho ou fêmea), mais importante será escolher o outro cão do casal para a reprodução, devendo este ter um valor no **"extremo verde"**, preferencialmente.

Figure 1. First page of the preliminary report given to breeders.



Você está recebendo uma lista dos valores genéticos de cada um de seus cães que participaram do projeto de pesquisa até o momento. A melhor maneira de tirar proveito destes dados para o melhoramento genético da displasia é a escolha de casais conforme já orientado. Assim, veja o exemplo abaixo:

Ótima escolha de casal:

(chances baixas de doença na ninhada)

Macho **x** **Fêmea**

0,32 **- 0,43**

Escolha razoável:

(chances ligeiramente aumentadas de doença na ninhada)

Macho **x** **Fêmea**

0,32 **- 0,02**

Escolha de risco (cuidado!):

(chances aumentadas de doença na ninhada, mesmo que pais sejam normais)

Macho **x** **Fêmea**

0,32 **0,21**

Figure 2. Second page of the preliminary report given to breeders.