Inbreeding may affect phenotypic traits in an Italian population of Basset Hound dogs

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Abstract The influence of inbreeding depression on phenotypic traits of a Basset Hound dog Italian population was evaluated. Moreover this paper reports the first results of a survey on morphological traits and analyse the genetic variability of the population using genealogical information. The following traits were studied: height at withers, height of chest, depth of chest, body length, length at rump, ischiatic width of rump, circumference of chest, circumference of cannon, length of ear, and length of nose. The inbreeding coefficient (F) of each dog was computed by genealogical data. Traits were taken from 75 adult (mean age 2.17±1.545 years) dogs (36 males and 39 females) belonging to 19 different Italian farms. A linear regression of each trait on inbreeding coefficient was used to estimate inbreeding depression. ANOVA was used to test the differences in morphological traits between the sexes, among breeders and among animals with different F level. Despite the good level of genetic variability and the low coefficients of inbreeding observed in the population, a significant weakly effect of inbreeding on the depth of chest was observed. In addition, the present study revealed no significant differences in morphological traits between sexes and among farms.

Keywords Basset Hound dog · Pedigree analysis · Morphological traits · Inbreeding depression

1 Introduction

The Basset Hound is a hunting dog, belongs to Group 6 (Segugi e cani per pista di sangue) of the ENCI (Ente Nazionale Cinofilia Italiana) and over 400 puppies are registered every year. Currently in Italy there are 32 official breeders, who breed dogs of American and British bloodlines. Recently Swedish and Dutch lines were also introduced. The breed standard shows rather accurate morphological and behavioural characteristics, although in this breed there are many variables for the height, for the colour of the coat and for the deportment. Basset Hound dog is also used as a model in studies on human hereditary diseases and their gene therapy (Switonski, 2012); in Italy is frequently used for pet therapy (Tomezzoli, 2015).

In the selection the inbreeding is used as a mating method because it allows to fix the characteristics and traits of the best representatives of a breed. However this mating method can lead to high rates of inbreeding with disadvantageous phenomena: in fact, inbreeding can increase genetic diseases (Ubbink et al. 1992), mortality of puppies (Van der Beek et al. 1999) and can cause inbreeding depression (Ubbink et al. 1998, Ólafsdóttir and Kristjánsson 2008). This phenomenon is often associated with fitness reduction (Keller and Waller 2002; Brzeski et al. 2014, Cecchi et al. 2016a) and can also lead to a decrease in selection response for economic traits in the livestock species (Khan et al. 2007, Gonzalez-Recio et al. 2007, Hossein-Zadeh 2012, Malhado et al. 2013, Niknafs et al. 2013, Silió et al. 2012, Mokhtari et al. 2014). The knowledge of the influence of inbreeding on reproductive traits and on the manifestation of specific diseases is crucial for breeders and veterinaries: over 1000 inherited conditions have been reported in dogs (Leroy, 2011) and veterinarians can contribute to the solution of the problem of hereditary disorders in dogs by diagnosing these diseases and helping breeders in the mating management. A better management of the existing genetic variability should constitute an important concern for clubs and breeders (Nicholas et al. 2011). Moreover, it is well known that dog breeders choose animals on the basis of standard characteristics and the beauty of a breed is often equivalent to the functionality and also to the health of an animal. For example the primary function of a Basset Hound is hunting and dogs must follow traces in ravines, brambles and scrubs. So his skin should not be a hindrance to movement and should not be excessive to be entangled and injured. The ears must be long in order to capture the smells of the ground but not too long, thus risking becoming an obstacle to the movement. Considering the health aspect of the animal dogs with excessive skin can more easily meet dermatitis or too much loose skin that falls on the forehead, inevitably leads to the formation of entropion and a laxity of the lower palpebral fissure makes the eye too exposed to atmospheric agents and predisposed to ulcers and conjunctivitis (Società Basset Hound Italiana, 2011). For all these reasons the purposes of the present study were to explore the effects of inbreeding on morphological traits in order to estimate the magnitude of changes associated with an increase in inbreeding and to analyse the genetic variability and morphological traits of a Basset Hound population.

2 Materials and methods

The research was carried out on 19 different Basset Hounds dog Italian farms (most of these had 1-3 dogs and/or one sex). Genealogical and morphological data of 75 adult (mean age 2.17±1.545 years) dogs (36 males and 39 females) were monitored. For each male and female body measurements were carried out using a Lydtin stick and tape measure; dogs were put on a flat floor and held by the respective owners (Cecchi et al. 2015). The ten body measurements obtained were: height at withers (WH), height of chest (ChH), depth of chest (ChD), body length (BL), length at rump (RL), ischiatic width of rump (RIsW), circumference of chest (ChC), circumference of cannon (CaC), length of ear (EL), and length of nose (NL).

Concerning genealogical data the number of inbred dogs and the inbreeding coefficient and the average numerator relationships of each dog were obtained using CFC software (Sargolzaei et al. 2006). A linear regression was used do predict each morphological trait based on inbreeding coefficient to estimate inbreeding depression. Values were considered statistically significant for $P<0.05$ (Confidence Interval 95%). Solutions were given per 1% increase of inbreeding.

For the analysis of the genetic variability of the population all measured dogs constitutes the Reference Population (RP), while the complete genealogy of the RP constitutes the whole population (WP), containing all founders, ancestors and their offspring; the base of population (BP) was defined as individuals with one or both unknown parents. The distribution of inbreeding in the whole population was analysed. Different levels of inbreeding were identified and dogs were divided into nine classes according to its own F level: class 1 including non-inbred animals (F = 0); all the other eight classes include inbred animals (class 2: dogs with an F value between 0 and 0.05; class 3: dogs with an F value between 0.05 and 0.10; class 4: dogs with an F value between 0.10 and 0.15; class 5: dogs with an F value between 0.15 and 0.20; class 6: dogs with an F value between 0.20 and 0.25; class 7: dogs with an F value between 0.25 and 0.30; class 8:

dogs with an F value between 0.30 and 0.35. A multivariate analysis of variance was used to test the effect of sex, inbreeding level and farm on each morphological trait, including dog age at the time of the study as covariate. Three variables were entered as fixed factors: sex in the first model, different inbreeding class levels and sex in the second model and farm and in the third model. In this last one model we considered only the farms (n=5) who breed more than 5 dogs (27 animals in total, 11 males and 16 females); it was no possible consider sex factor because some of these farms have only females. Morphological data were analysed by SAS-JMP software version 5.0 (2002).

3 Results and discussion

Table 1 reports morphological data in males and females. For all traits, between males and females, no statistical significantly differences were observed. These results were also confirmed by the measures of sexual dimorphism (m/f) that ranged from 0.99 for ChC, RIsW and NL to 1.02 for CaC. In the breed standard (ENCI), the height at withers is the only parameter for which range is reported: from 33 to 38 cm (with no differences between males and females). In this research the average withers height was 35.8 ± 1.57 cm in females and 36.0 ± 1.76 cm in males. These values fall exactly in the expected ranges defined by the current breed standard. Only one male in the sample exceeded the maximum value (39 cm) while a female had a lower value (32 cm). The age at measurement did not show significant effects as well as no significant differences in the traits were observed among dogs belonging to different breeders. A few number of study have been performed on the morphological parameters of dog breeds; these studies have been conducted with breed dogs with a very different morphology, such as Spanish water dogs (Barba Capote et al. 1996), Bolognese dogs (Beretti et al. 2008), Lagotto dogs (Vaccari Simonini et al. 2007) and Bracco Italiano dogs (Cecchi et al. 2015). Also Jordana et al. (1999) had analysed several morphological and behavioural characters of a series of breeds, including Basset Hound, in order to improve the knowledge of relationships among these breeds. However, scores were assigned to each state of different characteristics in an arbitrary manner and no analytical measurements were conducted. In our study 35 dogs out 75 (46.7%) of the Reference Population were inbred and all had an inbreeding coefficient less than 0.15 (Table 2). Therefore, considering the complete database, 47 dogs were inbred. Of these dogs, 22 dogs (68.75% of the inbred) showed an inbreeding value lower than 5% while only 3 dogs (9.37% of the inbred) showed an inbreeding value higher than 20%.

A significant regression equation was found for the depth of chest (ChD=32.6-0,659F) with a R^2_{ADJ} of 13.98%. Dogs' depth of chest decreased 0.659 ($p<0.05$) for each 1% increase of inbreeding. No statistically significant effects were detected for all other traits. Table 3 reports the morphological differences among animals with various F levels. The depth of chest was significantly lower in animals with F values included between 5% and 10% ($P<0.05$) in comparison to animals with $F<5\%$; this effect increased in animals with F values included between 10% and 15% ($P<0.01$). A weakly reduction of ChC due to inbreeding was also observed; this effect was even highlighted by Gandini et al. (1992) in Haflingers horse breed. The effects of inbreeding on morphological traits have been studied in other horse breeds: Gomez et al. (2009) found significant inbreeding depression for several biometrical measurements in Spanish Purebred horses. On the other hand, Curik et al. (2003) in Lipizzan horse and Sierszchulski et al. (2005) in Arabian horse found no effect of inbreeding on morphological traits. Wolc and Balińska (2010) reported that inbreeding was associated with a decrease in whither height in Sieraków horse, but not in Dobrzyniewo and in Kobylniki horse. To our knowledge, there is only the paper by Cecchi et al. (2015) on the effect of inbreeding on traits in Bracco Italiano dog showing that no inbreeding depression, computed using the same model, was observed on the conformation traits. It is well known that different breeds and populations, as well as different traits, vary in their response to inbreeding: some populations may show a very pronounced effect of increased inbreeding for a trait, whereas other populations may not demonstrate much of an effect. For example, Jansson and Laikre (2014) did not find any correlation between inbreeding and health in 26 dog breeds in Sweden. As reported by Barczak et al. (2009), in a given population, "bad" and "good" inbreeding effects are mixed. Furthermore, the degree of inbreeding depression in a population depends on the extent of inbreeding, the original frequency of deleterious recessives, the environment, and inbreeding depression may be greater under more stressful conditions (Marr et al. 2006).

Table 4 summarizes the main genealogical parameters computed by CFC. Analysis of the pedigrees of the 75 studied dogs (RP) showed that the complete database resulted in 333 dogs (WP), distributed in ten traced generations. Sires and dams in total were 125 and 147, respectively, with a ratio dams-sires of 1.18. This value was smaller than reported on Bracco Italiano dog breed (1.63) (Cecchi et al. 2013) and on Bracco Francese dog breed (1.31) (Cecchi et al. 2016b). Number of animals in the base population (one or both unknown parents: absolute founders = ft) was 131. Average value of inbreeding (F) in the whole population (WP) was 1.1% while the average value of F in the reference population (RP) was 3.2% (7.7% in the inbred). Of the 19 considered farms, 12 had inbred animals with an average F ranging from 0.1 to 10.7% (data not shown). Many studies have explored inbreeding in dog breeds, showing different average value of the pedigree coefficient inbreeding both within and amongst breeds, which also varies across countries (Różańska-Zawieja et al. 2013). The results presented in this paper suggest that this population of Basset Hound had a good level of genetic variability. In fact, our results were generally smaller than those reported in many other dog breeds. In particular the average coefficient of inbreeding observed in this Basset Hound population for the RP (3.2%) was smaller than those reported by Cole et al. (2004) in a population of Labrador Retriever (F=22%) and German Shepherd (26.2%) guide dogs and by Glażewska (2008) for a small population of Polish Hounds born in the period 1970-2004 (F=26.5%-37.0%). Also Voges and Distl (2009) reported value of inbreeding coefficients ranging from about 4.5% for Bavarian Mountain Hounds to about 9.5% for Tyrolean Hounds. The average inbreeding coefficients estimated by Martinez et al (2011) for Cimarrón Uruguayo dog breed, reached about 4-6% while in a study on breeds raised in France (Leroy et al. 2006) the average coefficient of inbreeding ranged from 3.3% in Bouledougue Francais to 12.4% in Barbet breed dog. In an Italian population of Pit Bull Terrier dogs the average coefficient of inbreeding was 3.73% (Ciampolini et al. 2013), while the average coefficient of inbreeding in an Italian population of the dog Braque Français type Pyrénées was 4.35% (Cecchi et al. 2016b). In some Italian breeds F value ranged from 2.27% in Lagotto Romagnolo (Sabbioni et al. 2008), 6.29% in Bracco Italiano dog breed (Cecchi et al. 2013) to 10.81% in Bolognese dog breed (Sabbioni et al. 2007). On the other hand, values of inbreeding smaller than 1% were reported by Cecchi et al. (2009) in an Italian colony of guide dogs (0.45% in German Shepherd dogs, 0.38% in Labrador dogs and 0.49% for Golden Retriever dogs) and by Różańska -Zawieja et al. (2013) in the Hovawart dogs (0.26-0.31%).

4 Conclusion

Despite the good level of genetic variability and the low coefficients of inbreeding of this Basset Hound population, our data suggest that inbreeding has effect mainly on the depth of chest starting from the F values between 10% and 15%. It should be noted that according to the breed standard (ENCI), the chest should be neither narrow nor excessively descended. An inbreeding-related reduction in the depth of chest could thus be advantageous for those animals in which an excessive depth of chest is undesirable to the farmers. In fact, farmers considered this as an unpleased feature because Basset Hound was created to follow traces in ravines, brambles, scrubs and other place impossible to penetrate for other hounds; an excessive chest depth that rubs into the ground, is not the most suitable for hunting and would can cause difficulty in movements.

We do not know the effects that F values greater than 15% might have on these traits but it would be interesting to extend the sample size considering high inbred animals in order to verify the interesting results. Furthermore, it would be interesting to calculate inbreeding depression on other very important physiological aspects such as the neonatal survival, stress resistance, fertility, reproductive success, longevity, and birth weight.

Disclosure statement

The Authors report that they have no conflicts of interest. The Authors alone are responsible for the content and writing of this article.

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Table 1 Means, standard deviation (SD) and Sexual Dimorphism for each morphological trait in both males and females

Table 2 Distribution of inbreeding coefficients in the WP and in RP

Table 3 Mean and standard error (SE) for each morphological trait in dogs subdivided according to different inbreeding class

Table 4 Main genealogical parameters computed for dog pedigree

Table 1

		Male Statistics Mean ± SD	Female Statistics Mean ± SD	Farm	Sexual Dimorphism (m/f)
Animals	N°	36	39		
Traits					
WH	cm	36.0±1.76	35.8±1.57	ns	1.00
ChC	"	72.4±4.85	73.28±3.87	ns	0.99
CaC	"	5.6±1.00	5.5±1.12	ns	1.02
ChD		32.6±0.93	32.6±0.90	ns	1.01
ChH	"	17.5±0.38	17.3±0.40	ns	1.01
BL	"	58.5±1.08	58.01±4.90	ns	1.00
RL	"	22.8±0.50	22.8±0.57	ns	1.00
RIsW	"	31.5±1.23	31.7±0.70	ns	0.99
EL	"	23.2±0.63	23.1±0.94	ns	1.00
NL	"	10.9±0.52	11.00±0.55	ns	0.99

WH: height at withers; ChC: circumference of chest; ChH: height of chest; ChD: depth of Chest; CaC: circumference of cannon; BL: body length; RL: length at rump; RIsW: ischiatic width of rump; EL: length of ear; NL: Nose length. ns: not significant.

Significant values for $P \leq 0.05$.

m/f = ratio between mean values of males and females

Table 2

Range		WP*	RP**
		n°	n°
0.00 < F < 0.05	N°	22	14
0.05 < F < 0.10	"	6	6
0.10 < F < 0.15	"	16	15
0.15 < F < 0.20	"	0	0
0.20 < F < 0.25	"	2	0
0.25 < F < 0.30	"	0	0
0.30 < F < 0.35	"	1	0

*WP: whole population;

** RP: reference population

Table 3

		F=0	0<F≤0.05	0.05<F≤0.10	0.10<F≤0.15
		Mean ± SE	Mean ± SE	Mean ± SE	Mean ± SE
Animals	N°	40	14	6	15
Traits					
WH	cm	35.90±0.254	36.22±0.487	35.72±0.843	35.71±0.435
ChC	“	72.85^{a}±0.649	71.18^{ab}±1.243	71.00^{ab}±1.152	70.65^{b}±1.111
ChH	“	17.37±0.061	17.47±0.116	17.57±0.202	17.23±0.104
ChD		32.75^{Aa}±0.133	32.45^{Aa}±0.255	31.52^{Ab}±0.441	30.69^{B}±0.227
CaC	“	5.51±0.162	5.52±0.311	5.92±0.539	5.48±0.278
BL	“	57.99±0.551	58.48±1.055	58.25±1.828	58.85±0.943
RL	“	22.77±0.082	22.90±0.157	22.72±0.272	22.72±0.141
RIsW	“	31.42±0.131	31.54±0.249	31.97±0.432	31.90±0.223
EL	“	23.14±0.121	23.27±0.232	23.87±0.402	23.19±0.208
NL	“	10.83±0.080	10.98±0.153	11.27±0.266	11.27±0.137

WH: height at withers; ChC: circumference of chest; ChH: height of chest; ChD: depth of Chest; CaC: circumference of cannon; BL: body length; RL: length at rump; RIsW: ischiatic width of rump; EL: length of ear; NL: Nose length.

Different letters on the same row show significant differences: $^{A, B}P \leq 0.01$; $^{a, b}$ $P \leq 0.05$.

Table 4

	No.
Whole population (WP)	333
- Sires in total	125
- Dams in total	147
Inbreed in the whole population	47
Average F in the whole population	0.011
Average F in the inbred of the whole population	0.078
Reference population (RP)	75
Inbreed in the reference population	35
Average F in the reference population	0.032
Average F in the inbred of reference population	0.077
Base population (one or two unknown parents = f_t)(BP)	131