Investigating the relationship between inbreeding and life expectancy in dogs: mongrels live longer than pure breeds (#82902)

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Investigating the relationship between inbreeding and life expectancy in dogs: mongrels live longer than pure breeds

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This study aimed to investigate the establishment of a relationship between inbreeding and life expectancy in dogs. A dataset of N = 30563 dogs, containing information about their breed and longevity was subject to survival analysis. A Cox regression proportional hazards model was used to differentiate survivability in three groups of dogs (mongrel, cross-bred, and pure breed). The model was found significant (p<0.001) with mongrel dogs surviving longer than cross-bred and both these surviving longer than pure breeds. A second Cox regression was also found significant (p<0.001) differentiating the lifespan of different dog breeds, and correlating positively the hazard ratio and the Genetic Illness Severity Index for Dogs. The results show that survivability is higher in mongrel dogs followed by cross-bred with one of the ancestors only as a pure breed, and for the last pure breed dogs have the highest morbidity levels. Higher morbidity is associated with higher GISID scores, and therefore, higher inbreeding coefficients.

Investigating The Relationship Between Inbreeding And Life Expectancy In Dogs: Mongrels Live Longer Than Pure Breed

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Abstract

This study aimed to investigate the establishment of a relationship between inbreeding and life expectancy in dogs. A dataset of N = 30563 dogs, containing information about their breed and longevity was subject to survival analysis. A Cox regression proportional hazards model was used to differentiate survivability in three groups of dogs (mongrel, cross-bred, and pure breed). The model was found significant (p<0.001) with mongrel dogs surviving longer than cross-bred and both these surviving longer than pure breeds. A second Cox regression was also found significant (p<0.001) differentiating the lifespan of different dog breeds, and correlating positively the hazard ratio and the Genetic Illness Severity Index for Dogs. The results show that survivability is higher in mongrel dogs followed by cross-bred with one of the ancestors only as a pure breed, and for the last pure breed dogs have the highest morbidity levels. Higher morbidity is associated with higher GISID scores, and therefore, higher inbreeding coefficients.

Introduction

Dogs, the humans' best friends, have been domesticated from the wolf during the late Pleistocene more than 15.000 years ago (Horard-Herbin et al., 2014). Since the beginning of this process, we have understood that dogs could be useful to human activities in many ways, such as

33   hunting, guarding, herding, waste disposal, warfare, entertainment, pest control, transport,

34   clothing, and even food (Janssens et al., 2018). Having so many potential utilitarian roles led to

35   specialization, and humans started to shape dogs accordingly. More recently, in the past 200 to

36   300 years shape standards were envisaged, and dogs' morphology was manipulated through

37   closed population breeding (Axelsson et al., 2021). It was however, during the late 19th century,

38   in Victorian Britain, that dog breeding standards started to be implemented, and the pedigree and

39   pure blood concepts reached momentum (Worboys et al., 2018). The modern dog had been

40   'invented'.

41   The modern dog has a multitude of shapes, sizes, colors, and hair types, but also behaviors and

42   personalities, adapted to human needs. The closed population breeding of dogs is a modern

43   practice aiming at the fixation of traits of interest (Axelsson et al., 2021). This bottlenecking of

44   gene flow has also, however, undesirable consequences, as each individual carries deleterious

45   genes with the potential to cause harm and affect fitness and health (Mabunda et al., 2022). Most

46   of these genes are recessive and can affect the phenotype in homozygosity only. Inbreeding

47   decreases the genetic load and creates in the descendants' genome long homozygous regions,

48   increasing the potential for deleterious genes to express themselves (Bosse et al., 2019).

49   The deleterious defects in pure-breed dogs have long ago been identified, and the number of

50   problems identified is growing. Hodgman (1963) identified thirteen conditions, having

51   highlighted the most important being hip dysplasia, patella luxation, entropion, retinal atrophy,

52   and the elongated soft palate. More recently Asher et al. (2009) and Summers et al. (2010), in

53   two companion papers, identified almost 400. At present, the Online Mendelian Inheritance in

54   Animals (OMIA) database, (Nicholas & Tammen, 2023) identifies 856 trait disorders in dogs.

55   The lifespan of dogs in relation to breeds and types has been presented and discussed (e.g.

56   Patronek et al., 1997; Salvin et al., 2012) and very recently Teng et al. (2022) produced lifetables

57   based on a large UK population above 30.000 dogs. The enormous diversity of dog breeds,

58   ranging between the 1 kg Chihuahua and the 75 kg Saint Bernard, the 30 cm of the Dachshund

59   and the 85 cm of the Great Dane, determines some variation in the different breeds' lifespan

60   (Fleming et al., 2011). Several factors of variation have been identified by the different

61   epidemiological studies investigating lifespan in dogs: weight (Adams et al., 2010), neutering

62   status (Moore et al., 2001), breed (Teng et al., 2022), and breed purity (Proschowsky et al.,

63   2003).

64 Asher et al. (2009) and Summers et al. (2010) in their two companion papers introduced the

65 Generic Illness Severity Index for Dogs (GISID), where the severity of disorders is sensibly

66 scored. In addition, the authors provide an estimate of these scores for the most common breeds

67 in the UK. The authors classify the different disorders (inherited defects) as conformation related

68 (C), conformation exacerbated (CD), and not previously linked to conformation (D).

69 The present study used the lifespan data reported by Teng et al. (2022) to relate with the GISID

70 scores obtained by Asher et al. (2009) and Summers et al. (2010). This study aims to investigate

71 the establishment of a relationship between inbreeding and life expectancy in dogs.

72 Understanding this relationship can be used in the management of breeding for gains in dogs'

73 health and welfare. It is hypothesized that mongrel dogs may have a larger lifespan than

74 crossbred and pure breeds based on a decrease in inbreeding coefficients, associated with carriers

75 of deleterious genes.

76

77 Materials & Methods

78 Data are open access (Creative Commons, CC BY 4.0) and were retrieved from the Royal

79 Veterinary College, University of London, repository (O'Neill, 2022). The sample includes all

80 dogs under primary veterinary care at clinics participating in the VetCompass™ Program, UK

81 during 2016 (i.e., dogs with at least one clinical record in 2016) (Teng et al., 2022). The

82 VetCompass™ Program, UK centralizes in a repository de-identified clinical records from

83 veterinary practices in the UK (VetCompass™ Program, UK) and Australia (VetCompass™

84 Program, Australia). Data in this study includes dogs that had at least one clinical record in the

85 year 2016, in The VetCompass™ Program, UK. The dog breeds recognized by any of the Kennel

86 Club (KC), the American Kennel Club, and the Australian National Kennel Council were

87 considered purebred, while all others were considered crosses. Crosses with ancestors not

88 belonging to a recognized breed were considered mongrels. We have therefore obtained a

89 lifespan data set of dogs classified as 'pure breed', cross with at least a pure breed ancestor

90 ('cross bred'), and a cross without pure breed ancestors ('mongrel'). A total of N = 30563 entries

91 were found in the original dataset, which after data cleansing and elimination of outliers, resulted

92 in a sample of N = 30470 dogs (n = 2406 mongrel, n = 3962 crossbred, and n = 24102 pure

93 breed).

94 Outliers were identified after data transformation for a standard normal distribution, and when

95 their z score was above 3 or below -3 standard deviations. Data entered a Cox-regression

96   proportional hazards model for survival analysis with 'Lifespan' as the 'time to event' variable,

97   and 'Type of Dog' ('Mongrel', 'Cross Bred', and 'Pure Breed') as the factor to analyze. There

98   were no censored entries, and the 'event' is 'Age at Death' (years). An ANOVA with an LSD

99   test as post hoc was also used to differentiate means between 'Type of Dog'.

100   The different pure breed dogs were then compared with the inherited defects in pedigree dogs,

101   namely the disorders related (Asher et al., 2009), and not related (Summers et al., 2010) to breed

102   standards. At this stage, some breeds in the original dataset were eliminated from analysis once

103   to compare with Asher et al. (2009) and Summers et al. (2010) we had to consider the breeds

104   reported by these authors. The new dataset comprises N = 19172 dogs: Alaskan Malamute (n =

105   50), Basset Hound (n = 76), Beagle (n = 171), Bichon Frise (n = 338), Border Collie (n = 1018),

106   Border Terrier (n = 294), Boxer (n = 831), Bull Mastiff (n = 143), Bull Terrier (n = 435),

107   Bulldog (n = 501), Cairn Terrier (n = 107), Cavalier King Charles Spaniel (n = 1004), Chihuahua

108   (n = 405), Cocker Spaniel (n = 1063), Collie (Rough) (n = 84), Dalmatian (n = 149), Doberman

109   (n = 148), Dogue de Bordeaux (n = 152), German Shepherd (n = 1096), German Short-haired

110   Pointer (n = 41), Golden Retriever (n = 511), Great Dane (n = 83), Hungarian Vizsla (n = 44),

111   Irish Setter (n = 39), Labrador (n = 2501), Lhasa Apso (n = 282), Miniature Schnauzer (n = 211),

112   Poodle Miniature (n = 102), Poodle Standard (n = 84), Poodle Toy (n = 56), Pug (n = 196),

113   Rhodesian Ridgeback (n = 68), Rottweiler (n = 505), Scottish Terrier (n = 201), Shar Pei (n =

114   149), Shetland Sheep Dog (n = 61), Shih Tzu (n = 635), Springer Spaniel (n = 800), Staffordshire

115   Bull Terrier (n = 2344), Tibetan Terrier (n = 71), Weimaraner (n = 129), West Highland Terrier

116   (n = 1103), Whippet (n = 125), and Yorkshire Terrier (n = 1060).

117   The number of identified disorders in the different breeds (inherited defects), were divided by the

118   average scores obtained by the application of the GISID (Asher et al., 2009; Summers et al.,

119   2010) (for C, CD, D, and Total), to obtain the variables 'Rate C', 'Rate D', 'Rate CD' and 'Rate

120   Total'. These new variables entered a Cox-regression proportional hazards model for survival

121   analysis with 'Lifespan' as the 'time to event' variable, 'Breed' as a factor, and the 'Rate'

122   variables as covariates. Again, there were no censored entries, and the event considered is 'Age

123   at Death' (years).

124   The models were tested via the -2 Log likelihood test and their parameters via the Wald test. A

125   cumulative survival plot was also produced for the first model.

126   Data were initially entered in a spreadsheet (Microsoft® Excel® for Microsoft 365 MSO, version

127   2204 Build 16. 0. 15128. 20240, 64-bit) for cleansing and outlier detection and elimination.

128 Descriptive statistics were also produced with this software. The Cox regression proportional

129 hazards models were produced with the statistical package IBM Corp.® SPSS® Statistics,

130 Armonk, NY, USA. Version: 28.0.1.1 (15).

131

132 **Results**

133 The descriptive statistics of the variables entered in the first model are shown in Table 1. The

134 ANOVA test is significant (Z = 211.84, 2df, p<0.001) and all the means are significantly

135 different (p = 0.032 between 'Pure Breed' and 'Cross Bred', and p< 0.001 for the other

136 comparisons.

137 The first model differentiating 'Pure Breed', 'Cross Bred', and 'Mongrel' dogs was found to be

138 significant (-2 Log Likelihood 567623, χ^2 = 595, 2 df, p<0.001) and the parameter is also

139 significant (Wald 585, with 2 degrees of freedom, p<0.01). The full model parameterization is

140 shown in Table 2.

141 In a Cox proportional hazards model, a negative parameter is indicative of a decrease in the

142 hazard ratio (HR) and an increase in survival in relation to the baseline. The exponential of the

143 parameter (e^β) indicates the HR effect size and is interpreted as multiplicative effects on the

144 hazard. Therefore, a 'Cross Bred' dog has a negative β, indicative of a decrease in the HR in

145 relation to a 'Pure Breed' of e^β = 0.828 or 17.2%. 'Mongrel' dogs also have lower HR in relation

146 to pure breed and the effect size is larger when compared to 'Cross Bred'. The decrease in the

147 HR in mongrel dogs is 39%. These effects are evident in the survival functions plotted in Figure

148 1.

149 The second model differentiating dog breeds and using the 'Rates' calculated from the GISID

150 was also found to be significant (-2 Log Likelihood 335993, χ^2 = 5013 with 43 df, p<0.001). The

151 variable 'Breed' is significant (Wald 4314, with 42 df, p<0.01), as it is the covariate 'Total

152 Ratio' (Wald 65, with 1 df, p<0.001). The full model parameterization is shown in Table 3.

153 In the second model, the lower the parameter associated with the breed, the higher the HR.

154 Therefore the breed Dogue de Bordeaux is the breed with the lower HR and higher survivability,

155 while the Bulldog has the higher HR and the lower survivability. The breed Yorkshire Terrier is

156 the baseline, therefore negative parameters are associated with lower HR, and positive

157 parameters with higher HR, in relation to this breed. As the model includes over forty breeds any

158 plot of the survival function becomes impossible to read, therefore it is not presented for this

159 model.

160   The covariate 'Total Ratio' indicates that for an additional unit in the ratio, the HR is added by a

161   factor of 1.75% while holding age constant. In other words, the higher the GISID, the higher the

162   death hazard, therefore the lower the survivability. A negative correlation between GISID and

163   survivability becomes, therefore, established within this model.

164

165   **Discussion**

166   An increase in dogs' inbreeding coefficients is associated with a lower lifespan. In decreasing

167   order, dogs with longer lives are 'Mongrel' (mean and 95%CI 12.76 [12.68, 12.84]), followed by

168   'Cross Bred' (11.23 [11.16, 11.29]), and 'Pure Bred' (11.09 [11.06, 11.11]).

169   Some previous studies have reported this relationship. In a study based on questionnaires filled

170   by members of the Danish Kennel Club and representing a sample of 2928 dogs, Proschowsky et

171   al. (2003) reported differences between mixed breed (median and IQR 11 [8, 13]) and several

172   breeds with median varying between 7 and 11. These results were subject to a Kruskal-Wallis

173   test and significant differences were found, however, no post hoc tests are reported and,

174   therefore, the statement that differences between pure-breed and cross-bred dogs exist is not

175   robust. Also, a study in Britain (Michell, 1999) using questionnaires, reports that mongrel dogs

176   are between those with larger lifespans (median 14.0). This study, however, does not provide any

177   inferential statistical test and anchors the statement in descriptive statistics only. Patronek et al.

178   (1997) report statistical evidence of significant differences between mixed breeds and pure

179   breeds (medians 8.5 and 6.7 years, respectively), using a large sample (23,535 dogs) of data

180   collected in veterinary hospitals in the USA and Canada. Despite the high credibility of the

181   study, there is no definition of what a mixed breed is; it could eventually be a mongrel, a cross

182   between two pure breeds, or a cross between a mongrel and a pure breed.

183   Inbreeding is known by agglomerating homozygotic recessive genes in the genome of

184   individuals (Mooney et al., 2021), and particularly in pure-breed dogs, it has been shown that

185   higher inbreeding coefficients are associated with higher morbidity (Bannasch et al., 2021;

186   Yordy et al., 2020), due to a larger accumulation of deleterious genes associated with the most

187   common disorders (O'Neill et al., 2014).

188   The novelty in the present study is the clear differentiation between groups that are not pure

189   breeds. This differentiation allows the definition of three groups with different inbreeding

190   coefficients and therefore allows the clear establishment of a relationship between inbreeding

191   coefficients and lifespan. Being pure-breed dogs bred in a closed population, they have higher

192   inbreeding coefficients than mongrels; and cross-bred dogs with no more than one pure breed

193   ancestor have, obviously, intermediate inbreeding coefficients. The present study reports results

194   based on a continuous variable allowing the comparison and the report of significantly different

195   means in the three groups of dogs. Previous studies report median values only.

196   The life span differences between breeds have been the object of study and are well documented,

197   e.g. Bannasch et al. (2021), O'Neill et al. (2013), Teng et al. (2022), and Yordy et al. (2020). The

198   common report in lifespan differences between dog breeds is the size or weight of the breed.

199   Larger dogs are reported to have higher morbidity, e.g. Bannasch et al. (2021), Greer et al.

200   (2007), Michell (1999), and O'Neill et al. (2013). This trend is not evident in the present study.

201   The limitations of this study are associated with the sample. The sample is based on dogs that

202   attended veterinary practices in the UK, and for which both born, and death dates are known.

203   The generalization of the results for other geographies must be done carefully. Also, not all dogs

204   in the UK have records in veterinary practices and many that have records eventually don't show

205   born and/or death dates. The sample may, therefore, be somehow biased.

206   Nevertheless, ethical dog breeding must be implemented with respect for dog welfare. Broeckx

207   (2020) revised and elected two points of action: reduce the frequency of disorders and increase

208   genetic diversity. For example in a study (Douglas et al., 2015) of policy comparison between

209   the British Kennel Clube (BKC) and the German Kennel Club, Verband für das Deutsche

210   Hundewesen (VDH) it was demonstrated that it is possible to tackle some of the most common

211   problems faced by pure breeding by reducing the frequency of the disorder. Canine hip scoring

212   can effectively be used in selection programs to reduce the incidence of hip dysplasia. By

213   adopting VDH's system of mandatory hip scoring of breeding parents and only allowing those

214   with low scores to breed, it was demonstrated that it is possible to reduce faster, hip scores in

215   populations of pedigree dogs when compared with the BKC's voluntary system.

216

Conclusions

218   It was hypothesized that morbidity in dogs may be associated with inbreeding coefficients. The

219   results of this study confirm the hypothesis, showing that survivability is higher in mongrel dogs

220   followed by cross-bred with one of the ancestors only as a pure breed, and for the last pure breed

221   dogs have the highest morbidity levels. Higher morbidity was associated with higher GISID

222   scores, and therefore, higher levels of homozygotic recessive genes in the genomes of the

223 individuals, and inbreeding coefficients. Future research may be directed to dog breeding, to
224 decrease inbreeding coefficients and control deleterious genes.
225

Acknowledgments

229

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312

Table 1(on next page)

Descriptive statistics of the lifespan of the three groups of dogs analyzed with model 1 (mongrel, cross-bred, and pure breed).

1

Statistic	Mongrel	Cross Bred	Pure Breed
Observations	2406	3962	24102
Minimum	0.008	0.003	0.003
1st Quartile	11.006	8.909	9.126
Median	13.569	12.049	11.723
3rd Quartile	15.198	14.350	13.722
Maximum	20.561	21.884	21.539
Mean	12.761	11.225	11.086
Standard deviation	3.762	4.276	3.729
Mean CI (95% upper)	12.838	11.293	11.110
Mean CI (95% lower)	12.684	11.158	11.062

2
3

Table 2(on next page)

Parameters of the Cox proportional hazards model, modeling the survivability of three groups of dogs being studied (mongrel, cross-bred, and pure breed).

Pure breed is the baseline group.

1

	β	Wald	df	p-value	e^{β}	e^{β} 95% CI	
						Lower	Upper
Cross	-0.177	105.474	1	<.001	0.838	0.810	0.867
Mongrel	-0.494	527.621	1	<.001	0.610	0.585	0.637

Table 3 (on next page)

Parameters of the Cox proportional hazards model, modeling the survivability of different breeds of dogs with 'Rate Total' as a covariate. 'Rate Total' is a calculated rate based on the Genetic Illness Severity Index for Dogs.

Yorkshire Terrier is the baseline breed.

1

		β	Wald	df	p-value	Exp(β)	Exp (β) 95% CI	
							Lower	Upper
Covariate	Rate Total	0.162	64.58	1	<0.001	1.175	1.130	1.223
Breed	Dogue de Bordeaux	-12.105	44.271	1	<0.001	6^{-6}	1.565^{-7}	1.960^{-4}
	Whippet	-2.419	39.009	1	<0.001	0.089	0.042	0.190
	Rhodesian Ridgeback	-1.941	24.433	1	<0.001	0.144	0.067	0.310
	Staffordshire Bull Terrier	-1.806	40.143	1	<0.001	0.164	0.094	0.287
	Tibetan Terrier	0.483	13.633	1	<0.001	1.621	1.255	2.096
	Bull Mastiff	0.795	20.258	1	<0.001	2.214	1.566	3.129
	Shetland Sheepdog	1.546	61.335	1	<0.001	4.691	3.186	6.907
	Pug	1.599	411.244	1	<0.001	4.950	4.241	5.777
	Bull Terrier	1.629	102.357	1	<0.001	5.101	3.720	6.995
	Poodle Miniature	1.666	38.626	1	<0.001	5.292	3.129	8.950
	Poodle Toy	1.798	41.540	1	<0.001	6.037	3.494	10.429
	Labrador	1.874	57.486	1	<0.001	6.514	4.013	10.575
	West Highland Terrier	1.983	68.114	1	<0.001	7.265	4.536	11.634
	Irish Setter	2.103	78.054	1	<0.001	8.187	5.135	13.053
	Basset Hound	2.107	127.733	1	<0.001	8.225	5.707	11.853
	Cavalier King Chrles Spaniel	2.205	204.593	1	<0.001	9.071	6.705	12.270
	German Shorted-Hair Pointer	2.210	65.239	1	<0.001	9.119	5.333	15.592
	Chihuahua	2.286	182.833	1	<0.001	9.832	7.059	13.693
	Dalmatian	2.329	99.287	1	<0.001	10.270	6.495	16.239
	Springer Spaniel	2.423	85.607	1	<0.001	11.278	6.750	18.841
	Collie (Rough)	2.431	82.005	1	<0.001	11.376	6.721	19.255
	Hungarian Vizsla	2.444	82.177	1	<0.001	11.519	6.791	19.539
	Cairn Terrier	2.474	63.367	1	<0.001	11.865	6.453	21.815
	Border Collie	2.512	73.124	1	<0.001	12.334	6.935	21.938
	Shih Tzu	2.548	83.657	1	<0.001	12.779	7.402	22.059
	Poodle Standard	2.642	68.117	1	<0.001	14.036	7.496	26.285
	Bichon Frise	2.706	92.274	1	<0.001	14.963	8.615	25.987
	German Shepard	2.746	156.512	1	<0.001	15.582	10.134	23.959
	Shar Pei	2.813	349.604	1	<0.001	16.662	12.407	22.377
	Alaskan Malamute	3.012	132.368	1	<0.001	20.334	12.172	33.969
	Cocker Spaniel	3.030	96.623	1	<0.001	20.698	11.312	37.871
	Scottish Terrier	3.037	77.295	1	<0.001	20.845	10.591	41.024
	Lhasa Apso	3.346	89.761	1	<0.001	28.381	14.205	56.705
	Beagle	3.356	112.241	1	<0.001	28.661	15.406	53.320
	Golden Retriever	3.488	83.652	1	<0.001	32.730	15.499	69.118
	Miniature Schnauzer	3.747	87.736	1	<0.001	42.381	19.351	92.823
	Great Dane	3.912	235.326	1	<0.001	50.010	30.337	82.440
	Doberman	3.935	162.363	1	<0.001	51.146	27.923	93.682
	Boxer	3.983	130.334	1	<0.001	53.691	27.096	106.387
	Weimaraner	4.088	99.726	1	<0.001	59.640	26.734	133.048
	Rottweiler	4.247	151.288	1	<0.001	69.930	35.540	137.596
	Bulldog	4.446	201.831	1	<0.001	85.273	46.178	157.466

2

Figure 1

Representation of the survival functions of the Cox proportional hazards model, modeling the survivability of three groups of dogs being studied (mongrel, cross-bred, and pure breed).