

Comparative analysis of canine genomes in terms of chromosomal perspectives

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Abstract

The most well-known pet and one of the first domesticated animals is the dog. There are around 400 different dog breeds worldwide. There are many different breeds, each with its unique set of features. The dog's euchromatic genome is predicted to be 2.31 to 2.47 billion base pairs in size, which is somewhat smaller than the human genome but comparable to the mouse genome. The mean value and standard error mean of chromosomal length of five exotic breeds are estimated in this study: Labrador, Basenji, Tasha-Boxer, Mischka German shepherd, and Zoey Great Dane. The total mean value of autosomes is 58266084.83 and the standard error mean is ± 1522688.95 for five exotic breeds of dogs. The corresponding mean values for the X and Y chromosomes were 121774056 and 3937623, respectively.

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1. Introduction

Canis lupus familiaris, the dog, is one of the earliest domesticated animals and mankind's most familiar friend. There are around 400 different breeds of domesticated dogs, each with its own set of morphological, physiological, and behavioural features (Vaysse et al. 2011). Dog populations have evolved over thousands of years into hundreds of breeds, each with unique set of features and polymorphism range (Morrill et al. 2022). Each nucleus in dogs has 76 autosomes (non-sex chromosomes) plus the two sex chromosomes (X and Y), for a total of 78. Each of the 78 chromosomes contains hundreds of genes. Genes code for the machinery needed to produce proteins, which create the physical structure of the body (Szydowski 2022). Dogs are said to be faithful friends that protect their masters and their territory. There are many different breeds, each with its unique set of features. Labrador retrievers are distinguished by their broad head, droop ears, and large, expressive eyes. The thick but relatively short double coat, which is especially water resistant, and the well-known "otter tail" are two distinguishing characteristics of the Labrador retrievers. Colors range from black to chocolate, red/

yellow, and almost white. Labrador retrievers are excellent family dogs in general (<https://urlzs.com/RQNFv>). White feet and legs are common, often accompanied by a blaze and collar (Williams 2019). Boxers have regal, square heads that are distinctive in form. They have a large, deep chest and a short, powerful back. Boxer ears naturally lean over, but they are routinely cut to stand erect. They regularly dock and lift their tails. Their feet are little and their toes are arched. The boxer's coat is short and prone to shedding. Some boxers have a fawn colour, while others have a brindle colour (<https://urlzs.com/Mz3Dk>). German Shepherds are large, powerful dogs with a prominent square snout, bushy tails, and (usually) black masks. They are often tan/black or red/black, with "saddle" and "blanket" symbols across the back. Rare colours include sable, silver, liver, and panda. As herding dogs, German Shepherds have been bred for intelligence and independence. German Shepherds are fantastic guard dogs (<https://urlzs.com/BX6GW>). Africa's 'Barkless Dog,' the Basenji, is a tiny, sweet-faced hunter with intelligence and grace. They are one-of-a-kind and enticing pets, ideally suited to owners who can satisfy their activity requirements and enjoy the challenge of teaching this cat-like canine. Basenjis are petite, elegant hounds that

stand 16 to 17 inches at the shoulder. Their shimmering short coat, tightly curled tail, furrowed forehead, and expressive almond-shaped eyes portray a range of nuanced, humanlike emotions (<https://urlzs.com/Xmf9u>). The Tasha breed temperament is characterized by patience, calmness, bravery, and fearlessness. It is typically a calm, quiet, and obedient dog with an alert yet calm disposition. They were developed for battle and have a dignified demeanor and strong size, but are currently utilized as watchdogs. Tasha is calm and loving with his family but can be distant from outsiders. This breed is also naturally wary of other dogs and may respond violently to canines it perceives as invaders (<https://urlzs.com/F7YSF>). Great Danes are a type of working dog that originated in Germany and are recognized for their tall stature, huge heads and muzzles, long limbs, thin bodies, and short fur. The coat is available in a variety of colours and designs, the most well-known of which is the "harlequin" black-and-white patchwork pattern. Despite their gentle demeanour, Danes are vigilant house protectors. Intruders are frequently put off by the mere sight of these gentle giants (<https://urlzs.com/16vJS>). This article's goal is to outline the distinctions between the mean value and standard error means, two metrics used in descriptive and statistical analysis of normally distributed data.

2. Materials and methods

The chromosome length of five exotic dog breeds (namely, Labrador, Basenji, Tasha-Boxer breed, Mischka breed German shepherd, Zoey breed Great Dane) were noted from NCBI Genome (<https://www.ncbi.nlm.nih.gov/genome/?term=Dog>). The whole data were subjected to analysis of mean value and standard error means.

3. Results

The current study examined the mean values of chromosomal length in five exotic dog breeds. Table 1 shows the

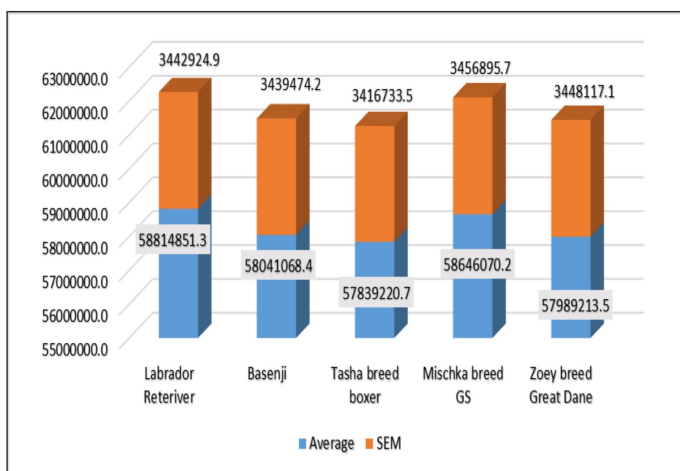


Fig. 1 Graph showing the average and standard error mean of chromosome length of exotic breeds of dog

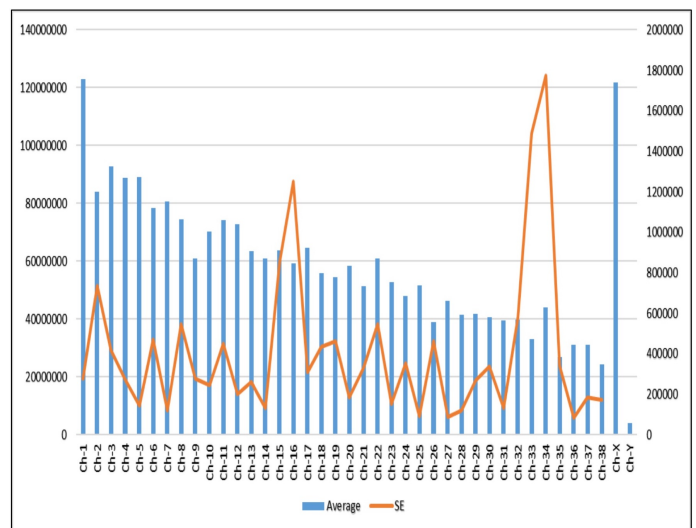


Fig. 2 Graph showing the total chromosomes average and standard error mean values of five exotic breeds of

chromosomal lengths of five exotic breeds, as well as the computed mean value and standard error mean (Fig. 1). The mean autosomal chromosomal lengths ranged from 24216329.4 (chromosome 38) to 122854885 (chromosome 1), whereas the corresponding sex chromosome lengths ranged from 3937623 to 121774056. The standard error mean of five exotic dog breeds varied from ± 83523.81 (chromosome 36) to ± 1774063 (chromosome 34). Figure 2 depicts the average and standard error mean of autosome and sex chromosomal lengths in five exotic breeds. In Labrador retrievers, Tasha breed boxer, Mischka breed German Shephard, and Zoey breed Great Dane, the mean mitochondrial DNA values are 16729, 16727, 16728, and 16756, respectively (Fig. 3). Basenji is devoid of mitochondrial DNA.

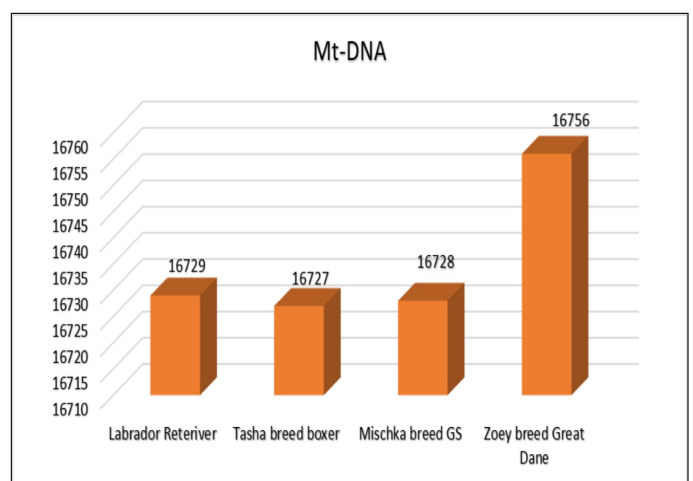


Fig. 3 Graph showing the average and standard error mean of mitochondrial DNA of five exotic breeds of dog

Table 2 Details of chromosome length and calculated mean and standard error mean value of five exotic breeds of dogs

Ch- No.	Labrador Retriever	Basenji	Tasha breed Boxer	Mischka breed German shepherd	Zoey breed Great Dane	Average	Standard error means
1	123313939	122495832	122014068	123556469	122894117	122854885	277523.16
2	86187811	83937118	82037489	84979418	82903020	84008971	734987.85
3	92870237	92105948	94329250	92479059	92032900	92763478	418928.61
4	89007665	88678928	87912527	89535178	88429730	88712805	272485.21
5	89573405	88932562	88913986	89562946	89245444	89245668	144243.76
6	78268176	77624785	80213190	78113029	77758088	78395453	469057.24
7	81039452	80731069	80419774	81081596	80745686	80803515	120175.93
8	75260524	73571895	73585679	76405709	74192687	74603298	545370.21
9	62002293	61088559	60315500	61171909	60772386	61070129	277285.45
10	70361000	70337451	69219345	70643054	70059352	70124040	244307.94
11	75541347	74079022	72832428	74805798	74036318	74258982	450582.34
12	73497294	72601125	72300020	72970719	72762459	72826323	200354.67
13	64037277	63189501	62895387	64299765	63682632	63620912	259856.94
14	61043064	60727891	60430354	61112200	61098034	60882308	132916.81
15	65200600	64291023	60430354	64676183	64289916	63777615	853302.61
16	62021213	59917745	54556944	60362399	59281881	59228036	1252723.3
17	65471548	64428229	63738581	65088165	64204256	64586155	310250.22
18	56883407	55524946	54357284	56472973	55934595	55834641	435652.58
19	55265241	54051281	52989165	55516201	53975570	54359491	462522.6
20	58896461	58423659	57984708	58627490	57931936	58372850	185290.44
21	52140716	51098066	50232922	51742555	50995378	51241927	328483.15
22	58896461	61548924	61822301	61573679	61534057	61075084	547197.81
23	53282923	52864858	52413914	53134997	52790355	52897409	150225.94
24	48838997	47805869	46832179	48566227	47687389	47946132	354206.06
25	51941001	51434566	51908704	51730745	51695226	51742048	90615.053
26	40674351	37989690	38725074	39257614	38422312	39013808	463621.45
27	46248802	46255058	46280981	46662488	46166038	46322673	87113.631
28	41862212	41327378	41264955	41733330	41338898	41505354	121757.02
29	42049852	41986439	40893792	42517134	42070705	41903584	269472.84
30	40414903	41986439	40067686	40643782	40358978	40694357	335806.78
31	39518933	39358666	39086971	39901454	39389883	39451181	132721.8
32	39023732	38764302	41857359	40225481	39041421	39782459	577188.28
33	39023732	31480421	31422675	32139216	31430699	33099348	1487224.4
34	42263871	42143512	51113282	42397973	42177406	44019208	1774062.7
35	26942268	26557760	26040529	28051305	26483662	26815104	340617.8
36	31065185	31053474	30723464	31223415	31110614	31035230	83523.807
37	30932408	30789429	31754289	30785915	30840041	31020416	185363.94
38	24102048	24377179	23973277	24803098	23826045	24216329	172427.75

Table 1 continued on next page

Table 2 Details of chromosome length and calculated mean and standard error mean value of five exotic breeds of dogs

Ch- No.	Labrador Retriever	Basenji	Tasha breed Boxer	Mischka breed German shepherd	Zoey breed Great Dane	Average	Standard error means
Average	58814851.3	58041068.4	57839221	58646070	57989214		
SEM	3442924.9	3439474.24	3416733.5	3456895.7	3448117.1		
Ch - X	127069619	125260708	108808365	124992030	122739558	121774056	
Ch - Y	3937623					3937623	
Mt. - DNA	16729		16727	16728	16756	16735	

4. Discussion

The selection of the reference genome becomes more important in subsequent canid variant studies due to the increasing availability of high-quality canid reference genomes. The Basenji's basal location makes it appropriate for variation analysis for targeted dog breed uses (Edwards et al. 2021). A scan of the dog genome sequence highlights the ability of sample sequencing for mammalian genome comparison research and the production of species-specific resources. More than 650 million base pairs (more than 25%) of the dog sequencing uniquely correspond to the human genome (Pontius et al. 2007). In recent years, molecular and cytogenetic technologies for extensive genetic examination of dogs have been created. Progress in the study of canine hereditary disorders suggests that additional diseases will be identified in the near future. It will have a significant influence on this species' reproduction strategy (Switonski et al. 2004). It is likely that certain recessive genes that cause hereditary disorders will be eradicated. It will help to enhance the dogs' welfare because many canine genetic disorders are not fatal but have a negative impact on life quality (blindness, deafness, hip dysplasia, epilepsy, and so on).

5. Conclusions

This is a brief study of the dog genome's chromosomal length. This study estimates the mean value and standard error mean of chromosomal length in five exotic breeds: Labrador, Basenji, Tasha-Boxer, Mischka German shepherd, and Zoey Great Dane. For five exotic dog breeds, the overall mean value of autosomes is 58266084.83, and the standard error mean is 1522688.95. For the X and Y chromosomes, the corresponding mean values were 121774056 and 3937623, respectively. More research into dog genomes is needed to uncover their hidden potential.

Declarations

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Conflict of interest: The author declares no conflict of interest

Ethical approval: Not applicable

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