



# Population Structure and Breed Composition of Indigenous Korean Donggyeong Dogs

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## ABSTRACT

Korean Donggyeong dogs hold the unique position with their short tails and the longest known history among indigenous Korean breeds. To fully elucidate the evolutionary process and breed composition of indigenous Korean dogs, we conducted an extensive genome-wide survey of 169 breeds on a dataset of 146,300 single nucleotide polymorphisms. Here we show that Donggyeong dogs share the significant amount of haplotypes with other indigenous Korean breeds, and a substantial degree of sharing was observed with other Asian breeds, notably Akita from Japan. Furthermore, we found the relatively high level of genetic diversity in a once-endangered breed, which possibly reflects the lack of concerted efforts of intense breeding practices that have created most modern dog breeds with desirable traits. Together, these results emphasize that characterization of diversity is an essential step towards understanding the genetic history and structure of Donggyeong dogs.

**Key words:** Population Structure, Korean Indigenous dogs, Haplotype Sharing

## INTRODUCTION

Dogs (*Canis lupus familiaris*) hold the unique position among domestic animals as they display the greatest levels of phenotypic diversity on the planet (Clutton-Brock and Serpell 1995). More than 450 breeds are recognized from multiple sections of the globe; and are characterized by distinct morphologic and behavioral phenotypes as the result of limited gene flow and generations of intense selection over the last 300 years (Ostrander and Kruglyak 2000). Genetic studies on domestic dogs have focused heavily on established breeds with a few exceptions including a recent population genetics study on New Guinea singing dogs (Surbakti et al. 2020).

Korean Donggyeong dogs (KDG) represent one of the indigenous Korean dog breeds originating from southeast Korea (Gyeongju) over 1,000 years ago. The KDG breed is uniquely characterized by a short tail which had given rise to incorrect and negative social perceptions. They are also distinctive among native Korean dogs, e.g. Jindo (KJD) and Poongsan (KPS) dogs, and have the oldest recorded history evidenced by their numerous appearance in historical documents. Unfortunately, KDG have experienced the dramatic loss of genetic diversity (Choi 2010).

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KDG, along with KJD and KPS originated in the Asian spitz clade (Choi et al. 2017, Parker et al. 2017); however, specific breed composition and hybridization in the history of Asian breeds remain uncertain. Descending from a very small founder population, KDG have experienced negative selection based on the wrong social perceptions, which have led to the population size decline to less than 500 dogs alive today, mainly bred for conservation efforts. Hence, the genomic data available today may represent a significant evolutionary unit essential for guiding future conservation and management and provide comprehensive insight into dog domestication in Korea. This study specifically attempts to assess the hybridization between KDG and 168 representative purebreds from around the world.

## **MATERIALS & METHODS**

### **Genotype Data and Haplotype Sharing Analysis**

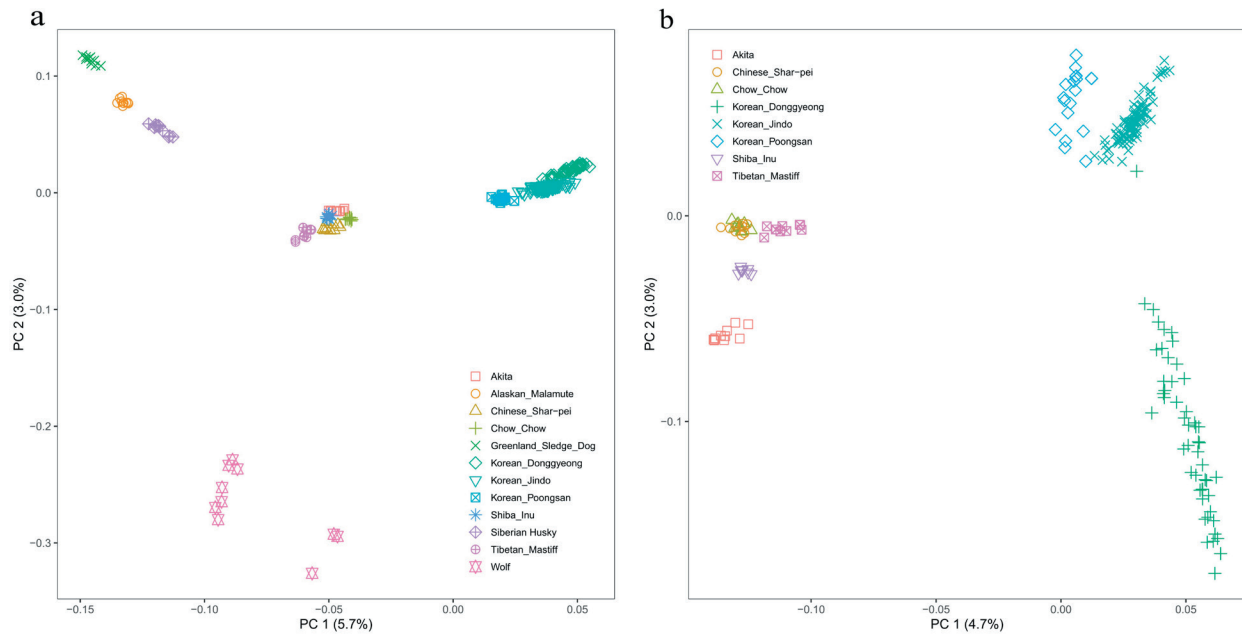
The raw data files for the single nucleotide polymorphism (SNP) genotype arrays reported in this paper are retrieved from previous publications (Choi, et al. 2017). The combined data included 146,300 SNPs in 1,545 individuals from 169 breeds. The genotype data were phased to infer the haplotype sharing using the Beagle v4.1 (Browning and Browning 2007) ibd option with sliding windows of 1,000 SNPs and 50-SNP overlap parameters. The identical-by-state haplotypes between every pair of dogs were predicted to be IBD, which are based on the excessive length and strong sharing with a LOD score greater than 3.0, following the previously published method (Parker, et al. 2017). The inferred IBD haplotypes for each pair were summed across the whole genome to determine the recent breed ancestry.

### **Population Structure Analysis**

We used the genome-wide complex trait analysis (GCTA) tool for PCA (Yang et al. 2011) which implements EIGENSTRAT (Price et al. 2006) to estimate eigenvectors, incorporating genotype data from all samples from breeds of the Asian/spitz clade. A second PCA was performed including only dogs originating from Asia: KJD, KPS, Akita, Shiba Inu, Chow Chow, Tibetan Mastiff, and Chinese Shar-pei. The inbreeding coefficient ( $F$ ) and nucleotide diversity (in windows of 10 Mb) statistics for each breed were estimated using VCFtools (v0.1.13) (Danecek et al. 2011).

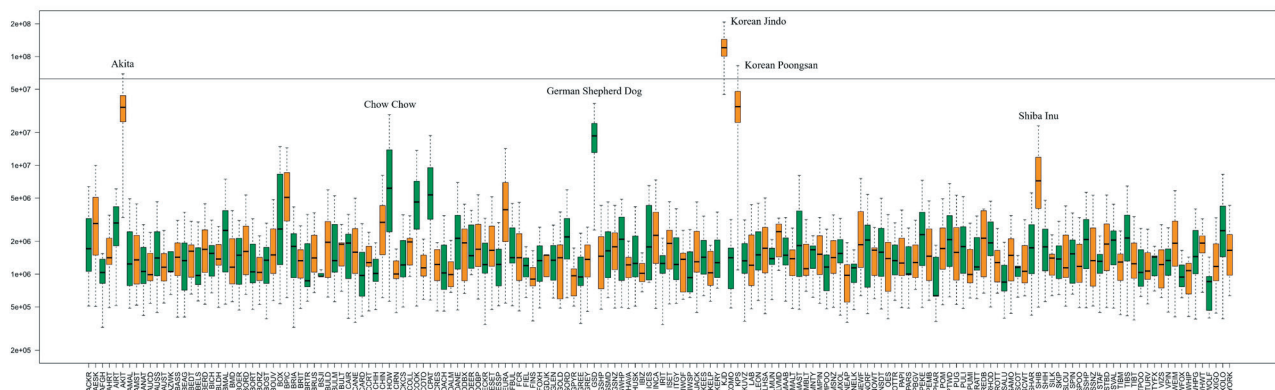
## **RESULTS & DISCUSSION**

Leveraging the publicly available data, we created a dataset of 1,545 dogs from 169 breeds including Korean indigenous breeds, KDG, KJD, and KPS (Supplementary Table S1). We first undertook Principal Component Analysis (PCA) of the autosomal genotype data from KDG and Asian and spitz breeds (Figure 1), which presented the global patterns of genetic structure. The analysis revealed clear structures and separations as samples from the same breed including KDG clustered together. The samples showed no evidence of admixture with each other. The wolf samples clearly constitute a distinct group, and the split within the population is due to independent Korean lineage formation stemming from a bottleneck. To further examine genetic relationships among Asian breeds, we conducted an independent PCA on KDG and Asian breeds, where PC 1 provided evidence that Korean indigenous breeds and Chinese and Japanese breeds are genetically discriminated. The wide distribution of Korean indigenous dogs, specifically DG, indicates the higher level of heterogeneity in this population than in other established Asian breeds.



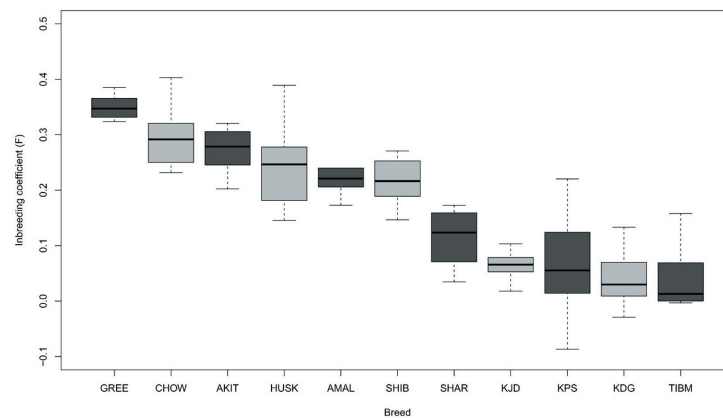
**Figure 1.** (A) PC1 of 235 dogs and composed of North America, East Asia breeds and wolves. Confirming population structure of breeds located in near-by geographical locations. (B) PC2 graph of East Asia breeds separated from PC1.

To capture a holistic view of the genetic and breed composition of KDG in comparison with all publicly available purebreds, we assessed possible hybridization using identical-by-descent (IBD) haplotype sharing. As expected, other indigenous Korean dogs such as KJD and KPS showed the significant amounts of shared haplotypes, reflecting the geographical and historical relatedness of these breeds. The Japanese breeds Akita and Shiba Inu and a Chinese breed Chow Chow also showed strong haplotype sharing with the KDG. The results corroborate with the ancient literatures, which state that most indigenous Korean dogs migrated to Japan and may have contributed to the genetic diversity of ancestral Japanese dog populations (Choi 2010). Finally, a European herding breed, German Shepherd dogs also indicated the unexpected substantial hybridization with KDG.

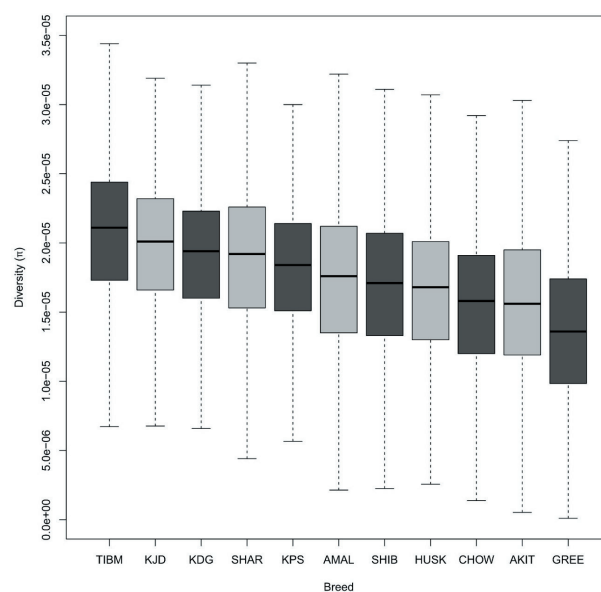


**Figure 2.** Box plots of IBD haplotype sharing from Korean Donggyeong dogs. Graph represents 168 breeds (excluding KDG) on the x-axis and total haplotype sharing on the y-axis, with 90% significance level. Breed abbreviation is provided in Supplementary Table S1.

We next examined the inbreeding coefficient ( $F$ ) in the KDG and Asian/spitz breeds (Figure 3). Of the eleven breeds estimated, Akita showed the one of the highest inbreeding coefficients, illuminating the strong and concerted closed breeding practices, as Akita was recognized as an official breed by the American Kennel Club (AKC) in 1972. On the other hand, Tibetan Mastiff had the lowest inbreeding coefficients, suggesting a relatively greater genetic diversity within the population compared to other established breeds. KDG were ranked tenth from eleven breeds tested and lower than both KJD and KPS. This may indicate that the current low current population size of KDG could be misleading in terms of the genetic diversity due to the limited efforts of controlled and selective breeding. This result was also supported by the nucleotide diversity analysis by each breed, which showed that KDG had a relatively high genome-wide diversity level compared to purebreds (Figure 4). Nucleotide diversity ( $\pi$ ) is defined as the average occurrence of nucleotide discrepancies per site between any two randomly chosen DNA sequences to estimate the degree of polymorphism within a population (Nei and Li 1979). The early ancestral population of KDG were not subject to intensive and closed breeding schemes and may have contributed to the rich nature of the standing genetic variation in the KDG population today.



**Figure 3.** Boxplots of individual inbreeding coefficient ( $F$ ) for eleven breeds.



**Figure 4.** Boxplots of genome-wide nucleotide diversity ( $\pi$ ) for eleven breeds.

The genomes of domestic dog breeds offer a lens through which to view genetic variation and understand evolutionary forces on an evolving population. Given the evidence of both drastic population decline and restoration, KDG represent a valuable resource for population genetic studies. Our results revealed KDG shared significant proportion of haplotypes across genome with geographically close populations including indigenous Korean breeds and a Japanese breed Akita. Finally, we observed a relatively high level of standing genetic variation in KDG when compared to closely related purebreds, although the negative selective pressure over time may have costed a substantial loss of genetic diversity. This study shows the value of comparative genomics in disentangling signals of the admixture and demographic footprints in the population history.

## CONFLICT OF INTEREST

The authors declare that they have no conflicting interest.

## REFERENCES

- Browning SR, Browning BL. 2007. Rapid and accurate haplotype phasing and missing-data inference for whole-genome association studies by use of localized haplotype clustering. *The American Journal of Human Genetics*.81:1084-1097.
- Choi BH, Wijayananda HI, Lee SH, Lee DH, Kim JS, Oh SI, Park EW, Lee CK, Lee SH. 2017. Genome-wide analysis of the diversity and ancestry of Korean dogs. *PloS one*.12:e0188676.
- Choi S. 2010. Studies on the origin and breed characteristics of Gyeongju Donggyeong dog Ph. D. Dissertation. Daegu University, Korea.
- Clutton-Brock J, Serpell J. 1995. Origins of the dog: domestication and early history. *The Domestic Dog: Its Evolution. Behaviour and Interactions with People*.7:20.
- Danecek P, Auton A, Abecasis G, Albers CA, Banks E, DePristo MA, Handsaker RE, Lunter G, Marth GT, Sherry ST. 2011. The variant call format and VCFtools. *Bioinformatics*.27:2156-2158.
- Nei M, Li W-H. 1979. Mathematical model for studying genetic variation in terms of restriction endonucleases. *Proceedings of the National Academy of Sciences*.76:5269-5273.
- Ostrander EA, Kruglyak L. 2000. Unleashing the canine genome. *Genome research*.10:1271-1274.
- Parker HG, Dreger DL, Rimbault M, Davis BW, Mullen AB, Carpintero-Ramirez G, Ostrander EA. 2017. Genomic analyses reveal the influence of geographic origin, migration, and hybridization on modern dog breed development. *Cell reports*.19:697-708.
- Price AL, Patterson NJ, Plenge RM, Weinblatt ME, Shadick NA, Reich D. 2006. Principal components analysis corrects for stratification in genome-wide association studies. *Nature genetics*.38:904-909.
- Surbakti S, Parker HG, McIntyre JK, Maury HK, Cairns KM, Selvig M, Pangau-Adam M, Safonpo A, Numberi L, Runtuboi DY. 2020. New Guinea highland wild dogs are the original New Guinea singing dogs. *Proceedings of the National Academy of Sciences*.117:24369-24376.
- Yang J, Lee SH, Goddard ME, Visscher PM. 2011. GCTA: a tool for genome-wide complex trait analysis. *The American Journal of Human Genetics*.88:76-82.

**Table S1.** List of Individuals by breed used in the analysis.

ABB	Breed Name	N	ABB	Breed Name	N
ACKR	American Cocker Spaniel	10	CHIN	Japanese Chin	4
AESK	American Eskimo Dog	6	CHOW	Chow Chow	10
AFGH	Afghan Hound	10	CIRN	Cirneco dell'Etna	5
AHRT	American Hairless Terrier	10	CKCS	Cavalier King Charles Spaniel	10
AIRT	Airedale Terrier	3	COLL	Collie	10
AKIT	Akita	10	COOK	Chinook	10
AMAL	Alaskan Malamute	10	COTO	Coton du Tulear	2
AMST	American Staffordshire Terrier	6	CPAT	Cane Paratore	2
ANAT	Anatolian Shepherd	6	CRES	Chinese Crested	10
AUCD	Australian Cattle Dog	10	DACH	Dachshund	10
AUSS	Australian Shepherd	10	DALM	Dalmatian	9
AUST	Australian Terrier	10	DANE	Great Dane	10
AZWK	Azawakh	5	DDBX	Dogue de Bordeaux	6
BASS	Basset Hound	10	DEER	Scottish Deerhound	10
BEAG	Beagle	10	DOBP	Doberman Pinscher	10
BEDT	Bedlington Terrier	7	ECKR	English Cocker Spaniel	10
BELS	Belgian Sheepdog	10	ESET	English Setter	10
BERD	Bearded Collie	3	ESSP	English Springer Spaniel	10
BICH	Bichon Frise	10	EURA	Eurasier	10
BLDH	Bloodhound	10	FBUL	French Bulldog	10
BMAL	Belgian Malinois	6	FCR	Flat-coated Retriever	10
BMD	Bernese Mountain Dog	10	FIEL	Field Spaniel	4
BOER	Boerboel	3	FINS	Finish Spitz	10
BORD	Border Collie	10	FOXH	Foxhound	10
BORT	Border Terrier	10	GDJK	Golden Jackal	2
BORZ	Borzoi	10	GLEN	Glen of Imaal Terrier	9
BOST	Boston Terrier	10	GOLD	Golden Retriever	10
BOUV	Bouvier des Flandres	8	GORD	Gordon Setter	10
BOX	Boxer	10	GPYR	Great Pyrenees	10
BPIC	Berger Picard	3	GREE	Greenland Sledge Dog	10
BRIA	Briard	10	GREY	Greyhound	10
BRIT	Brittany	10	GSD	German Shepherd Dog	10
BRTR	Black Russian Terrier	4	GSHP	German Shorthaired Pointer	10
BRUS	Brussels Griffon	2	GSMD	Greater Swiss Mountain Dog	6
BSJI	Basenji	10	GSNZ	Giant Schnauzer	10
BULD	Bulldog	10	GWHP	German Wirehaired Pointer	2
BULM	Bulmastiff	10	HAVA	Havanese	10
BULT	Bull Terrier	10	HUSK	Siberian Husky	10
CAIR	Cairn Terrier	10	IBIZ	Ibizan Hound	10
CANE	Cane Corso	9	ICES	Icelandic Sheepdog	2
CARD	Cardigan Welsh Corgi	10	INCA	Peruvian Hairless dog	10
CCRT	Curly Coated Retriever	6	IRIT	Irish Terrier	7
CHIH	Chihuahua	10	PTWD	Portuguese Water Dog	10
ISST	Irish Setter	9	PUG	Pug Dog	10
ITGY	Italian Greyhound	10	PULI	Puli	4
IWOF	Irish Wolfhound	10	PUMI	Pumi	5
IWSP	Irish Water Spaniel	10	RATT	Rat Terrier	2
JACK	Jack Russell Terrier	10	REDB	Redbone Coonhound	2
KDG	Korean Donggyeong	51	RHOD	Rhodesian Ridgeback	9
KEES	Keeshond	10	ROTT	Rottweiler	10
KELP	Kelpie	2	SALU	Saluki	19
KERY	Kerry Blue Terrier	4	SAMO	Samoyed	10
KJD	Korean Jindo Dog	117	SCOT	Scottish Terrier	10



**Table S1.** List of Individuals by breed used in the analysis (to be continued).

ABB	Breed Name	N	ABB	Breed Name	N
KPS	Korean Poongsan	19	SHAR	Chinese Shar-pei	10
KUVZ	Kuvasz	10	SHIB	Shiba Inu	8
LAB	Labrador Retriever	10	SHIH	Shih Tzu	10
LEON	Leonberger	10	SILK	Silky Terrier	4
LHSA	Lhasa Apso	10	SKIP	Schipperke	10
LMUN	Large Munsterlander	3	SLOU	Sloughi	5
LVMD	Levriero Meridionale	2	SPIN	Spinone Italiano	2
MAAB	Mastino Abruzzese	2	SPOO	Poodle - Standard	10
MALT	Maltese	10	SSHP	Shetland Sheepdog	10
MAST	English Mastiff	10	SSNZ	Standard Schnauzer	10
MBLT	Miniature Bull Terrier	10	STAF	Staffordshire Bull Terrier	10
MNTY	Toy Manchester Terrier	2	STBD	Saint Bernard	10
MPIN	Miniature Pinscher	10	SVAL	Swedish Valhund	6
MPOO	Poodle - Miniature	10	TIBM	Tibetan Mastiff	10
MSNZ	Miniature Schnauzer	10	TIBS	Tibetan Spaniel	10
MXOL	Xoloitzcuintle - Miniature	5	TIBT	Tibetan Terrier	10
NEAP	Neapolitan Mastiff	6	TPOO	Poodle - Toy	10
NELK	Norwegian Elkhound	10	TURV	Belgian Tervuren	10
NEWF	Newfoundland	10	TYFX	Toy Fox Terrier	4
NORF	Norfolk Terrier	10	VIZS	Vizsla	7
NOWT	Norwich Terrier	10	VPIN	Volpino Italiano	4
NSDT	Nova Scotia Duck Tolling Retriever	10	WEIM	Weimaraner	10
OES	Old English Sheepdog	10	WFOX	Wire Fox Terrier	10
OTTR	Otter Hound	9	WHIP	Whippet	10
PAPI	Papillon	10	WHPG	Wirehaired Pointing Griffon	6
PARS	Parsons Russell Terrier	2	WHWT	West Highland White Terrier	10
PBGV	Petit Basset Greffon Vendeen	10	WOLF	Wolf	10
PEKE	Pekingese	10	XIGO	Xigou	5
PEMB	Pembroke Welsh Corgi	10	XOLO	Xoloitzcuintle	5
PHAR	Pharoah Hound	2	YORK	Yorkshire Terrier	10
POM	Pomeranian	10			