**Molecular Genetic Diversity of the Gyeongju Donggyeong Dog in Korea**

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**ABSTRACT.** The present study was conducted to analyze the genetic characteristics of the Donggyeong dog and establish parentage conservation systems for it by using 10 microsatellite markers recommended by the International Society for Animal Genetics (ISAG). A total of 369 dogs from 12 dog breeds including the Donggyeong dog were genotyped using 10 microsatellite loci. The number of alleles per locus varied from 5 to 10 with a mean value of 7.6 in the Donggyeong dog. The observed heterozygosity and expected heterozygosity ranged from 0.4706 to 0.9020 (mean 0.7657) and from 0.4303 to 0.8394 (mean 0.7266), respectively. The total exclusion probability of 10 microsatellite loci was 0.99955. Of the 10 microsatellite markers, the AHT121, AHTH260 and CXX279 markers had relatively high PIC values (≥0.7). This study found that there were specific alleles, 116 allele at AHT121 in the Donggyeong dog when compared with other dog breeds. Also, the results showed two (Korean native dogs and the foreign dog breeds) distinct clusters. The closest distance (0.1184) was observed between the Donggyeong dog and Jindo dog, and the longest distance (0.3435) was observed between the Donggyeong dog and Bulgaa.

The Korean native dog breeds have comparatively near genetic distances between each other. The Korean native dogs and the foreign dog breeds showed genetic distances of more than 0.13 and 0.2, respectively. Also, the genetic distances between the Donggyeong dog and Korean native dogs were more than 0.19. This study found that there were specific alleles, 116 allele at AHT121 in the Donggyeong dog when compared with other dog breeds. Also, the results showed two (Korean native dogs and the foreign dog breeds) distinct clusters. The closest distance (0.1184) was observed between the Donggyeong dog and Jindo dog, and the longest distance (0.3435) was observed between the Donggyeong dog and Bulgaa.

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**KEYWORDS:** Donggyeong dog, genetic distance, microsatellite marker

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Dogs had been with us longer than any other domestic animals. Men and dogs share the closest and most intimate relationship. About 400 breeds are distributed worldwide, and more than 150 breeds are bred in Korea [2, 5, 19]. Other than the Jindo dog, known native Korean dogs include the Poongsan dog, Sapsaree (Sapsal dog) and Jeju dog. The standard height of the male Jindo dog is 48 to 50 cm, and that of the female Jindo dog is 45 to 50 cm. The front view of the head is octagonal or inverted triangular, with the eyes pointing upward and generally dark brown. The tail is curled up, and the coat color is usually yellow and white [6, 7]. The Sapsaree is a medium-sized dog that can be categorized as the ‘Chung-Sapsaree (Blue Sapsaree)’ and ‘Hwang-Sapsaree (Yellow Sapsaree)’. The Chung-Sapsaree has a long black coat with a mix of gray patches. Overall, it is dark gray, but in the moonlight, its coat glows blue. The Hwang-Sapsaree looks yellow, with a yellow coat and patches of white and black hairs. Its height is generally greater than that of the Chung-Sapsaree. It also has drop ears [6, 7, 11]. The Jeju dog is very similar to the Jindo dog. Its height is generally 40 to 45 cm, and it has a fox-shaped head with a wide bulging forehead and narrow muzzle. Its tail points upward. Generally, the Jeju dog has a yellow coat, but rarely, a white or black Jeju dog can be found. The Poongsan dog is a large-sized dog with a height of 55 to 60 cm and length of 60 to 65 cm. It has a white coat, and its head is round with a long muzzle. The Poongsan dog is characterized by a pea-sized bump under its chin that is hard to find in other breeds [3].

The Donggyeong dog is being bred in Gyeongsang province, and only 300 are known to exist. They are friendly toward people, clean, agile and fast. The height of the female Donggyeong dog is 45.46 ± 0.68 cm, and that of the male Donggyeong dog is 49.28 ± 0.71 cm. The length of the female is 53.27 ± 0.67 cm, and that of the male is 57.36 ± 0.63 cm. The Donggyeong dog is characterized by a very short or no tail, and it can be categorized into the yellow coat, white coat, black coat and leopard coat types. The Donggyeong dog is categorized into the short tail type, if the length of the tail from the anus to the tip of the tail is between 4 cm and 15 cm. The number of the tail bones is the important radiographic evaluation index that can be used to identify short tail from no tail. The no-tail Donggyeong dog has 4 or less tail bones, while short-tail Donggyeong dog has 5 to 10 tail bones [3, 4].

Currently, the importance of native genetic resources is being emphasized around the world. Steady effort to preserve and industrialize genetic resources is also in progress. Native genetic resources should be considered to be of more importance rather than just viewed from the perspective of breed conservation. Because it is impossible to revive a breed once it has been lost, protecting and cultivating native genetic resources are nationally important projects. For these reasons, the Donggyeong dog is being researched to preserve its unique characteristics and genuineness. Amongst the native Korean dogs that exist today, the Donggyeong dog is the native Korean dog with the longest history. It is also considered a genetic resource with high cultural value. However, due to hybridization with other breeds, such as the Jindo dog,
studies are required to preserve and manage its pedigree [3, 4]. The aim of this study was to identify the genetic traits of the Donggyeong dog and analyze its phylogenetic relationships to help with the lineage preservation.

MATERIALS AND METHODS

Sample collection and DNA extraction: Genomic DNAs were prepared from whole blood samples, which were collected from 369 individuals of twelve dog breeds (sample sizes are shown in parentheses), the Donggyeong dog (102), Jindo dog (46), Sapsaree (65), Poongsan dog (65), Bulgae (17) and foreign dog breeds (110), to compare native dog breeds, which had been identified based on the dogs’ certified pedigrees (Table 1). Genomic DNAs from samples were extracted using a MagExtractor System MFX-2000 (Toyobo, Osaka, Japan) according to the manufacturer’s protocols [20].

Microsatellite markers and analysis: Ten microsatellite markers, AHT121, AHTH171, AHTk211, AHTk253, AHTk260, CXX279, FH2054, INRA21, REN162C04 and REN54P11, were used for analysis of the dog breeds, and the annealing temperatures are given in Table 2. PCR was accomplished in a total volume of 10 µl of the following mixture: 40 ng of genomic DNA, 10 pmole primer mix, PCR Premix buffer (Qiagen, Hilden, Germany) and distilled water. PCR amplification was performed as follows: the first step was performed by initial denaturation for 3 min at 95°C, followed by 25 cycles at 95°C for 30 sec, 53 to 60°C for 30 sec and 72°C for 40 sec. An extension step of 72°C for 10 min was added after the final cycle. Single PCR was performed in a GeneAmp PCR System 9700 (Applied Biosystems, Foster City, CA, U.S.A.). PCR products were denatured with formamide, and electrophoresis was carried out on an ABI 3130xl Genetic Analyzer (Applied Biosystems). The internal size standard GeneScan 500 RIZ (Applied Biosystems) was used for sizing alleles. In addition, sample No. 1 from the International Society for Animal Genetics (ISAG) 2010 canine comparison test was used as a reference to standardize allele sizes (base pairs).

Statistical analysis: Allelic frequencies, the number of alleles per locus, observed heterozygosity and expected heterozygosity were estimated using Microsatellite Toolkit Ver.3.1.1 program (Microsoft®, Redmond, WA, U.S.A.) [18], and polymorphic information contents (PIC) was computed using the CERVUX software [13, 15]. After checking the relationship of the expected allele and genotype frequency, the Chi-square value and P-value were evaluated to check the compatibility of the genetic distribution in the pool with the Hardy-Weinberg equilibrium.

Genetic differences among populations were estimated by calculating the DA genetic distance [15]. Phylogenetic trees were constructed from the DA genetic distance matrix according to the neighbor-joining (NJ) method [19] using the DISPAN software [17]. Also, each breed’s genetic distance based on allele sharing was analyzed using the Microsat software [14].

Table 1. Lists of dog breeds and numbers used in this study

| Population       | Number | Collection Place |
|------------------|--------|------------------|
| Donggyeong dog   | 102    | Gyeongju         |
| Jindo dog        | 46     | Ansung           |
| Sapsaree         | 65     | Daegu (farm)     |
| Poongsan dog     | 29     | Ulsan (farm)     |
| Laika            | 14     | Ulsan (dog school) |
| Pointer          | 22     | Ulsan (dog school) |
| Shepherd         | 17     | Gyeongju (dog school) |
| Labrador retriever| 12   | Ulsan (dog school) |
| Golden retriever | 12     | Ulsan (dog school) |
| Malinois         | 15     | Gyeongju (dog school) |
| Bulgae           | 17     | Youngju (farm)   |
| Border collie    | 18     | Ulsan (dog school) |

| Total            | 369    |

Table 2. Annealing temperature of the 10 microsatellite loci used in this study

| Loci      | Size Range (bp) | Dye   | Annealing (°C) |
|-----------|-----------------|-------|----------------|
| FH2054    | 135–179         | NED   | 55             |
| AHT121    | 68–118          | FAM   | 57             |
| REN162C04 | 192–212         | PET   | 58             |
| REN54P11  | 224–242         | FAM   | 58             |
| AHTk211   | 83–101          | VIC   | 60             |
| INRA21    | 87–111          | PET   | 63             |
| CXX279    | 109–133         | NED   | 63             |
| AHTk253   | 277–297         | FAM   | 63             |
| AHTk260   | 236–254         | PET   | 63             |
| AHTH171   | 215–239         | VIC   | 63             |

RESULTS

Analysis of the genetic diversity of the Donggyeong dog: As shown in Table 3, there were 7.6 alleles out of 10 microsatellite markers in 102 Donggyeong dogs. The CXX279 locus and AHT121 locus were observed with comparably high genotypes, while the INRA21 locus and AHTk211 locus were observed with the fewest genotypes of 5 alleles. The average value of the observed heterozygosity was 0.7657, with the highest value in the AHT121 locus and the lowest value in the AHTk211 locus. The average value of the expected heterozygosity was 0.7266, with the highest value in the FH2054 locus and the lowest value in the AHTk211 locus. The average microsatellite marker PIC value was 0.6913. Nine markers, excepting the AHTk211 locus, had a PIC value higher than 0.5000, and among these values, the AHTk253 locus and AHTH260 locus were observed with PIC values higher than 0.7000. The PE (exclusion probability) value was observed to have the highest value in the CXX279 locus and the lowest value in the AHTk211 locus. The average PE value was 0.7058.

The estimated results of object identification and paternity evaluation efficiency for the 10 microsatellite markers in the order of priority of PIC values are shown in Table 4. To verify the object identification and paternity evaluation efficiency
for the markers, exclusion power 1 (the possibility of not knowing either of the parents) was accumulated with a marker based on the order of PIC values. The product was called accumulated exclusion power 1, which was accumulated with a single marker in the order of the FH2054, CXX279, AHT121, AHTh260, REN54P11, AHTk253, INRA21, REN162C04, AHTh171 and AHTk211 loci and was observed with values in the order of 0.49599, 0.74437, 0.86883, 0.92042, 0.94759, 0.96445, 0.97583, 0.98315, 0.98677 and 0.98827. Accumulated exclusion power 2 (the possibility of knowing one of the parents) was accumulated with a single marker in the order of the FH2054, CXX279, AHT121, AHTh260, REN54P11, AHTk253, INRA21, REN162C04, AHTh171 and AHTk211 loci and was observed with values in the order of 0.66762, 0.8842, 0.96193, 0.98370, 0.99220, 0.99610, 0.99805, 0.99897, 0.99938 and 0.99955. Accumulated exclusion power 2 (the possibility of knowing one of the parents) was accumulated with a single marker in the order of the FH2054, CXX279, AHT121, AHTh260, REN54P11, AHTk253, INRA21, REN162C04, AHTh171 and AHTk211 loci and was observed with values in the order of 0.66762, 0.8842, 0.96193, 0.98370, 0.99220, 0.99610, 0.99805, 0.99897, 0.99938 and 0.99955.

**Table 3. Number of alleles, heterozygosity and PIC values of the 10 microsatellite markers in 102 the Donggyeong dogs**

| Marker      | No. of Alleles | OHet  | EHet  | PIC    | PE    |
|-------------|----------------|-------|-------|--------|-------|
| AHTh260     | 8              | 0.8039| 0.7794| 0.7432 | 0.7590|
| FH2054      | 7              | 0.8627| 0.8394| 0.8135 | 0.8400|
| AHTk253     | 7              | 0.7843| 0.7362| 0.6902 | 0.6830|
| AHTh171     | 9              | 0.6863| 0.5992| 0.5704 | 0.6040|
| CXX279      | 10             | 0.8529| 0.8309| 0.8067 | 0.8430|
| INRA21      | 5              | 0.8137| 0.7300| 0.6866 | 0.6870|
| REN54P11    | 8              | 0.7157| 0.7357| 0.6795 | 0.7180|
| REN162C04   | 7              | 0.7647| 0.7226| 0.6702 | 0.6540|
| AHTk211     | 5              | 0.4706| 0.4618| 0.4303 | 0.4330|
| AHT121      | 10             | 0.9020| 0.8302| 0.8045 | 0.8370|

Mean 7.6 0.7657 0.7266 0.6913 0.7058

OHet, observed heterozygosity; EHet, Expected heterozygosity; PIC, Polymorphism Information Content; PE, Exclusion probability.

**Table 4. Exclusion power of each microsatellite marker and accumulated exclusion power**

| Marker | PIC  | Excl (2) | AccExcl (2) | Excl (1) | AccExcl (1) |
|--------|------|----------|-------------|----------|-------------|
| FH2054 | 0.81350 | 0.66800 | 0.66762 | 0.49600 | 0.49599 |
| CXX279 | 0.81010 | 0.66400 | 0.88842 | 0.49300 | 0.74437 |
| AHT121 | 0.80820 | 0.65900 | 0.96193 | 0.48700 | 0.86883 |
| AHTh260 | 0.79190 | 0.57200 | 0.98370 | 0.39300 | 0.92042 |
| REN54P11 | 0.77310 | 0.52100 | 0.99220 | 0.34100 | 0.94759 |
| AHTk253 | 0.75920 | 0.49900 | 0.99610 | 0.32200 | 0.94759 |
| INRA21 | 0.74890 | 0.49900 | 0.99805 | 0.32000 | 0.96445 |
| REN162C04 | 0.73900 | 0.47400 | 0.99897 | 0.30300 | 0.97583 |
| AHTh171 | 0.72030 | 0.43700 | 0.99938 | 0.21500 | 0.98315 |
| AHTk211 | 0.69130 | 0.26700 | 0.99955 | 0.11400 | 0.98677 |

PIC, polymorphism information content; Excl (1), the exclusion power when we do not know parents; AccExcl (1), the accumulated exclusion power when we do not know parents; Excl (2), the exclusion power when we do not know parent; AccExcl (2), the accumulated exclusion power when we do not know parent.

As shown in Table 7, Wilcoxon test to check Bottleneck, the criteria of population statistics that verifies the degree of genetic loss in decreased population size, had evaluated TPM (Two Phase Microsatellite Mutation) value of 0.19336 for the Donggyeong dog. For other native Korean dogs, the TPM values were in the order of 1.00000 for the Bulgae (red dog), 0.49219 for the Poongsan dog, 0.16016 for the Jindo dog and 0.00293 for the Sapsaree. For nonnative dogs, the TPM values were in the order of 0.76953 for the pointer, 0.62500 for the border collie, 0.49219 for the shepherd, 0.43164 for the Laika and 0.00977 for the Malinois.

The DISPAN software was used to verify the phylogenetic relationship of 12 breeds. Estimated genetic distances, the minimum genetic distances and standard genetic distances are shown in Tables 8 and 9. Calculation of the minimum genetic distances between the native dog, Donggyeong dog and other native Korean dogs revealed that the Jindo dog and Donggyeong dog shared the closest minimum genetic distances (0.1184). The minimum genetic distances between...
the Sapsaree and Donggyeong dog was 0.1589, and that between the Poongsan dog and Donggyeong dog was 0.161, showing that they shared comparably close minimum genetic distances. However, the minimum genetic distances between the Bulgae and Donggyeong dog was observed to be 0.3435, showing that they did not have a close minimum distances.

Similar results were found for the standard genetic distances between the Donggyeong dog and other native dogs. A minimum genetic distance dendrogram and standard genetic distance dendrogram were created by UPGMA (Unweighted Pair Group Method with Arithmetic mean) clustering and NJ with the previously analyzed genetic matrix. The dendrograms are shown in Figs. 1 and 2. Overall, the standard genetic distance was 0.327, and the minimum genetic distance was 0.193. Comparing the dendrograms, the 369 dogs of the 12 breeds formed two groups: one centered among native Korean dogs including the Donggyeong dog and the other centered among a group consisting of foreign dogs and the Bulgae.

The Donggyeong dog shared the closest phylogenetic relationship with the Jindo dog compared with the breeds, with a standard genetic distance of 0.095 and minimum genetic distance of 0.059. On the other hand, the Bulgae did not share as close genetic distances with native Korean dogs and was assumed to be very heterogeneous from native Korean dogs.

Table 6. F statistics between 5 Korean native dog breeds and 7 Foreign dog breeds

| Allelic | Obs Hz | Unbiased Hz | Fis | Fit |
|---------|--------|-------------|-----|-----|
| Korean native dogs | 3.514 | 0.723 | 0.744 | 0.028 | 0.067 |
| Foreign dogs | 3.248 | 0.637 | 0.700 | 0.090 | 0.140 |
| Total | 0.320 | 0.097 | 0.200 | 0.506 | 0.170 |

Korean native dogs: Donggyeong dog, Jindo dog, Sapsaree, Poongsan dog; Foreign dogs: Laika, pointer, shepherd, Labrador retriever, golden retriever, Malinois, Bulgae, border collie. Obs Hz, observed heterozygosity; Fis, inbreeding coefficient of an individual (I) relative to the subpopulation (S); Fit, inbreeding coefficient of an individual (I) relative to the total (T) population.

Table 7. Bottleneck phenomenon for each group

| Population | Sign Test | SD Test | Wilcoxon Test |
|------------|-----------|---------|--------------|
|            | I.A.M.    | TPM     | S.M.M        | I.A.M.    | TPM     | S.M.M        |
| DG         | 0.15014   | 0.15435 | 0.06519      | 0.00171   | 0.08896 | 0.01248      | 0.00488   | 0.19336 | 0.23242 |
| JD         | 0.04544   | 0.16201 | 0.18155      | 0.00323   | 0.12354 | 0.02316      | 0.01855   | 0.16016 | 0.92188 |
| SS         | 0.00554   | 0.04089 | 0.17482      | 0.00096   | 0.03681 | 0.10891      | 0.00098   | 0.00293 | 0.16016 |
| PS         | 0.15368   | 0.61723 | 0.05924      | 0.01674   | 0.32235 | 0.01200      | 0.00488   | 0.49219 | 0.16016 |
| LC         | 0.16500   | 0.17097 | 0.37498      | 0.02574   | 0.22573 | 0.21677      | 0.00977   | 0.43164 | 0.76953 |
| PT         | 0.04287   | 0.17550 | 0.01518      | 0.06917   | 0.40401 | 0.00104      | 0.00293   | 0.76953 | 0.00684 |
| BG         | 0.09523   | 0.44198 | 0.19762      | 0.15654   | 0.31126 | 0.05898      | 0.27539   | 1.00000 | 0.43164 |
| BC         | 0.57844   | 0.17687 | 0.01254      | 0.19418   | 0.22974 | 0.00074      | 0.37500   | 0.62500 | 0.03223 |
| MN         | 0.04423   | 0.04813 | 0.04400      | 0.00058   | 0.00718 | 0.09390      | 0.00195   | 0.00977 | 0.08398 |
| SP         | 0.15060   | 0.63012 | 0.05781      | 0.03466   | 0.28465 | 0.10176      | 0.00977   | 0.49219 | 0.23242 |

DG, Donggyeong dog; JD, Jindo dog; SS, Sapsaree; PS, Poongsan dog; LC, Laika; PT, pointer; SP, shepherd; MN, Malinois; BG, Bulgae; BC, border collie; SD, standard deviation; I.A.M., Infinite Allele Model; TPM, Two Phase Microsatellite Mutation; S.M.M., Stepwise Mutation Model.

Similar results were found for the standard genetic distances between the Donggyeong dog and other native dogs.

A minimum genetic distance dendrogram and standard genetic distance dendrogram were created by UPGMA (Unweighted Pair Group Method with Arithmetic mean) clustering and NJ with the previously analyzed genetic matrix. The dendrograms are shown in Figs. 1 and 2. Overall, the standard genetic distance was 0.327, and the minimum genetic distance was 0.193. Comparing the dendrograms, the 369 dogs of the 12 breeds formed two groups: one centered among native Korean dogs including the Donggyeong dog and the other centered among a group consisting of foreign dogs and the Bulgae.

The Donggyeong dog shared the closest phylogenetic relationship with the Jindo dog compared with the breeds, with a standard genetic distance of 0.095 and minimum genetic distance of 0.059. On the other hand, the Bulgae did not share as close genetic distances with native Korean dogs and was assumed to be very heterogeneous from native Korean dogs.

An NJ phylogenetic dendrogram was created for the
population using the TreeView program based on simple allele-sharing measurements. As shown in Fig. 3, the Donggyeong dog formed a cluster with uniform genetic distances. Based on the dendrogram, it is believed that the Donggyeong dogs are mainly distributed in one neighbor group.

**DISCUSSION**

After researching over 400 breeds and looking into the history of each breed around the world, the Donggyeong dog was by far an excellent dog with unique characteristics and a rich history. Historical records and evidence could only be found for the Donggyeong dog and a few other dogs. The historical data showed that only the Donggyeong dog had formed the unique characteristic of having a short to no tails and been able to retain it. Overall, a dog as special as the Donggyeong dog was not found anywhere else in the world [3, 4].

To analyze the genetic polymorphism of the Donggyeong dog, 102 Donggyeong dogs were evaluated with 10 microsatellite loci. The results showed that each marker had 5 to 10 alleles, with the average being 7.6 alleles. The number of alleles is used as criteria to evaluate how many alleles are found in each locus. This can be utilized as the simplest method to compare and estimate the purity of a breed. Generally, as more alleles are observed, it is possible to estimate that more interbreeding has occurred. However, because the number of alleles can also increase with higher marker PIC values and larger populations, simply determining the purity with the number of alleles can lead to unreasonable conclusions. Thus, in the genetic characterization of breeds, rather than characterizing breeds with the number of alleles in each marker, the number of alleles should be used to evaluate the reasonability of each marker based on the PIC values.

Heterozygosity rises when multiple groups are combined together, but when they are not, heterozygosity is related to mutations. Heterozygosity increases when the percentage of mutations is high, or when the size of the group becomes larger [16].

The heterozygosity of the Donggyeong dog was analyzed, and the average value was 0.7266. The heterozygosity was lower compared with that (0.7588) in the research done by Lee et al. [12] in 2008 with 51 Donggyeong dogs, but it was higher compared with that (0.6350) in the research done by Cho et al. [2] with 44 Milyang dogs. Also, the heterozygosity values were calculated using the standard genetic distances and standard errors observed among the populations.

### Table 8. Matrix of minimum genetic distances and standard errors observed among the populations

|      | DG  | JD  | SS  | PS  | LC  | PT  | SP  | LR  | GR  | MN  | BG  | BC  |
|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| DG  | -   | 0.1184 | 0.1589 | 0.1610 | 0.2694 | 0.2960 | 0.2672 | 0.3148 | 0.3454 | 0.2224 | 0.3435 | 0.3459 |
| JD  | -   | -   | 0.1184 | 0.1589 | 0.1610 | 0.2694 | 0.2960 | 0.3148 | 0.3454 | 0.2224 | 0.3435 | 0.3459 |
| SS  | -   | -   | -   | 0.1589 | 0.1610 | 0.2694 | 0.2960 | 0.3148 | 0.3454 | 0.2224 | 0.3435 | 0.3459 |
| PS  | -   | -   | -   | -   | 0.1610 | 0.2694 | 0.2960 | 0.3148 | 0.3454 | 0.2224 | 0.3435 | 0.3459 |
| LC  | -   | -   | -   | -   | -   | 0.2694 | 0.2960 | 0.3148 | 0.3454 | 0.2224 | 0.3435 | 0.3459 |
| PT  | -   | -   | -   | -   | -   | -   | 0.2694 | 0.2960 | 0.3148 | 0.3454 | 0.2224 | 0.3435 |
| SP  | -   | -   | -   | -   | -   | -   | -   | 0.2694 | 0.2960 | 0.3148 | 0.3454 | 0.2224 |
| LR  | -   | -   | -   | -   | -   | -   | -   | -   | 0.2694 | 0.2960 | 0.3148 | 0.3454 |
| GR  | -   | -   | -   | -   | -   | -   | -   | -   | -   | 0.2694 | 0.2960 | 0.3148 |
| MN  | -   | -   | -   | -   | -   | -   | -   | -   | -   | -   | 0.2694 | 0.2960 |
| BG  | -   | -   | -   | -   | -   | -   | -   | -   | -   | -   | -   | 0.2694 |
| BC  | -   | -   | -   | -   | -   | -   | -   | -   | -   | -   | -   | -   |

DG, Donggyeong dog; JD, Jindo dog; SS, Sapsaree; PS, Poongsan dog; LC, Laika; PT, pointer; SP, shepherd; LR, Labrado retriever; GR, golden retriever; MN, Malinois; BG, Bulgae; BC, border collie.

### Table 9. Matrix of standard genetic distances and standard errors observed among the populations

|      | DG  | JD  | SS  | PS  | LC  | PT  | SP  | LR  | GR  | MN  | BG  | BC  |
|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| DG  | -   | 0.1365 | 0.2046 | 0.2334 | 0.4857 | 0.5019 | 0.5472 | 0.5841 | 0.5471 | 0.4221 | 0.5854 | 0.6318 |
| JD  | -   | -   | 0.1365 | 0.2046 | 0.2334 | 0.4857 | 0.5019 | 0.5841 | 0.5471 | 0.4221 | 0.5854 | 0.6318 |
| SS  | -   | -   | -   | 0.2046 | 0.2334 | 0.4857 | 0.5019 | 0.5841 | 0.5471 | 0.4221 | 0.5854 | 0.6318 |
| PS  | -   | -   | -   | -   | 0.2334 | 0.4857 | 0.5019 | 0.5841 | 0.5471 | 0.4221 | 0.5854 | 0.6318 |
| LC  | -   | -   | -   | -   | -   | 0.4857 | 0.5019 | 0.5841 | 0.5471 | 0.4221 | 0.5854 | 0.6318 |
| PT  | -   | -   | -   | -   | -   | -   | 0.5019 | 0.5841 | 0.5471 | 0.4221 | 0.5854 | 0.6318 |
| SP  | -   | -   | -   | -   | -   | -   | -   | 0.5841 | 0.5471 | 0.4221 | 0.5854 | 0.6318 |
| LR  | -   | -   | -   | -   | -   | -   | -   | -   | 0.5841 | 0.5471 | 0.4221 | 0.5854 |
| GR  | -   | -   | -   | -   | -   | -   | -   | -   | -   | 0.5841 | 0.5471 | 0.4221 |
| MN  | -   | -   | -   | -   | -   | -   | -   | -   | -   | -   | 0.5841 | 0.5471 |
| BG  | -   | -   | -   | -   | -   | -   | -   | -   | -   | -   | -   | 0.5841 |
| BC  | -   | -   | -   | -   | -   | -   | -   | -   | -   | -   | -   | -   |

DG, Donggyeong dog; JD, Jindo dog; SS, Sapsaree; PS, Poongsan dog; LC, Laika; PT, pointer; SP, shepherd; LR, Labrado retriever; GR, golden retriever; MN, Malinois; BG, Bulgae; BC, border collie.
Heterozygosity was evaluated to be as much higher compared with that (0.5581) in the research done by Huson et al. [8] with 141 purebred Alaskan sled dogs.

Generally, in genetic characterization of breeds with a microsatellite marker, heterozygosity can be used as a standard value in estimating how much of the targeted breed is mixed with the other breed. Typically, the heterozygosity value is low for a purebred and high for mixed breed. However, one characteristic feature of heterozygosity is that the value can increase with an increase in population. Therefore, judging the purity of a breed with just the heterozygosity value can lead to unfair results. However, considering that the research of 141 purebred Alaskan sled dogs performed by Huson et al. [8] showed a heterozygosity value of 0.5581, while the 102 Donggyeong dogs in the present study showed higher heterozygosity, it could be safe to simply assume that the Donggyeong dog has more genetic diversity.

With each marker’s PIC value as the standard value, a marker’s validity and credibility can be estimated. When the PIC value is higher than 0.5000, a marker’s credibility can be judged as reliable in pedigree analysis, and when the PIC value is higher than 0.7000, the analysis is universally valid and capable of providing credible results [1].

The 10 microsatellite marker PIC values used in this study had an average value of 0.6913. Generally, genetic characterization with a microsatellite marker for pedigree identification, pedigree analysis and paternity testing is considered reliable when the PIC value is higher than 0.5000. When the value is higher than 0.7000, genetic characterization is considered to be very credible. Considering these facts, the markers in this study could be identified as credible, with the exception of the AHTk211 marker, which had a PIC value of 0.4303. Furthermore, the results of the present study suggest that the AHTh260 (0.7432), FH2054 (0.8135), CXX279 (0.8067) and AHT121 (0.8045) markers, which had PIC values higher than 0.7000, can be effectively utilized in the future the Donggyeong dog evaluation studies [10].

Comparing the heterozygosity of the Donggyeong dog with those of the other native Korean dogs like the Jindo dog, Poongsan dog, Sapsaree and Bulgae, the Donggyeong dog’s 10 microsatellite marker values were generally lower.
than those of the Jindo dog. However, excluding the Jindo dog, the marker values of the Donggyeong dog were higher than those of the other native Korean dogs. It is estimated that either the Donggyeong dogs were bred with less fixity than other native dogs that were raised in the same province, like the Bulgae or Sapsaree, or the collected blood samples affected the screening results.

In this study, after the genetic distribution was checked, the compatibility of the genetic distribution in the pool was checked with the Hardy-Weinberg equilibrium. The compatibility of the genetic distribution and Hardy-Weinberg equilibrium were checked by measuring Chi-square values. The results showed that markers, except for AHTh171, were evaluated to have low Chi-square values. This means that the genetic distributions do not change as time changes; for the AHTh171 marker, the Hardy-Weinberg equilibrium must not have applied due to increasing inbreeding. Since there are only 300 Donggyeong dogs left, inbreeding might have increased to increase the number of Donggyeong dogs. Therefore, the equilibrium of the marker might not have been reached, and this implies the possibility of loss of genes in the future. However, the rate of inbreeding was still lower than for other native Korean dogs or foreign dogs, and this also implies the possibility of improvements in the Donggyeong dogs.

Although not much research has been done on native Korean dogs and Donggyeong dogs, Lee et al. [11], Jeong et al. [9], and Ha and Kim [6] performed similar studies on genetic distance and concluded that the Sapsaree and Jindo dog are the most closely related dogs. In this study, the Donggyeong dog and Jindo dog were found to be more closely related, while the Sapsaree dog and Poongsan dog were found to be closely related.

It was also found that among the neighboring genetic relationships of the 369 dogs, the Donggyeong dogs were clustered into two uniform groups. This emphasizes the need to categorize the Donggyeong dog into two groups in the future based on physical and genetic characteristics. Also, if two genetically diverse groups could be formed, then with planned selection, inbreeding could be prevented. If the key to avoiding inbreeding could be found, then the Donggyeong dog could retain its characteristics. Also, the standard genetic distance and minimum genetic distance proved that the Donggyeong dog shares its lineage with other breeds of dog, and it is genetically closest to the Jindo dog. This information can be used as fundamental data for meeting the demands of future breeding programs, and further investigation are required using more microsatellite markers or other markers, such as SNP.

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