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ИТТЕРДИН ЖҮРҮМ-ТУРУМУН ЖАНА АЛАРДЫН ГЕНЕТИКАЛЫК НЕГИЗДЕРИН ИЗИЛДӨӨ

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Аннотация: Жаныбарлар адамдын жашоосу үчүн зарыл. Алар менен чогуу жашоо үчүн алардын жүрүм-турумун түшүнүү маанилүү. Бул изилдөө анкета жана геномдук маалыматтардын негизинде жаныбарлардын жүрүм-турум өзгөчөлүктөрүн алдын ала баалоо мүмкүнчүлүгүн көрсөтөт. Жаныбарлардын жүрүм-турум сапаттарын сандык аныктоо үчүн биз анкета жана фактордук анализди колдондук. Ошондой эле, биз жүрүм-турум өзгөчөлүктөрү менен байланышкан полиморфизмдерди аныктоо үчүн геномдук маалыматтарды талдадык. Биз бул ыкмаларды колдонууну жана изилдөөнү башка үй жаныбарларына жайылтууну пландаштырып жатабыз.

ИССЛЕДОВАНИЕ ПОВЕДЕНЧЕСКИХ ЧЕРТ СОБАК И ИХ ГЕНЕТИЧЕСКИХ ОСНОВ

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Аннотация. Животные необходимы для человеческой жизни. Чтобы жить с ними лучше, важно понимать их поведение. В данном исследовании показана возможность предварительной оценки поведенческих признаков животных на основе анкетных и геномных данных. Для количественной оценки поведенческих признаков животных мы использовали анкетные опросы и факторный анализ. Также мы проанализировали геномные данные для поиска полиморфизмов-кандидатов, связанных с поведенческими признаками. Мы планируем применить эти методики и распространить исследования на других домашних животных.

AN INVESTIGATION OF DOG BEHAVIORAL TRAITS ANS THEIR GENETIC UNDERPINNINGS

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Abstract: Animals are necessary for human life. To live better with them, understanding their behaviors is important. This study shows the possibility to assess the animals' behavioral traits in advance from questionnaire and genomic data. To assess animals' behavioral traits quantitatively, we used questionnaire surveys and factor analyses. In addition, we analyzed genome-wide data to find candidate polymorphisms related to behavioral traits. We plan to apply these techniques and expand research to other domestic animals.

Ключевые слова: поведение, опросник, однонуклеотидный полиморфизм (SNP), GWAS, собака

Негизги сөздөр: жүрүм-турум, анкета, бир нуклеотиддик полиморфизм (SNP), GWAS, ит.

Key words: behavior, questionnaire, single nucleotide polymorphism (SNP), GWAS, dog

Since ancient times, humans have used many animals in their daily lives. Even today, humans and animals live together and influence each other. For coexistence, it is important to know the behavior of such animals well, and hence they are frequently studied. Just as each human beings are different from one another, so too are the individual differences within non-human species. Knowledge of individual behavioral traits may provide clues to better managing and living with animals. Research has been conducted on individual differences in behavior and their genetic backgrounds in several animal species, including humans [1]. In recent years, more research is being conducted using whole genome data. Analyses of genome-wide single nucleotide polymorphisms (SNPs) are especially increasingly implemented for non-human species as well. Genome-wide association studies (GWAS), a method to find SNPs throughout the genome of an individual that correlate with phenotypic traits, has been applied to study the genetic background of behaviors [5, 6].

In this study, we searched for genes associated with behavioral tendencies in Dachshunds and Toy Poodles, the most common breeds kept as pets in Japan.

MATERIAL AND METHOD

Samples: All dogs in this study are purebred Miniature Dachshunds and Poodles raised in Japanese households. There were 301 Toy Poodles (140 males and 161 females) and 183 Dachshunds (103 males and 78 females). All of them are between 7and 12 years old, with an average age of 10 years.

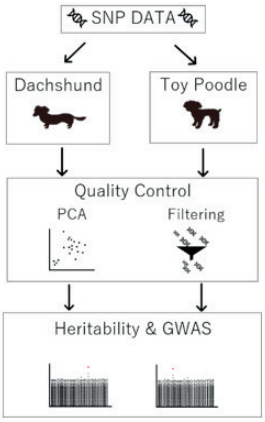

Figure 1. Flow to GWAS in this study

Questionnaire survey: We conducted a questionnaire survey to assess the dogs' personality traits between 2019 and 2022. The questionnaire consists of 39 items asking about the dogs' usual behavior and personality, and each item is rated on a 6-point scale from 1 to 6. This questionnaire is a more detailed version of the one used to evaluate the character of Akita inu dog [7].

Factor analysis on questionnaire data: All analyses on questionnaire data were conducted in R version 4.2.3 [8]. Before the analysis, we calculated Measures of Sampling Adequacy (MSA) using the psych package version 2.1.6 [9]. The average MSA was 0.86. This value suggests this questionnaire data is adequate for exploratory factor analysis. An exploratory search for the number of factors and rotation of factors was conducted for the questionnaire survey data. The number of factors was determined using psych package.

In addition, factor rotation was performed using the GPArotation package version 2014.11.1 [2].

DNA extraction and genotyping: DNA was extracted from the aforementioned buccal swabs, and a Canine 230K BeadChip Array (Illumina, CA, USA) for genome-wide SNP genotyping was used according to standard protocols provided by the manufacturer. The CanFam 3.1 reference genome was used for genome mapping.

Heritability: Heritability was calculated as the ratio of the variance of polymorphisms to the variance of traits (factor scores) using Genome-wide Complex Trait Analysis (GCTA) version 1.93.2 beta Windows [11].

GWAS: We controlled the quality of the SNP dataset based on existence accurate sex information, PCA, filtering with quality of SNPs raw data using the PLINK software version 1.90b6 [3].

Finally, we conducted GWAS with linear mixed models considering kinship using GEMMA software version 0.98.4 [12]. We did a GWAS for each breed with personality factor scores used as traits. Manhattan plots were plotted by the R package qqman [10]. We adopted the default value, p = 10-5, as the suggestive level and p = 10-8, as the significant level when evaluating the effect of individual SNPs on behavioral traits.

RESULTS

We found a seven-factor structure from the personality questionnaire results, denoted Factors 1 ~ 7. Dachshund's Factor 1 and Toy Poodle's Factor 5 were the only ones affecting the factor score with heritability exceeding 0.4 ($p < 0.1$). This difference in heritability among breeds may be due to different selection pressures during the breeding process. The Factor 1 includes aggressiveness. Dachshunds were originally bred for hunting and reported more aggressive than Toy Poodles [4].

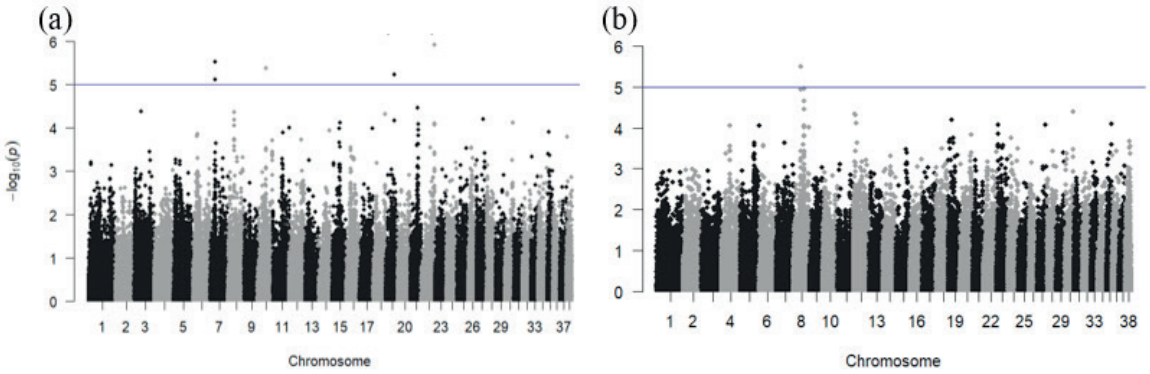

Figure 2. Manhattan Plots of (a) Dachshund's Factor 1 and (b) Toy Poodle's Factor 5

We found several suggestive SNPs possibly related to those traits, though we found no SNPs with significant levels. One of the SNPs we found was located on an intron region of one protein coding gene which regulate G protein signaling.

CONCLUSIONS

We assessed dogs' behavioral traits quantitatively and their genetic background. We found differences in heritability of behavioral traits between two breeds. We also succeeded to find some SNPs possibly related to behavioral traits in the breeds. Although a large sample size is required, whole-genome SNP analysis can provide insight into population composition and search for mutations involved in behavior, as in this study. Whole genome sequence data can also be used to analyze genetic backgrounds of other phenotypes, such as diseases and physical traits, as well as demographic history (e.g. estimation of past population sizes) and genetic differentiation from other species. In the future, we plan to apply these techniques to understand the genetic background of phenotypes and population genomic patterns of other domesticated species, with hopes to deepen our knowledge of each species and their relationships with human beings.

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