Tests for diseases and advances in genetics

From the point of view and in the interest of the Yakutian Laika breed.

E. Ramenska,
member of the Presidium
of the National Breed Club of Yakutian Laika [1]

No time to read the whole article? Here are the NBC YL recommendations:
click here

Breeders and owners of Yakutian Laika dogs very often wonder - how to maintain the health of this native breed and how to conduct its selection, taking into account the available information about the dogs' health. And almost always these questions arise: in what cases should instrumental tests be carried out (radiography, electroretinography, etc.), and in which case it makes sense to conduct genetic tests in order to identify inherited diseases?

If everything is quite clear about instrumental tests - the veterinarian recommends them when establishing a clinical diagnosis - for what concerns genetic tests, it is still a complex and constantly developing branch of science.

Here are our thoughts. As you know, there are several methods of genetics:

- genetic and genealogical methods[2]
- twin genetics
- cytogenetic, which reveals only chromosomal mutations,
- biochemical,
- population statistics[3]
- molecular genetic method
- others

Breeders carefully engaged in breeding, mainly use the genealogical method.

We are interested in molecular genetic method, which also has several types, the most famous and common of which are the PCR method and DNA sequencing methods. However, here it is not our task to study the technology of genetic tests. **We are interested in: what kind of hereditary diseases are detectable by applying molecular genetic tests.** Here we will try to answer this question.

---

[1] *hereinafter called : NBC YL*

[2] *proposed in 1865, F. Galton*

[3] *proposed in 1956 by Tiyo and Levin 3 first applied in 1908 population statistics*

First some general information. DNA is “divided” into chromosomes; in mammals, each chromosome is represented by two copies: one from the father, the other from the mother. They are almost identical except for single changes that may either not affect the body, or lead to phenotypic differences, or lead to diseases.

The size of the dog’s genome consists of 2.4 billion nucleotide[4] (base) pairs, which have a fixed sequence. Scientists have introduced the designation A, T, G, C - the first letter of the nucleotide’s name – to describe the genome sequence. These 2.4 billion nucleotides can be compared to 3,000 volumes of a thick book such as “War and Peace” (2080 pages each volume, information from Leo Uspensky’s book “A Word About Words”). A person is not able to read it, I made an approximate calculation: even browsing (scrolling pages) would take 75 years.

Therefore, the genome is studied in parts and using powerful computer resources. The whole genome was read, but not decrypted, that means, science does not yet know the purpose of each point in the genome. By the way, significant sequences that “encode” DNA make up about 1.5% of the genome, the rest is a mass of objects that are called “junk” DNA, their functions, if any, have not been established, but they are not denied, are not left out either.

Methods for identifying genetically specific diseases:

1. In order to search for a mutant allele that leads to a disease, geneticists examine an animal with symptoms of the disease. (If it comes to collect scientific research, it is highly advisable to first have data on the hereditary nature of the disease using the genealogical method, that means that it is useful to have data on whether the ancestors had the disease). The DNA sequence of this animal is examined piece by piece until the defective gene is found in a certain place.

Or the principle of analogy with other animals is used, using studies that describe the genetic nature of the disease. In this case, the initial search can be narrowed down to the analysis of only a gene (a group of genes) in which mutations can be involved in the development of the disease.

At the same time, scientists, identifying a genetic disorder for the first time, use a purely formal method (that is, a comparison of forms): they compare several, sometimes quite numerous, sections of DNA in one animal, comparing them later with areas of other sick animals, as well as the same sections of DNA healthy animals, which serve as a sample for normal condition. With the help of such studies, ancient, already known, mutations underlying the hereditary disorders in many breeds, and breed-specific diseases have been identified. Currently, expensive genome-wide sequencing

[4] Nucleotides - complex organic compounds, the building material for DNA, RNA and other biological compounds, store information about the structure of the protein and heritable traits.

has been simplified, and chips have appeared (general panels, screen panels), on which DNA sections with already established points are placed. If an animal is examined for already known genetic diseases, then mutations, if any, will be found.

2. Another way to detect mutations is a scientific study aimed at identifying diseases in animals that do not have clinically established pathologies (that is, by a veterinarian). This method can be called a fortuitous search, because the search is carried out in the genome (do not forget about the size!) and can end with the discovery of only ancient mutations. It is not surprising that the scientists themselves use the following words in their articles: “sorting out”, “stumble”. This is a rather expensive method and it is used purely for scientific purposes - for investigating new diseases or for the development of fundamental science.

a) there are “small” chips on which it is really possible to identify already known mutations, they are sometimes used just for diagnostic purposes“ on stream ”- each point has clinical meaning - usually such chips include dozens, sometimes hundreds of points, but they do not make sense to search for new mutations;

b) there are “large” chips - they try to “shove” all the described mutations that have ever been encountered during sequencing of genomes. And it is not necessary that the mutations under study have any known clinical meaning, such chips can include hundreds of thousands and millions of points, and comparing the results of such chips between sick and healthy animals can provide new information about the relationship of the mutation with the disease.

Both methods are quite expensive, the first, of course, became cheaper with the advent of chips, however, it is also used in practice in relation to an animal that has suspected genetic diseases.

Biologist's opinion: Excellent, very effective methodologies, called positional gene cloning have been developed. This method is based on the fact that for all chromosomes there is a whole set of DNA markers scattered along the entire length of the chromosome. Sorting through such DNA markers and observing how they are inherited in families, with or without illness, and without separately associating with the disease, one can stumble upon such a site, such a genome locus, where we really see that this marker is inherited along with the disease. There are diseases, such as hemophilia, when all genes and the spectrum of mutations are quite well known. The more common diseases, all the same, apparently have a polygenic nature, most likely caused by mutations or certain changes in the DNA in several sites or in several genes.

Known clinical meaning - a diagnosis made by a veterinarian. From an interview with Professor of Biological Sciences Evgeny Rogaev.

Ancient (common) mutations.

Some diseases that arose long ago spread to a large number of breeds. Currently, about 200 mutations have been identified that underlie hereditary diseases. Some mutations are considered very ancient. They took place at an early stage in the evolution of the dog’s ancestors from the wolf to modern dog breeds and are common regardless of the breed. For example,

PRA (Progressive Retinal Atrophy) occurs in ~ 100 breeds. DM (degenerative myelopathy), drug sensitivity in the MDR gene (multidrug resistance gene), malignant hyperthermia (reaction to anesthesia) are found in almost all breeds. The last two diagnoses are not a disease, this is an animal's reaction to drugs.

Breed-specific mutations.

Other mutations are found only in some groups of related breeds. This gives rise to the assumption that these violations preceded the final separation of modern dog breeds. For example, CEA (Collie Eye Anomaly) is found in dogs of several shepherd breeds, and PLL (Primary Lens Dislocation) is distributed mainly among terrier breeds. Finally, many mutations were found only among dogs of the one breed, for example, BFJE (Juvenile Epilepsy) in Lagotto Romagnolo. ***

Now, based on the above, we will try to understand how things are with new breeds that do not have a Breed ID, that is, do not have at least a partially known genome. In order to establish mutations, a sick animal is examined and the gene responsible for the mutation is searched. It is either found or not. If the researchers find it, then an ancient or breed-specific disease is established. If they do not find it, then the genetic cause of the disease is called into question - either it exists and it wasn't found, or the disease is not hereditary, but acquired for other reasons. For example, genes responsible for joint dysplasia have not yet been found.

This is further complicated by the fact that diseases similar in symptoms can be caused by different mutations. For example, in the human cystic fibrosis gene about 200 disease-causing mutations are described. Or, if we talk about dogs, then, for example, the already mentioned PRA can be caused by more than more than 20 mutations that have a different distribution in breeds.

The Yakutian Laika breed has never been examined for the detection of mutations inherent in the breed, however, when studying the diseases of breeds in general, scientists always focus on close and related species, genera. Therefore, we can consider what diseases were identified in the breeds related to the Yakutian Laika. Moreover, as we already understood, it makes no sense to examine a healthy dog, if he does not have any ancestors in the pedigree (or rather, parents, the mutation could be not-transmitted from more distant ancestors) suffering from any disease caused by a gene mutation, and then all the work will be worthless.

So, we will consider diseases of dog breeds related to the Yakutian Laika.

Diseases inherent in northern dog breeds:

1. **Vision**

First of all, attention should be paid to the disease - progressive retinal atrophy (disease code: XLPRA1), which is characteristic of Samoyeds and

Siberian Husky. XLPRA1 can be described as a late-onset PRA form. The first symptoms do not appear before the dog turns three to five years old. The main clinical symptom is constantly dilated pupils to maximize light capture, the so-called "tunnel vision" develops. Diagnosis is by systematic fundus examination and electroretinography (ERG). In practice, such a dog has an enlarged pupil, and also he may not see objects located to the side of his head. XLPRA1 is also characterized by adhesion to the female chromosome. For the purpose of breeding, if a clinical diagnosis is made, it is possible to conduct a genetic analysis of bitches in order to identify the carriage of a mutated gene. We could not find the disease statistics for the northern breeds, we focus on the fact that the disease is inherent in about 100 breeds and has more than 20 mutations. It should be also noted that there are other diseases of the PRA retina inherent in the northern breeds: achromatopsia - degeneration of the cone CDAMAL (Siberian Husky, Alaskan Malamute), oculoskeletal dysplasia osd2 / drd2 (Samoyed), progressive degeneration of the cone PRCD (American Eskimo Dog, Karelian Bear Dog, Norwegian Elkhund, Swedish Laphund), generic retinal dysplasia RD (Nenet Laika[5], Norwegian Elkhund), early retinal degeneration ERD (Norwegian Elkhund).[6]

PRA Selection Work.

When a known mutation is detected by the molecular genetic method (a gene - in 99.9%, everyone always has the same genes, even in humans and dogs, but the mutations in them, alleles, are what distinguishes us - A. Markov), female should not be bred. However, taking into account the fact that the disease is diagnosed in adulthood, it is not always possible to avoid this, so the genealogical method of genetics should also be used, removing daughters of this bitch from breeding, since 50% of them will be affected (carriage or defect).

The question remains about the controlled use of carriers in breeding: exclusion from breeding of all carriers can lead to degradation of the breed due to a decrease in the number of dogs and an increase in the degree of inbreeding, which will lead to the identification of new mutations, extremely rare in large populations.

There is no point in doing genetic tests for these diseases without a serious suspicion of their presence (i.e., healthy dogs ones).

It should also be borne in mind that in the Yakutian Laika breed there are no diseases associated with vision.

Conclusion: NKP "Yakutskaya Laika" recommends performing eye tests using electroretinography. Genetic analysis should only be carried out if there is a clinical diagnosis made by a veterinarian.

---

5 Instrumental research of the Nenet Laika (Dr. Perepechaev): http://9265231897.ru/product/lens15d/lens15d.pdf?fbclid=IwAR2LWCLM1JDybsk43w- hNaIsoaOMWbGDH0JcJdg1YClVvyPK72T8_TQwWU

6 Retinal Disease Table: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3942498/table/T1/? report = objectonly Table in Russian: http://ramenska.com/tablitsa_pra

2. Hearing

First of all, owners of white dogs and white-headed dogs - that is, with extreme white piebold (extreme white spotting) and wite piebold (white spotting) - should pay attention to hearing,. In each case, it is necessary (if possible) to identify the nature (not the cause) of deafness - congenital or acquired.

Acquired deafness can be caused by injuries, infectious and other diseases, they can be a result of senile degenerative processes or of an exposure to toxic substances.

Congenital deafness in dogs can be acquired (caused by intrauterine infection, ototoxic drugs, for example, gentamicin, liver diseases or other toxic factors that affected the body before birth or soon after) or hereditary.

Hereditary deafness is associated with a defective gene that ican be autosomal dominant, recessive, sexually linked, or polygenic (more on this later). It is usually not possible to determine the cause of congenital deafness. Observing and using the genealogical method of genetics can help establish the hereditary nature of deafness.

Causes of Hereditary Deafness

Especially often two pigmentation genes are associated with deafness of dogs: the marble color gene M (Merle factor) and the extreme white spotting gene. But not all breeds carrying these genes suffer from this defect (this is, rather, a question of incomplete penetrance, which manifests itself differently in different breeds).

Deafness, which develops, as a rule, in the first few weeks after birth, when the auditory canal is not yet open, is usually the result of a partial interruprion of the blood supply to the cochlea of the inner ear (vascular strip). cochlear nerve cells, which leads to irreversible deafness. The cause of vascular degeneration is unknown, but it appears to be related to the lack of pigment (melanin) produced by melanocytes (pigment cells) in the blood vessels. The functions of these cells have not yet been fully studied, but their role in maintaining a high level of potassium concentration in the fluid surrounding the hair cells of the cochlea of the inner ear is known.

These pigment cells are absolutely essential for the maintenance of the vascular bed (stria vascularis). It should be noted that, from a genetic point of view, the transmission risk of the defect to offspring is the same for one-sided hearing dogs as for two-sided deaf dogs.

Deafness Selection Work

Note: The following information is based on materials from the Department of Comparative Biomedical Research of the Veterinary Faculty of the University of Pieces. Louisiana, as well as other sources.

In terms of simple Mendelian inheritance, each dog has a double set of genes, one from each of the parents. Assuming that deafness is

transmitted autosomally recessive gene (d), by mating two hearing carriers of the deafness gene (Dd), we get an average of 25% deaf dogs (dd), 50% carriers (Dd) and 25% of dogs free from the defective gene (DD). Mating a carrier with a dog that has no defective gene will cause all dogs to hear, but 50% will be carriers and 50% will be free of a defective gene. Mating a deaf dog and carrier will result in 50% of the dogs being deaf, 50% being carriers of deafness.

There will be no dogs free of a defective gene. And ultimately from mating a deaf dog with a dog free of a defective gene, we get 100% carriers, not a single deaf and not a single dog free of a defective gene. But if deafness is transmitted by a simple autosomal dominant gene (D), mating a deaf dog (Dd) with a dog with no defective gene (dd) will result in an average of about 50% of dogs being deaf and 50% free of a defective gene. Dogs with the genotype DD are unlikely to be born, unless someone specifically mates two deaf individuals.

If more than one gene (recessive and / or dominant) is involved in the mechanism of deafness, the possible combinations become much more complex. In humans, more than 50 different autosomal recessive or dominant genes of deafness or their loci have been identified. Children of two deaf parents with two different recessive types of deafness can be hearing, but will be carriers of both genes. If deafness in dogs arises from the presence of more than one recessive gene, the possible mating results will be more diverse and determining the mechanisms of its transmission will be difficult.

As mentioned above, deafness is often associated with the Merle gene, however, we consider here the mechanism of inheritance of deafness in dogs with the spotting (sp) or extreme spotting (sw) gene, for example, as in Dalmatians (8% of deafs according to the US statistics), which not yet clear. These sp and sw genes affect the number and distribution of white areas. Deafness in Dalmatians cannot be called autosomal dominant, as deaf puppies are born from hearing parents. It cannot be called a simple recessive trait: in fact, two deaf Dalmatians were mated, as a result of which some puppies were born hearing in one and some in both ears, while with a simple recessive transmission mechanism they should be all deaf.

These results can be explained by the polygenic mechanism, the presence of two different autosomal recessive deafness genes, or the syndrome with the presence of incomplete penetrance. Further researches (they are ongoing) will aim to identify of such mechanisms.

Not every visually white dog has an extreme spotting gene sw – the white color of the coat can be due to a weakened red one, etc.

It is known that at the S locus exist the gene of continuous color S and the gene of pie color sp. The extreme white spot gene sw and the Irish spotted gene si have not been found at present; they were established theoretically by geneticists through genealogical analysis. Scientists are still searching. There are still a lot of questions with the S locus, and it is possible because the

spotting, like the white color, is determined by mutations in different genes and the concept of “locus” here is more likely to be genealogical than molecular.

By the way, the blue eyes with sw do not indicate the absence of hearing or the presence of a mutation leading to deafness. Thus, it is currently impossible to verify the mutation by the molecular genetic method.

At this time, the NBC YL is investigating the issue of the mandatory BAER test, statistics are being collected, after which a decision will be made whether there is reason for concern or not.

In any case, taking into account the insufficiency of scientific research (which does not allow to establish the exact nature of deafness (hereditary or not), with negative results (lack of response of brain structures to sound stimulus) of the BAER test, deaf dogs should be removed from breeding.

Conclusion: NBC YL recommends: It is necessary to check puppies by simple means (reaction to noise), In case of suspicion - do a BAER test.

3. Dysplasia of the joints

Hip dysplasia (HD) and elbow dysplasia (ED) affect the health and well-being of all dogs.

Scientists disagree on the origin of joint dysplasia. Some are of the opinion that one should distinguish between:

1. True dysplasia (hereditary).
2. Secondary dysplasia associated with impaired joint formation as a result of excessively fast puppy growth, excessive condition and significant physical loads on the unformed joint, injuries.

It should be borne in mind that to distinguish between these two species is very complicated.

Another group of scientists believes that the disease is hereditary, and the external environment is responsible for the severity (expression) of the disease. The heritability coefficient, according to American and European researchers, is 25%. An interesting example is the study of 150 thousand German shepherds in Germany. According to the results of statistical analyzes of the end of the last century, the role of hereditary factors in the occurrence of dysplasia for the German shepherd population in Germany is estimated at less than 20%. Computer data processing has confirmed these statistical findings. It is noteworthy that among dogs born from June to September, the percentage of dysplasia is slightly less than that born in other months. The weight of this factor (month of birth) was determined to be 5%. Thus, if the manifestation of dysplasia is determined by 20% hereditary factors, by 5% by the month of birth, then 75% is left to the environment.

Classical programs offering to use only dogs with completely healthy joints for breeding do not allow the disease to be eradicated quickly due to the nature of its inheritance and the presence of healthy carriers in the population of dogs. Also, a sharp exclusion from the breeding sphere of a large number of dogs, highly valuable for other characteristics, will cause irreparable and

disproportionate damage to the breed. First of all: catastrophic decrease in biodiversity in the breed.

Despite nearly a century of research, the complex etiology and optimal paradigm of treatment for HD/ED disease remain unclear. As originally proposed by dr. Schnell at a meeting of the New York Veterinary Medical Society in the 1930s, joint dysplasia is most likely a series of hereditary and environmental[7] degenerative diseases that affect the morphology and function of the joint of a dog in different ways.

A study by the University of California and the University of Illinois[8] evaluated the effectiveness of using phenotypic selection[9] to improve the condition of the hips and elbows using the complete database of the Orthopedic Animal Fund, covering the period 1970–2015. Assessments (pictures) of sixty breeds (about a million dogs) were studied taking into account gender, age, correlation between joints (knees-elbows), heredity assessment, estimated breeding value (EBV) and maternal / paternal selection efficiency.

A weak and breed-specific influence of gender and older age on joint dysplasia was noted. The influence of gender on heritability is not straightforward - in some breeds there were more favorable estimates of the femur for fathers, in others for mothers. An increase in age affected an increase in cases of dysplasia, but that was a little above average.

An interesting conclusion is made in connection with the estimated breeding value. A lower breeding value means an increased likelihood of good hips, and vice versa.

The study revealed breeds with a higher (Boxer) and lower (Cavalier King Charles Spaniel) heritability. The 5 breeds with the highest prevalence of HD were identified: Newfoundland, Bloodhound, American Staffordshire Terrier, Bullmastiff and Rottweiler, as well as the 5 breeds with the lowest prevalence: German Pointer, Smooth Retriever, Belgian Tervueren, Belgian Shepherd and Scottish Shepherd.

In the absence of direct genetic tests for joint dysplasia, phenotypic selection was effective, that is, data for all breeds indicate a steady improvement. In addition, the data emphasizes that selection schemes should be specific to each breed.

A few words about inbreeding: a 2013 study by the Kennel Club Center for Genetics (UK) and the University of Edinburgh in 2013 indicated that the influence of the inbreeding coefficient was generally very slight.[10] However, in a 2018 study by Genoscoper Laboratories (Finland) and Wisdom Health (UK),

---

[7] The environment that affects the expression of dysplasia is nutrition, growth rate, improper physical activity, total body weight, etc.

[8] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5325577/#pone.0172918.s002

[9] Phenotypic selection - selection of dogs according to their individual indicators: productivity, appearance, constitution, general development. In this study, there is the term phenotypic radiographic assessment. In this sense, phenotypic selection in this study means selection by x-ray indicators.

[10] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3599011/

conclusions were drawn about the effect of repeated inbreeding factors such as limited gene pool, genetic founder effect, intensive selection, overuse of popular producers.[11]

It is known that the inheritance of this disease cannot be established by the molecular genetic method. Therefore, an X-ray study is used to establish a clinical analysis.

The Russian Cynology Federation recently approved a new Regulation on testing for hip dysplasia (HD) and / or elbow dysplasia (ED) (decision of the Presidium of the RCF of 05.29.2018):

Evaluation of HD dysplasia (hip joints):

HD A - healthy joint

HD B - predisposition stage

HD C - stage of initial destructive changes HD D - stage of pronounced destructive changes HD E - stage of severe destructive changes.

Evaluation of ED dysplasia (elbow joint):

0 - no dysplasia of the elbow joint

1 - mild arthritic changes

2 - average arthritic changes

3 - severe arthritic changes

Dysplasia HD/ED Selective Work:

Despite the fact that recent research by scientists suggests that the selection of dogs for joint assessment leads to a decrease in the incidence of dysplasia, selective work requires special attention, since health improvement should be considered several factors:

• Genetic diversity.

Complete exclusion of dogs with dysplasia can lead to the opposite result, because with small sizes of the population, other, no less dangerous gene diseases can appear. Genetic diversity always causes a decrease in any incidence.

• Disease polygenesis. Genetics have found a large number of chromosomes showing a relationship with dysplasia, and different breeds are specific. These can be genes that affect the shape of the joint, the composition of cartilage, soft tissues, up to genes that affect the hormonal background. Therefore, heritability is possibly variable and varies.

• The breeding value of the stud dogs should be taken into account, since often a positive quality (for example, a stable psyche) can change if it is not taken into account during the selection, and only the joints assessment (for example, German shepherds) is taken into account.

Since recently breeders have been actively involved in screening of the hips and elbows, and the results indicate a favorable breed condition in the area of dysplasia (single cases D and the absence of E), therefore, at the moment there is no reason to introduce a mandatory screening for dysplasia,

[11] https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1007361

The NKP, however, recommends a reproductive selection based on an x-ray assessment and a subjective assessment of the pedigree.

Conclusion: NBC YL recommends conducting X-ray examination of the hip and shoulder joints of dogs of the Yakutian Laika breed, reaching the age of 1 year. Dogs with HD-D and HD-E dysplasia, as well as ED-3, should not be allowed for breeding.

4. Other diseases of the northern breeds

Genoscoper Laboratories and WisdomHealth have assembled the world's largest dog disease database, Mybreeddata, which contains both ancient and breed-specific mutations identified through genetic analysis of more than 100,000 dogs.

In this database, for each breed, the gene diseases inherent in it are indicated, but an impressive list of genetic disorders that have been tested in all these dogs but have not been found is also published. I counted 209 diseases, including: blood disorders 34, neurological 38, visual impairment 35, etc., and I went through several related breeds and identified breed-specific diseases.

Four disorders were found in the examined Samoyeds, 2 of them breed-specific: oculoskeletal dysplasia (causing dwarfism of the extremities OSD2 and retinal hypoplasia, which I mentioned in the chapter on PRA and other eye defects), and nephropathy XLHN.

In the East Siberian Laika breed, 2 types of degenerative myelopathy were found. It should be noted that, based on the statistical table in this study, among 100,000 dogs, this disease (DM) occupies the 1st place in frequency.

In a conversation with the Zoogen laboratory, they explained to me that the 1st place of this disease is logical. Not because of aggressiveness, but because of late manifestation. Symptoms of this disease begin to manifest in old age, so culling of affected dogs is not performed, or is done late when the dog gave birth many times.

And it occurs in a large number of breeds because, most likely, it came from wolves, which in principle do not live up to that age in the wild, and the disease does not undergo natural selection. (A. Markov)

In the examined dogs of the Russian-European Laika breed, prcd-PRA disease was found.

Of the 30 individuals of the West Siberian Laika, there is not one that would have discovered any gene disease.

The Alaskan Husky breed has 2 genetically related diseases, one of which is inherent in this breed - Alaskan Husky Encephalopathy (AHE) - a serious disease of the central nervous system.

In the examined dogs of the Alaskan Malamute breed, 4 mutations were found, 2 of which are inherent in this breed: cone degeneration (CD), also called "daytime blindness", also mentioned in the PRA chapter, and early progressive polyneuropathy.

And finally, the Siberian Husky breed suffers DM degenerative myelopathy and GM1 gangliosidosis (neuromuscular disorder).

In this database, there is no such Siberian Husky breed disease as hereditary juvenile cataract and corneal dystrophy, since they cannot be established by a genetic test. In addition, when examining the Siberian Husky breed, no PRA was found. I think this is due to the rarity with which this breed is exposed to the disease. According to the American College of Veterinary Ophthalmologists, in 1995, out of 1345 examined Siberian husky dogs, 107 dogs had hereditary cataract (8%), 44 dogs had corneal dystrophy (3%), and 4 dogs had progressive retinal atrophy (less than 1%).[12]

The Mybreed data base continues to grow, and I'm glad to inform you that the Yakut Like appeared in the list of breeds, although there is not a single examined individual there, and we hope that our dogs will be examined soon!

The FCI website has a list of DNA tests recommended by the British Kennel Club (UK) for specific breeds:

- Siberian Husky - DM, micropenia, GM-1, vision (prcd-PRA, CD, PRA-XL);
- Samoyed - DM, HN, vision (PRA and OSD);
- Alaskan Malamute - AMPN, DM, Vision (CD, PRA).

If case that diseases similar to related breeds will be detected in the Yakutian Laika breed, it would be advisable to collect such biomaterial and examine it purposefully for known mutations - this may provide additional material for further work. In addition, of course, compiling a registry of hereditary diseases confirmed by pedigrees would be very useful in the future.

Conclusion: NBC YL recommends to perform the tests mentioned in this chapter ONLY if there is a clinical diagnosis, since randomly taking tests without proper justification makes no sense. Such large-scale studies are possible and meaningful for scientific purposes.

In conclusion, we draw attention to the fact that scientists warn against a thoughtless use of genetic tests:

"In recent years, breeders, breeding organizations, and other stakeholders have expressed concern about the use and marketing of DNA tests for breeds in which the results have not been properly validated." [13]

Even well-known tests require proof in order to apply them to other breeds:

"*Essentially, detailed clinical and pathological follow-up studies are needed to ultimately confirm whether the option is relevant for different breeds and should be considered in veterinary care and breeding."*[14]

---

[12] https://www.shca.org/shcahp4d.htm?fbclid=IwAR0jIuEtS3FymHTQjdNJ2nmmDwyPnWB20XAe- OQik-FJ3Csu-V7sK1Lvp6U

[13] https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1007361

[14] https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1007361

Currently, no DNA test is relevant for the Yakutian Laika breed (neither in the field of disease, nor in the field of origin identification), except for the test for establishing parents/ family relationship.

Elena Ramenska,
member of the Presidium of the Nation Breed Club
of Yakutian Laika

The author is grateful to:
Dr. M.Sotskaya, Associate Professor, Department of General Psychology, Moscow State Pedagogical University, Scientific Advisor on Genetics, RKF and to mr. A.Markov, the head of the Zoogen laboratory, for critical review of the manuscript and remarks, mrs. A. Pushkar, deputy pre-director of the Status Praesens medical resource, for editing, mrs. G. Morosetti, Health Officer at the Official Veterinary Services of Bolzano (Italy), for translation.

And read on NBC YL recommendations:

Tests for diseases

Recommendations of the National Breed Club of the Yakutian Laika (NBC YL)

The Yakutian Laika breed is indigenous and is characterized by good health, however, the NBC Yakutian Laika has approved the prevention of dog morbidity as one of its priorities.
NBC YL recommends the following instrumental tests for establishing hereditary diseases in dogs:

Vision

1.1. Retinal Atrophy Progression XL PRA1. The first symptoms of the disease appear in the dog no earlier than 3-5 years of age. Diagnosis is by systematic fundus examination and electroretinography (ERG). Based on the established diagnosis, it is possible to conduct a genetic test of bitches in order to identify the carriage of a mutated gene. The female carrier should be removed from the breeding.
1.2. If there is a doctor's testimony that indicates the presence of symptoms of other types of PRA (see Article -"Vision" chapter), it is also possible to conduct appropriate tests.
No diseases associated with visual impairment have been reported in the breed.

Hearing

1.1. It is necessary to check born puppies, especially white and white-headed ones, by simple means (reaction to noise, etc.). If you suspect - do a BAER test. At present, NBC YL is investigating the issue of the mandatory BAER test, statistics are being collected, after which a decision will be made whether there is reason for concern or not. In case of negative results of the BAER test (lack of response of brain structures to a sound stimulus) breeder should remove deaf dogs from breeding.
1.2. It should be borne in mind that genetic tests for testing deafness including associated with the extreme spotting gene sw do not currently exist.
1.3. If possible, the nature of deafness (acquired or congenital (acquired or hereditary)) should be established. Sometimes the nature of deafness is not related to heredity.

Joint Dysplasia HD and ED

NBC YL recommends an X-ray examination of the hip and shoulder joints of dogs at least 12 months old. Dogs with a dysplasia degree of HD-D and HD-E and ED-3 should not be allowed for breeding.

Other diseases

Other diseases (see Article) are found in related breeds, therefore it is necessary in each individual case of the manifestation of symptoms similar to the symptoms of these diseases, undergo a medical examination and follow the doctor's recommendations.

***

NBC YL together with the ZOOGEN laboratory performs FREE testing of DISEASED dogs with visual and hearing impairment that have a clinical diagnosis. Retinal atrophy can be determined genetically, but genetic testing for deafness is not possible because the sw gene has not yet been identified. However, it is necessary to collect biomaterial for future use. Genetics moves forward on all sails. The biological material of the dogs should be sent here: http://zoogen.org/eng/index.php (select language). For healthy dogs, it is necessary to pass a test for gene A, gene K, a gene for hair length. In the application, indicate as the «Customer : National Breed Club of the Yakutian Laika» to receive a discount on payment. For sick dogs, it is necessary to pass the appropriate to the disease test, without payment.

NBC YL collects statistical material on diseases. Please forward your results (scans of documents) or simply the breeder's information about the presence of problem dogs to yras@sakha.ru Information is confidential. For foreign breeders - please select the person in charge of the country for the collection of information.
These actions are necessary to compile a register of diseases in the Yakutian Laika breed, the hereditary nature of which is confirmed by the genealogical or genetic method.