MyDogDNA Technical Sheet – Design, Technology and Performance Data

Contents

1 Summary

The MyDogDNA canine DNA analysis is based on a custom-designed microarray with over 7000 SNP markers combined with internationally approved ISAG/AKC short tandem repeat markers to simultaneously detect and measure

- 100+ disease and trait variants
- genetic diversity, genetic relationships and population structure
- DNA identification profile

The analysis leverages licensed state-of-art technology based on Illumina Infinium HD Ultra platform for SNP genotyping and provides robust results combined with an advanced bioinformatics and interactive reporting system.

2 Overview of the MyDogDNA testing process

Advances in genetic research and technology enable efficient and comprehensive DNA testing of dogs and breeds for different health risks and breeding purposes. Given the growing number of available single gene tests made possible by active international canine genetics research, there is a clear need to move from single gene tests to more comprehensive test panels. Panel testing of genetic mutations has been called for by renowned experts within the field as a next generation testing concept that would finally enable cost-efficient screening for the multitude of known hereditary disorders (1). The MyDogDNA canine DNA analysis aims to provide the means to meet this need, while simultaneously providing the necessary tools for utilizing genome-wide DNA information in practice in breeding selections and programs.

The fundamental idea of the MyDogDNA service is to provide a comprehensive and cost-efficient analysis of the dog genome to help dog owners, breeders, veterinarians and breed clubs better understand their dogs' and breed's genetic health risks and population structures. This supports the setup of sustainable breeding plans. As the first service on the market, the MyDogDNA test combines disease gene testing with an advanced measurement of genetic diversity and relationships.

The MyDogDNA service involves a multi-step process including sample collection, DNA isolation and quality control, genomic analysis by genotyping, data quality control, bioinformatics and dynamic reporting (Figure 1). The test results are easily accessible, and can be utilized for the benefit of the individual dog and the breed.

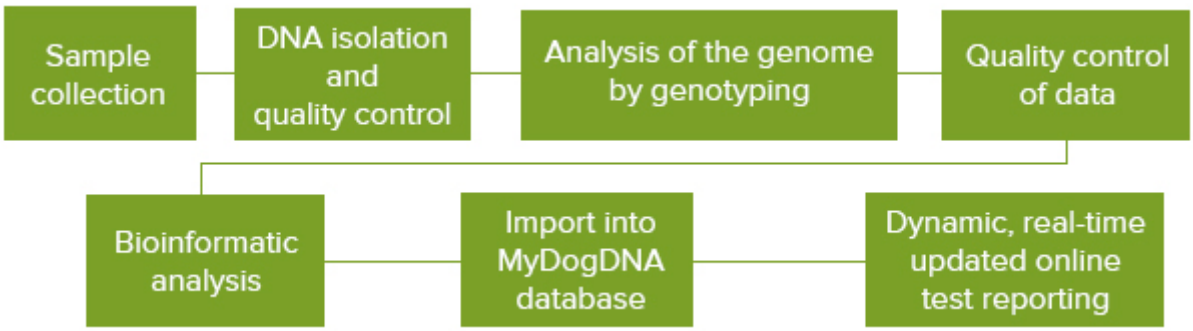

Figure 1. Overview of the MyDogDNA testing process involving multiple steps from sampling to reporting.

3 Design

The test panel design is based on scientific literature and includes 100+ canine diseases and traits (coat colour, coat type, size, etc.) from publicly available Online Mendelian Inheritance in Animals (OMIA), PubMed and MEDLINE databases (2-3). All assayed mutation sites have been defined according to the information provided by the retrieved original publications and the database entries.

Over 7000 markers covering each of the 39 chromosome pairs in the dog genome were selected for the assessment of genetic diversity and relationships. Markers were selected from the public SNP (single nucleotide polymorphism) databases generated as part of the dog genome project (4) and utilized in the development of the widely used Illumina Canine HD Beadchip arrays (5-7). The MyDogDNA test contains on average 160 SNP markers per chromosome with a median intermarker distance of 269 kilobases. Additional markers were selected on chromosome 12 around the DLA (dog leukocyte antigen; major histocompability complex [MHC]) -region for better coverage of this particular genomic region with known functional importance.

4 Technology

The MyDogDNA test panel uses a custom-designed beadchip array, which is run on the robust, reliable and widely utilized Illumina Infinium HD Ultra platform (5-7). The vast majority of the designed assays directly measure known mutations, including point mutations or small insertions and deletions. Specific breakpoint assays have been developed for the larger genomic rearrangements underlying some disorders. Each disease and trait marker is replicated up to three times on the array to ensure accurate and reproducible results. A separate standard DNA fragment analysis is included to provide an STR (short tandem repeat) –based unique DNA profile using internationally approved ISAG (International Society for Animal Genetics) and AKC (American Kennel Club) marker panels for DNA identification and parentage verification.

5 Performance

The scientific team behind the MyDogDNA testing concept is strongly committed to providing high-quality test results. Therefore, a comprehensive pilot study was carried out to validate the performance of the test array. Any set of produced data is subjected to stringent routine quality control before sophisticated bioinformatics analyses can be performed, and the results can be reported to customers. These processes are described in detail in the following sections.

5.1 Validation

A pilot study including around 2000 dogs from 50 breeds was carried out prior the launch of the MyDogDNA testing service to validate the test and to monitor its performance. The validation process included source sample type comparisons, analyses on replicate concordance and test-retest reproducibility (Table 1). Overall, observed call rates on the microarray were very high considering the varying levels of experience of the sample takers (dog owners, breeders and veterinarians). No significant difference was observed in the call rates between blood and buccal cell samples, similarly to other published canine sample type comparison studies (8). Replicate concordance (measuring the number of times replicates of the same assay yield the same result) for individual markers was excellent (99.8%). The test panel is highly reproducible as evidenced by a

median test-retest (rerun of the same sample) concordance of 99.8%. Moreover, high quality samples with previously known genotypes replicated the original genotyping results effectively validating the new array in terms of sensitivity and specificity. Additionally, obtained genotypes for different traits (e.g. for coat colour and -type) correlated well with the expected breed characteristics and breed variation in the phenotype, matching the true phenotypes.

For disorders for which we did have validation samples available *a priori*, clearly discernible genotype clusters and signals were a requisite for including the test among the reported disorders. The identified carrier and affected genotypes for such disorders were also subjected to *a posteriori* validation by routine Sanger sequencing with 100% concordance, further validating the array. Similar sequencing confirmation will always be applied in the future to any novel discovery of a known mutation in new breeds.

Although we have validated the test for a large number of individual disorders in the array, we acknowledge that some rare disorders remain unvalidated due to lack of validation samples with known genotypes. In some cases, such control samples would be available only to the academic research groups having published the original mutations. We continue efforts to establish validation experiments for all disorders on the array.

Given the robust, validated and established performance of the MyDogDNA technology as described herein, we are confident in the capacity of the array to give accurate data on all markers. The key validation steps passed by the MyDogDNA array are summarized in Table 2. The performance of the array is continuously monitored to guarantee delivery of highest quality data for customers.

Table 1.

Summary of microarray performance data based on analysis of >2000 tested samples	
Median call rate (blood samples)	98.1%
Median call rate (buccal swab samples)	98.2%
Average replicate concordance	99.8%
Reproducibility	99.8%
Sensitivity and specificity*	100%

*based on known validation genotypes for >30 different disorders

Table 2.

Key steps in the validation process successfully passed by the MyDogDNA test
Source sample validation (buccal cell vs. blood)
Validation of known genotypes for disorders and traits
Validation of MyDogDNA array genotypes by another technology
Concordance validation across arrays
Concordance validation within an array (replicate markers)
Independent international validation
Stringent continuous quality control measures for sample quality
Established and widely utilized technology (Illumina)
Careful selection of markers based on scientific documentation
Successful identification of different breeding lines and geographic differences
Successful identification of crossbred litter in the diversity analysis

5.2 Independent validation

The MyDogDNA microarray was also subjected to an external blind evaluation by an independent commercial DNA testing laboratory. Heterozygous or affected homozygous genotypes were successfully identified for 20/21 tested genetic disorders and traits. The test failed to identify carrier genotypes for a complex repeat mutation, which we had also observed to behave inconsistently. The test was subsequently removed from the panel.

5.3 Sample collection and DNA quality control

The MyDogDNA test kit includes sampling brushes and detailed instructions for easy collection of buccal cell samples. Careful sampling according to instructions is the key to obtaining intact DNA that yields high quality results, and to avoiding resampling. DNA quality is monitored by standard measurements of DNA concentration and purity (e.g. Nanodrop). Whenever poor sample quality gives reason to believe that the analysis results are imperfect, we prefer redoing the analysis on a new sample from the same dog.

5.4 Genotyping quality control

Every set of raw genotyping data produced on the MyDogDNA microarray is routinely subjected to manual inspection using Illumina's GenomeStudio® Data Analysis Software (9; Figure 2). Genotypes for all tested disorders and trait markers are manually curated. Any result with replicate discordance is discarded. Poor DNA sample quality (e.g. due to high bacterial DNA load or low DNA quantity) influences the consistency and reliability of the results. An example of the effect of poor DNA quality on genotyping results is shown in the scatter plot in Figure 2B. We require a minimum overall call rate of 95% (meaning >95% of the tested markers successfully yielding results) for all analysed samples. An observed lower success rate leads to a reanalysis on a new sample from the dog. Similarly, whenever a dog appears as a genetically different outlier compared to the rest of its breed, a novel analysis is requested unless there is a clear explanation for the finding (e.g. suspected mixed breed ancestry). In practice, call rates for high quality samples are around 99%.

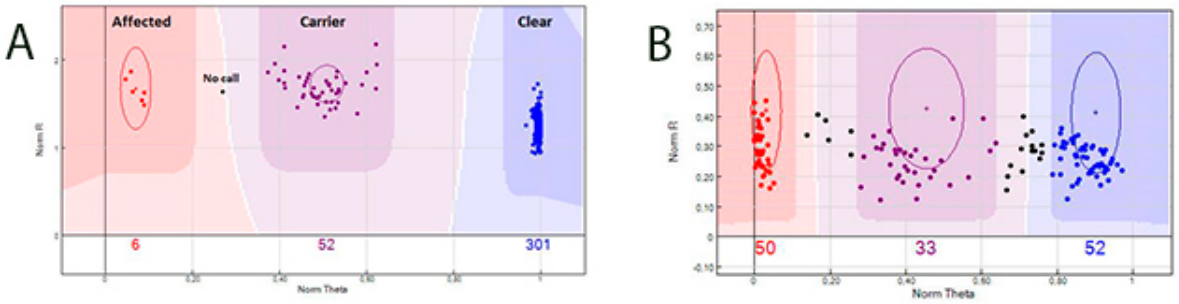

Figure 2. An example of the validation and quality control analysis of raw genotyping data using Illumina's GenomeStudio® Data Analysis Software.
A. Good quality DNA samples (depicted by red, purple and blue signal dots) yield clearly distinguishable genotype clusters and reliable results.
B. Low quality DNA results in unclustered and ambiguous data, which necessitates rerun of the samples.

6 Reporting

The wealth of information gathered from more than 7000 genomic regions of each MyDogDNA-tested dog requires a unique database combined with an online reporting system. Real-time, interactive reporting provides the most holistic view available on the market to the tested dog's genetic properties, helping owners and breeders to understand not only their dogs' health risks but also the genetic structure and relationships of the entire breed. All test results stored within the MyDogDNA database are confidential and their sharing is fully controlled by the dog owner. Additional functionalities built into the MyDogDNA online system encourage breeder networking and the exchange of both phenotypic and genetic information that is needed for improved and sustainable breeding plans. The reporting is continuously being developed, and new functions added to provide more insight into the canine genome on both the level of individual dogs and breeds. The following sections describe the main features of the MyDogDNA reporting system in more detail.

6.1 Reporting architecture: Dog profile

Each dog owner is granted a personal secured user account in the MyDogDNA database, and each of the owners' own tested dogs appears within the account. The owner has to provide mandatory basic information on the tested dog(s) such as breed, registration ID, microchip/tattoo number, gender, geographic region and date of birth. Such information is required for an official DNA identification profile, as defined by the standards of several national Kennel Clubs. In addition to the mandatory information, dog owners can upload photos of their dog, and provide additional information about their dog that can be shared with other users via the MyDogDNA Breeder™ dog matchmaking interface (described in section 6.3).

6.2 Reporting architecture: Test results

Due to the large amount of collected genome-wide data of different nature, the genetic testing results for an individual dog are reported under four separate main sections: "Summary", "Disorders", "Traits" and "Genetic Diversity and Relationships". In addition, it is separately indicated that a unique DNA identification profile (either ISAG or AKC) now exists for the dog.

"Summary". The "Summary" provides a quick overview of the dog's test results, summarizing results for the known disorders in the breed, potential new disorders discovered in the breed, key conformational traits and main genetic diversity and relationships statistics.

"Disorders". A separate "Disorders" section lists test results for around 100 mutations underlying known canine genetic disorders that are simultaneously screened on the MyDogDNA microarray. This result listing is divided into three major categories to highlight and acknowledge the different nature and significance of the test results (see an example of disorders reporting in Appendix 1).

Test results for the "**Known disorders in the breed"** appear first on the list in separate table. Although genetic research continuously identifies new mutations and the number of tests for inherited disorders grows rapidly, most of the currently known mutations can still be considered breed-specific.

The second category **"New potential disorders in the breed"** includes novel discoveries previously unknown to the scientific community. The MyDogDNA panel testing concept has proven to be a powerful discovery platform with regard to screening for the presence of known mutations in breeds in which these have not been previously encountered. Several novel discoveries were made already during the pilot study and new findings for further research emerge in almost every genotyping run. In order to understand the significance of the novel findings for the health of the

breed, the presence and penetrance of the new mutations need to be validated through several protocols (see chapter 7).

The third and final category of test results lists **"Additional tested disorders found in other breeds"**. There are at least two main reasons to screen for many known mutations in the same panel test. First, although many mutations are breed-specific or affect a limited number of breeds, this is the only cost-efficient approach today to test any dog for the growing number of individual mutations known within breeds. Second, despite actively ongoing research around the world, no one has ever tested for all of known mutations in all breeds. Academic research is often limited to a few breeds available during the study at hand. Strikingly, as demonstrated already during our pilot study, some of mutations originally published as breed-specific appear to be widespread and common in other breeds as well. These discoveries are important because unknown mutations can potentially be severe existing or emerging health risks. Once these mutations are revealed, breeders are empowered to control their prevalence within breeds. However, we acknowledge that the new mutation findings have to be validated for each breed as discussed below in more detail (see chapter 7).

"Traits". This section includes test results for conformational characteristics such as coat colour, coat type and size. Some of the reported morphological traits are genetically complex, involving multiple loci and interactions between genetic variants. We strongly recommend users to familiarize themselves with our test documentation, and the provided literature references for a more complete understanding of the significance of the test results.

"Genetic Diversity and Relationships". A genome-wide analysis provides a tangible view to a dog's genetic diversity and the breed's genetic structure. The MyDogDNA visualization of genome-wide measured diversity shows heterozygosity levels within and across breeds illustrating how an individual tested dog relates to that information. Heterozygosity varies significantly across breeds. The MyDogDNA pilot study yielded consistent results in measurements of heterozygosity levels when comparing MyDogDNA data with data from some of the same dogs that had been previously studied with other methods to assess genetic diversity (STR analysis and DLA-haplotyping; 10). We found that the breeds that had shown the highest levels of heterozygosity upon examination with STRs or DLA haplotypes were also the genetically most diverse ones with MyDogDNA chip SNPs. A second line of evidence that supports the efficient performance of the diversity analysis with SNP markers comes from an example of a crossbreeding trial in the Kromfohrländer breed. Figure 3A demonstrates the level of original genetic diversity within the Kromfohrländer breed, and indicates clearly increased heterozygosity in dogs crossbred to Standard Poodle. Similarly, the crossbred litter clusters separately in the genetic relationships plot (Figure 3B).

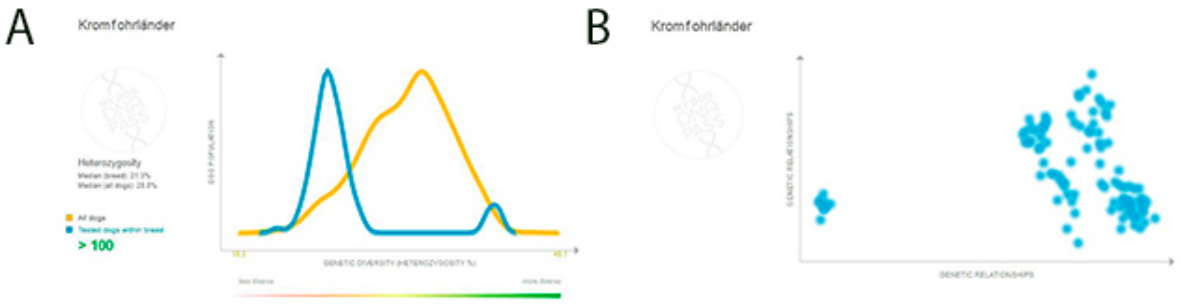

Figure 3. An example of the genetic diversity and relationship measurements of the MyDogDNA test
A. This graph shows average heterozygosity of the Kromfohrländer population at 21% and demonstrates how efficiently the MyDogDNA test measures differences in genetic diversity by identifying a second peak at 32%. The second peak designates a crossbred (Kromfohrländer-Standard Poodle) litter.
B. This graph shows the genetic relationships of the Kromfohrländers on the right, with the crossbred litter on the left. Each dot denotes a dog. The more distance between two dogs in the plot, the more genetically different they are.

In the “Genetic Relationships” plot, we visualize the tested dog’s genomic structure in relation to the other dogs in the breed, or across breeds. This analysis is based on the measured genome-wide data, with the high number of investigated SNP markers providing an accurate high resolution view. The plot provides multiple lines of useful information for breeders and breed clubs for improved understanding and development of their breeds. First, MyDogDNA analysis enables identification of different hidden sub-populations within breeds, including breeding lines such as working- and show line dogs (Figure 4). Second, genetic differences and distances of dogs between countries can be visualized. This is useful, as new “blood” from other countries may be valuable for maintaining and increasing a breed’s genetic diversity and expanding the gene pool. Third, knowledge on the origin and “purity” of their dog is of interest to breeders and dog owners. The MyDogDNA analysis helps to evaluate whether a dog clusters among the “core” group of dogs of the breed or stands out as an ‘outlier’. Outliers may have a “mixed” genetic background. On the other hand, ‘outliers’ may bring important genetic diversity into the breed when used for breeding, which is why identification of such dogs is important and supports breeding strategies that aim at preserving genetic diversity. The breadth in which MyDogDNA visualizes diversity data was previously available only to researchers, but now this information can be made available to any dog enthusiast.

Figure 4. Genetic structures of the Labrador Retriever and Golden Retriever breeds. The MyDogDNA test identifies two different breeding lines within these breeds, corresponding to working and show line dogs.

Genetic diversity and relationship reporting in the MyDogDNA database is real-time, relative, dynamic and interactive. Whenever a new dog is tested, the bioinformatics analyses are recalculated. This updates statistics on genetic distances between individuals and breeds, and the graphs shown.

6.3 Reporting architecture: MyDogDNA Breeder™

Breeding decisions should never be made only on the basis of genotypes. Optimally, it is based on the careful consideration of both phenotypic and genotypic characteristics. Phenotypic characteristics to consider may include information from health checks such as eye examinations and hip radiographs, various field trials, behavioural tests, conformation, show results, and other personal preferences of the breeder. MyDogDNA provides a comprehensive genomic analysis collecting data from thousands of markers spread across all chromosomes. This data enables, for the first time, the most holistic utilization of genetic data as a tool to support breeding selections. To efficiently handle the large amount of data generated and utilize it to improve a breed’s genetic health, sophisticated bioinformatics and computational tools are needed. For this purpose, the MyDogDNA database hosts a custom-developed bioinformatics tool named MyDogDNA Breeder™ (patent pending).

The fundamental idea of the MyDogDNA Breeder™ tool is to compare the genomic data between dogs and make suggestions for optimal breeding choices. The comparison of the dogs focuses on two important features: i) the genome-wide measured difference between the owner's dog and other tested dogs of opposite gender in the database and ii) the tested disorder carrier statuses of the dogs. The dogs which are genetically most different from the owner's dog and do not carry the same mutations rank on the top of the list as the best mating matches. The majority of the tested disorders are recessive and in order to manifest in the puppies, both parents would need to carry the mutation. At the same time a responsible breeder wants to maintain or increase genetic diversity in order to produce healthy puppies while sustainably managing the gene pool of the breed. This undertaking can be efficiently facilitated with the MyDogDNA Breeder™ tool when selecting genetically different partners for breeding while taking tested mutations into account. Breed history is often tricky and even with nearly complete pedigree data it is difficult to know how similar two dogs are to each other genetically. In particular, complex pedigrees with multiple popular sires may be misleading. However, it is again important to keep in mind that genetic ranking of suitable partners is only one side of the coin. As stated above, no breeding decision should be based only on genotype data, and the phenotypes of the potential breeding partners also have to be carefully considered.

7 Multistep validation process of novel MyDogDNA discoveries

During the MyDogDNA pilot study that included around 2000 samples from 50 breeds, the panel screening revealed several known mutations in new breeds, demonstrating that the MyDogDNA analysis is a powerful discovery tool. It allows cost-efficient and rapid screening of over 100 known mutations in any breeds, moving beyond what is typically feasible in an original study first describing a mutation. New discoveries provide important knowledge that may have implications for breed health, and they may affect breeding plans. However, new discoveries always require a stringent multistep validation process, such as the one the MyDogDNA scientific team has adopted (Figure 5), before their clinical significance in the new breeds is proven. It is known that the same mutation may not manifest similarly in other breeds for several reasons.

The first step of the MyDogDNA validation process is to confirm presence of the observed mutation by an alternative method such as Sanger sequencing or in some cases, real-time PCR genotyping.

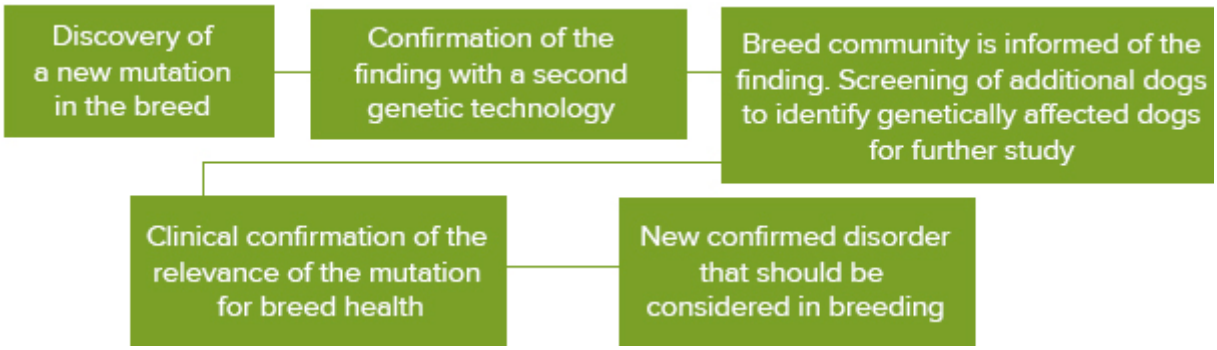

Figure 5. MyDogDNA is a powerful discovery platform for known mutations in new breeds, but new discoveries require a careful validation process to prove that the mutation has clinical significance in the new breeds.

Once the finding has been confirmed, we establish collaborations with dog owners, breeders, breed clubs to screen more dogs for the mutation and to collect more health information on genetically affected dogs. This step involves often also collaboration with veterinarians and academic researchers. The collaborative characterization that follows a new discovery made by the MyDogDNA research team is essential before it can be stated that a mutation is clinically relevant in the breeds. Clinical relevance is needed to provide proper breeding advices.

As a demonstration of our efficient validation process, functional results from a clinical MyDogDNA validation study in Canine Factor VII Deficiency are shown in Figure 6.

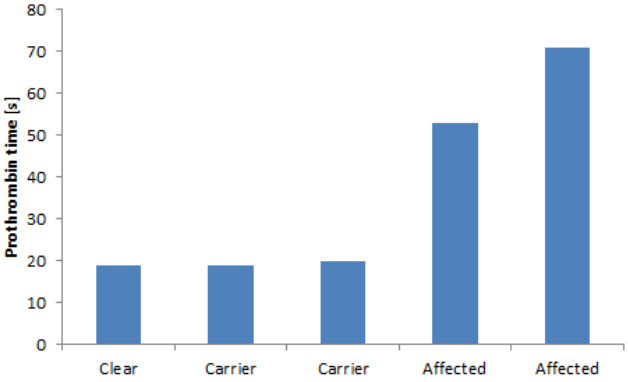

Figure 6. An example of a functional MyDogDNA validation study on Canine Factor VII Deficiency (cFVII) in Welsh Springer Spaniels. The MyDogDNA test identified several Welsh Springer Spaniels carrying the cFVII mutation known to cause a mild to moderate bleeding disorder. The recessively inherited mutation was originally described in Beagles (11). Additional screening of dogs in the breed identified a litter with genetically affected dogs. The litter was recruited for a clinical study to measure blood coagulation time on plasma samples. The functional experiment revealed that genetically "affected" homozygous dogs indeed show 2-3 times linger prothrombin times than their "clear" or "carrier" littermates, indicating a cFVII deficiency. Taken together, the study strongly suggests clinical relevance of the mutation in a novel breed. Further laboratory measurements are in progress in collaboration with scientists originally involved in describing the mutation.

8 Understanding the MyDogDNA test results: pros and cons

MyDogDNA provides the most holistic analysis of a dog's genome available to the general public. In addition, it is a powerful screening tool for discovering known mutations in new breeds. However, it is still important to understand some basic limitations related to the service, obtained results and their potential application in order to avoid unnecessary misconceptions and misinterpretations related to the potential health risks or breeding value of the tested dogs. In essence, it is important to know what the MyDogDNA analysis does, and what it does not do.

First, although the MyDogDNA analysis provides a comprehensive genetic analysis of your dog, it does not test the entire disease heritage of any breed, nor is it a complete health check. This is simply because most disease mutations have not been found yet, and consequently they cannot be tested for yet. Moreover, the most common genetic health issues in breeds are often polygenic. Identification of causative genetic risk factors for polygenic disorders, and application of such information to DNA testing and sustainable breeding, is still a focus of intensive research. For these reasons, genetic testing is currently limited to the set of known disease genes, which unfortunately does not necessarily address the most important health risks of the breed. On another note, efforts of making a panel screen as comprehensive as possible are also complicated by patents restricting the commercial use of certain tests. Taken together, it is not useless to test for as much as possible

despite the limitations described above. The results just have to be understood in a proper perspective of health risks for an individual dog, and breeds.

Second, the MyDogDNA analysis tests only for the listed, previously known, mutation sites in a dog's genome. It does not screen entire disease genes for any other possible mutations. This would require other genetic methods and approaches. Therefore, even if a dog tests clear for all assessed mutations, it is possible that there are other mutations in the same gene elsewhere in the genome that causes the same or a similar disorder, causing a dog to manifest a disorder despite a "clear" test result in MyDogDNA. However, unlike in human in whom tens or hundreds of different mutations in the same gene may cause the same disorder, the strong historical founder effects in dogs are thought to reduce the spectrum of existing mutations (=genetic heterogeneity). Though some notable exceptions exist (e.g. pyruvate kinase deficiency, polyneuropathy, multifocal retinopathy, von Willebrand's disease), the same major mutation underlying a disorder is often spread worldwide within a dog breed, or even across dog breeds.

Third, the MyDogDNA analysis contains over 7000 SNP markers and it could potentially be used as a research tool in genetic association studies to map new disease associations, given availability of proper case and control samples. Although this allows a chance for successful mapping of disease mutations, the marker density is not comparable to e.g. Illumina Canine HD Beadchip array (172 000 markers, 6) commonly used in research.

Fourth, the MyDogDNA analysis does efficiently screen for known mutations across breeds as demonstrated in the pilot study. However, it is important to realize the necessity of the multistep validation process described above (Figure 5) before the significance of the finding for the breed is fully understood.

Finally, the MyDogDNA analysis does open up the door to a completely novel level of real-time reporting that helps us visualize and understand the genetic structure and diversity of individual dogs and breeds. The maintenance and development of the genetic diversity is of utmost importance for maintaining the health, vitality and breeding potential of our breeds. Each breed suffers from a multitude of conditions of varying genetic complexity and it is difficult to control genetic health only by focusing on the control of individual disease mutations in specific conditions. While setting up a breeding program for eradicating a disease, selection may result instead in an increase in frequency of other conditions. Therefore, the development and enrichment of overall allelic architecture remains an important goal in any breed. Breeders should use the latest genetic tools to identify "new blood" or alleles within the breed in different lines or across countries, or use controlled crossbreeding as in the example of Figure 3. The MyDogDNA analysis and database enables this type of understanding of diversity, and its development.

References

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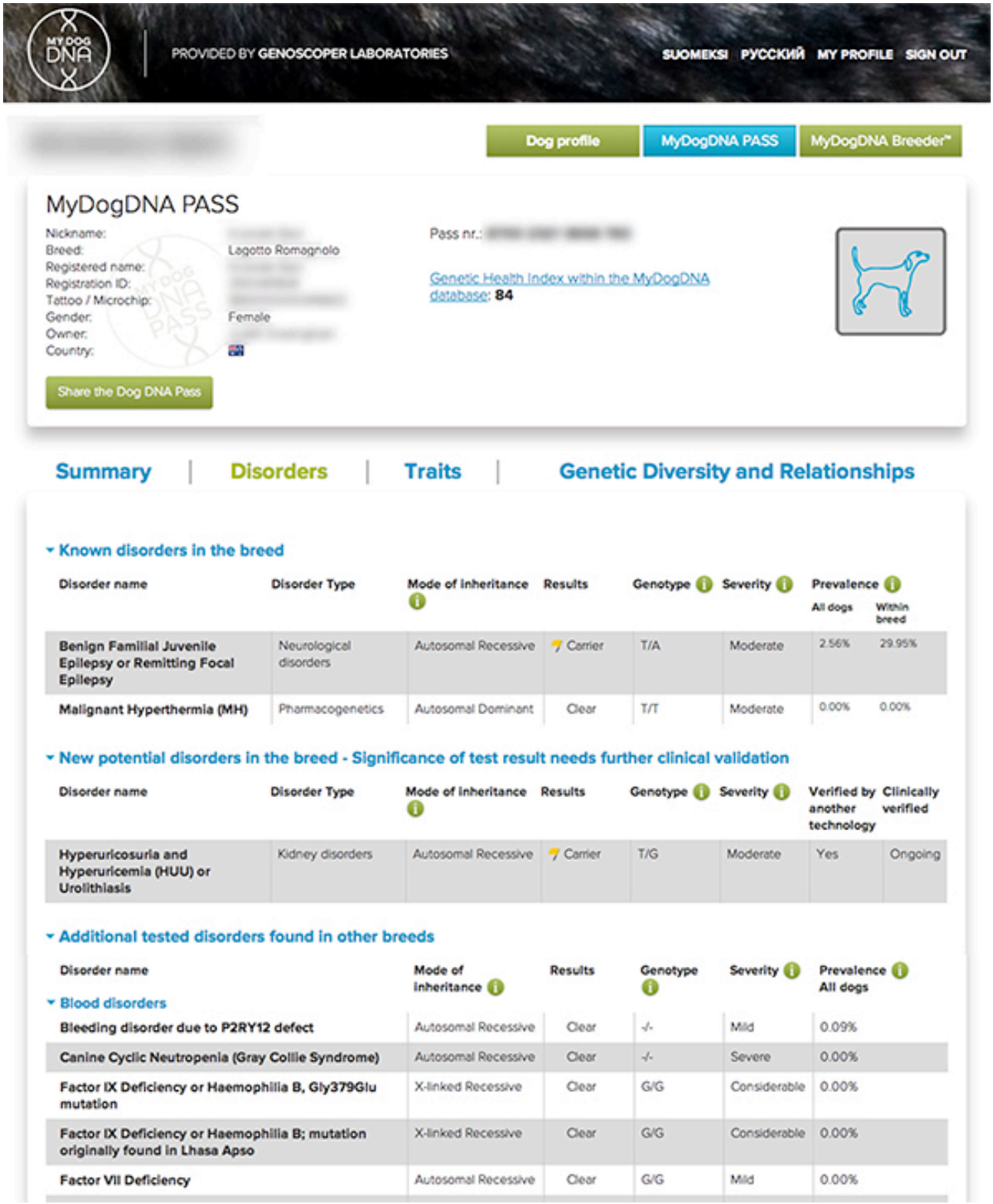
Appendix 1.



Appendix 1. An example of reporting of the test results in the “Disorders” section.