Many direct-to-consumer canine genetic tests can identify the breed of purebred dogs

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OBJECTIVE
To compare pedigree documentation and genetic test results to evaluate whether user-provided photographs influence the breed ancestry predictions of direct-to-consumer (DTC) genetic tests for dogs.

ANIMALS
12 registered purebred pet dogs representing 12 different breeds.

METHODS
Each dog owner submitted 6 buccal swabs, 1 to each of 6 DTC genetic testing companies. Experimenters registered each sample per manufacturer instructions. For half of the dogs, the registration included a photograph of the DNA donor. For the other half of the dogs, photographs were swapped between dogs. DNA analysis and breed ancestry prediction were conducted by each company. The effect of condition (ie, matching vs shuffled photograph) was evaluated for each company’s breed predictions. As a positive control, a convolutional neural network was also used to predict breed based solely on the photograph.

RESULTS
Results from 5 of the 6 tests always included the dog’s registered breed. One test and the convolutional neural network were unlikely to identify the registered breed and frequently returned results that were more similar to the photograph than the DNA. Additionally, differences in the predictions made across all tests underscored the challenge of identifying breed ancestry, even in purebred dogs.

CLINICAL RELEVANCE
Veterinarians are likely to encounter patients who have conducted DTC genetic testing and may be asked to explain the results of genetic tests they did not order. This systematic comparison of commercially available tests provides context for interpreting results from consumer-grade DTC genetic testing kits.

Keywords: genetic testing, direct-to-consumer, canine genetics, breed ancestry, deep learning

Clinical genetic testing is an invaluable tool for human and veterinary medicine.1,2 The study of genetic disease in animal models has a long history, and commercial genetic testing has been used to guide agricultural breeding practices for over 20 years.3 Commercial testing for genetic risk factors has been common for dogs4 for over a decade, and animal genetic testing is a booming industry that is expected to grow over the next 5 years.5 Increasingly, the decision to conduct genetic testing of both humans and companion animals occurs outside of the clinic. Direct-to-consumer (DTC) genetic tests allow consumers to collect a specimen (usually a buccal swab) at home and ship it to the company to be processed, sequenced, and analyzed. The company then returns a report about the individual’s ancestry and, in some cases, the likelihood of possessing genetic traits (eg, hair color) or risk of developing genetic diseases.

With canine genetic testing, ancestry estimates focus on the individual’s breed makeup. Dogs were the first domesticated animal and in the approximately 20,000 years6 since domestication have been specialized for a plethora of phenotypes, such as herding and tracking abilities.7 As a result of these breeding practices, modern dog breeds have significantly higher levels of homozygosity, leading to less genomic variation between individuals of the same breed, and therefore
dog breeds are more easily differentiated than sub-populations of many other species. Individual breeds are associated with distinct genetic signatures, allowing the breed ancestry of a particular dog to be estimated on the basis of the presence of genetic variants associated with specific breeds. Most DTC genetic tests assay single-nucleotide polymorphisms using microarray-based profiling, though some use other genotyping techniques (Table 1). In all cases, the stated goal is to identify genetic variants in an individual dog that are compared to genetic variants sampled from a variety of breeds. The genetic variants are assigned to 1 or more breeds and then deconvolved into measured sources of genetic ancestry. Therefore, these analyses depend on 3 variables: first, the density of markers analyzed; second, the set of breeds included in the reference panel; and third, diversity of individuals from each breed available within the panel. Typically, however, the specific approach used is proprietary, and the consumer receives only a report outlining their dog’s estimated breed ancestry and/or genetic risk variants. As a result, the specifics of how these estimates are made and their accuracy remains largely unknown.

This lack of transparency raises questions, especially in cases in which different tests produce different results. Crowd-sourced DTC dog genetic testing results on Reddit (https://www.reddit.com/r/DoggyDNA) suggest that some dogs receive wildly different breed assignments from different companies, beyond what would be expected on the basis of known methodological differences. One potential source of variation could be that all companies either allow or require the user to upload a photograph of the dog, despite the tests being advertised as being based on genetics only. If the photographic information is incorporated into the breed identification pipeline, it could bias the results. Because most of the dogs whose results are uploaded to the DoggyDNA subreddit are mixed breed, these crowd-sourced results cannot easily be used to compare different companies’ genetic ancestry estimates because there is no ground truth available. Therefore, we sought to assess whether the photograph uploaded with a purebred dog’s DNA sample influenced estimates of their breed ancestry. We considered alternative designs using F1 or F2 dogs with known purebred ancestry but after examining feasibility felt that finding sufficient examples from diverse breed combinations was impractical.

We evaluated the 6 DTC tests on the market at the end of 2021 (when our study began). We recruited 12 purebred dogs and submitted their buccal DNA samples along with a photograph to each company. For half of the dogs, the sample was submitted with a photograph of the DNA donor. For the other half, photos were between dogs so that each DNA sample was submitted with a photograph of a different purebred dog. To evaluate whether the photograph affected ancestry estimation, we checked whether breed predictions matched the donor’s registered breed. We also established a photograph-only baseline using a deep neural network trained to assign dog breeds to photographs. This design allowed us to compare breed ancestry estimation across different platforms.

**Methods**

Dogs were recruited by word of mouth between July and November 2022. Registration eligibility of each dog was confirmed by manually viewing the dog’s breed organization paperwork or locating the dog in the American Kennel Club database. Recruitment was structured to ensure full coverage across dog breed clades. As our goal was to evaluate the influence of photographs, we divided dogs into 2 groups. We considered these groups a control condition, in which the photograph matched the dog, and a treatment condition, in which the photograph was swapped with a different dog in the group. Thus, the term treatment refers to the photo and no treatment was applied to the dogs themselves. Randomization was performed using the RANDBETWEEN() function in Excel (Microsoft Corp.). All enrolled dogs came from different households.

We selected DTC tests that indicated an ability to predict breed that were identified as being available in 2021, when the study was initiated, and that we were able to purchase through our institutional purchasing systems or processes. Direct-to-consumer genetic tests (Table 1) were purchased directly from each company’s website. Kits were registered according to the instructions provided, using the dog’s own photograph (control) or the photograph of a dog paired on the basis of enrollment order (treatment). When the information was requested, dogs were listed as mixed breed. For some companies, this may support a search for additional minor-breed signature differences. Each dog owner was instructed to collect buccal swabs for each kit according to manufacturer instructions and mail the samples using the company-provided packaging. Genetic testing was conducted by each company according to their own protocols. The breed determination results were returned to the investigators and harmonized across

**Table 1:** Comparison of direct-to-consumer canine ancestry identification services. At the time of study design (end of 2021), 6 tests were commercially available.

<table>
<thead>
<tr>
<th>Company</th>
<th>Markers used</th>
<th>Reference panel</th>
<th>Ancestry assignment algorithm</th>
</tr>
</thead>
<tbody>
<tr>
<td>Embark</td>
<td>200,000+ SNPs, microarray</td>
<td>350+ breeds</td>
<td>Unknown</td>
</tr>
<tr>
<td>Wisdom Panel</td>
<td>SNPs, microarray</td>
<td>350+ breeds, 21,000+ samples</td>
<td>BCSYS</td>
</tr>
<tr>
<td>Orivet</td>
<td>SNPs</td>
<td>350+ breeds, 15,000 samples</td>
<td>Unknown</td>
</tr>
<tr>
<td>Darwin’s Ark</td>
<td>688,000 SNPs, whole-genome sequencing</td>
<td>101 breeds</td>
<td>Unknown</td>
</tr>
<tr>
<td>DNA My Dog</td>
<td>Copy-number variants</td>
<td>350+ breeds, 190 samples</td>
<td>SupportMix</td>
</tr>
<tr>
<td>Accu-Metrics</td>
<td>Unknown</td>
<td>300 breeds</td>
<td>Unknown</td>
</tr>
</tbody>
</table>

SNP = Single-nucleotide polymorphism.
studies using the Vertebrate Breed Ontology (VBO) version 20230601.\textsuperscript{27,28} The VBO was created to provide a standardized resource of breed names of many animals, including dogs. If a breed assignment corresponded to a variety rather than a breed, per the Fédération Cynologique Internationale,\textsuperscript{29} the corresponding breed was used instead. Qualitative assignments (ie, ranges of percentages) were converted to numerical values (Supplementary Table S1).

As a positive control for use of the photograph, we also analyzed each sample/photograph pair using a pre-trained convolutional neural network, NASNet, that has shown particularly robust performance for dog breed identification.\textsuperscript{30-32} We loaded the NASNet model NASNetLarge from the Python package PyTorch Image Models (torchvision, version 0.6.12)\textsuperscript{33,34} and used it to classify each of the dog photos, adapting code from a tutorial.\textsuperscript{35} The classifier estimates many categories with a very long tail, so only hits with a score > 1% were included in the analysis.

To evaluate the effect of the photograph on each test’s predictions, the proportion of results matching the registered breed was evaluated using an OR in the R package vcd (The R Project for Statistical Computing).\textsuperscript{36} The Haldane-Anscombe correction\textsuperscript{37} was applied when appropriate.\textsuperscript{38} Independence was assessed with a 1-tailed hypergeometric test. Rejection of the null, corresponding to a P value of < .05, would indicate a potential relationship between condition and outcome.

In a post hoc analysis, we also compared the results to the DNA donor and photograph at the level of breed clade.\textsuperscript{26} For breeds not assigned to a clade,\textsuperscript{26} a determination was made on the basis of the closest genetic relatives assigned. Each predicted breed was classified on the basis of whether it matched the DNA donor, the paired dog’s breed (in the treatment condition, this was also the photo), or neither. Odds ratios and the P values associated with the hypergeometric tests were calculated in R using vcd, and the results were visualized using ternary.\textsuperscript{39}

**Results**

Twelve purebred dogs were recruited from households around the US (Table 2). Most results were returned from the companies between August 2021 and June 2023. Results were not received for 4 samples. One, sent to Darwin’s Ark, was lost, with the company providing updates and offering to replace it. The remaining 3 lost samples were sent to Accu-Metrics, and as of June 2023, no status update could be obtained.

**Mapping to standardized terminologies enables cross-test comparisons**

Test results were usually directly mapped to VBO terms.\textsuperscript{27,28} However, 4 breed estimates mapped ambiguously to terms in the VBO (Supplementary Table S2). In 1 case, the result returned by NASNet (“Lhasa Apso”) was not a known dog breed, so “Lhasa” was assumed to be the intended breed. In the other 3 cases, 2 or more potential VBO terms could correspond to the breed result. For 2 cases, VBO developers were consulted to select the best mapping. The last ambiguous breed estimate was Catahoula Leopard Dog (DNA My Dog, estimated for German Shorthaired Pointer [GSP] DNA submitted with an Italian Greyhound photo). The Catahoula Leopard Dog is a breed with a complex history that could correspond to 3 VBO entries. However, as this result was returned only by 1 test for 1 dog, we selected the closest VBO term to the exact phrasing used in the breed result. The translation of qualitative to quantitative results is provided in Supplementary Table S1, and the standardization of NASNet’s predictions are shown in Supplementary Table S3.

Another difference in the way results were reported across tests was that Darwin’s Ark provided a 2-component breed prediction. As Darwin’s Ark evaluates ancestry and genetic diversity separately, they provided not only the most genetically similar breeds but also explicitly predicted whether each dog was purebred. We used their determinations of breed, rather than the ancestry percentages (Figure 1), to assess whether Darwin’s Ark’s result matched the registered breed (Table 3). Of the 11 samples for which results were returned, Darwin’s Ark identified all donors as purebred, even if some ancestry was resolved to another breed.

**Table 2**—Background information on the 12 canine participants.

<table>
<thead>
<tr>
<th>Breed</th>
<th>VBO identifier</th>
<th>Breed clade</th>
<th>Registry organization</th>
<th>Condition</th>
<th>Photograph</th>
</tr>
</thead>
<tbody>
<tr>
<td>Beagle</td>
<td>VBO:0200131</td>
<td>Scent Hound</td>
<td>UKC</td>
<td>Control</td>
<td>Self</td>
</tr>
<tr>
<td>Border Terrier</td>
<td>VBO:0200194</td>
<td>Terrier</td>
<td>AKC</td>
<td>Control</td>
<td>Self</td>
</tr>
<tr>
<td>Golden Retriever</td>
<td>VBO:0200610</td>
<td>Retriever</td>
<td>AKC</td>
<td>Control</td>
<td>Self</td>
</tr>
<tr>
<td>Pomeranian</td>
<td>VBO:0201043</td>
<td>Small Spitz</td>
<td>AKC</td>
<td>Control</td>
<td>Self</td>
</tr>
<tr>
<td>Shetland Sheepdog</td>
<td>VBO:0201217</td>
<td>UK Rural</td>
<td>AKC</td>
<td>Control</td>
<td>Self</td>
</tr>
<tr>
<td>Shih Tzu</td>
<td>VBO:0201223</td>
<td>Asian Toy</td>
<td>CKC</td>
<td>Control</td>
<td>Self</td>
</tr>
<tr>
<td>Brittany</td>
<td>VBO:0200238</td>
<td>Pointer/Setter</td>
<td>AKC</td>
<td>Treatment</td>
<td>Chinese Crested</td>
</tr>
<tr>
<td>Chinese Crested</td>
<td>VBO:0200345</td>
<td>American Toy</td>
<td>AKC</td>
<td>Treatment</td>
<td>Brittany</td>
</tr>
<tr>
<td>German Shorthaired Pointer</td>
<td>VBO:0200583</td>
<td>Pointer/Setter</td>
<td>AKC</td>
<td>Treatment</td>
<td>Italian Greyhound</td>
</tr>
<tr>
<td>Italian Greyhound</td>
<td>VBO:0200713</td>
<td>UK Rural</td>
<td>AKC</td>
<td>Treatment</td>
<td>German Shorthaired Pointer</td>
</tr>
<tr>
<td>Bulldog</td>
<td>VBO:0200258</td>
<td>European Mastiff</td>
<td>AKC</td>
<td>Treatment</td>
<td>Labrador Retriever</td>
</tr>
<tr>
<td>Labrador Retriever</td>
<td>VBO:0200800</td>
<td>Retriever</td>
<td>AKC</td>
<td>Treatment</td>
<td>Labrador Retriever</td>
</tr>
</tbody>
</table>

All dogs were registered with a breed organization. Breed clade was assigned on the basis of phylogeny\textsuperscript{14} as opposed to the breed groups used by breed organizations such as the American Kennel Club.

AKC = American Kennel Club. CKC = Continental Kennel Club. UKC = United Kennel Club. VBO = Vertebrate Breed Ontology.
Figure 1—Breed ancestry predictions from 6 direct-to-consumer dog genetic testing companies as well as a pre-trained image classifier. For the control condition, the breeds of the donor and photograph match, so the registered breed is depicted as purple. In the treatment condition, these are separated into blue (DNA donor) and red (photographed breed). All other breeds are represented in other colors as identified in the legend.
Artificial intelligence–based prediction with canine photographs was accurate with breeds included in training

The neural network NASNet was, as expected, unable to predict DNA donor breed in the treatment condition, in which the photograph and DNA sample did not match (Figure 1). While the neural network was often able to correctly identify the registered breed of the dog in the photographs it was provided, it sometimes identified breeds that were neither the DNA donor nor the photographed dog. This pattern was likely influenced by the limited number of breeds in the training data, and thus category labels, used by ImageNet. For example, ImageNet does not include the Chinese Crested and Bulldog breeds, and therefore NASNet also failed to identify these breeds (Figure 1; Supplementary Table S4).

Most tests accurately reflected purebred dogs’ registered breeds

For all dogs, the registered breed was always the majority estimate across tests (Figure 1; Supplementary Table S4). However, most tests did not match every dog with its registered breed at 100%. This primary outcome, selected a priori (Table 3), therefore did not capture apparent qualitative differences in breed predictions. In several cases, the breeds predicted by a test matched neither the DNA nor the photograph. This pattern was particularly apparent for both the image classifier and 1 DTC genetic test (ViaPet by Accu-Metrics). In the case of this genetic test, this pattern may have been influenced by the fact that the test predicted the registered breed zero times across both the control and treatment conditions.

Reevaluating the results at the level of breed clades (Figure 2) suggested potential explanations for results.

Table 3—Comparison of predictions from direct-to-consumer genetic tests and pretrained image classifier (NASNet) against the registered breed of each dog. Estimates were recorded as a match only when there was 100% concordance.

<table>
<thead>
<tr>
<th>Breed prediction approach</th>
<th>Overall results matching breed</th>
<th>Control matching</th>
<th>Treatment matching</th>
<th>Odds ratio (P)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wisdom Panel</td>
<td>12/12 (100%)</td>
<td>6/6 (100%)</td>
<td>6/6 (100%)</td>
<td>1.0 (1.00)</td>
</tr>
<tr>
<td>Darwin’s Ark</td>
<td>11/11 (100%)</td>
<td>6/6 (100%)</td>
<td>5/5 (100%)</td>
<td>1.2 (1.00)</td>
</tr>
<tr>
<td>Embark</td>
<td>10/12 (83%)</td>
<td>5/6 (83%)</td>
<td>5/6 (83%)</td>
<td>1.0 (.773)</td>
</tr>
<tr>
<td>DNA My Dog</td>
<td>8/12 (67%)</td>
<td>4/6 (67%)</td>
<td>4/6 (67%)</td>
<td>1.0 (.727)</td>
</tr>
<tr>
<td>Orivet</td>
<td>7/12 (58%)</td>
<td>3/5 (60%)</td>
<td>4/7 (57%)</td>
<td>1.1 (6.689)</td>
</tr>
<tr>
<td>NASNet</td>
<td>2/12 (17%)</td>
<td>2/6 (33%)</td>
<td>0/6 (0%)</td>
<td>7.2 (.227)</td>
</tr>
<tr>
<td>Accu-Metrics</td>
<td>0/9 (0%)</td>
<td>0/4 (0%)</td>
<td>0/5 (0%)</td>
<td>1.2 (1.00)</td>
</tr>
</tbody>
</table>

Note that for Orivet, the conditions were not balanced because, due to experimenter error, 1 control subject (Golden Retriever) was submitted with 2 photographs (the photograph of the DNA donor and of the Pomeranian). Also, due to sample loss, only 11 dogs were tested using Darwin’s Ark and 9 for Accu-Metrics versus 12 for the other tests.

Figure 2—Ternary plots identifying the breed clades of results predicted by each test. Each dog is represented by a circle in blue (control) or red (treatment). The position of the circle relative to the 3 axes indicates the percentage of results belonging to the breed clade of the DNA donor, photographed dog, or other clades. A result that is 100% concordant with the DNA donor’s registered breed will be placed at the apex of the triangle. A result that is 100% concordant with the photographed dog’s breed (in the treatment condition only) will be located at the top left. Offset from these positions can be interpreted by looking at the position relative to the other 2 vertices on a 0 to 100 scale. Darker colors indicate multiple circles mapping to the same position.
that matched the breed of neither the DNA donor nor the photograph. When the tests were evaluated on the basis of whether they predicted any breed in the same clade as the DNA donor at any percentage, NASNet performed with 100% accuracy in the control condition and 0% accuracy in the treatment condition, corresponding to an OR of 13 (Supplementary Table S5). Accu-Metrics identified breeds in the same clade as the donor twice in the control condition and zero times in the treatment condition, corresponding to an OR of 11. However, these results are only suggestive, as neither met our predefined threshold for significance. Given that NASNet assigned breeds solely on the basis of the photograph, it was expected to incorrectly predict the treatment samples (which had shuffled photos). The fact that a similar effect was observed for predictions made by Accu-Metrics suggests that the photograph may have also influenced breed predictions made by this DTC genetic test.

**Discussion**

Applying an experimental paradigm to evaluate DTC canine genetic tests revealed qualitative and quantitative differences in the breed ancestry estimates from 6 companies. By modulating whether DNA was submitted with a matched or mismatched photograph, we assessed whether this nongenetic information influenced breed predictions. In complement, a pretrained convolutional neural network, NASNet, provided a baseline of predictions made from the photograph alone. Ultimately, this analysis revealed a low rate of consensus across tests in estimating the breed makeup, even of registered purebred dogs, and suggested that at least 1 company is influenced by the photograph provided.

Both NASNet and Accu-Metrics were unlikely to identify the registered breed as 100% of the ancestry, regardless of condition. When breed ancestry estimates were evaluated at the clade level, there were elevated odds that the clades of the breeds predicted by these 2 tests matched the photograph rather than the DNA donor (Figure 2). For NASNet, which is an image recognition tool, this result was expected; however, Accu-Metrics requires a DNA sample. The lack of a relationship between the company’s breed predictions and the provided DNA samples suggests issues with the accuracy of the company’s tests.

In overall performance, Accu-Metrics was less successful in predicting a dog’s breed than NASNet, with an overall rate of 0% versus 17% (Table 3). NASNet may have had even higher performance if more breeds were included in its training dataset, given that it did not have any point of reference for some of the breeds examined in this study (eg, Chinese Crested). The Chinese Crested photograph was, incidentally, the only photograph that Accu-Metrics identified as 100% matching the registered breed of the photographed dog (Supplementary Table S4); in this case, however, the photograph of the Chinese Crested was submitted along with DNA from a Brittany.

Among the remaining 5 DTC testing services, the rate of predicting the registered breed of the DNA donor was very high, regardless of the condition. This result suggests that these companies are analyzing DNA as the basis for their breed ancestry predictions. Additionally, we did not find any evidence that the photographed breed (or its close relatives) were disproportionately likely to be included in the predictions. All the same, these 5 tests often differed in their breed predictions, and among the 12 purebred dogs tested, some received more consistent predictions than others. For more than half of the dogs, there was consensus among these 5 DTC genetic tests (excluding Accu-Metrics) about their breed (Table 3). Among the others, though the registered breed was always the major ancestry estimate from each of the 5 DTC tests, they often differed in what other breeds were predicted to contribute to ancestry.

While it is interesting to explore differences in their predictions, it is important to note that this study was not designed to evaluate the accuracy of the tests’ genetic ancestry predictions. Pedigrees are not infallible, and therefore mistaken parentage could be a source for some of this variation. For example, in the case of the Labrador Retriever tested here, Embark and Darwin’s Ark both predicted that she carried approximately 5% non-Labrador DNA, suggesting admixture approximately 5 generations ago. This result is plausible within breeding and registration practices; the higher-resolution markers used by these tests may be revealing present but minor ancestries or that annotating purebred dogs as a mixed breed is inducing a source of error in testing. Therefore, even with the ground truth provided by using registered dogs, some sources of genetic variation are difficult to determine. Wisdom Panel returned a prediction that matched the DNA donor’s registered breed 100% of the time, but this does not mean it is more accurate than the other 4 tests. Differences among tests, such as the number of markers analyzed (Table 1) are expected to contribute to differences in test resolution and breed prediction capabilities. Additionally, the specific breeds and specific dogs included in a company’s reference panel can have a strong effect on breed assignment. Importantly, these results underscore the complexity of using genetic ancestry to infer membership in a socially defined population (ie, breed).

These results highlight some of the challenges in developing genetic tools for genetic prediction of breed. As an example, tests that identified the GSP as having 100% GSP ancestry were more commercially popular than the tests that identified mixed ancestry. This pattern could arise if some of the genetic variants the dog carries have not been sampled for the GSP reference panels used by the smaller companies (ie, ascertainment bias). In another example of disagreement in breed estimation, DNA My Dog was alone in reporting that the purebred Bulldog had 10% to 20% wolf ancestry. This result would be consistent with a full wolf ancestor 3 generations ago. While not all tests evaluate the genome for non-dog contributions, Embark, Wisdom Panel, Orivet, and DNA My Dog all do. Therefore, it would be surprising for all the other tests to miss such a high percentage of wolf
ancestry. One possible explanation is that DNA My Dog uses copy number variation, whereas the other tests use single-nucleotide polymorphisms (Table 1). It is well known that different genetic tools can paint different pictures of a population’s history. However, a recent media report indicated that DNA My Dog failed to identify the species of a sample, assigning dog breeds to human DNA. While our analysis provides evidence that the company did sequence the DNA samples we submitted, it is possible that other issues (e.g., contamination) could cause issues in both species identification and breed prediction.

This analysis demonstrates the complexity of and lack of standardization in the DTC dog genetic testing market. In the case of Accu-Metrics, the results we received appeared to be independent of the DNA submitted. Unfortunately, the average consumer is unlikely to have the necessary information or training to critically evaluate such aspects when selecting a DTC genetic test.

Dog breed ancestry can have social and economic consequences. Many home insurance companies refuse to cover certain dog breeds such as Pitbulls (e.g., American Staffordshire Terriers) and Rottweilers. In our current sample of 12 purebred dogs (none of which are banned by more than 5% of insurance companies), 4 dogs were identified by at least 1 test as having ancestry banned by more than 50% of home insurance companies. DNA My Dog identified the Bulldog as a wolf hybrid and the Beagle as part Rottweiler. Accu-Metrics identified both the GSP and Golden Retriever as part American Staffordshire Terrier. Dog owners using these tests to establish ancestry could face financial repercussions in terms of home insurance and even housing rental eligibility if the results of a DTC test are viewed as definitive. Given that DTC genetic services are being used by some rental companies for pet waste identification, it is not difficult to envision landlords conducting or requiring breed testing as well. Additionally, it is legal for companies to decline to insure or to raise premiums for dog owners who they believe own a restricted breed. While insurance companies do not typically require DNA tests, some sources advise renters and homeowners to submit their dog’s results if they believe they were erroneously rejected for coverage. While breed discrimination in renting and insurance is controversial, unreliable breed ancestry tests will only serve to further muddy an already complicated issue.

For more than a decade, concerns have been raised about the potential pitfalls of human DTC genetic testing, especially when combined with limited regulatory oversight. Now, veterinary medicine faces related issues. Our systematic comparison of DTC genetic testing for dogs suggests that consumers must approach DTC test results with caution. Veterinarians are likely to be placed in a position where they need to educate pet owners about genetic tests that the veterinarians did not order or recommend. This study shows that breed predictions from at least 1 vendor can be at odds with the dogs’ pedigree registration, even for American Kennel Club–registered dogs (10 out of the 12 participants). As DTC testing for pets becomes increasingly popular, veterinarians may face increasing calls to educate owners about the limits of genetic testing.

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References


**Supplementary Materials**

Supplementary materials are posted online at the journal website: avmajournals.avma.org.

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