Comparison of Adoption Agency Breed Identification and DNA Breed Identification of Dogs

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Comparison of Adoption Agency Breed Identification and DNA Breed Identification of Dogs

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Governmental and other agencies may require dog caregivers (owners) to provide breed identification of their dogs. This study compares breed identification by adoption agencies with identification by DNA analysis in 20 dogs of unknown parentage. Of the 20 dogs who had been adopted from 17 different locations, the study identified 16 dogs as having (or probably having) 1 or 2 specific breed(s) in their ancestry. DNA analysis of these dogs indicated that 25% (4/16) did in fact contain genetic evidence of an adoption agency’s identified breed as one of the predominant breeds in a dog’s ancestry. DNA analysis did not detect all specified breeds in 14 of these dogs. That is, 87.5% of the dogs identified by an adoption agency as having specific breeds in their ancestry did not have all of those breeds detected by DNA analysis. The discrepancies between opinions of adoption agencies and identification by DNA analysis suggest that it would be worthwhile to reevaluate the reliability of breed identification as well as the justification of current public and private policies pertaining to specific dog breeds.

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In the past few decades, influential papers have ranked breeds of dogs identified as responsible for bites, serious injuries, and fatalities of people (Gershman, Sacks, & Wright, 1994; Sacks, Sattin, & Bonzo, 1989; Sacks, Sinclair, Gilchrist, Golab, & Lockwood, 2000; Schuller, DeBess, Lapidus, & Hedberg, 2008; Wright, 1985). With the intent of reducing harm to people and property, landlords, housing associations, governments, and insurance agencies have enacted breed-specific regulations that prohibit ownership of, or impose constraints on, ownership of specific breeds or mixed breeds (Bandow, 1996; Ledger, Orihel, Clarke, Murphy, & Sedlbauer, 2005). One source of information regarding the possible breed composition of dogs is a dog adoption facility or service. This study was undertaken to compare breed identification of dogs of unknown parentage by adoption agencies with identification by DNA analysis.

**MATERIALS AND METHODS**

The Institutional Animal Care and Use Committee at Western University of Health Sciences reviewed and approved the protocol for this study. Faculty, staff, and students in the College of Veterinary Medicine at Western University of Health Sciences were sent an email by the investigators offering them the opportunity to participate in a dog breed-identification study. Caregivers (owners) were asked to fill out an application form requesting the following information: age, size, sex, weight, and source of dog; in addition, they were asked how the breed had been identified. Of the 50 dogs who were volunteered, 40 met the entrance criteria of (a) being mature enough to have fully erupted canine teeth; (b) being obtained from a shelter, rescue, or animal control or similar adoption agency; and (c) being available to have blood drawn on a specific day. The 40 dogs were assigned to one of 4 weight ranges: <20 lb, 21–40 lb, 41–60 lb, and >60 lb. The study enrolled 5 dogs, randomly selected from each weight range.

On the day the blood sample was taken, the owners were asked how old their dogs were when acquired from the adoption agency and, again, how the adoption agency had identified the dog. The dogs were also weighed. All dogs were within the weight ranges provided by the owners.

Two ml of blood were drawn from each dog, transferred to heparinized test tubes, and immediately refrigerated. Later that day, the blood samples were boxed with cold packs and sent overnight to the processing/analyzing laboratory (MARS VETERINARY™, Lincoln, NE 68501), where the DNA analyses were performed. All breeds of dogs identified by the adoption agencies were in the MARS Wisdom Panel™ DNA database. DNA contributions from ancestral breeds that are less than 12.5% are not reported (Markwell, 2007).
The Mars Veterinary Wisdom Panel MX™ utilizes a set of 300 known genetic markers called single nucleotide polymorphisms to assess the breed compositions in a DNA sample submitted for testing. The polymorphic markers were selected from a set of more than 13,000 references, dogs from more than 130 American Kennel Club registered breeds obtained from the United Kingdom and the United States (Jones et al., 2008). The assignment of breed mixtures is based on a statistical model that infers ancestral breeds from the pattern of alleles across the set of 300 markers. The study determined strength of match to each breed signature by using a maximum likelihood model that quantifies the percentage of the marker panel that matches each breed. In 2007, the Wisdom Panel MX™ reported “an average of 84% accuracy in first-generation crossbred dogs of known parentage” (WISDOM Panel™ Analysis Summary, 2007). The positive predictive value (True Positives/True Positives + False Positives) defines the accuracy measure (Jones et al., 2008; Markwell, 2007).

RESULTS

Twenty dogs entered the study (Table 1). There were 12 spayed females, 1 intact female, and 7 castrated males. Their ages ranged between 5.5 months and 12 years—with an average age of 4.6 years. The dogs had been acquired between 6 weeks and 5 years of age and between 2.5 months and 11.5 years prior to this study. They had been adopted on different days and from 17 different agencies.

The adopting agencies identified all dogs as mixed breeds. Sixteen dogs had been described by specific breed(s). Three of these 16 had two breeds indicated. Five dogs were identified by “type” (two shepherd mixes and three terrier mixes). One dog (Number 1) had been identified as both a specific breed (Chow Chow) and a “type” (terrier).

This report classified DNA detectable breeds as either “Predominant” or “Less Dominant,” dependent on which breed(s) comprised highest reportable percentage. For example, in Dog 1, the highest percentage of any identified breed is 25% and there are two breeds in this percentage group; therefore, both are classified as most predominant breeds identified. A third breed is identified at 12.5% and is called a less dominant breed. In Dog 2, four breeds are identified at 25% each; in this case, all four breeds are classified as most predominantly identified breeds. The highest percentage of any breed identified in Dog 5 is 12.5%; therefore, all five of the breeds are classified as most predominant breeds identified.

The percentage of DNA identified breeds usually does not add up to 100% of the dogs’ makeup. This is likely because the dogs have highly mixed ancestral breeds that now are below the reportable 12.5% detection limit or have ancestral stock who never were purebreds.
TABLE 1  
Signalment, Adoption Agency Identification, DNA Breed Identification

<table>
<thead>
<tr>
<th>Dog ID #</th>
<th>Sex</th>
<th>Approximate Age at Time of Study</th>
<th>Breed or “Type” Identification by Adoption Agency</th>
<th>Approximate Age When Adopted</th>
<th>Percentage of DNA Identification of Predominant Breed(s)/Highest Percentage of Breed Makeup</th>
<th>DNA Identification of Less Dominant Breed(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>FS</td>
<td>3 years old</td>
<td>“Terrier”/Chow Chow</td>
<td>7.5 months</td>
<td>American Staffordshire Terrier (25%) Saint Bernard (25%)</td>
<td>Shar-Pei (12.5%)</td>
</tr>
<tr>
<td>2</td>
<td>FS</td>
<td>9 years old</td>
<td>Cocker Spaniel</td>
<td>5 years</td>
<td>Rottweiler (25%) American Eskimo Dog (25%) Golden Retriever (25%) Nova Scotia Duck-Tolling Retriever (25%)</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>MC</td>
<td>5 years old</td>
<td>Border Collie</td>
<td>7 weeks</td>
<td>English Springer Spaniel (25%) German Wirehaired Pointer (25%)</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>MC</td>
<td>2.5 years old</td>
<td>“Shepherd”</td>
<td>11 weeks</td>
<td>Lhasa Apso (25%)</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>FS</td>
<td>12 years old</td>
<td>German Shepherd/Labrador</td>
<td>1 year</td>
<td>German Shepherd (12.5%) Australian Shepherd (12.5%) Siberian Husky (12.5%) Chow Chow (12.5%) Dalmatian (12.5%)</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>FS</td>
<td>5 years old</td>
<td>Labrador</td>
<td>2 years</td>
<td>Chow Chow (12.5%) Dachshund (12.5%) Nova Scotia Duck-Tolling Retriever (12.5%)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Age</td>
<td>Breed</td>
<td>Age</td>
<td>Mixed Breeds (%)</td>
<td></td>
</tr>
<tr>
<td>----</td>
<td>----</td>
<td>------</td>
<td>----------------------------</td>
<td>------</td>
<td>--------------------------</td>
<td></td>
</tr>
</tbody>
</table>
| 7  | MC | 10 months old | Corgi | 3 months | Pomeranian (12.5%)  
|    |    |      |     | | Tibetan Terrier (12.5%)  
|    |    |      |     | | Shih Tzu (12.5%)  
|    |    |      |     | | Black Russian Terrier (12.5%)  
|    |    |      |     | | American Water Spaniel (12.5%) |
| 8  | FS | 2 years old | German Short-Haired Pointer | 5 months | French Bull Dog (25%)  
|    |    |      |     | | Chow Chow (25%)  
|    |    |      |     | | Great Dane (12.5%)  
|    |    |      |     | | Gordon Setter (12.5%)  
|    |    |      |     | | Dalmatian (12.5%)  
|    |    |      |     | | Clumber Spaniel (12.5%)  
|    |    |      |     | | Boxer (12.5%)  
|    |    |      |     | | Chow Chow (12.5%)  
|    |    |      |     | | New Foundland (12.5%)  
| 9  | FS | 7 years old | “Terrier” | 3 months | Dalmatian (25%)  
|    |    |      |     | |  
| 10 | MC | 5.5 years old | Silky Terrier | 3.5 years | Pekingese (25%)  
|    |    |      |     | | Australian Shepherd Dog (25%)  
| 11 | MC | 3 years old | Chow Chow | 6 weeks | German Shepherd Dog (25%)  
|    |    |      |     | | American Staffordshire Terrier (25%)  
| 12 | FS | 1.5 years old | “Shepherd” | 1 year | Boxer (12.5%)  
|    |    |      |     | | Dalmatian (12.5%)  
|    |    |      |     | | Dachshund (12.5%)  
|    |    |      |     | | Glen of Imaal Terrier (12.5%)  
|    |    |      |     | | Australian Shepherd Dog (12.5%)  
| 13 | MC | 3.5 years old | Australian Shepherd Dog | 4 months | Alaskan Malamute (12.5%)  
| 14 | FS | 3.5 years old | Australian Shepherd Dog | 3 months | Standard Schnauzer (25%)  
|    |    |      |     | | German Shepherd Dog (25%)  
|    |    |      |     | | English Setter (12.5%)  

(continued)
<table>
<thead>
<tr>
<th>Dog ID #</th>
<th>Sex</th>
<th>Approximate Age at Time of Study</th>
<th>Breed or “Type” Identification by Adoption Agency</th>
<th>Approximate Age When Adopted$^a$</th>
<th>Percentage of DNA Identification of Predominant Breed(s)/Highest Percentage of Breed Makeup</th>
<th>DNA Identification of Less Dominant Breed(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>15</td>
<td>FS</td>
<td>7 years old</td>
<td>Labrador</td>
<td>5 years</td>
<td>St. Bernard (12.5%) Gordon Setter (12.5%) Chow Chow (12.5%) Golden Retriever (12.5%)</td>
<td></td>
</tr>
<tr>
<td>16</td>
<td>F</td>
<td>5.5 months old</td>
<td>Australian Shepherd Dog/Labrador</td>
<td>3 months</td>
<td>Australian Shepherd Dog (12.5%) Boxer (12%) Golden Retriever (12.5%)</td>
<td></td>
</tr>
<tr>
<td>17</td>
<td>FS</td>
<td>2 years old</td>
<td>King Charles Spaniel Mix</td>
<td>1 year</td>
<td>Cavalier King Charles Spaniel (12.5%) Chihuahua (12.5%) Shih Tzu (12.5%)</td>
<td></td>
</tr>
<tr>
<td>18</td>
<td>FS</td>
<td>10 months old</td>
<td>Miniature Pinscher/ Poodle “Terrier”</td>
<td>3 months</td>
<td>Miniature Pinscher (50%)</td>
<td>Dachshund (12.5%)</td>
</tr>
<tr>
<td>19</td>
<td>FS</td>
<td>12 years old</td>
<td>“Terrier”</td>
<td>6 months</td>
<td>Border Collie (25%)</td>
<td>Cocker Spaniel (12.5%) Bassett Hound (12.5%) Pekingese (12.5%) Cocker Spaniel (12.5%) Miniature Schnauzer (12.5%)</td>
</tr>
<tr>
<td>20</td>
<td>MC</td>
<td>6 years old</td>
<td>Tibetan Terrier</td>
<td>5 years</td>
<td>Shih Tzu (25%)</td>
<td></td>
</tr>
</tbody>
</table>

*Note. FS = female spay; MC = male castrate; F = female intact.*

*Approximate age when adopted and identified by adoption agency.*
Table 1 contains background information of the dogs and breed identification by the adoption agencies and DNA analyses. Dogs in whom there is agreement between the adoption agencies identification and DNA identification of most predominant breed(s) are shown in Table 2.

There are several ways to organize these results; readers can examine the raw data and tabulate variables they find interesting. Owners of mixed breeds are often asked to provide information as to the predominant genetic makeup of their dog. For example, “What kind of dog is it, mostly?” Therefore, an interesting relationship to examine is the relationship between what owners were told was (or likely was) the breed makeup of their dog and the most predominant breed identified by DNA analysis. It is also interesting to examine if there is any agreement between adoption agencies’ speculations and DNA analyses.

Of the 16 dogs the adoption agency identified only by specific breed, 4 dogs (5, 16, 17, and 18) are also identified by DNA as having those breeds as one of the most predominant in their ancestry (Table 2). Therefore, there is an agreement between the adoption and DNA identification of a predominant breed.

### Table 2

<table>
<thead>
<tr>
<th>Dog ID #</th>
<th>Adoption Agency Identification of Breed(s)</th>
<th>Adoption Identification by &quot;Type&quot; of Breed(s)</th>
<th>Most Predominant Breed(s) Identified by DNA Analysis That Were in the &quot;Type&quot; Identified by Adoption Agency</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>&quot;Terrier&quot;</td>
<td>YES American Staffordshire Terrier (25%)</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>German Shepherd Dog/Labrador</td>
<td>YES German Shepherd Dog (12.5%)</td>
<td></td>
</tr>
<tr>
<td>12</td>
<td>&quot;Shepherd&quot;</td>
<td>YES Australian Shepherd Dog (12.5%)</td>
<td></td>
</tr>
<tr>
<td>16</td>
<td>Australian Shepherd Dog/Labrador</td>
<td>YES Australian Shepherd Dog (12.5%)</td>
<td></td>
</tr>
<tr>
<td>17</td>
<td>King Charles Spaniel</td>
<td>YES King Charles Spaniel (12.5%)</td>
<td></td>
</tr>
<tr>
<td>18</td>
<td>Miniature Pinscher/Poodle</td>
<td>YES Miniature Pinscher (50%)</td>
<td></td>
</tr>
</tbody>
</table>
25% of the time. In 3 of these 4 dogs, the matching DNA identification comprises only 12.5% of the dog. These 3 dogs are also comprised of several other breeds (also at 12.5% of composition) that were not mentioned by the adoption agencies.

There is an agreement between DNA detection of a less dominant breed and adopter identification in one of these 16 dogs (Dog 11). Therefore, in 31% of the dogs identified by an adoption agency, DNA analysis detected the named breeds somewhere in the dogs’ ancestry.

In this sample, there does not appear to be a relationship between the age of the dog (and breed identification) at the time of adoption and DNA identification. Discrepancies between adoption and DNA identification occur in dogs several years old as well as very young puppies.

Fourteen of the 16 dogs (87.5%) identified by agencies as having one or two specific breeds in their ancestry did not have each of those breeds detected by DNA analysis as either a predominant or less predominant breed. Fifteen of these 16 dogs (93.75%) did not have the specified breeds detected as the most predominant breeds by DNA analysis.

Five dogs were identified by the adoption agencies by a generic “type”: 3 “terriers” (Dogs 1, 9, 19) and 2 “shepherds” (Dogs 4 and 12). DNA analysis indicates that 2 of these 5 dogs do contain a breed categorized within those types. Dog 1 is 25% American Staffordshire Terrier, and Dog 12 is 12.5% Australian Shepherd dog. Therefore, classification by type is corroborated by DNA analysis 40% of the time. If, however, “shepherd” was meant to be German Shepherd Dog, then classification by type is only corroborated by DNA analysis for 20% of the dogs.

**DISCUSSION**

Unless a dog is a registered purebred or the known offspring of a registered dog, it varies considerably who determines a mixed-breed dog’s composition and how the decision is reached. Dog trainers, groomers, animal control officers, veterinary medical personnel, and victims or witnesses of dog bites are often asked to assign a breed, or predominant breed, to a dog. When dog-bite statistics are compiled, the identity of the dog could have been assigned by anyone. If people are unsure what breed a dog is, they may be forced to guess and generate “the breed the dog looks most like” to them. A dog adopted from a shelter or adoption agency usually comes with a probable breed composition or type assigned, be it from a previous owner or the shelter/rescue staff. It is not unreasonable to assume that thereafter this becomes how the dog may be identified.

This study cannot be interpreted to suggest that personnel at adoption agencies do not know what purebred dogs look like or that they are worse at identifying
breeds of dogs than other people who work in dog-related professions. More than 44 years ago, Scott and Fuller (1965) published pictures demonstrating that the phenotypic morphology (what a dog looks like) of a mixed-breed dog may not resemble either one of the parents. Yet, insurance company forms, animal control registration, veterinary medical and hospital records, bite reports, and surveys frequently require a “forced choice” breed identification. Subjective breed identification by a wide range of people have been collected as factual data and subsequently used to enact breed-specific legislation to establish insurance guidelines and housing regulations. This study and those of Scott and Fuller indicate that the information on which these actions are based is highly likely to be inaccurate.

Presently, accuracy of DNA identification of breeds is not perfect either. The design of this study does not allow one to conclude that the commercial breed test used in this study is necessarily a gold standard that always accurately identifies the ancestral breed heritage for all mixed-breed dogs; nor does the company that performs the test claim to be 100% valid (Jones et al., 2008; Markwell, 2007). Furthermore, different companies performing canine DNA analyses may report different results; this depends on which dogs were used to form the reference-breed standards; in addition, laboratories’ statistical genetic algorithms and computer programs may analyze samples differently (Kochan, 2008).

Genetic basis for breed identification lies in the frequency and ordering of specific combinations of polymorphic nucleotides in the canine genome that are shared by members of the registered purebred dogs used to establish the database. Because sexual reproduction results in only subsets of the parental chromosomes passed to offspring, the ability to interpret the genetic test in the context of breed must rely on statistical models that assign a specific breed to particular portions of the mixed-breed genome being tested. As the number of different breeds in a mixed-breed dog increase, the ability of the test to identify any breed decreases. Furthermore, because different breeds of dog share common ancestry with some breeds and not others, it is possible that two dogs with similar genetic profiles may be classified as having ancestors of the same breed, even if the two dogs do not. Furthermore, as the companies performing DNA breed analyses add more breeds to their databases and refine their identification processes, it is possible that an individual dog might generate different ancestral reports at separate points in time.

**CONCLUSION**

However, what is clear is that discrepancies between breed identification of dogs, based on people’s opinions and the identification of breed ancestry by DNA
analysis, need to be further studied and differing results reconciled. Clearly, the assignment of breed identification to mixed-breed dogs is complex, and public health and private polices that depend on identification of dog breeds must take these issues into account.

ACKNOWLEDGMENTS

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REFERENCES


