Canine Behavioral Genetics: Pointing Out the Phenotypes and Herding up the Genes

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An astonishing amount of behavioral variation is captured within the more than 350 breeds of dog recognized worldwide. Inherent in observations of dog behavior is the notion that much of what is observed is breed specific and will persist, even in the absence of training or motivation. Thus, herding, pointing, tracking, hunting, and so forth are likely to be controlled, at least in part, at the genetic level. Recent studies in canine genetics suggest that small numbers of genes control major morphologic phenotypes. By extension, we hypothesize that at least some canine behaviors will also be controlled by small numbers of genes that can be readily mapped. In this review, we describe our current understanding of a representative subset of canine behaviors, as well as approaches for phenotyping, genome-wide scans, and data analysis. Finally, we discuss the applicability of studies of canine behavior to human genetics.

The domestic dog displays greater levels of morphological and behavioral diversity than have been recorded for any land mammal (Figure 1) and holds the unique distinction of being the first species to be domesticated.[1] The phenotypic radiation of the dog has been the product of restricted gene flow and generations of intense artificial selection.[2] These factors have generated the astounding level of diversity noted among the more than 350 breeds of dog recognized worldwide, many of which were developed for highly specialized tasks such as herding, hunting, and retrieving.[3] Indeed, breeds are often defined by a combination of their specialized morphological and behavioral traits[4] (Figure 2).

The American Kennel Club (AKC) in the United States recognizes 157 distinct breeds of dog. For a dog to be a registered member of a breed, both of its parents must have been registered members of the same breed, meaning that many modern breeds, although all members of the same species *Canis familiaris*, represent closed breeding populations, often characterized by high levels of genetic homogeneity. Domestic dog breeds are thus ideal for studying the genetic basis of morphology, disease susceptibility, and behavior. Indeed, captured within the 157 U.S.-recognized breeds are heights that vary from nine inches (Pekingese) to three feet (Irish wolf hound); snouts that may be long and pointed (greyhound and collie) or short and flattened (pug and bulldog); coat colors, length, and textures galore; and variation at every level imaginable. Indeed, tail position alone has over a dozen recognized descriptors (plumed, ringed, snapped, whipped, sickle, curled, double curled, etc.).

Behavioral variation is similarly captured within different breeds. Differences between breeds that herd versus guard livestock illustrate this point particularly well. Herding breeds, such as the border collie, are used to manage the movement and behavior of livestock. As their name implies, guarding breeds, such as the kuvasz, live among the livestock, usually unattended, and guard against predators. Both types of dog have been developed to work with livestock; however, they present radically divergent behavioral responses to their charges. Herding breeds strongly express predatory motor patterns such as stalking. More advanced aspects of the canine hunting sequence (grabbing) are differentially developed among herding dogs, with breeds like the Australian cattle dog, which is used to work typically stubborn cattle, strongly expressing grab-biting behaviors.[5] In contrast, livestock-guarding breeds only weakly express predatory motor patterns. Good livestock-guarding dogs do not chase, stalk, or even attempt to play with livestock.[5]

Consideration of other breeds defines an array of additional behaviors, such as such as pointing, retrieving, tracking, and drafting, that are presumably controlled, as least in part, by strong genetic components. In addition, dogs display an amazing range of emotions to which humans respond, including loyalty and affection, for which a genetic basis has often been postulated.[6]

With recent completion of a 1.5× survey sequence of the standard poodle, a 7.5× high-quality draft sequence of the boxer,[7,8] and databases highlighting 2.1 million canine-specific single-nucleotide polymorphisms (SNPs), as well as the availability of platforms for doing whole-genome association studies, canine genetics is now poised to significantly advance our understanding of mammalian behavior. These facts, combined with increasing knowledge about how dog breeds relate one to another,[9,10] as well as how variation in the dog genome is organized,[11,12] allow us to hypothesize that we can unravel the genetic basis of both simple and complex canine behaviors with currently available tools. In the following sections, we first review dog domestication and describe ongoing experiments to identify behavioral genes. We discuss phenotypes of interest and highlight the features of the canine population that make it amenable to mapping studies. We also discuss

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DOI 10.1016/j.ajhg.2007.12.001.

Figure 1. Canine Variation
Shown are examples of the cane corso and a Chihuahua mix (A). The cane corso is a large breed weighing, on average, 110 lbs (males) in contrast to the Chihuahua, one of the smallest, sometimes weighing under 3 lbs. Also shown are (B) the pug and (C) Afghan hound, which exhibit dramatic differences in head shape. Most dog breeds were developed in Europe within the last 300 years. The AKC recognizes nearly 157 breeds, although there are about 350 noted worldwide. Breeds differ in phenotype in terms of overall body size, coat color, length and texture, head shape, leg length, and dozens of other attributes.

what is known about genetic variation within the canine genome and how that may relate to behavioral genetics. Finally, we discuss examples of both normal and aberrant behaviors of interest to both human and companion-animal geneticists and the potential for identifying causative genes via the canine system.

Canine Domestication

Domestication is both the process and condition of genetic and environmentally induced developmental adaptation to humans and captivity.[13] Initial studies of mitochondrial DNA (mtDNA) from domestic dogs suggested the potential for multiple domestication events and an origin of perhaps >100,000 years ago.[14] More recent studies, however, suggest that dogs were domesticated 15,000 to 40,000 years before present (YBP).[15] Although fossil records show an association between prehistoric man and wolves, which are precursors of domesticated dogs,[15,16] as far back as 400,000 YBP,[1] most of archeological data support a true domestication event date of about 15,000–20,000 YBP.

Domestication brought about several distinct changes in the appearance of the wolf, as demonstrated by the remains of the earliest dogs found in Russia and Germany, dated at 13,000–17,000 and 14,000 YBP, respectively,[1,17] as well as fossils from Iraq and Israel dated at 12,000 YBP.[1] During the early Holocene period, between 10,000 and 7,000 YBP, dogs spread across much of the globe and were found even in the Americas. Remains of these early dogs are characterized by their smaller cranial volumes and mandibles, compacted teeth, and smaller auditory bulla (bony enclosure of the inner and middle ear). Other morphological changes included widened snouts, decreased tooth size, decreased body size, altered coat color and pattern, and altered tail and ear carriage.

The development of cooperative hunting techniques together with the utilization of projectile hunting implements are believed to have significantly increased hunting efficiency during the Mesolithic period.[1] Hence, humankind's relationship with the dog increased in sophistication, resulting in selection of dogs exemplifying more refined traits adapted for specialized aspects of the hunt. As a result, modern hunting dogs have been selectively bred to point, track, chase, hold at bay, retrieve, and flush.

The Farm-Fox Experiment

A remarkable resource for understanding the behavioral and morphological changes associated with early domestication is the so called "farm-fox experiment," which has been conducted for the last 50 years at the Institute of Cytology and Genetics of the Russian Academy of Sciences (ICG) in Novosibirsk, Russia. In the 1950s, Dmitry Belyaev and colleagues established a colony of silver foxes (*Vulpes vulpes*) with a goal of domesticating the animals so that they would be easier to handle by furriers seeking to develop products from the animal's unique silver coat.[18] Foxes were selected on the basis of a key component of domestication, tameness. Yet, despite rigorous selection

Figure 2. Herding Behavior
Dogs have been bred for a large number of behaviors including hunting, pointing, herding, guiding, etc. Shown is an example of the border collie herding livestock. Photo by Dan Weber.

based solely on behavior, several morphologic traits that typically distinguish domestic dogs from their wild progenitors began to appear in the foxes,[19,20] including widened skulls, shortened snouts, floppy ears, shortened tails, curly tails, and altered coat color patterns. In aggregate, these data suggest a link between selection for behavior and generation of a subset of morphological traits observed in modern domestic dogs.

ICG researchers began their breeding program with 100 females and 30 males.[19] Behavioral classes ranged from foxes exhibiting aggressive avoidance behaviors, such as biting and growling, to the highest tameness class, which included animals that actively sought human contact and exhibited dog-like behaviors such as tail wagging and licking. By the tenth generation, 18% of foxes were in the highest tameness class. By the 30–35th generations, 70%–80% of foxes were in the highest tameness class[19] and the animals behaved like modern domestic dogs.[19,21,22]

While developing the tame fox strain, ICG researchers also maintained a population of foxes that retained the aggressive behavioral conformation typical of wild-type foxes.[19,20,23] Newly developed quantitative measures are now used to define both tame and aggressive strains. These measurements rely on the assessment of video-recorded behavioral tests and can be reproducibly measured and quantified.[23] Examples include the frequency of occurrence of specific vocalizations and the relative positions of highly communicative body parts, such as the tail. Each of these has been used in a principal-component analysis (PCA), which classifies the variation of correlated traits into linear combinations. Principal components (PCs) are, thus, genetically accessible phenotypes. Nearly 50 traits have been defined that distinguish the tame and aggressive fox populations and can be summarized into two PCs, explaining 47.3% and 6.4% of the variance between the populations.[23]

Recently, a fox meiotic linkage map was constructed that covers the entire haploid set of 16 fox autosomes as well as the X chromosome.[24] With this key resource now available, several experimental pedigrees have been generated to map the fox loci for both aggression and tameness.[24] The research community is anxiously awaiting results of this 50 year study, which are expected within the next two years.

Mechanisms for Generating Variation

The above experiment is one of many that have forced scientists to question the rate at which phenotypic change is possible in the dog. Simply put, does the wild canine genome carry all the possible alleles needed to create the diversity of phenotypes observed in domesticated dogs today? Alternatively, do canids have a mechanism for rapid generation of nonlethal mutations that are then available for selection? Experiments by Fondon and Gardner address this issue.[12,25] These investigators measured skulls of 20 breeds of dog as well as several mongrels. They then analyzed the DNA sequences of 37 microsatellite-repeat-containing regions from 17 genes hypothesized to be involved in craniofacial development. Strikingly, they found fewer perfect repeats in dogs than in humans, suggesting that evolution of microsatellite repeats might occur faster in dogs, thus accelerating the development of new alleles available for selection.[12,25] Given these results, it is easy to imagine how rapid mutation among strategically positioned microsatellite repeats in genes encoding neurotransmitters and their receptors, ion channels, synaptic-vesicle proteins, and axon-guidance molecules could play a role in behavioral variation as well. Indeed, such a role has already been suggested for a microsatellite within the promoter of the vole vasopressin 1a receptor gene. This regulatory polymorphism has been shown to be associated with both inter- and intraspecific differences in mating behavior among voles.[26] A similar role has been hypothesized in humans for a microsatellite within the D4 dopamine receptor, which was hypothesized to play a role in so called "thrill-seeking" behaviors.[27,28]

Also of interest are canine small interspersed nuclear elements (SINEs), which litter the canine genome.[11] These elements are retrotransposons derived from a frequently occurring tRNA-Lys.[7,29,30] Canine narcolepsy, first described in the Doberman pinscher,[31] is caused by insertion of a canine-specific SINE element (SINEC_Cf)[30,32,33] within the hypocretin receptor-2 gene.[34] As with *Alu* repeats in the human genome, SINE elements seem to be frequently located in positions affecting gene expression. Other examples include the insertion of a SINEC_Cf element into the canine *PTPLA* and *SILV* genes. The insertion into *PTPLA* has been found to cause centronuclear myopathy in the Labrador retriever.[35] The insertion of a SINE_Cf element into the *SILV* gene, which plays a role in the formation of premelanosomes, causes the merle coat coloring of several breeds.[36]

As with the microsatellites, it is easy to hypothesize a role for SINE elements in canine behavioral variation if they are stragetically placed in the same classes of genes mentioned above (neurotransmitters, ion channels, synaptic-vesicle proteins, etc.). Indeed, the number of phenotypes found to be associated with SINEC_Cf element insertion compared to the number of mutations identified to date is sufficiently large that it might be prudent to map the locations of such elements and then determine which adjacent genes may be hypothesized to be of relevance for behavior. Whether insertion of similar elements plays a role in human behavioral variation remains to be examined.

Behavioral Phenotyping

A long-stated goal of behaviorists is to identify genes that control behavioral traits. Traits that define specific breeds, such as those associated with hunting and herding, are of interest, as are those observed in particular dogs or lineages of dog, such as obsessive-compulsive behaviors in the bull terrier.[37] Because of its inherent complexity, developing reliable behavioral metrics for dogs has been difficult. Currently, four general approaches have been employed to study canine behavior: test battery, owner-directed

survey, expert rating of breeds, and observational study,[38] with test battery being the most frequently used.[39–43] In this method, dogs are exposed to novel stimuli, and their responses are recorded.

The owner-directed-survey approach is also commonly used to assess canine behavioral attributes.[44–49] Such surveys capitalize on the expertise of owners and caregivers in the evaluation of their own dogs. By combining the responses of many independent owners and caregivers, individual bias can be overcome.[38,47] This approach is less useful for characterizing individual variation but excellent for studying breed-specific behavioral variation. Less commonly used is the expert-rating approach,[50–55] whereby veterinarians or others with recognized expertise rate breeds, as opposed to individual dogs, for specific traits.

The final approach is the observational test,[56] which relies on expert observation of individual dogs under natural circumstances, such as during video-recorded walks.[56] Thus, both observational tests and test batteries can be useful for measuring individual- and breed-specific variation.

For genetic studies, owner-directed surveys offer the most high-throughput approach for behavioral phenotyping. Because these studies can be conducted by phone, mail, or internet or in person, researchers have tremendous flexibility in data collection. If breed prototypes form the basis of phenotypes for a mapping study, large numbers of dogs can be easily characterized. Although individual variation cannot practically be taken into account, this approach is useful for characterizing binary traits or those phenotypes of large and essentially fixed differences (i.e., pointing).

Because they require each dog to be observed in a familiar or natural environment by an expert, observational tests are the most low-throughput method. By comparison, test batteries are more applicable because standardized novel environments can be used in administering the tests, thus accommodating larger numbers of dogs.[42] Using this approach, researchers have found general behavioral axes of variation for the domestic dog relating to aggression, playfulness, fear, sociability, and chase-proneness. Indeed, playfulness, fear, sociability, and chase-proneness were all related and create the broad behavioral dimension of shyness-boldness, which is comparable to that found in humans.[57]

Behavioral Variation

Perhaps the most striking behavioral variation observed in dogs is that observed across breeds.[5,42,51,53–55,58] In their now classic study, Scott and Fuller[58] examined interbreed differences in behavior in the American cocker spaniel, basenji, beagle, Shetland sheepdog, and wire-haired fox terrier. In general, dogs were reared in a standardized environment, although a subset was also cross fostered (across breed) to study the effect of maternal environment and some were reared in private homes to ensure that the performance of the laboratory animals was comparable to dogs in natural social settings.

The study revealed several interesting results. Specifically, the authors found that the cocker spaniel and Shetland sheepdog have much lower reactivity than the beagle, basenji, or wire-haired fox terrier. Reactivity relates to dogs' response to sudden changes in stimuli, such as a doorbell ring. They also found differences in trainability, depending on the specific task. One training task was learning the sit-stay command, which the cocker spaniel and wire-haired fox terrier learned much more quickly than the basenji, with the performance of the beagle and Shetland sheepdog falling in the middle. Breeds were also tested for problem-solving abilities with mazes, manipulation, spatial-orientation, detour, and trailing tests. Interestingly, no breed universally outperformed all the other breeds on all of the tests. Not surprisingly given the tasks, the beagle ranked first for speed of trailing a scent. The basenji ranked first for all the various manipulation tests of pulling strings and moving objects to reveal food items. Because of differences on a number of phenotypic axes, American cocker spaniels and basenjis were crossed to generate experimental, reciprocal backcross populations. F1 and F2 hybrids showed a strong tendency to be intermediate in performance on behavioral tests. Similarly, backcross progeny were intermediate relative to F1 and parental animals. In summary, although a limited number of breeds were characterized, the results of this work represents direct empirical evidence of the pronounced and reproducible behavioral diversity of the dog as well as the existence of genetic components of behavior.

Candidate Genes

As with human behavior, the candidate-gene approach has also been applied to the study of dog genetics, but with very limited success. Studies involving putative behavioral genes, such as those involved in serotonergic, catecholaminergic, and glutamatergic pathways,[59–61] have failed to find variants of certain significance, largely because of a small number of study subjects and a lack of functional assays. Screening the coding sequences and intron and exon boundaries of three serotonergic genes in the hopes of understanding aggression in golden retrievers[62] has been similarly frustrating. Although interbreed differences in allele frequency are found for some SNPs,[59–62] none of the studies clearly defined phenotypes with which to contextualize results and none included sufficiently large numbers of animals to achieve statistical significance.

Whole-Genome Association Studies

Whole-genome association studies (WGASs) can bypass many of the weaknesses associated with candidate-gene studies because WGASs take an unbiased approach to assessing the entire genome. Two studies suggest that WGAS studies in the dog will require significantly fewer SNPs than similar studies in humans because linkage disequilibrium (LD) extends for megabases in the dog, whereas it extends for only kilobases in humans.[8,63] In an initial set of experiments, Sutter and colleagues

examined five breeds of dog at five unlinked loci and reported a 10-fold range in LD in breeds that ranged from popular to rare and whose individual histories differed in key features such as use of popular sires and occurrence of population bottlenecks. In addition, they showed that, on average, LD extends for about 2 Mb in dogs compared with the frequently quoted number of 0.28 Mb for humans.[64,65] These differences reflect not only the breed barrier that defines dog breeds, but also the fact that many breeds originated from small numbers of founders, thus restricting genetic diversity. In addition, the gene pool of many breeds suffers from overrepresentation of popular sires—that is, dogs who do well at performance events and from whom frozen sperm has been collected, producing theoretically hundreds of progeny. Finally, the fact that dog breeds wax and wane in popularity, sometimes increasing or decreasing by as much as 100,000 new registrations per year in less then two decades, as was the case with the rottweiller, affects the gene pool as well. The length of LD in any region will ultimately reflect the alleles that passed through the bottlenecks. The implications of these findings are important for experimental design and suggest that a WGAS in the dog would require as few as 10,000–30,000 SNPs, compared to the 500,000 required for human studies.[66,67]

These results were validated and expanded in a much larger study by Lindblad-Toh and colleagues as part of the boxer sequencing effort.[8] These investigators reported that the dog genome consists of megabase-size regions that are alternatively homozygous and heterozygous. In addition, they reported on characteristics of over 2.1 million SNPs in the dog. Finally, as did Sutter et al.,[63] Lindblad-Toh and colleagues highlighted the fact that haplotype sharing between breeds was a common occurrence, although haplotype diversity was more rare then expected.[8] This important result suggests that a single SNP chip could be developed and used for mapping in all breeds of dogs. As a result, several such resources have been or are being produced, including the now widely available Affymetrix chip that contains nearly 127,000 SNPs.

One caveat to the above is that although long-range LD makes the identification of initial loci less problematic than similar studies in humans, it is likely to make the move from linked marker to gene more challenging. Initial findings of linkage may extend for megabases and span nearly a hundred genes.[68] Multiple strategies will probably be needed to overcome this problem. The first is the use of cross-breed comparisons. Parker et al. have shown that modern dog breeds can be divided into five major groups, with the members of each groups sharing some common ancestry.[9,10] As was demonstrated by the identification of two disease mutations relevant for canine vision disorders[9,69] and identification of a gene for body size,[70] the analysis of haplotypes from affected dogs belonging to breeds from the same group allows for significant reduction in the region of linkage. The use of samples that are from dog lineages from that same breed but that are either comparatively out bred, or that share few common founders or popular sires between lines, can produce the same results.

Ultimately, however, functional studies will be needed to develop a complete understanding of how any germline variant affects behavior. It has been suggested that the development of cross-bred lines of dogs would be useful in this regard. Although this is theoretically true, the development and maintenance of a behavioral colony of dogs is extremely expensive and, frankly, an unpopular concept because of spiraling animal-care costs, long-term funding worries, and animal-welfare concerns. In addition, it is well recognized that many social behaviors in dogs do not appear in a colony setting and require interaction to develop. Much more likely will be the incorporation of mouse or other behavioral models to test putative behavioral variants.

Where Will the Causative Variants Be?

Many behavioral-mapping studies are likely to reveal a role for changes in noncoding and regulatory regions. Indeed, given that coding regions are typically under the most selective constraint, these sequences typically evolve at a slower rate than noncoding sequences. As a result of the recent divergence of dogs from wolves and the subsequent radiation of the dog, it is likely that substitutions in noncoding regulatory regions that control transcription levels, message stability, and localization, as well as splicing, will be important. Two studies have examined differential gene expression in the canine brain.[71,72] In the study of Saetre and colleagues, brain regions thought to be important in emotion and cognition, such as the hypothalamus, amygdala, and frontal cortex, were compared in postmortem brain samples from ten each of dogs and coyotes, and from five wolves, by use of a cDNA microarray containing 7762 genes. Divergence in gene expression in the frontal lobe correlated with the evolutionary distances between species. Expression profiles of the amygdala were differentiated, but did not correlate with evolutionary distance or domestication. In contrast, gene expression in hypothalamus, which controls specific emotional and endocrinological responses, was highly conserved among the wild canids, yet divergent in the dog. Saetre et al.[71] have postulated that behavioral selection for domestication may be the result of simple changes in gene regulation by genes in the hypothalamus.

Lindberg and colleagues examined gene expression for three brain regions in tame and unselected foxes from the colony in Noversebirsk, as well as foxes living in the wild.[72] Whereas they found large differences between the wild and farm animals, only small differences were seen between the tame and nonselected farm lines. This suggests that the behavioral and physiological changes caused by selection for tameness might be associated with only limited changes in gene expression in the fox brain.

What's Wrong with My Dog?

Questions regarding abnormal behaviors in dogs are among the most frequently asked questions of behaviorists.

Although there is little evidence for complex disorders like bipolar disease, dog-behavior experts have long treated dogs for anxiety and depression. Also, as described above, sleep disorders, which are prevalent in humans, occur in dogs.[73] Indeed, the genetic study of canine narcolepsy is an excellent demonstration of how canine genetics can inform our understanding of common human diseases. Although inherited narcolepsy is rare in both humans and canines, sleep disorders are extremely common in humans. In 1999, long-term studies by Mignot and colleagues revealed that canine narcolepsy, which segregated in a colony of Doberman pinchers, was caused by a mutation in the hypocretin (orexin) receptor 2 gene.[34] This important discovery lead to subsequent findings[74,75] that regard the molecular biology of sleep modulation and that have proven critical for more general studies of sleep disorders in humans.

The dog is also likely to contribute to our understanding of the pathways involved in obsessive-compulsive disorder (OCD). Although human OCD is often believed to have at least a partial a hereditary component, both candidate-gene and linkage studies have yet to identify causative mutations, genes, or pathways underlying the disorder.[76] OCD has been described in several dog breeds, particularly the bull terrier and related breeds.[37] Affected dogs display an obsessive tail-chasing behavior that responds to treatment with serotonin-reuptake inhibitors such as clomipramine hydrochloride, suggesting that they are true obsessive-compulsive disorders and not the result of a seizure. Although the gene for this disorder has not yet been found, the fact that the disorder occurs in only a small subset of related terrier breeds (bull terriers, miniature bull terrier, American Staffordshire terrier, and Jack Russell terrier) makes it a good candidate for either a family-based linkage study or a WGAS.

How many other human disorders can we learn about by studying anomalous behavior in dogs? Certainly aggression has been considered at length.[62] However, the social and political ramifications of identifying genes that control this complex behavior are not lost on either the companion animal or human-genetics communities. Dog fanciers argue that there are "no bad dogs, only bad dog owners" and that laws that would outlaw so-called "aggressive" dog breeds within city limits are discriminatory to owners of those breeds. In terms of human genetics, the considerations are much more complex. Ethicists will be faced with difficult discussions about both individual and social responsibilities for violent actions on the part of individuals carrying certain mutations. More likely to be palatable to both communities are studies of depression and anxiety, which clearly exist in humans and dogs and for which a genetic understanding would be welcome.

Performance-Enhancing Polymorphisms

Although behavioral studies are often couched in the negative (i.e., what is wrong with my dog?), of equal interest to canine behaviorists are studies of performance genetics. We recently showed that two copies of a protein-truncating mutation in the myostatin gene (*MSTN*) are found in whippet dogs with a heavily muscled phenotype known as "bully" whippets.[77] However of even greater interest is the observation that heterozygotes, who carry only one copy of the mutation and who are, on average, more muscular than the typically lean wild-type, compete more successfully in racing events than individuals who lack the mutation. These results highlight the importance of "performance-enhancing polymorphisms" as well as raise questions about the role of *MSTN* and similar genes in human athletics.[77] We found only one report of a human who is a homozygote for mutations in *MSTN*, a child who is heavily muscled and whose mother was reportedly an Olympic-class swimmer.[78] How many athletes are heterozygotes for mutations in this or other performance-enhancing genes? It is difficult to even speculate, but certainly several.

Conclusions

For years the dog has been suggested as an ideal system for studies of behavioral genetics.[79] With the genome now mapped and sequenced and tools for building haplotypes and studying expression at hand, it is time to tackle the hard experiments. Why is the basset hound less effective at herding sheep or an Anatolian shepherd less effective as a hunting dog? More importantly, why do Australian shepherd dogs herd and greyhounds chase, both in the absence of instruction? Why did the domestication of dogs lead to a level of loyalty and devotion unrivaled among modern mammals?

For many geneticists, the most interesting behaviors in dogs are those that are highly breed associated, such as herding and pointing. For others, the challenge is to understand the genetic variation that contributes to the individual variation between dogs (personality). Still others see in man's best friend a mirror of our best (loyalty, steadfastness, trainability, strong work ethic) and worst (stubbornness, aggression, and anxiety) qualities. An understanding of the genetics of all of these traits is likely to produce a better understand of not only the canine species, but the human species as well.

Acknowledgments

We thank the many dog owners, breeders, and colleagues who have provided DNA samples for our studies of canine health. We acknowledge the AKC Canine Health Foundation and the Intramural Program of the National Institutes of Health for Support.

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