

See all ›
5 Citations

See all ›
163 References

Share

Download full-text PDF

Genetics of Domesticated Behavior in Dogs and Foxes

Article · December 2014 *with* 407 Reads

DOI: 10.1016/B978-0-12-394586-0.00010-X



1st [Anna V Kukekova](#)

il 26.61 · University of Illinois, Urbana-Champaign



2nd [Lyudmila N. Trut](#)



3rd [Gregory M. Acland](#)

Abstract

Dog domestication involved long-term genetic selection for behavior. The genetics-centered view of domestication is supported by experimental selection of farm-foxes (*Vulpes vulpes*) that began in the 1950s. Selection of foxes, separately, for tame and for aggressive behavior, has yielded two strains with markedly different, genetically determined behavioral phenotypes. Tame-strain foxes communicate with humans in a positive manner and are eager to establish human contact. Foxes from aggressive strains are aggressive to humans and difficult to handle. Although selected solely for behavior, changes in physiology, morphology, and appearance with significant parallels to characteristics of the domestic dog, were observed in tame-strain. Ongoing research is focused on identification of molecular genetic mechanisms associated with selection of foxes for behavior. Identification of behavioral loci in the fox genome in the region which is homologous to the region in the dog genome that differentiates dogs from wolves lead to the hypothesis that domesticated behavior in dogs and foxes may have similar genetic bases.

Genetics of Domesticated Behavior in Dogs and Foxes

Anna V. Kukekova*, Lyudmila N. Trut[†], and Gregory M. Acland[‡]

*Department of Animal Sciences, University of Illinois at Urbana-Champaign, Urbana, IL, USA; [†]Institute of Cytology and Genetics of the Russian Academy of Sciences, Novosibirsk, Russia; [‡]Baker Institute for Animal Health, Cornell University, Ithaca, NY, USA

INTRODUCTION

This chapter offers an overview of recent studies in behavior and behavioral genetics of dogs, wolves, and foxes with the aim of providing insight into the complex structure of domesticated behavior in canids.

All domesticated animals have common behavioral features, becoming not only tame to humans but showing lower levels of aggression toward each other. It is not too much of a stretch to wonder if these behavioral features have something in common with the species-specific differences between the behavior of humans, and their two closest extant “cousin species”—the chimpanzee and bonobo, leading to the suggestion that the evolution of modern humans may have been a process of self domestication (Brüne, 2007; Hare *et al.*, 2012; Shipman, 2010).

Behavior is a preeminent phenotype that drives and is driven by the selective pressures of both domestication and evolution. Domestication is a microcosm of evolution. Driven by directed or natural selection, it causes divergence of a founder population into new populations that can exploit new and/or different environmental niches. Once selection takes hold, the genetic aspects of behavioral differences are reinforced, as specialized subpopulations become better adapted to specific niches. Domestication thus provides a window in which the processes involved in the genetics of behavior can be observed at close range providing phenotypes that are accessible to the modern tools of molecular genetics.

The intraspecific and interspecific (i.e. human directed) social behavior of domesticated animals differs dramatically from their wild ancestors (Price, 2002). The paradigmatic example is provided by the domesticated dog (*Canis familiaris*) and its progenitor species, the gray wolf (*Canis lupus*). Although

the differences in social behavior of dogs and wolves are undeniably genetic, little is known about the evolutionary processes that led to these behavioral modifications. In the mid-20th century, the Russian geneticist, Dmitry Belyaev, argued for a primary role of selection for behavior in animal domestication. To test this hypothesis, experimental selection of the silver fox (color morph of the red fox, *Vulpes vulpes*), a close relative of the dog, was started in 1959 (Belyaev, 1969, 1979; Trut, 1999, 2001, 2009). The experiment led to the development of a strain of foxes that show friendly, dog-like behavior to humans. Selecting foxes for behavior constituted a completely novel long-range approach to the genetics of behavioral modification that preceded the demonstration that dogs evolved from wolves (Axelsson *et al.*, 2013; Leonard *et al.*, 2002; Savolainen *et al.*, 2002; Vilà *et al.*, 1997; vonHoldt *et al.*, 2010).

THE DOG IS THE FIRST DOMESTICATED SPECIES

The dog was the first species to be domesticated. In fact, this “event” took place so early that it is arguable that the dog self-domesticated itself, and provided the example that humans subsequently followed in deliberately domesticating other species.

Archeological evidence for the coexistence of dogs with humans has been identified from as early as 14,000–17,000 ybp in Russia (Sablin and Khlopachev, 2002); 14,000 ybp in Germany (Nobis, 1979); 12,000 ybp in Israel (Dayan, 1994; Davis and Valla, 1978; Tchernov and Valla, 1997); and 5000 ybp (Olsen, 1985) in China. Recent findings identified remains of dog-like canids living prior to the Last Glacial Maximum (*c.* 26,500–19,000 cal BP) in southern Siberia (Altai Mountains, Russia) dated *c.* 33,000 cal BP (Ovodov *et al.*, 2011), and Western Europe (Goyet, Belgium) dated 36,000 cal BP (Germonpré *et al.*, 2009). Although these incipient dogs may represent domestication events that were terminated by climatic changes associated with the Last Glacial Maximum, and thus may have not given rise to modern dogs, molecular analysis of these remains may still shed light on the evolution of domestication in the dog. Identification of further dog-like canid remains in different parts of Eurasia supports a hypothesis of recurrent, multiregional dog domestication (Ovodov *et al.*, 2011).

Molecular data suggest that the divergence of dogs from wolves took place as recently as 15,000 years ago (Savolainen *et al.*, 2002; Skoglund *et al.*, 2011). Initial molecular analyses, based on mitochondrial DNA and Y-chromosome markers from dog breeds and wolf populations from different geographical locations, suggested an East-Asian origin for canine domestication (Brown *et al.*, 2011; Ding *et al.*, 2012; Pang *et al.*, 2009; Savolainen *et al.*, 2002; Oskarsson *et al.*, 2012); while genomic DNA analysis supports the Middle East (vonHoldt *et al.*, 2010) as the most likely center. Studies of ancient dog remains from Latin America and Alaska, and dog breeds

indigenous to North America, establish the origin of New World dogs as from Old World wolves (Leonard *et al.*, 2002; Vilà *et al.*, 1999; vonHoldt *et al.*, 2010). Village dogs from Africa that did not experience the population bottleneck associated with modern breed formation, and the Australian dingo and New Guinea singing dogs, were also sourced to ancient dogs domesticated in Eurasia (Ardalan *et al.*, 2012; Boyko *et al.*, 2009; Larson *et al.*, 2012; Oskarsson *et al.*, 2011; Savolainen *et al.*, 2004). The multiple recent studies of dog ancestry differ in their estimate of how many domestication events led to the emergence of modern dog lines (Larson *et al.*, 2012; Savolainen *et al.*, 2002; Vilà *et al.*, 1997), and further document recent admixture events between dogs and wolves (Anderson *et al.*, 2002; Anderson *et al.*, 2009; Vilà *et al.*, 1997, 2003; Vilà and Wayne, 1999; vonHoldt *et al.*, 2010; Wayne and vonHoldt, 2012). For example, shared genomic regions between some European breeds and European wolves indicate admixture events between the two species after the divergence of dogs from wolves in the course of dog domestication (vonHoldt *et al.*, 2010; Wayne and vonHoldt, 2012).

Despite the differences in detail cited above, it is clear that dog domestication occurred at a time when modern *Homo sapiens* were hunter-gatherers, and soon after the first entry of modern humans into geographical regions populated by the wolf (Clutton-Brock, 1995). A long co-existence of dogs with humans is supported by recent findings of genomic signatures in the genome of the dog, but not the wolf, associated with the adaptation to a starch-rich diet (Axelsson *et al.*, 2013). Although just how humans and pre-dog wolves benefitted mutually from their new-found coexistence is still an open question, several scenarios have been proposed (Coppinger and Coppinger, 2001; Lorenz, 1954). Significant modification of the dog domestication picture came with recognition of the genetic basis of differences in the social behavior of dogs and wolves (Acland and Ostrander 2003; Coppinger and Coppinger, 2001; vonHoldt *et al.*, 2010). The current hypothesis proposes that dog domestication was a genetic selection for specific behaviors in the course of a long-term co-existence of pre-dog wolves with humans (Acland and Ostrander, 2003; Coppinger and Coppinger, 2001; Hare *et al.*, 2002; Miklosi *et al.*, 2003). Formation of this genetics-centered view of dog domestication was influenced in large part by the farm-fox domestication experiment (Trut 1999, 2001; Trut *et al.*, 2009) which is reviewed in this chapter.

The importance of dogs to human society is reflected in ancient art (Olsen, 1985; Zeuner, 1963) and by ancient co-burial of humans with dogs (Davis and Valla, 1978). Wall paintings of dogs in ancient Egypt show that distinct types of dogs had already existed 2500–4500 ybp (Zeuner, 1963). The morphotypic range of such ancient dogs remain with us today among modern breeds such as mastiffs, hounds, and toy breeds, indicating that distinctly different dog types first appeared thousands of years ago

(Cesarino, 1975; Clutton-Brock, 1981, 1995; Harcourt, 1974; Pionnier-Capitan *et al.*, 2011; Zeda *et al.*, 2006). Significantly, many of these ancient paintings and other works of art portray dogs and humans in contexts of social interaction between the two species, and evidence exists from prehistoric times for task-related interactions between humans and dogs. Dogs have been and remain present in almost every human culture and population as our close companions, assisting us in many tasks. This has led to the concept that dogs and humans are co-evolved species, each influencing the development of the other (Hare *et al.*, 2012; Shipman, 2010).

DOGS ARE MORE COMPETENT THAN WOLVES IN SOCIAL INTERACTION WITH HUMANS

When we talk about dogs we often describe their behavior in anthropomorphic terms. Dogs actively participate in our lives using their unique abilities to understand words from our language, the tone of our voice, and our body language (Grassmann *et al.*, 2012; Kaminski *et al.*, 2004, 2009; Pilley and Reid, 2011; Pongrácz *et al.*, 2001a, 2004, 2005a). Humans and dogs have developed mutual skills for cross-species communication (Ellingsen *et al.*, 2010; Pongrácz *et al.*, 2001a, 2001b, 2005b) that have led to development of the unique social interaction between the dog and its master. No other species is so routinely used as guides for blind people (Naderi *et al.*, 2001; Serpell and Hsu, 2001) and as assistants for people with other disabilities (Eddy *et al.*, 1988; Guest *et al.*, 2006; Lanea *et al.*, 1998; Rintala *et al.*, 2008).

Dogs develop attachment to their owners after a short period of interaction (Gacsi *et al.*, 2001, 2004; Topál *et al.*, 2005), in contrast to home-raised wolves who do not show patterns of attachment to humans similar to those observed in dogs, even after extensive socialization from an early age (Gacsi *et al.*, 2004; Topal *et al.*, 2005). Attachment is one of the basic phenomena of human social relationships (Bowlby, 1958) and one of the obvious features of the human–dog attachment is its resemblance to the human parent–child relationship (Hare and Tomasello, 2005; Scott and Fuller, 1965; Topál *et al.*, 1998, 2005).

In the laboratory, the social skills of dogs and wolves and their ability to communicate with humans are commonly tested using the object-choice paradigm. In this test the canid should choose between two containers using the experimenter's tap, point, or gaze cues. The correct choice is rewarded. The work of Brian Hare and colleagues (2002) has shown that dogs are more skillful than hand-reared wolves at using human social cues. Dogs presented with the object-choice task showed competence in reading proximal point, proximal point and gaze, and all three types of cues (tap, point, and gaze) combined. The wolves in the same test demonstrated abilities to identify a correct container above the random chance level only when provided with

combined gaze and proximal point cues (Hare *et al.*, 2002). The number of successful trials in this test was lower for the wolves than for the dogs (Hare *et al.*, 2002).

Subsequent studies showed that wolf performance in the object-choice test is strongly influenced by the level of wolf socialization with humans (Miklósi *et al.*, 2003; Udell *et al.*, 2008; Virányi *et al.*, 2008). Udell *et al.* showed that highly socialized hand-reared wolves from a population bred in captivity for many generations can successfully use distal point cues to make a correct choice. In this particular test, the wolves tested outdoors in a familiar area outperformed dogs tested outdoors in an unfamiliar area (Udell *et al.*, 2008). A group in Hungary studied highly socialized hand-reared wolves from a different population and demonstrated that these wolves had the skills to identify the correct container using tapping cues and some of these wolves were competent in reading proximal point cues (Gácsi *et al.*, 2009; Miklosi *et al.*, 2003; Virányi *et al.*, 2008). Virányi *et al.* have found that wolves can reach a level of untrained dogs in following distal pointing gestures after several months of formal training (Virányi *et al.*, 2008). Importantly, this study has also demonstrated a variation among the hand-reared wolves in their ability to follow human cues, suggesting that the variability in the wolves' communicative behavior might have provided the raw material for selection during domestication (Virányi *et al.*, 2008).

Several studies have shown that dogs are competent in the recognition of human attention status (Bräuer *et al.*, 2004; Call *et al.*, 2003; Gacsi *et al.*, 2004). Dogs use the orientation of the body, the orientation of the head, and the visibility of the eyes to distinguish between “attentive” and “inattentive” humans (Gacsi *et al.*, 2004; Viranyi *et al.*, 2004). Comparison of dog behavior across several tests led to the conclusion that dogs can rely on the same set of human facial cues that are used by humans to understand the attention status of other humans (Gacsi *et al.*, 2004).

Dogs also look to humans for assistance and direction more than wolves. When human-reared dogs and wolves trained to solve a simple manipulative task were presented with an impossible version of the same test (e.g., opening a locked box with food inside), dogs looked at the human almost immediately and then directed their gaze between the human and the box, while wolves did not look to the human but continued to attempt to solve the problem on their own (Miklosi *et al.*, 2003). The ability and desire of dogs to look at a human's face is one of the key differences between dogs and wolves in initializing and maintaining communicative interaction with humans (Miklosi *et al.*, 2003).

Differences in the behavior of dogs and wolves in social interactions with humans are recognized early in the postnatal period. The amount of interaction required for socialization of a wolf is dramatically different from and greater than the amount of interaction required for the socialization of a dog (Coppinger and Coppinger, 2001). Successful socialization of wolf puppies

requires the puppy's separation from the family before the eyes open and intense socialization with a human caregiver (Coppinger and Coppinger, 2001). Competence of dog and hand-reared wolf puppies in their interaction with humans was tested in multiple tests at 3, 4, and 5 weeks of age (Gacsi *et al.*, 2005). Significant differences in their behavior have been recorded at each time point. Dog puppies showed more communicative behavior with humans. Wolf puppies were more often aggressive to humans and more often demonstrated avoidance behavior (Gacsi *et al.*, 2005).

These reviewed experiments argue for a domestication hypothesis (Hare *et al.*, 2002) proposing that canine competence in interaction with humans has been acquired in the course of long-term selection for communicative skills. Differences between dogs and wolves in their skills of communication with humans strongly suggest a genetic basis for these behaviors. Early socialization improves the competence of wolves for interaction with humans but a dramatic difference in wolf and dog behavior remains (Coppinger and Coppinger, 2001). Variation in social skills among individuals in each species, domesticated and wild, is caused by a complex interplay of genetic determinants, life experiences, and environmental factors. Selection for specific behaviors can lead to genetically determined modifications of these behaviors, furthermore, it can lead to unexpected modifications of other behavioral aspects as well.

ANALYSIS OF TEMPERAMENT TRAITS IN DOGS

Selection for breed-specific behaviors has clearly played an important role in the course of the formation of the working breeds of dogs. Although reliable historical records on breed origins barely exist for most breeds, there is substantial evidence that breed formation was associated with cultural and economical developments in human societies (Clutton-Brock, 1995; Willis, 1999). Modern breeds were officially registered relatively recently, less than 200 years ago, but a gamut of breeds recognized for their unique behavioral skills had existed for a much longer period of time (Leighton, 1910). Dogs with similar working skills but differences in terms of the specific functions they served as well as differences in appearance were recognized as independent breeds and received official breed standards when registries were created by dog clubs (AKC, 2006; Dalziel, 1897). The migration of Europeans and their dogs to the New World promoted the formation of new working breeds descended from the old breeds or their crosses, incorporating new combinations of desirable skills which were better adapted to new needs and places (Clark, 2003; Cummins, 2002; Huson *et al.*, 2012).

The development of herding breeds is inevitably linked to the growth of livestock farming. Herding breeds differ among the geographical regions, as well as the species they herd and the types of tasks they perform (Combe, 1987). Genetically, working sheepdog breeds that originated in Great Britain

are more related to each other than to any other breed category selected for different working tasks in Great Britain or other countries (Parker *et al.*, 2004, vonHoldt *et al.*, 2010).

The use of dogs for hunting is reflected in paintings and historical records from ancient times (Clutton-Brock, 1995). Although, we do not have evidence that modern hunting breeds are descendants of these ancient dogs, it is instructive to note that the sight hound breeds, perhaps the oldest type of hunting dogs, are genetically closely related to each other (vonHoldt *et al.*, 2010), even those from different geographical locations. Likewise, hunting breeds sharing highly specialized behavioral repertoires, such as retrieving breeds, are more closely related genetically to each other than to breeds such as scent hounds selected for different hunting skills (vonHoldt *et al.*, 2010).

It is well established that humans have deliberately preserved specific valuable genetic variants in domestic animals from ancient times (Andersson, 2009; Andersson *et al.*, 2012; Rosengren Pielberg *et al.*, 2008). For example, all breeds characterized by the chondrodysplastic dwarfism phenotype carry the same, identical by descent, *FGF4* gene mutation (Parker *et al.*, 2009) since prehistoric times. These dwarf breeds were developed in different countries, at different times, and do not share recent common ancestry (Parker *et al.*, 2004, 2007). For example, the Pekinese is an ancient Chinese breed while Basset Hounds are traced back to Medieval Western Europe. This *FGF4* allele would clearly be disadvantageous for free-living canids, and has been maintained in the dog population by artificial selection favoring the phenotype.

To assume a similar scenario for behavioral traits is more difficult. In contrast to some morphological and appearance traits that are often determined in dogs by a small number of genes with large effects (Boyko *et al.*, 2010; Cadieu *et al.*, 2009; Hoopes *et al.*, 2012; Sutter *et al.*, 2007), behavior is most likely influenced by a large number of genes, each of which has a relatively small effect on the trait (Anholt and Mackay, 2009; Flint, 2003). However, the close relationships among dog breeds with specific working skills argues for the preservation of genetic variants for behavioral genes among these breeds.

Selection for breed-specific behaviors in the course of breed development was inevitably linked to selection for morphology, appearance, and other characteristics that were important for the dog's ability to perform specific tasks (Coppinger and Schneider, 1995). Guard dogs had to have tough bodies to fight enemies or predators. Sight hounds had to have gracile bodies and high endurance for fast running and long hours of hunting. A white coat color was favored by shepherds because it helped to distinguish herding dogs from wolves (Coppinger and Coppinger, 2001). A thick insulating coat was important for dogs in many geographical regions in order to survive the cold weather outside.

These days, each dog breed has a strictly defined standard that is much more focused on morphologic appearance than on dog behavior. In fact, many behaviors for which working breeds were originally selected became inconvenient in modern life and are not supported by current breeding practices. Behavioral characteristics for which the breeds were known historically thus often do not correspond to the behavioral characteristics of these breeds today. For example, Kubinyi *et al.*, analyzed temperament traits in different breeds in Europe and found significant differences for some breeds between behavioral characteristics provided by the breed standard and behavioral profiles of same breeds based on the owners reports (Kubinyi *et al.*, 2009).

In the Kubinyi *et al.* (2009) study, 93.3% of the respondents representing 14,004 dog owners indicated the “family member” category as the function of their dogs. These results are consistent with other studies in Europe, Australia, and the US, indicating that the majority of dog owners acquire dogs not for specific working tasks but for companionship (Bennett and Rohlf, 2007; Ellingsen *et al.*, 2010; Jagoe and Serpell, 1996; Serpell, 2004). Although the strict demand for working skills is reduced, some breed clubs are making an effort to preserve these skills through behavioral tests and incorporating the results of these tests into breeding programs. This sometimes leads to the development of two independent lines of breeding, one for show and pet dogs, but another one for working dogs, as in, for example, the Border Collie breed.

Programs implemented by organizations to evaluate specific aspects of dog behavior (e.g., herding, protection, detection of drugs or explosives) or for general behavioral assessment (e.g., to screen potential breeding populations for dogs with undesirable behavioral characteristics), have yielded valuable data for scientific evaluation of dog temperament. Svartberg and Forkman (2002) identified five factors (dimensions) underlying canine temperamental traits using data from 1175 dogs of 47 different breeds tested in the dog mentality assessment (DMA) test designed by the Swedish Working Dog Association (Svartberg and Forkman, 2002). The factors were labeled as “Playfulness,” “Curiosity/Fearlessness,” “Chase-proneness,” “Sociability,” and “Aggressiveness,” and accounted for 37% of common variation in the test. The first four factors were related to one other higher-order factor, which was interpreted as shyness–boldness. The same broad factors with slight variations were identified in an analysis of 15,329 dogs from 164 breeds performed for each of eight FCI (Fédération Cynologique Internationale) breed groups (Svartberg and Forkman, 2002). These data argue that personality factors underlying dog behavior in the DMA test are universal among breeds and not related to specific characteristics of FCI breed groups. Consistency of these behaviors over repeated tests for individual dogs was observed (Svartberg *et al.*, 2005). A heritability of 0.25 for the shyness–boldness dimension was reported (Saetre *et al.*, 2006).

Another common approach for assessment of dog behavior is the collection of information from dog owners by questionnaires (Arhanta *et al.*, 2010; Bennett and Rolf, 2007; Ellingsen *et al.*, 2010; Hsu and Serpell, 2003; Kubinyi *et al.*, 2009; Serpell and Hsu, 2001; Svartberg *et al.*, 2005; Vas *et al.*, 2007). This approach assumes that the dog owner knows its dog's typical behavior and that by asking appropriate questions this information can be extracted in a reasonably accurate, quantitative, and reliable manner (Hsu and Serpell, 2003; Serpell and Hsu, 2001). Using 132 items from a questionnaire filled by owners of 2054 dogs, Hsu and Serpell identified 11 factors that accounted for 57% of common variance in the scored items (Hsu and Serpell, 2003). The factors have been labeled based on the most significant traits contributing to each factor. The factors identified by Hsu and Serpell (2003) arguably describe narrower behavioral categories than the factors identified in the study by Svartberg and Forkman (2002). For example, the study by Hsu and Serpell identified three factors related to aggression: stranger-directed aggression, owner-directed aggression, and dog-directed fear or aggression.

Kubinyi used a 48-item questionnaire adapted for the dog from a questionnaire for human personality assessment (Kubinyi *et al.*, 2009) and, in parallel, a second questionnaire collecting demographic information for the owners and their dogs. In total, the study included owner reports for 14,004 dogs. Factor analysis identified four dimensions of dog personality: calmness, trainability, sociability, and boldness. Each dimension was shown to be influenced by other variables: calmness was influenced by age, neutered status, and the number of professional training courses the dog had experienced; trainability was influenced by training experience, age, and the reason for keeping the dog; sociability to other dogs was mainly determined by age, sex, training experience, and time spent together; boldness was affected by the sex, age of the dog, and the age of the dog at acquisition (Kubinyi *et al.*, 2009). Differences in trainability and boldness among the dog groups were identified: herding dogs were more trainable than Hounds, Working dogs, Toy dogs, and Non-sporting dogs, while Terriers were bolder than Hounds and Herding dogs (Turcsán *et al.*, 2011).

Assessment of dog behavioral phenotypes using data from either tests conducted either by dog organizations or by owner-filled questionnaires has some pitfalls (for a review, see Hall and Wynne, 2012; Jones and Gosling, 2005). The former, biased towards dog populations whose owners are interested in dog training, are often focused on specific behavioral characteristics and target-limited set of breeds. The latter do not provide results of direct observation of dog behavior in a defined period of time; and are sensitive to owner experience in judging dog behavior, and to the validity of the questionnaire. There are practical difficulties in observing dogs in their owners' homes. It is rare for such studies to be undertaken on dogs maintained in research facilities where their behavior is observed in a controlled familiar

environment in a systematic manner. There are almost no dog studies that take into account developmental aspects of behavior and the dogs' life experiences (Coppinger and Coppinger, 2001). One exception stands out: the long-term study of dog behavior conducted at Jackson Laboratory in Bar Harbor in the mid-20th century (Scott and Fuller, 1965).

THE BAR HARBOR EXPERIMENT

In this 13-year-long study in Bar Harbor, the behavior of five different dog breeds (Basenji, Beagle, Cocker Spaniel, Shetland Sheepdog, and Wire-haired Fox Terrier) was studied in great detail from birth to approximately one year of age. The experiment was designed to gain insight into the genetics of social behavior; the dog was selected as a model because dog social behavior was regarded as resembling human behavior, and there was a large amount of variation in behavior among the dogs (Hahn and Wright, 1998; Scott and Fuller, 1965). The results of this experiment had a profound effect not only on our understanding of dog behavior but on other disciplines including human psychology, genetics, and evolutionary biology. Here we describe a few of the Bar Harbor experiments and findings as examples that clearly illustrate the complexity of dog behavior and the necessity of applying a systematic approach for understanding basic biological principles underlying it.

A detailed analysis of canine behavioral development from the early postnatal period identified a critical period in dog socialization (Freedman *et al.*, 1961). The importance of this discovery to the field of dog behavior is paramount. The role of the environment during the socialization period was subsequently shown to be important for the development of other aspects of dog behavior, such as herding behavior (Coppinger and Coppinger, 2001).

Analysis of social relationships among littermates revealed different behavioral mechanisms of aggression. By 11 weeks of age, 95% of litters developed a food-related dominance hierarchy. Fox terriers formed more dominance relationships than cocker spaniels or beagles. Significantly more male fox terriers and basenjis formed dominance relationships than did females, whereas beagles and cocker spaniels did not show gender-specific differences in dominance relationships. Shelties (Shetland sheep dogs) developed strong territorial rather than food-related dominance relationships, whereas basenjis showed the opposite pattern: absence of territorial aggression but escalated aggression over food (Hahn and Wright, 1998; Scott and Fuller, 1965).

Measuring emotional reactivity showed significant differences among the breeds: terriers, beagles, and basenjis were consistently more emotional than shelties and cockers. Although significant differences in breed reactivity were observed, a variation in reactivity was also very apparent among individuals from the same breed. This reactivity showed very little change with age and no differences between males and females.

Problem-solving behavior was studied in different tests including a maze test. Fox terriers and shelties made more errors and required a longer time in moving through the maze. Basenjis had the best time in the first day of learning but beagles appeared superior on overall scores through multiple trials. The authors suggested that the beagles' success was attributable to their avoidance of stereotyped habits and their demonstrated random exploration of their surroundings.

Differences in trainability were observed among both breeds and individuals from an early age. Some individuals showed response to training at 5 weeks of age (forced training to be quiet on the weight platform); by the age of 16 weeks nearly 70% of the cocker spaniels were remaining quiet in the test while only 10% of the fox terriers were. All dogs learned to walk appropriately on a leash within a 10-day training period, but different breeds differed in the course of their learning: basenjis were outstanding in their vigorous resistance to restraint, shelties interfered excessively with the handler by leaping on him and winding between his legs; and beagles demonstrated excessive vocalization during the initial stages of training. These experiments show that the basic trainability characteristics of the different breeds tend to be specific to particular test situations and that they are based on a large variety of capabilities. The authors concluded,

In short, the effect of heredity upon trainability is highly complex, both because of the number of specific basic abilities involved and because of the complicated interaction between them made possible by behavioral adaptation.

Scott and Fuller (1965)

Genetic inheritance of several behavioral characteristics was demonstrated by experimental crossbreeding among breeds with distinctive behavioral repertoires. Fearful behavior was analyzed in crosses between basenjis (all tested individuals exhibited some fearful behavior) and cocker spaniels (62% of tested individuals exhibited fearful behavior). F1 dogs exhibited behavior broadly similar to that of the basenji parents, although the inheritance of different specific behavioral characteristics in this cross varied significantly. In several training and spatial-orientation tests the F1 offspring were superior relative to both parents suggesting a complex interplay in inheritance of different behavioral characteristics.

Furthermore, this study clearly demonstrated the influence of genotype-by-environment interaction on dog behavior. As summarized in a recent review:

The most intriguing result was the interaction of genotype and experience (Freedman, 1958). Puppies were raised in isolation and exposed to either tolerant humans or disciplinary humans who made the puppies sit and wouldn't play with them. Later the puppies were presented one by one with a bowl of food. If they approached, the handler would clap his hands to frighten them away. The handler then left the room so the puppies were free to eat the food. The basenjis did, no

matter how they had been handled. The Shetland sheepdog never did, no matter how they had been handled. The disciplined beagles ate the food, but not the tolerantly treated ones. The conclusion is that identical handling will have different effects on different genotypes of dogs.

Houpt (2007)

The Bar Harbor experiment clearly shows the complexity of dog social behavior in terms of its development and inheritance. A strong maternal effect was shown for several behavioral characteristics. In particular, Scott and Fuller demonstrate how easily behavior can be misjudged in terms of its genetic origin or gene–environment interaction nature. Underestimation of critical parameters underlying the formation of dog behavioral traits can lead to serious pitfalls in an attempt to identify genes implicated in these behaviors.

GENETIC ANALYSIS OF BEHAVIORAL TRAITS IN DOGS

In contrast to the genetic analysis of morphological traits (Boyko *et al.*, 2010; Cadieu *et al.*, 2009; Chase *et al.*, 2002; Hoopes *et al.*, 2012; Sutter *et al.*, 2007) and inherited diseases (Miyadera *et al.*, 2012; Ostrander and Beale, 2012; Parker *et al.*, 2010; Rimbault and Ostrander, 2012) success in the identification of loci and genes influencing dog behavior has been noticeably more modest.

Breed stereotypes, characteristics for which dog breeds were selected for (i.e. size, skull shape, and ear type), were successfully used as phenotypes for mapping morphological traits (Boyko *et al.*, 2010; Schoenebeck *et al.*, 2012; Sutter *et al.*, 2007). One study used a similar approach for genetic mapping of breed behavioral characteristics (i.e. herding, pointing, boldness, and trainability) defined by a dog trainer as phenotypes (Jones *et al.*, 2008). Several genomic regions that showed statistically significant association with breed behavioral characteristics were identified. Several candidate genes were suggested but no follow up analyses of involvement of these genes in dog behavior were performed.

Recent studies of performance in Alaskan sled dogs identified genetic loci associated with two main racing styles segregating in this breed: sprinting *versus* long-distance racing (Huson *et al.*, 2012). The Alaskan sled dog is a relatively recent breed originating from Alaskan Malamute, Siberian Husky, German Shorthaired Pointer, and Borzoi-type dogs bred for performance, rather than appearance. The racing style in this breed was shown to correlate with the contribution of parental breeds: increase in Alaskan Malamute and Siberian Husky ancestry correlated with increased endurance while contribution from Pointer and Borzoi-type dogs was associated with enhanced speed (Huson *et al.*, 2010). Genetic comparison between sprint-type versus long-distance racing Alaskan sled dogs identified several genomic regions associated with differences in racing style and pinpointed a variant of *MYH9* gene significantly associated with increased heat tolerance in sprint-type dogs (Huson *et al.*, 2012).

Multiple efforts have adopted a candidate gene approach to identify genes associated with behavioral traits in dogs, with mostly negative results (recently reviewed in [Hall and Wynne, 2012](#) and [Haupt, 2007](#)). Positive associations were identified for: Activity–Impulsivity with *DRD4* and *TH* in German Shepherds; with *DAT*, *DBH*, *DRD4* in Belgian Tervuren ([Hejjas et al., 2007, 2009](#); [Kubinyi et al., 2012](#)); activity level with *SLC1A2* and *COMT* in Labrador Retrievers ([Takeuchi et al., 2009a](#)); human-directed aggression with *DRD1*, *HTR1D*, *HTR2C*, and *SLC1A1* in English Cocker Spaniels ([Våge et al., 2010](#)); aggression with *SLC1A2* in Shiba Inu ([Takeuchi et al., 2009b](#)), but with *AR* in Akita Inu ([Konno et al., 2011](#)). All these studies were performed in relatively small dog samples and none has been validated in independent data sets. Taking into account the complexity of dog behavior, the validity of this single gene approach may be questionable.

Comparison of dog and wolf genomes identified several regions where the two species differ most significantly ([Axelsson et al., 2013](#); [vonHoldt et al., 2010](#)). From purely genomic data it is almost impossible to determine whether any of these regions are causally associated with behavioral differences between dogs and wolves. One such region identified in the [vonHoldt et al. \(2010\)](#) study is homologous to the region on human chromosome 7, where a deletion causes Williams–Beuren syndrome in humans, a complex disorder associated with exceptional gregariousness ([Doyle et al., 2004](#); [Jarvinen-Pasley et al., 2008](#)). Identification of a selection signal in the corresponding canine genomic region does suggest that this region may harbor genes influencing behavior in both species. However, as dogs diverged from wolves so long ago and have been selected for so many different traits, one would certainly expect their genomes to harbor multiple species-specific selection signals not necessarily associated with behavioral differences. What is clearly needed to complement such studies as these, is evidence of co-segregation of genomic changes with behavior, and expression differences of implicated genes that correlate with differences of behavior. The opportunity to obtain such information is provided in studies that recapitulate canine domestication in the silver fox.

THE FARM-FOX EXPERIMENT

The silver fox is a coat color morph of the red fox (*Vulpes vulpes*). In contrast to the dog that was domesticated prehistorically, the fox was domesticated in controlled farm conditions. Experimental domestication of farm-bred foxes was started by Dmitry Belyaev and Lyudmila Trut at the Institute of Cytology and Genetics (ICG) of the Russian Academy of Sciences, in Novosibirsk, Russia, in the late 1950s and is still ongoing, as has been reviewed in several publications ([Trut, 1999; 2001](#); [Trut et al., 2004, 2009](#)). Belyaev proposed that selection for behavior was the primary force in the

course of animal domestication. He further hypothesized that selection for an unusual behavior in wild species, that is, a tame response to humans, may affect many physiological processes in animals under selection (i.e. activity of hypothalamic-pituitary-adrenal axis) and lead to the emergence of variation in morphology, a common feature of domesticated species (Belyaev, 1979; Belyaev and Trut, 1989; Trut 1988). The fox was selected as a model to test this hypothesis.

When the fox domestication experiment began, foxes had been bred in captivity for over 50 years. Fox-fur farming was pioneered on Prince Edward Island in Southeastern Canada, beginning in the 1890s (Westwood 1989). Farmers on Prince Edward Island primarily raised the silver–black coat color variant of red foxes, which had the greatest economic value and were subsequently used to stock fur farms in many areas of North America and Eurasia (Bespyatih, 2009; Nes *et al.*, 1988; Westwood 1989; Petersen 1914). Mitochondrial DNA analysis has identified Eastern Canada as the primary, if not sole, source of ancestry for farm-bred fox populations maintained at the ICG in Novosibirsk (Statham *et al.*, 2011).

SELECTION OF FOXES FOR TAME BEHAVIOR

In the beginning of the experiment, 130 foxes that showed less fearful and aggressive responses to humans were identified at several commercial fox farms across the former Soviet Union and brought to the experimental farm at the ICG to become the founders for the experimental population. The response to human presence was the sole selection criteria in this population. At first the selection was focused against aggressive responses to humans, as summarized in Trut *et al.*, 2004:

The main task at this stage of selection was eliminating defensive reactions to humans. In order to reveal variability in the expression of these reactions more completely, the animals in the selected population were subjected to more intensive contacts with humans than in usual practice. During these contacts, the pups were subjected to a number of tests: the experimenter attempted to hand feed, stroke or handle them. This type of human–animal communication continued for the first three to four months of life of the animals. As a result, the emotionally negative defensive reactions to humans in these foxes weakened, disappeared or, in some of the animals, emotionally positive reactions were formed. The foxes that retained aggressive–fearful reactions to humans in spite of the 3-month period of human contacts with them, were eliminated by selection from the population as soon as in 2 to 3 generations (Trut, 1980a, 1980b; Trut, 1999). In generation 4 of selection, the first pups appeared that did not form aggressive–fearful reactions to humans as a result of positive contacts with them. On the contrary, these pups demonstrated emotionally positive response to humans: when the experimenter approached them, they whined and wagged their tails anticipating a positive contact.

Results of the selection against defensive aggression became apparent after a few generations of selective breeding. Subsequently, selection for an emotionally positive (“friendly”) response to humans was applied. Behavior of all foxes was evaluated in a test with five consecutive stages: (1) observer approaches the cage; (2) observer stands near the closed cage; (3) observer opens the cage door and stands near by; (4) observer attempts to touch the fox; (5) observer closes the cage door, then stays near the closed cage (Trut, 1980a; Trut *et al.*, 2004). Fox behavior in this test was scored based on their response to humans using a categorical system (Table 10.1A). Behavior of young animals was tested several times during development and the final test was given to all pups at 7–8 month of age. Only the tamest individuals in each generation, less than 10%, were bred. At the same time a deliberate effort was made to avoid inbreeding (Kukekova *et al.*, 2004; Trut, 1999, 2001; Trut *et al.*, 2004). The response to selection was extremely rapid (Table 10.2). Improvement of behavioral scores recorded in fox pedigrees clearly showed genetic inheritance of tame behavior. It is important to note that except for the first few generations of selection, foxes from the population selected for tame behavior did not receive special handling. All human contacts were, and continue to be limited to maintenance and testing procedures. Foxes from the tame population show a friendly response to humans as early as one month postnatal and remain friendly throughout their entire lives. Tame foxes are eager to establish human contact, whimper to attract attention, and sniff and lick similar to dogs (Figure 10.1A). The behavior of tame foxes can be observed on the webpage: <http://cbsu.tc.cornell.edu/ccgr/behaviour/Index.htm>.

TABLE 10.1A System for Scoring Behavior in Tame Fox Population and Selecting the Most Tame Foxes for the Breeding Program

Animal Reaction	Scores
Passive-protection response; fox avoids experimenter or bites if stroked or handled, comes if offered food.	0.5–1.0
Foxes let themselves be petted and handled, but show no emotionally friendly response to experimenter.	1.5–2.0
Foxes show emotionally positive, friendly, response to experimenter, wagging tails and whining.	2.5–3.0
Foxes are eager to establish human contact, whimpering to attract attention and sniffing and licking experimenters like dogs. They start displaying this kind of behavior before one month postnatal age.	3.5–4.0

Tame behavior is scored from zero (representing “neutral” behavior; an absence of both active aggressive and tame responses directed towards the observer) to 4 (representing the most tame behavior).

Source: Trut (1980a).

(A) (B)

FIGURE 10.1 (A) Behavior of a fox from the tame population. (B) Behavior of a fox from the aggressive population. (*Photographs: Darya Shepeleva*)

SELECTION OF FOXES FOR AGGRESSIVE BEHAVIOR

In parallel with selection for tameness, selective breeding of farm foxes for aggressive behavior began in 1970s. Because there is deliberate selection on commercial farms against animals that show excessively aggressive responses to humans, selection of the aggressive strain at ICG was undertaken to preserve this behavior for research. Fifty farm-bred silver foxes with the most aggressive responses to humans were selected from several fox farms and used as founders of the aggressive population. The critical distance between experimenter and caged animal and the intensity of fox aggressive response were the major criteria for measuring aggression in the fox population, and to select animals for producing the next generation (Table 10.1B). Progress in selection for aggressive behavior did not follow the same pattern as selection for tame behavior, being slower in comparison (Trut 1980a, b). Foxes from the aggressive population are, however, consistently and distinctly aggressive towards humans and difficult to handle (Figure 10.1B).

BEHAVIORAL AND PHYSIOLOGICAL CHANGES ASSOCIATED WITH SELECTION FOR TAME BEHAVIOR

The genetic basis of fox tame and aggressive phenotypes has been clearly demonstrated in multiple experiments which included experimental cross-breeding of tame and aggressive animals, cross-fostering of newborn pups, and embryo transplantation (Kukekova *et al.*, 2008, 2011a; Trut, 1980a, b, 2001). Although selection of foxes for tame behavior was strictly limited to defined behavioral criteria, further developmental and behavioral differences emerged in tame foxes. Opening of the eyelids and the external auditory canal was accelerated; the sensitive period for socialization persisted past 60 days of age (compared to less than 45 days in unselected foxes); and play activity (normally only seen in infantile wild type foxes) extended into

TABLE 10.1B System for Scoring Behavior in Aggressive Fox Population and Selecting the Most Aggressive Foxes for the Breeding Program

Animal Reaction	Scores
Fox shows teeth, snarls, growls at first sight of human . When experimenter is near closed cage fox attacks experimenter and other objects in field of view. Bared teeth and fixed dilated pupils.	−4.0
When experimenter is near closed cage , fox shows teeth, snarls, growls, tries to attack both the experimenter and other objects in field of view. Bared teeth and fixed dilated pupils.	−3.5
When experimenter is near open cage , fox shows teeth, snarls growls, attacks experimenter and other objects in the field of view. Bared teeth and fixed dilated pupils.	−3.0
When experimenter is near the open cage , fox growls but does not attack.	−2.5
When experimenter, near the open cage , moves protected arm towards fox, it growls and tries to bite.	−2.0
As experimenter opens cage, fox is calm, but attempts to touch the fox provoke it to show teeth and snarl.	−1.5

The score is based on the critical distance between the experimenter and the caged fox when the animal first demonstrates an aggressive reaction to the experimenter's presence. Originally the scoring system was based on a range from zero (least aggressive) to −4 (most aggressive). However, after multiple generations of selection, no current individuals exhibit behavior scoring between −1.5 and 0.

Source: [Trut \(1980a\)](#).

TABLE 10.2 The Number and Proportion of Elite-Behavior Progeny at Different Stages of Selection

Year of Study (Generation of selection)	Number of Progeny Scored	Out of them, Elite Animals	
		<i>Number</i>	<i>Proportion (%)</i>
1965 (F ₆)	213	4	1.8
1970 (F ₁₀)	370	66	17.8
1980 (F ₂₀)	1438	503	35.0
1990 (F ₃₀)	1641	804	49.0
2002 (F ₄₂)	902	642	71.2

Source: [Trut et al. \(2004\)](#).

adulthood ([Belyaev et al., 1985](#); [Plyusnina et al., 1991](#); [Trut, 2001](#)). Tame foxes developed a novel repertoire of vocalizations toward humans ([Gogoleva et al., 2009, 2011](#)). Significant differences in corticosteroid and neurotransmitter levels were found between tame and control foxes

(Oskina and Tinnikov, 1992; Popova *et al.*, 1997). Significant differences in hypothalamic–pituitary–adrenocortical (HPA) system reactivity in ontogenesis were observed between foxes from tame and unselected populations (Oskina, 1996; Trut and Oskina, 1985). Significantly lower density of serotonin 5-HT_{1A} receptors was observed in the hypothalamus; and significantly higher levels of serotonin and tryptophan hydroxylase were detected in the midbrain and hypothalamus of domesticated strain of foxes (Popova *et al.*, 1997, 2007; Trut, 2001). The transformation of the seasonal reproductive pattern was also observed. Some foxes from the tame population showed sexual activity outside of the regular breeding season and a few females have been mated twice in a year, a pattern which was not recorded for foxes in nature or in commercial bred populations (Belyaev and Trut, 1983; Trut 1980b).

Several *de novo* traits were detected in the fox population selected for tameness. In particular, coat color changes such as the appearance of a white spot on the head (Star phenotype) and loss of pigment in other areas began to appear in the eighth selected generation (Belyaev *et al.*, 1981). It is intriguing that white spotting, which appeared without direct selection or inbreeding in the tame fox population, is frequently observed as a distinctive difference between domesticated animals of several species (dogs, cats, cattle, horses, etc.) and their wild progenitors. Other morphological characteristics also arose in the same manner: some foxes had floppy ears until significantly older age than foxes from commercial populations, some had rolled tails, some had changes in the skull shape that made them look more like dogs (Trut *et al.*, 1991, 2009).

The basis of the morphological and physiological changes that occurred in the course of selection for tame behavior in the farm fox population is unclear. Genetic drift is plausible, as is genetic hitchhiking, especially if genes involved in development or physiology are located on the same chromosomes and in close proximity to genes involved in behavior. Selection acting on behavioral genes would inevitably act as well on tightly linked neighboring genes. In-phase alleles for both behavioral genes and neighboring genes on the same haplotype would be inherited together until sufficient generations passed for the haplotype to be broken by recombination events. Selection for rare alleles of genes involved in development and physiology could promote the development of novel phenotypes or increase the frequency of rare ones. Indeed, the higher rate of atypical phenotypes was observed during the early stages of selection for behavior. Alternatively, genes involved in behavior could have a pleiotropic effect and be involved in regulatory processes not only restricted to behavior, but that play an important role in animal development and physiology (Belyaev, 1879; Trut, 1999, 2001; Trut *et al.*, 2009). Support for this hypothesis comes from the observation that multiple behavioral and morphological changes observed in tame foxes are associated with delayed or truncated development (Trut, 1999, 2001; Trut *et al.*, 2009). This concept of neoteny, the retention of

puppy-like traits into adulthood, is widely used to explain behavioral, morphological, and physiological changes associated with dog domestication as well (Coppinger and Coppinger, 2001; Wayne, 1986).

The multifaceted changes observed in the course of selection of foxes for tame behavior affirm the destabilizing hypothesis of Dmitry Belyaev (1979). The molecular mechanisms underlying these phenomena are best addressed by analyzing the genetic architecture of fox behavior.

IDENTIFICATION OF LOCI AND GENES IMPLICATED IN FOX BEHAVIOR

The strains of tame and aggressive foxes provide a robust model for identification of genes and loci involved in behavioral differences between the two populations. Unlike modern dogs, the strain of domesticated foxes was created rapidly by selection focused exclusively on specific behavioral traits. Although these fox strains have been carefully studied for several decades, only recently has it become possible to consider a systematic approach to identify the loci and molecular mechanisms controlling these behaviors. Classical genetic approaches to genome mapping had derived a rudimentary map of the fox genome by 1998, with a well-defined fox karyotype (Graphodatsky *et al.*, 1981, 1995; Yang *et al.*, 1999) and sparsely populated linkage groups (for a review, see Rubtsov, 1998). To begin an attack on the molecular genetics of behavior in these foxes, however, further resources were essential, including a set of suitable pedigrees for mapping, an adequate set of suitable molecular markers, and a robust method for measuring behavior in re segregating pedigrees.

RESOURCES FOR MAPPING FOX BEHAVIOR

Accordingly, a program was instituted at ICG to crossbreed foxes from the tame and aggressive strains, producing an F1 population, and subsequently generating informative backcross and intercross pedigrees. Simultaneously, the canine genome sequence and linkage map were exploited to identify a set of microsatellite markers shared between the dog and the fox (Kukekova *et al.*, 2004). Approximately 60% of canine markers proved useful for interrogating the fox genome.

To construct a meiotic linkage map of the fox genome, 286 individual foxes (180 animals in the third generation) from 37 pedigrees were genotyped, for a total of 320 markers (Kukekova *et al.*, 2007). A second generation of the fox meiotic linkage map was then developed using an extended set of fox three-generation pedigrees, including a total of 916 progeny in informative generations, and adding a further 93 microsatellite markers adapted from dog genome sequence and the recently published genetic maps of the dog genome (Sargan *et al.*, 2007; Wong *et al.*, 2010). This increased

the total number of markers on the map to 408 (Kukekova *et al.*, 2011a, 2012), 405 of which could be uniquely identified in the 7.6x genome sequence of the dog. The resulting fox linkage map is thus directly anchored to the dog genome sequence, enabling detailed comparisons to be made between corresponding chromosomal fragments of the two species and indirect comparisons between fox and human chromosomes. The resulting sex-averaged map comprises 1548.5 cM (Kukekova *et al.*, 2011a) that covers 16 fox autosomes and the X chromosome. Alignment of the fox meiotic map against the 7.6x canine genome sequence revealed high conservation of marker order between homologous regions of the two species and provides a robust method for predicting the chromosomal location of the fox orthologs of genes identified in the canine or human genome sequences (Kukekova *et al.*, 2007, 2011a, 2012).

MEASUREMENT OF FOX BEHAVIORAL PHENOTYPES

In the course of the selective breeding program, the behavioral phenotypes in the selected tame and aggressive populations quickly diverged, and separate scoring systems for assignment of fox behavioral phenotypes were developed for the tame (Table 10.1A) and the aggressive population (Table 10.1B) (reviewed in Kukekova *et al.* 2005; Trut 1980a, b, 1999, 2001). However, a single, unified scoring system was required for measuring behavior in experimental pedigrees descended from crosses of the tame and aggressive strains. Individuals in such pedigrees have a wide range of behaviors and often exhibit fragmented or reshuffled elements of the behavioral patterns characteristic of the founder populations.

A new method was devised that could measure the variation in quantitative behavioral phenotypes between different fox populations as well as the resegregation of behaviors in experimental pedigrees. This new system was rooted in the traditional behavioral test used for selective breeding (Vasilieva and Trut, 1990; Trut 1980b, Trut *et al.*, 2004, see Table 10.1). Fox responses to humans were evaluated in a standard series of four sequential steps that were videotaped (Kukekova *et al.*, 2008, 2011a).

- Step A: observer stands calmly near the closed cage but does not deliberately try to attract the animal's attention;
- Step B: observer opens the cage door, remains nearby but does not initiate any contact with the fox;
- Step C: observer attempts to touch the fox;
- Step D: observer closes the cage door, then stays calmly near the closed cage.

Because all foxes live under consistent conditions including similar interactions with humans and because their behavior is tested at precise time points using standard tests under constant conditions, the environmental factors that might influence behavior were held to a strict minimum.

An ethological survey of these videotaped tests identified over 300 discrete behavioral observations (traits) which could be reproducibly scored from video records in a binary fashion, e.g., presence or absence. Examples, each simply scored Yes or No, include: “Wagging Tail?”; “Stays at the front wall of the cage?”; and “Ears pinned?” (Kukekova *et al.*, 2008). Evaluation of these traits for informativeness, redundancy, reproducibility, and consistency identified two overlapping sets of traits: (i) a minimal set of 50 traits that reliably distinguished fox populations along a tame–aggressive axis (Kukekova *et al.*, 2008); and (ii) a larger, 98-trait set (Kukekova *et al.*, 2011a), that includes all traits from the minimal trait set plus additional traits that capture other dimensions of fox behavior (Kukekova *et al.*, 2011a).

Behavior of foxes from parental (tame and aggressive) and crossbred pedigrees was evaluated using this standardized testing protocol and videotaped. The resulting videotape dataset comprised a total of 1003 foxes (83 tame foxes, 80 aggressive, 93 F1, 293 backcross-to-tame, 202 backcross-to-aggressive, and 252 F2 foxes). Video records were analyzed to deconstruct fox behavior by scoring for the presence or absence of each of 98 specific binary traits (Kukekova *et al.*, 2011a). Principal-components (PC) analysis was then used (Kukekova *et al.*, 2011a), to identify independent (i.e. uncorrelated) underlying factors (i.e. the principal components) that accounted for decreasing amounts of the total variance in observed behavior (Kukekova *et al.*, 2011a). Specific methodological aspects of the PC analysis are described in Kukekova *et al.*, 2008 and 2011a.

In this large data set, the first two principal components, PC1 and PC2, accounted for 33% and 9% of the total behavioral variation, respectively (Kukekova *et al.*, 2011a). PC1 clearly distinguished tame foxes from aggressive foxes; F1 foxes yield intermediate values that extend into the ranges of both the tame and aggressive foxes. The scores of the backcross generations reaggregate (Figure 10.2A) such that mean values of PC1 in the different populations defined a linear gradient of heritable behavior, ranging from aggressive to tame, that clearly corresponds to the relative proportions of aggressive to tame ancestry in each population (Figure 10.2A).

PC2 did not follow a similar gradient (Figure 10.2B). Review of the discrete behavioral traits that contribute to these two principal components demonstrated that PC1 and PC2 are comprised of very different aspects of behavior (Figure 10.3). PC1 is comprised of traits that distinguish overall aggressiveness from tameness, whereas most of the traits important to PC2 can be interpreted as distinguishing bold from shy behavior (independent of the degree to which a fox was tame or aggressive).

QTL MAPPING OF FOX BEHAVIOR

These two principal components of behavior were used as phenotypes to identify associated quantitative trait loci (QTL) in informative fox pedigrees

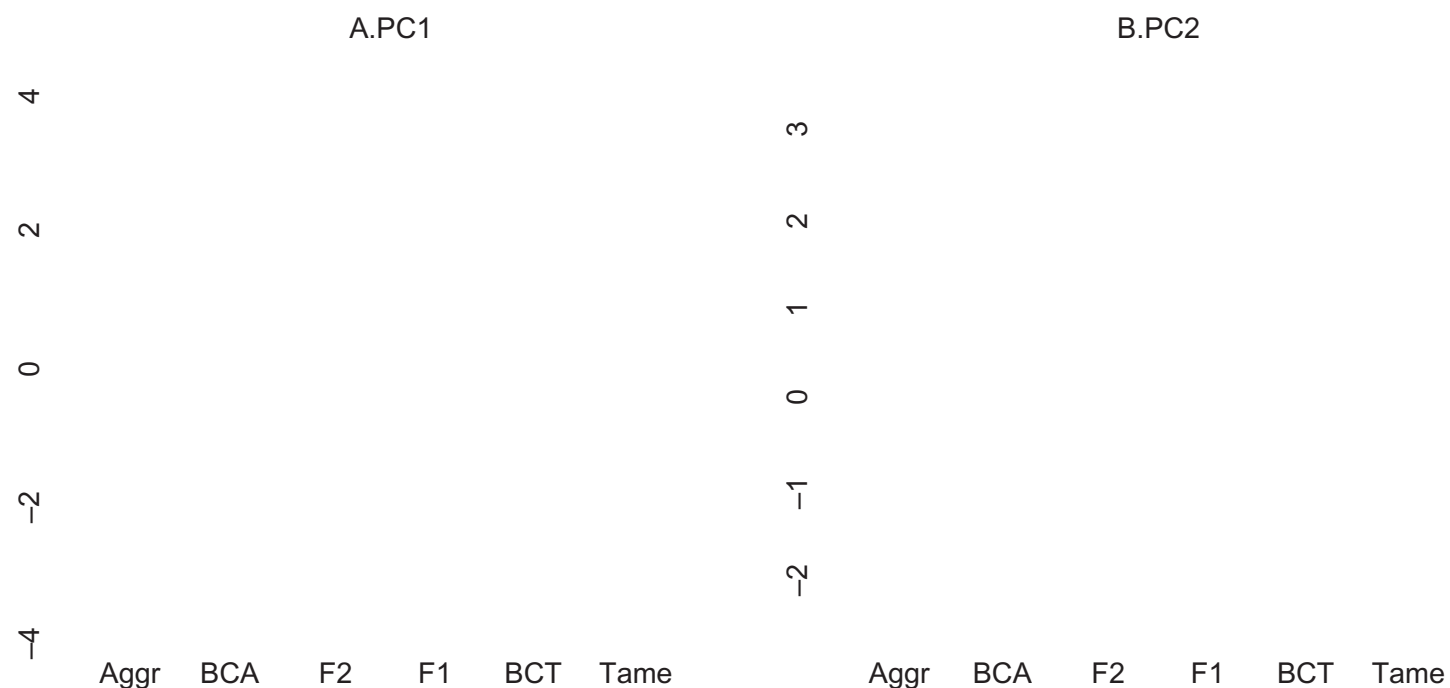


FIGURE 10.2 Population distributions for the first two principal components of silver fox behavior. (A) Distributions for principal component 1 (PC1). (B) Distributions for PC2. Aggr = “aggressive” founder population; BCA = backcross-to-aggressive; F2 = F2 population (F1 × F1); F1 = F1 population (“tame” × “aggressive”); BCT = backcross-to-tame population; Tame = “tame” founder population. Horizontal bars within each box indicate the population median. Confidence intervals for the medians are shown as notches such that two distributions with non-overlapping notches are significantly different (at $P < 0.05$). The bottom and top edges of the boxes indicate the 25th and 75th percentiles. The whiskers indicate the range of data up to 1.5-times the interquartile range. Outliers are shown as individual circles. In each of the populations, the PC1 distribution pattern conforms to that expected for a heritable trait reflecting the proportional contributions from “Tame” and “Aggressive” ancestry. This is clearly not the case for PC2.

by interval mapping. Fox informative pedigrees included three populations: backcross-to-tame (293 progeny), backcross-to aggressive (202 progeny), and intercross (F2) (250 progeny) (Kukekova *et al.*, 2011a).

Interval mapping in the combined data set, which included all the experimental pedigrees, identified a locus for PC1 on fox chromosome 12 (VVU12), located in a region between 10 and 60 cM (Figure 10.4A). Intriguingly, part of this QTL interval on VVU12 is homologous to canine chromosome 5 (Figure 10.5) and includes a region corresponding to a genomic location recently implicated in domestication of dogs from wolves (VonHoldt *et al.*, 2010). On the fox meiotic map, this conserved syntenic region lies between markers CM5.41 and CM5.60, or between 27.2 and 28.4 cM, respectively. Among individual behavioral traits that map precisely to this interval are B3 (touches observer’s hand) and C17 (allows observer to touch belly), both traits of trustfulness that will be immediately familiar to persons familiar with dogs and other domesticated species.

In contrast to PC1, PC2 did not yield a significant peak on VVU12 using the combined data set. However, PC2 also mapped to VVU12 when only the backcross-to-tame segregants were used for interval mapping (Figure 10.4B). This result provides insight into the complex expression of behavioral phenotypes in different populations. It suggests that, although independent by

A. (Sorted by C.PC1)				B. (Sorted by C.PC2)			
Trait	Trait description	C.PC1	C.PC2	Trait	Trait description	C.PC1	C.PC2
*	C37 Aggressive sounds	-86	8	C7	Observer can first touch fox in zones 5-6	-2	-41
	C34 Follows the hand (aggr.)	-84	14	C38	Fox remains only in zones 3-5-6	-1	-39
	C31 Attack alert	-83	12	C4	Spends more than 30 seconds in zones 3-4-5-	-3	-33
	C32 Pinned ears (aggr.)	-56	8	C35	Narrow ears directed back	3	-26
	C36 Triangle ears directed back (aggr.)	-42	4	C3	Fox is in zones 3-4-5-6 at the beginning of step C	-4	-24
	C33 Trying to bite	-33	12	C13	Fox allows observer to touch the rear part of its back	49	-18
	C30 Attack	-33	20	C14	Fox allows observer to touch its back	73	-15
	C55 Leans on back or side walls in zones 5-6	-5	-14	C55	Leans on back or side walls in zones 5-6	-5	-14
	C3	-4	-24	C16	Fox allows observer to touch its head	105	-12
	C4 Spends more than 30 seconds in zones 3-4-5-6	-3	-33	C15	Fox allows observer to touch its nose	115	-10
**	C7 Observer can first touch fox in zones 5-6	-2	-41	C8	Lies down during a contact for at least 5 seconds	88	0
	C38 Fox remains only in zones 3-5-6	-1	-39	C50	Tail is up for at least for 3 seconds	-1	1
	C50 Tail is up for at least for 3 seconds	-1	1	C6	Observer can first touch fox in zones 3-4	18	4
	C35 Narrow ears directed back	3	-26	C36	Triangle ears directed back (aggr.)	-42	4
***	C39 Moved forward at least one zone during the step	3	29	C12	Tame ears	107	7
	C2 Fox is in zones 1-2-3-4 at the beginning of step C	6	24	C37	Aggressive sounds	-86	8
	C6 Observer can first touch fox in zones 3-4	18	4	C32	Pinned ears (aggr.)	-56	8
	C204 Tame sounds (combined)	18	10	C204	Tame sounds (combined)	18	10
	C19 Comes into zone 2 at the end of step C	21	19	C33	Trying to bite	-33	12
	C25 Wagging tail	25	13	C31	Attack alert	-83	12
	C18 Fox holds observer's hand with its mouth	26	14	C25	Wagging tail	25	13
	C17 Fox rolls onto its side, inviting observer to touch its belly	27	20	C18	Fox holds observer's hand with its mouth	26	14
	C29 Comes to and sniffs observer's hand at the end of step C	32	14	C29	Comes to and sniffs observer's hand at the end of step C	32	14
	C24 Loud breathing	36	20	C34	Follows the hand (aggr.)	-84	14
	C13 Fox allows observer to touch the rear part of its back	49	-18	C19	Comes into zone 2 at the end of step C	21	19
	C14 Fox allows observer to touch its back	73	-15	C30	Attack	-33	20
	C8 Lies down during a contact for at least 5 seconds	88	0	C17	Fox rolls onto its side, inviting observer to touch its belly	27	20
	C16 Fox allows observer to touch its head	105	-12	C24	Loud breathing	36	20
	C12 Tame ears	107	7	C2	Fox is in zones 1-2-3-4 at the beginning of step C	6	24
****	C15 Fox allows observer to touch its nose	115	-10	C39	Moved forward at least one zone during the step	3	29

FIGURE 10.3 Comparison of behavioral traits contributing to the first two principal components of silver fox behavior at test step C (C.PC1 and C.PC2). All observations from one step of the test (Step C “Observer attempts to touch the fox”) are shown. Behavioral observations (traits) contributing to C.PC1 and C.PC2 are ranked according to their loadings (eigenvalues) from principal component analysis. The significances for each trait loading for C.PC1 and C.PC2 are shown as the number of standard errors from zero (negative or positive) as established by bootstrap trials. Note in particular the difference in ranking for the traits marked with asterisks. C.PC1 and C.PC2 are very different behavioral gestalts. PC1 is comprised of traits that contribute to overall aggressiveness (*) or tameness (****), whereas PC2 represents traits that are marked by either passivity (**) or activity (***).

definition, the phenotypes measured by PC1 (tameness *vs* aggressiveness) and PC2 (bold *vs* shy) are not entirely unrelated, as PC2 can enhance the observed expression of PC1. That is, if an animal is aggressive, passive behavior will reduce the perceived expression of that trait whereas active behavior will enhance the expression, and the same effect applies if an animal is tame. In backcross populations the distribution of behavior is skewed toward the extreme of the recurrent parent, reducing the range of tame *vs* aggressive behaviors. Under these circumstances, PC2 acts to increase that range. We would therefore expect that whereas PC1 and PC2 are distinct principal components in a matrix composed of all populations, they could be correlated in particular backcross populations. This is in fact the case for the backcross-to-tame populations ($r = 0.75-0.8$). In contrast, in F2 populations where the behaviors are more normally distributed, this is not the case ($r = -0.06$). It could well be, therefore, that the PC2 QTL on VVU12 in the backcross-to-tame population reflects enhancement of the expression of PC1.

TRANSCRIPTOME ANALYSIS

A good example of an approach that can be applied for identification of genes and regulatory elements involved in fox behavioral phenotypes is the

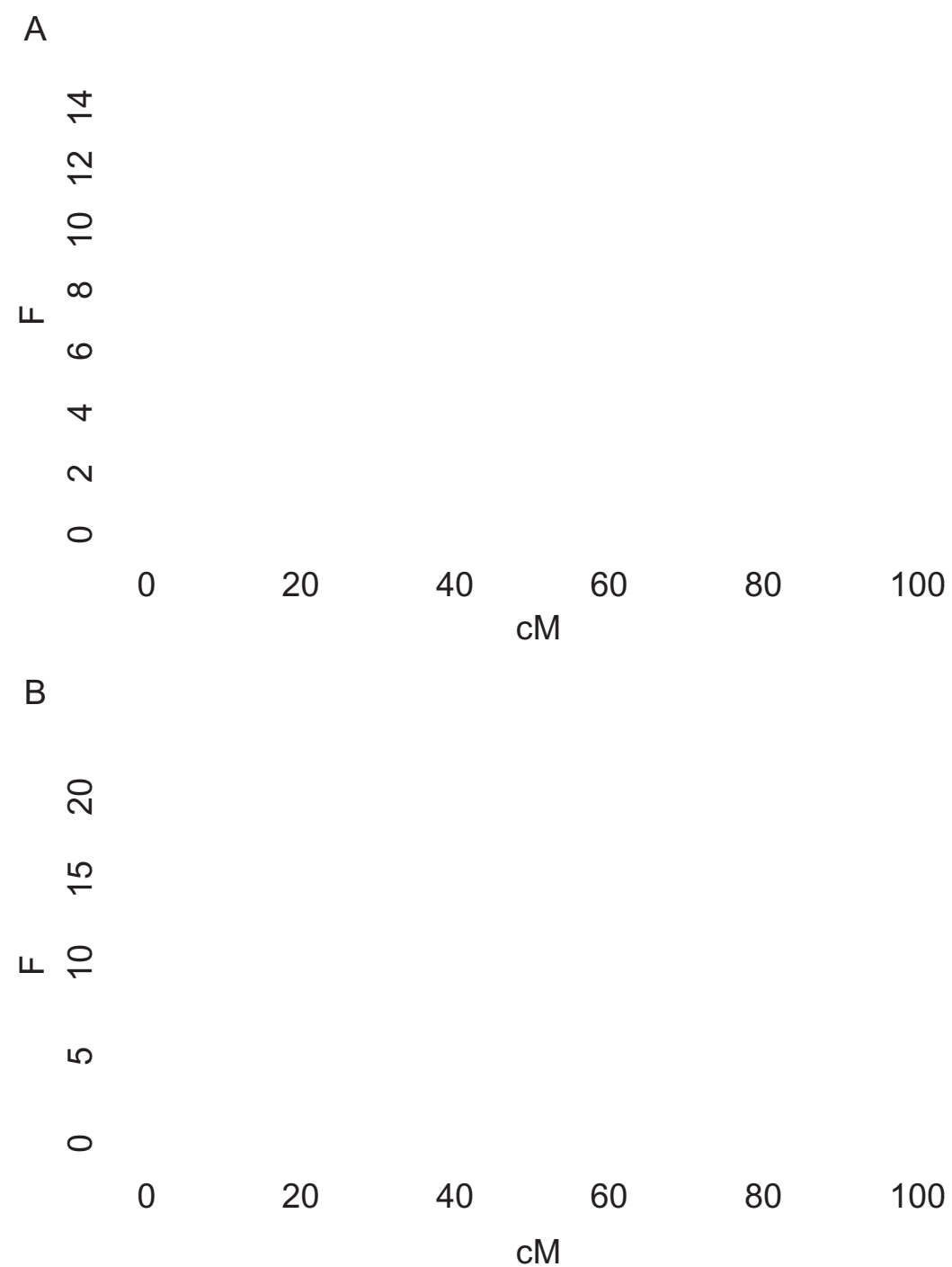


FIGURE 10.4 Interval mapping of the first two principal components of silverfox behavior (PC1, PC2) to Fox chromosome 12 (VVU12). Interval mapping using GridQTL software, was undertaken on (A) a combined data set including all experimental silver fox populations; and (B) Backcross-to-tame population only (i.e. excluding backcross-to-aggressive, and F2). Solid lines = PC1, dashed lines = PC2. The F stat (y-axis) is graphed as a function of cM distance across VVU12 (data and map distances from: Kukekova *et al.* 2011). Horizontal lines (solid = PC1, dashed = PC2) = thresholds for genome wide significance at $P < 0.01$. Interval mapping across all populations (A) yields support for PC1-associated loci on VVU12, located broadly between 10 and 60 cM, that exceeds the threshold for genome-wide significance; but support for PC2 does not achieve significance. Interval mapping restricted to backcross-to-tame populations (B) yields support for PC2-associated loci on VVU12, located broadly between 10 and 60 cM, that exceeds the threshold for significance; but support for PC1 does not achieve significance.

analysis of the transcriptome of tame and aggressive foxes. High-throughput genetic sequencing of all the gene transcripts expressed in a specific tissue sample yields that sample's transcriptome, and provides quantitative information about gene expression in different tissues. Comparative analysis of gene expression in tame and aggressive foxes will highlight the expressed parts of the genome that differentiate the strains. Furthermore, comparison of gene expression profiles and loci (QTL) identified in the course of genetic

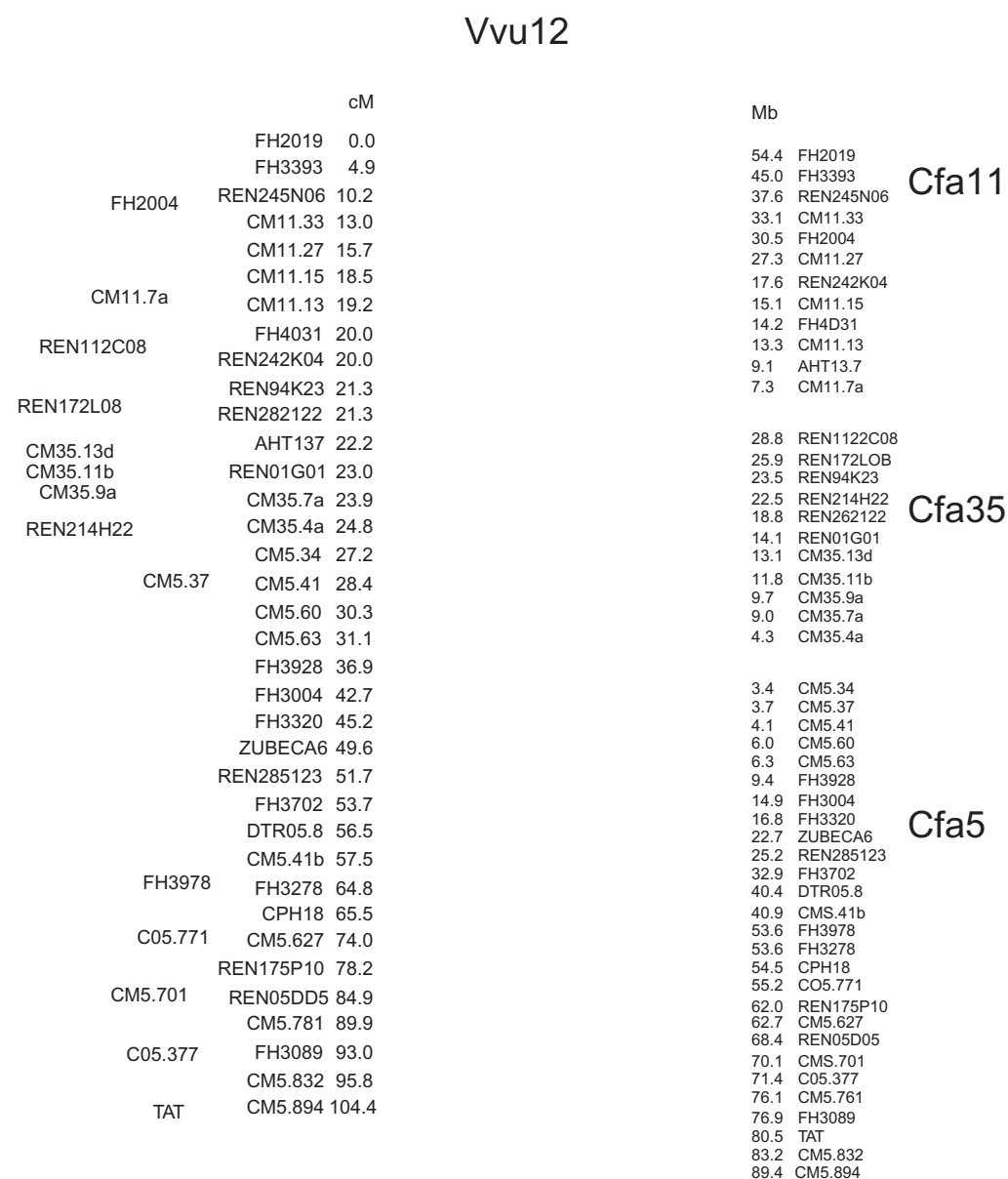


FIGURE 10.5 A locus for the first principal component of behavior (PC1) on Fox chromosome 12 (VVU12). The meiotic linkage map of VVU12 (left side of figure) is aligned to the genome sequence of the homologous canine chromosomes (CFA11, CFA35, CFA5) on the right side of the figure (data and map distances from Kukekova *et al.*, 2011). In the middle of the figure, the gray interval indicates the broad support interval for PC1 in the silverfox, and the black interval a region homologous to a locus on CFA 5 identified with domestication of the wolf (VonHoldt *et al.*, 2010).

mapping will help to identify genes under selection for behavior. Transcriptome sequencing of brain samples from tame and aggressive foxes has recently been initiated (Kukekova *et al.*, 2011b). Although only preliminary results have so far been reported, this has provided significantly expanded genomic resources for the fox, a species without a sequenced genome; as well as significant insights into the gene expression profile of the fox prefrontal cortex, expression differences between fox samples, and a catalog of potentially important gene-specific sequence variants (Kukekova *et al.*, 2011b). This approach can provide valuable insights into the molecular mechanisms implicated in behavioral differences between the two strains.

WHAT THE FARM-FOX EXPERIMENT TELLS US ABOUT BEHAVIOR

One of the most striking results of the farm-fox experiment is the clear demonstration of the influence of genes on behavior (Kukekova *et al.*, 2008, 2011a; Trut, 1980a, b, 2001).

The farm-fox experiment showed that modification of a specific behavior (friendly response to humans) can affect other aspects of behavior as well. Tame foxes are eager to establish human contact from a very early age (Trut, 1999), develop close attachment to their owners when raised in human homes (Trut, personal communication), and are as skillful as dog puppies in using human point-and-gaze gestures for finding the hidden food (Hare *et al.*, 2005; Hare and Tomasello, 2005). Behavioral testing of kits from two farm-bred populations (i.e. the unselected population and the population selected for tame behavior), using the object-choice test, demonstrated that although fox communicative skills had not been used as a selection criterion (Trut *et al.*, 2009), the tame foxes were as skillful in reading proximal point cues as age-matched puppies of domestic dogs and outperformed foxes from the unselected population. These results suggest that reduced fear and/or aggression to humans may be a prerequisite for the development of advanced inter-specific communicative skills in canids and the ability and willingness of tame foxes to read human cues has appeared as a by-product of, or is associated with, the selection for tame behavior (Hare *et al.*, 2005). Thus, the fox experiment provides an independent line of evidence for the argument that reducing fear and aggression can support the development of interactive behaviors.

Play activity of tame foxes persists into adulthood and they actively seek communication with humans and other foxes (Belyaev *et al.*, 1985; Kukekova and Trut, 2010; Plyusnina *et al.*, 1991). Many other differences of behavior between tame and aggressive foxes that are not directly related to their response to humans remain to be investigated.

Selection of foxes for positive responses to humans led rapidly to the development of a behavioral repertoire with significant parallels to that of domestic dogs. The prehistoric domestication of the dog from the wolf may have taken a longer time and more generations but in all probability was similarly achieved through selection for behavioral modifications. The similarities between the behaviors of domesticated foxes and dogs suggest that the behavioral response to humans in these two species could involve similar sets of genes.

SUMMARY

Archeological and molecular data have well documented the long history of coexistence of humans and dogs. Although the full scenario of historical dog domestication remains to be determined, the behavioral differences between dogs and wolves strongly argue that selection for behavior was the force that created “Man’s best friend”. The fox domestication experiment demonstrated that many behavioral characteristics that differentiate dogs from wolves can be obtained by selection solely for a friendly response to humans. The rapid progress in selection of foxes for tame behavior strongly suggests that selection was acting on genetic variation pre-existing in the founder fox population. These results support dog domestication hypotheses that suggest that pre-dog

wolves underwent natural selection for behavioral traits that allowed them to coexist with humans. Genetic variants pre-existing in wolf populations were likely targets of this selection. Support for this theory of selection for pre-existing variants also arises from recent studies of size in dogs. While all small breeds of dogs are fixed for a specific variant of the *IGF1* gene (Sutter *et al.*, 2007) the same allele was found to segregate in a modern population of gray wolves from the Middle East (Gray *et al.*, 2010) and in Portuguese Water dogs, a breed in which the size variation takes place (Chase *et al.*, 2002).

Identification of loci that both influence tame behavior in foxes and are homologous to regions in the dog genome supporting genetic signals related to selection of dogs from wolves leads to the intriguing hypothesis that domesticated behavior in dogs and foxes may have similar genetic bases.

Not only do dogs differ in their behavior from wolves, but different breeds of dog are characterized by genetically determined differences in behavior. Although the latter differences are highly characteristic and readily recognized, in fact each such behavioral pattern likely represents a synthesis of many discrete behaviors. This synthesis has been clearly demonstrated in the fox study. For example, the apparently simple response to human presence can be influenced by many behavioral characteristics at once: interplay of discrete mechanisms captured by the tame–aggressive (PC1) and bold–shy (PC2) dimensions are just two of the most obvious ones that influence the test outcome. However, a detailed understanding of the genetic basis of behavior in dogs requires well-defined phenotypes, as well as control of environmental factors and gene–environment interactions that can strongly influence behavioral outcomes. These are not as easily implemented as in the fox study.

Although domestication has, for many years, been of great interest to scientists, most notably including Darwin, until recently basic questions concerning the genetic mechanisms involved have been difficult to address. With modern advances in molecular genetic technologies, however, it is now feasible to pursue research on diverse organisms to find the links between genes, brain function, and a wide range of social behaviors (Robinson *et al.*, 2005, 2008).

We expect that identification of the molecular mechanisms underlying domesticated behavior in foxes and dogs will help us to understand basic biological principles guiding social behavior in mammals and to provide insights into our own behavior as well.

ACKNOWLEDGMENTS

We thank Dr. K. Gordon Lark, Kevin Chase, and Anastasiya V. Kharlamova for insightful discussions and to Dr. Lark for critical reading of the manuscript. We would like to express profound gratitude to members of Dr. Trut, Dr. Acland, and Dr. Kukekova's

groups and all personnel of the ICG experimental farm for many years of dedicated work on this project. We gratefully acknowledge NIH grants RO1MH077811, R24GM082910, RO1EY006855, and FCP84-74 for support.

REFERENCES

- Acland, G.M., Ostrander, E.A., 2003. The dog that came in from the cold. *Heredity* 90, 201–202.
- American Kennel Club, *The Complete Dog Book: Official Publication of the American Kennel Club* (Howell Book House, New York, ed. 20, 2006).
- Anderson, T., vonHoldt, B.M., Candille, S.I., et al., 2009. Molecular and evolutionary history of melanism in North American gray wolves. *Science* 323 (5919), 1339–1343.
- Andersone, Z., Lucchini, V., Randi, E., et al., 2002. Hybridisation between wolves and dogs in Latvia as documented using mitochondrial and microsatellite DNA markers. *Mamm. Biol.* 67, 79–90.
- Andersson, L., 2009. Studying phenotypic evolution in domestic animals: a walk in the footsteps of Charles Darwin. *Cold Spring Harb. Symp. Quant. Biol.* 74, 319–325.
- Andersson, L.S., Larhammar, M., Memic, F., Wootz, H., Schwochow, D., Rubin, C.J., et al., 2012. Mutations in *DMRT3* affect locomotion in horses and spinal circuit function in mice. *Nature* 488 (7413), 642–646, Aug 30.
- Anholt, R.R.H., Mackay, T.F.C., 2009. *Principles of Behavioral Genetics*. Elsevier Academic Press, Oxford, UK.
- Ardalan, A., Oskarsson, M., Natanaelsson, C., Wilton, A.N., Ahmadian, A., Savolainen, P., 2012. Narrow genetic basis for the Australian dingo confirmed through analysis of paternal ancestry. *Genetica* 140 (1–3), 65–73, Mar.
- Arhanta, C., Bubna-Littitzb, H., Bartelsc, A., Futschikd, A., Troxlera, J., 2010. Behaviour of smaller and larger dogs: effects of training methods, inconsistency of owner behaviour and level of engagement in activities with the dog. *Appl. Anim. Behav. Sci.* 123 (3–4), 131–142.
- Axelsson, E., Ratnakumar, A., Arendt, M.-L., Maqbool, K., Webster, M.T., Perloski, M., et al., 2013. The genomic signature of dog domestication reveals adaptation to a starch-rich diet. *Nature*. Published online January 23.
- Belyaev, D.K., 1969. Domestication of animals. *Science (Russ.)* 5, 47–52.
- Belyaev, D.K., 1979. Destabilizing selection as a factor in domestication. *J. Hered.* 70, 301–308.
- Belyaev, D.K., Trut, L.N., 1983. Reorganization of the seasonal rhythm of reproduction in the silver black foxes during their selection for the capacity to domestication. *Zh. Obshch. Biol.* 42, 739–752, In Russian.
- Belyaev, D.K., Trut, L.N., 1989. The convergent nature of incipient forms and the concept of destabilizing selection. In: Ovchinnikov, Y.A., Rapoport, I.A. (Eds.), *Vavilov's Heritage in Modern Biology*. Nauka, Moscow, pp. 155–169.
- Belyaev, D.K., Ruvinsky, A.O., Trut, L.N., 1981. Inherited activation–inactivation of the star gene in foxes: its bearing on the problem of domestication. *J. Hered.* 72 (4), 267–274, Jul–Aug.
- Belyaev, D.K., Plyusnina, I.Z., Trut, L.N., 1985. Domestication in the silver fox (*Vulpes fulvus Desm*): changes in physiological boundaries of the sensitive period of primary socialization. *Appl. Anim. Behav. Sci.* 13, 359–370.

- Bennett, P.C., Rohlf, V.I., 2007. Owner–companion dog interactions: relationships between demographic variables, potentially problematic behaviours, training engagement and shared activities. *Appl. Anim. Behav. Sci.* 102, 65–84.
- Bespyatih, O.Y., 2009. The consequences of amber acid feeding in different genotypes of farm-bred foxes. *VOGIS (Russian)* 13 (3), 639–646.
- Bowlby, J., 1958. The nature of the child’s tie to his mother. *Int. J. Psychoanal.* 39, 350–371.
- Boyko, A.R., Boyko, R.H., Boyko, C.M., Parker, H.G., Castelhano, M., Corey, L., et al., 2009. Complex population structure in African village dogs and its implications for inferring dog domestication history. *Proc. Natl. Acad. Sci. U.S.A.* 106 (33), 13903–13908.
- Boyko, A.R., Quignon, P., Li, L., Schoenebeck, J.J., Degenhardt, J.D., Lohmueller, K.E., et al., 2010. A simple genetic architecture underlies morphological variation in dogs. *PLoS Biol.* 8 (8), e1000451, Aug 10.
- Bräuer, J., Call, J., Tomasello, M., 2004. Visual perspective taking in dogs (*Canis familiaris*) in the presence of barriers. *Appl. Anim. Behav. Sci.* 88 (3), 299–317.
- Brown, S.K., Pedersen, N.C., Jafarishorijeh, S., Bannasch, D.L., Ahrens, K.D., Wu, J.T., et al., 2011. Phylogenetic distinctiveness of Middle Eastern and Southeast Asian village dog Y chromosomes illuminates dog origins. *PLoS ONE* 6 (12), e28496.
- Brüne, M., 2007. On human self-domestication, psychiatry, and eugenics. *Philos. Ethics. Humanit. Med.* 2, 21.
- Cadiou, E., Neff, M.W., Quignon, P., Walsh, K., Chase, K., Parker, H.G., et al., 2009. Coat variation in the domestic dog is governed by variants in three genes. *Science* 326 (5949), 150–153, Oct 2.
- Call, J., Bräuer, J., Kaminski, J., Tomasello, M., 2003. Domestic dogs (*Canis familiaris*) are sensitive to the attentional state of humans. *J. Comp. Psychol.* 117 (3), 257–263, Sep.
- Cesarino, F., 1975. *Il Molosso: Viaggio Intorno Al Mastino Napoletano*. Casa editrice Faustino Fiorentino, Napoli, p.203.
- Chase, K., Carrier, D.R., Adler, F.R., Jarvik, T., Ostrander, E.A., Lorentzen, T.D., et al., 2002. Genetic basis for systems of skeletal quantitative traits: principal component analysis of the canid skeleton. *Proc. Natl. Acad. Sci. U.S.A.* 99 (15), 9930–9935, Jul 23.
- Clark, N.R.A., 2003. *1840–2000, Dog Called Blue: The Australian Cattle Dog and the Australian Stumpy Tail Cattle Dog*. WrightLight Publishers, Wallacia, NSW.
- Clutton-Brock, J., 1981. *Domesticated Animals from Early Times*. British Museum (Natural History)/Heinemann, London.
- Clutton-Brock, J., 1995. Origins of the dog: domestication and early history. In: Serpell, J. (Ed.), *The Domestic Dog: Its Evolution, Behaviour, and Interactions with People*. Cambridge Univ Press, Cambridge, UK, pp. 7–20.
- Combe, I., 1987. *Herding Dogs, Their Origins and Development in Britain*. Faber & Faber Ltd., London.
- Coppinger, R., Schneider, R., 1995. Evolution of Working Dogs. In: Serpell, J. (Ed.), *The Domestic Dog: Its Evolution, Behaviour and Interactions with People*. Cambridge University Press, pp. 21–50.
- Coppinger, R., Coppinger, L., 2001. *Dogs: A Startling New Understanding of Canine Origin, Behavior & Evolution*. Scribner, New York, NY.
- Cummins, B.D., 2002. *First Nations, First Dogs : Canadian Aboriginal Ethnology*. Detselig Enterprises, Calgary, p.351.
- Dalziel, H., 1897. *British Dogs: Their Varieties, History, Characteristics, Breeding, Management, and Exhibition*. “The Bazaar” Office, London.
- Dayan, T., 1994. Early domesticated dogs of the Near East. *J. Archaeol. Sci.* 21, 633–640.

- Davis, S.J.M., Valla, F.R., 1978. Evidence for the domestication of the dog 12,000 years ago in the Natufian of Israel. *Nature* 276, 608–610.
- Ding, Z.L., Oskarsson, M., Ardalan, A., Angleby, H., Dahlgren, L.G., Tepeli, C., et al., 2012. Origins of domestic dog in southern East Asia is supported by analysis of Y-chromosome DNA. *Heredity (Edinb)* 108 (5), 507–514, May.
- Doyle, T.F., Bellugi, U., Korenberg, J.R., Graham, J., 2004. “Everybody in the world is my friend”: hypersociability in young children with Williams syndrome. *Am. J. Med. Genet.* 124A, 263–273.
- Eddy, J., Hart, L.A., Boltz, R.P., 1988. The effects of service dogs on social acknowledgments of people in wheelchairs. *J. Psychol.* 122 (1), 39–45.
- Ellingsen, K., Zanella, A.J., Bjerkås, E., Indrebø, A., 2010. The relationship between empathy, perception of pain and attitudes toward pets among norwegian dog owners. *A Multidisciplinary Journal of The Interactions of People & Animals* 23 (3), 231–243.
- Flint, J., 2003. Analysis of quantitative trait loci that influence animal behavior. *J. Neurobiol.* 54 (1), 46–77.
- Freedman, D.G., King, J.A., Elliot, O., 1961. Critical period in the social development of dogs. *Science* 133 (3457), 1016–1017, Mar 31.
- Gácsi, M., Miklósi, Á., Varga, O., Topál, J., Csányi, V., 2004. Are readers of our face readers of our minds? Dogs (*Canis familiaris*) show situation-dependent recognition of human’s attention. *Anim. Cogn.* 7, 144–153.
- Gácsi, M., Győri, B., Miklósi, Á., Virányi, Z., Kubinyi, E., Topál, J., et al., 2005. Species-specific differences and similarities in the behavior of hand-raised dog and wolf pups in social situations with humans. *Dev. Psychobiol.* 47, 111–122.
- Gácsi, M., Győri, B., Virányi, Z., Kubinyi, E., Range, F., et al., 2009. Explaining dog wolf differences in utilizing human pointing gestures: selection for synergistic shifts in the development of some social skills. *PLoS ONE* 4 (8), e6584.
- Germonpré, M., Sablin, M.V., Stevens, R.E., Hedges, R.E.M., Hofreiter, M., Stiller, M., et al., 2009. Fossil dogs and wolves from Palaeolithic sites in Belgium, the Ukraine and Russia: Osteometry, ancient DNA and stable isotopes. *J. Archaeol. Sci.* 36 (2), 473–490.
- Gogoleva, S.S., Volodin, I.A., Volodina, E.V., Kharlamova, A.V., Trut, L.N., 2009. Kind granddaughters of angry grandmothers: the effect of domestication on vocalization in cross-bred silver foxes. *Behav. Processes* 81, 369–375.
- Gogoleva, S.S., Volodin, I.A., Volodina, E.V., Kharlamova, A.V., Trut, L.N., 2011. Explosive vocal activity for attracting human attention is related to domestication in silver fox. *Behav. Processes* 86, 216–221.
- Graphodatsky, A.S., Beklemisheva, V.R., Dolf, G., 1995. High-resolution GTG-banding patterns of dog and silver fox chromosomes: description and comparative analysis. *Cytogenet. Cell. Genet.* 69 (3–4), 226–231.
- Grassmann, S., Kaminski, J., Tomasello, M., 2012. How two word-trained dogs integrate pointing and naming. *Anim. Cogn.* 15 (4), 657–665, Jul.
- Gray, M.M., Sutter, N.B., Ostrander, E.A., Wayne, R.K., 2010. The IGF1 small dog haplotype is derived from Middle Eastern grey wolves. *BMC Biol.* 8, 16. 10.1186/1741-7007-8-16, Feb 24.
- Guest, C.M., Collis, G.M., McNicholas, J., 2006. Hearing dogs: a longitudinal study of social and psychological effects on deaf and hard-of-hearing recipients. *J. Deaf. Stud. Deaf. Educ.* 11 (2), 252–261.
- Hahn, M.E., Wright, J.C., 1998. The influence of genes on social behavior of dogs. Chapter 10. In: Grandin, T. (Ed.), *Genetics and the Behavior of Domestic Animals*. Academic Press, San Diego.

- Hall, N.J., Wynne, C.D., 2012. The canid genome: behavioral geneticists' best friend? *Genes. Brain. Behav.* Sep 14.
- Harcourt, R.A., 1974. The dog in prehistoric and early historic Britain. *J. Archeol. Sci.* 1, 151–175.
- Hare, B., Brown, M., Williamson, C., Tomasello, M., 2002. The domestication of social cognition in dogs. *Science* 298 (5598), 1634–1636.
- Hare, B., Plyusnina, I., Ignacio, N., Schepina, O., Stepika, A., Wrangham, R., et al., 2005. Social cognitive evolution in captive foxes is a correlated by-product of experimental domestication. *Curr. Biol.* 15 (3), 226–230.
- Hare, B., Tomasello, M., 2005. Human-like social skills in dogs? *Trends. Cogn. Sci.* 9, 439–444.
- Hare, B., Wobber, V., Wrangham, R., 2012. The self-domestication hypothesis: evolution of bonobo psychology is due to selection against aggression. *Anim. Behav.* 83, 573–585.
- Hejjas, K., Vas, J., Topal, J., Szantai, E., Ronai, Z., Szekely, A., et al., 2007. Association of polymorphisms in the dopamine D4 receptor gene and the activity–impulsivity endophenotype in dogs. *Anim. Genet.* 38, 629–633.
- Hejjas, K., Kubinyi, E., Ronai, Z., Szekely, A., Vas, J., Miklósi, Á., et al., 2009. Molecular and behavioral analysis of the intron 2 repeat polymorphism in the canine dopamine D4 receptor gene. *Genes. Brain. Behav.* 8, 330–336.
- Hoopes, B.C., Rimbault, M., Liebers, D., Ostrander, E.A., Sutter, N.B., 2012. The insulin-like growth factor 1 receptor (IGF1R) contributes to reduced size in dogs. *Mamm. Genome.* 23 (11–12), 780–790, Dec.
- Haupt, K., 2007. Genetics of canine behavior. *Acta. Vet. Brno.* 76, 431–444.
- Hsu, Y., Serpell, J.A., 2003. Development and validation of a questionnaire for measuring behavior and temperament traits in pet dogs. *J. Am. Vet. Med. Assoc.* 223 (9), 1293–1300.
- Huson, H.J., Parker, H.G., Runstadler, J., Ostrander, E.A., 2010. A genetic dissection of breed composition and performance enhancement in the Alaskan sled dog. *BMC Genet.* 11, 71, Jul 22.
- Huson, H.J., vonHoldt, B.M., Rimbault, M., Byers, A.M., Runstadler, J.A., Parker, H.G., et al., 2012. Breed-specific ancestry studies and genome-wide association analysis highlight an association between the MYH9 gene and heat tolerance in Alaskan sprint racing sled dogs. *Mamm. Genome.* 23 (1–2), 178–194, Feb.
- Jagoe, A.J., Serpell, J., 1996. Owner characteristics and interactions and the prevalence of canine behaviour problems. *Appl. Anim. Behav. Sci.* 47, 31–42.
- Jarvinen-Pasley, A., Bellugi, U., Reilly, J., Mills, D.L., Galaburda, A., Reiss, A.L., et al., 2008. Defining the social phenotype in Williams syndrome: a model for linking gene, the brain, and behavior. *Dev. Psychopathol.* 20, 1–35.
- Jones, A.C., Gosling, S.D., 2005. Temperament and personality in dogs (*Canis familiaris*): a review and evaluation of past research. *Appl. Anim. Behav. Sci.* 95, 1–53.
- Jones, P., Chase, K., Martin, A., Davern, P., Ostrander, E.A., Lark, K.G., 2008. Single-nucleotide-polymorphism-based association mapping of dog stereotypes. *Genetics* 179 (2), 1033–1044, Jun.
- Kaminski, J., Call, J., Fischer, J., 2004. Word learning in a domestic dog: evidence for fast mapping. *Science* 304, 1682–1683.
- Kaminski, J., Tempelmann, S., Call, J., Tomasello, M., 2009. Domestic dogs comprehend human communication with iconic signs. *Dev. Sci.* 12 (6), 831–837, Nov.
- Konno, A., Inoue-Murayama, M., Hasegawa, T., 2011. Androgen receptor gene polymorphisms are associated with aggression in Japanese Akita Inu. *Biol. Lett.* 7, 658–660.

- Kubinyi, E., Turcsán, B., Miklósi, Á., 2009. Dog and owner demographic characteristics and dog personality trait associations. *Behav. Processes* 81, 392–401.
- Kubinyi, E., Vas, J., Hejjas, K., Ronai, Z., Brúder, I., Turcsán, B., et al., 2012. Polymorphism in the tyrosine hydroxylase (TH) gene is associated with activity–impulsivity in German Shepherd Dogs. *PLoS ONE* 7 (1), e30271.
- Kukekova, A.V., Trut, L.N., Oskina, I.N., Kharlamova, A.V., Shikhevich, S.G., Kirkness, E.F., et al., 2004. A marker set for construction of a genetic map of the silver fox (*Vulpes vulpes*). *J. Hered.* 95, 185–194.
- Kukekova, A.V., Oskina, I.N., Kharlamova, A.V., Chase, K., Erb, H.N., Aguirre, G.D., et al., 2005. In: Ostrander, E.A., Giger, U., Lindblad-Toh, K. (Eds.), *The Dog and Its Genome*. Cold Spring Harbor Laboratory Press, Woodbury NY, pp. 515–538.
- Kukekova, A.V., Trut, L.N., Oskina, I.N., Johnson, J.L., Temnykh, S.V., Kharlamova, A.V., et al., 2007. A meiotic linkage map of the silver fox, aligned and compared to the canine genome. *Genome. Res.* 17 (3), 387–399.
- Kukekova, A.V., Trut, L.N., Chase, K., Shepeleva, D.V., Vladimirova, A.V., Kharlamova, A.V., et al., 2008. Measurement of segregating behaviors in experimental silver fox pedigrees. *Behav. Genet.* 38 (2), 185–194.
- Kukekova A.V., Trut L.N., 2010. Analysis of fox interspecific and intraspecific behavior in selectively bred strains of silver foxes (*Vulpes vulpes*). 15th European Conference in Personality. Brno, Czech Republic, July 20–24, 2010.
- Kukekova, A.V., Trut, L.N., Chase, K., Kharlamova, A.V., Johnson, J.L., Temnykh, S.V., et al., 2011a. Mapping Loci for fox domestication: deconstruction/reconstruction of a behavioral phenotype. *Behav. Genet.* 41, 593–606.
- Kukekova, A.V., Johnson, J.L., Teiling, C., Li, L., Oskina, I.N., Kharlamova, A.V., et al., 2011b. Sequence analysis of prefrontal cortical brain transcriptome from tame and aggressive strains of the silver fox (*Vulpes vulpes*). *BMC Genomics* 12 (1), 482.
- Kukekova, A.V., Temnykh, S.V., Johnson, J.L., Trut, L.N., Acland, G.M., 2012. Genetics of behavior in the silver fox. *Mamm. Genome* 23 (1–2), 164–177.
- Lanea, D.R., McNicholas, J., Collis, G.M., 1998. Dogs for the disabled: benefits to recipients and welfare of the dog. *Appl. Anim. Behav. Sci.* 59 (1–3), 49–60.
- Larson, G., Karlsson, E.K., Perri, A., Webster, M.T., Ho, S.Y., Peters, J., et al., 2012. Rethinking dog domestication by integrating genetics, archeology, and biogeography. *Proc. Natl. Acad. Sci. U.S.A.* 109 (23), 8878–8883, Jun 5.
- Leighton, R., 1910. *Dogs and All About Them*. Cassell and Company, Ltd., London.
- Leonard, J.A., Wayne, R.K., Wheeler, J., Valadez, R., Guillén, S., Vilà, C., 2002. Ancient DNA evidence for old world origin of New World dogs. *Science* 298, 1613–1616.
- Lorenz K. *Man Meets Dog*. 1954.
- Miklósi, Á., Kubinyi, E., Topál, J., Gácsi, M., Virányi, Z., Csányi, V., 2003. A simple reason for a big difference: wolves do not look back at humans but dogs do. *Curr. Biol.* 13, 763–766.
- Miyadera, K., Acland, G.M., Aguirre, G.D., 2012. Genetic and phenotypic variation of inherited retinal diseases in dogs: the power of within- and across-breed studies. *Mamm. Genome* 23 (1–2), 40–61, 2012 Feb.
- Naderi, S., Miklósi, Á., Dóka, A., Csányi, V., 2001. Co-operative interactions between blind persons and their dogs. *Appl. Anim. Behav. Sci.* 74, 59–80.
- Nes, N., Einarsson J., Lohi O., Jarosz S., Scheelje R., 1988. *Beautiful Fur Animals and their Color Genetics*, Scientifur, 60 Langagervij, DK-2600 Glostrup, Denmark.
- Nobis, G., 1979. Der älteste Haushunde lebte. *Umschau* 79, 610.

- Olsen, S.J., 1985. *Origins of the Domestic Dog: The Fossil Record*. Univ. of Arizona Press, Tucson, USA.
- Oskarsson, M.C., Klütsch, C.F., Boonyaparakob, U., Wilton, A., Tanabe, Y., Savolainen, P., 2012. Mitochondrial DNA data indicate an introduction through Mainland Southeast Asia for Australian dingoes and Polynesian domestic dogs. *Proc. Biol. Sci.* 279 (1730), 967–974.
- Oskina, I.N., 1996. Analysis of the function state of the pituitary–adrenal axis during postnatal development of domesticated silver foxes (*Vulpes vulpes*). *Scientifur* 20, 159–161.
- Oskina, I.N., Tinnikov, A.A., 1992. Interaction between cortisol and cortisol-binding protein in silver foxes (*Vulpes fulvus*). *Comp. Biochem. Physiol. Comp. Physiol.* 101, 665–668.
- Ostrander, E.A., Beale, H.C., 2012. Leading the way: finding genes for neurologic disease in dogs using genome-wide mRNA sequencing. *BMC Genet.* 13, 56. 10.1186/1471-2156-13-56.
- Ovodov, N.D., Crockford, S.J., Kuzmin, Y.V., Higham, T.F.G., Hodgins, G.W.L., van der Plicht, J., 2011. A 33,000-year-old incipient dog from the Altai Mountains of Siberia: evidence of the earliest domestication disrupted by the last glacial maximum. *PLoS ONE* 6 (7), e22821, Open Access.
- Pang, J.F., Kluetsch, C., Zou, X.J., Zhang, A.B., Luo, L.Y., Angleby, H., et al., 2009. mtDNA data indicate a single origin for dogs south of Yangtze River, less than 16,300 years ago, from numerous wolves. *Mol. Biol. Evol.* 26 (12), 2849–2864.
- Parker, H.G., Kim, L.V., Sutter, N.B., Carlson, S., Lorentzen, T.D., Malek, T.B., et al., 2004. Genetic structure of the purebred domestic dog. *Science* 304 (5674), 1160–1164, May 21.
- Parker, H.G., Kukekova, A.V., Akey, D.T., Goldstein, O., Kirkness, E.F., Baysac, K.C., et al., 2007. Breed relationships facilitate fine-mapping studies: a 7.8-kb deletion cosegregates with Collie eye anomaly across multiple dog breeds. *Genome. Res.* 17 (11), 1562–1571, Nov.
- Parker, H.G., VonHoldt, B.M., Quignon, P., Margulies, E.H., Shao, S., Mosher, D.S., et al., 2009. An expressed *fgf4* retrogene is associated with breed-defining chondrodysplasia in domestic dogs. *Science* 325 (5943), 995–998.
- Parker, H.G., Shearin, A.L., Ostrander, E.A., 2010. Man’s best friend becomes biology’s best in show: genome analyses in the domestic dog. *Annu. Rev. Genet.* 44, 309–336.
- Petersen, M., 1914. *The Fur Traders and Fur Bearing Animals*. The Hammond Press, Buffalo, New York, USA, 364.
- Pilley, J.W., Reid, A.K., 2011. Border collie comprehends object names as verbal referents. *Behav. Process.* 86, 184–195.
- Pionnier-Capitan, M., Bemilli, C., Bodu, P., Célérier, G., Ferrié, J.-G., Fosse, P., et al., 2011. New evidence for Upper Palaeolithic small domestic dogs in South-Western Europe. *J. Archaeol. Sci.* 38 (9), 2123–2140.
- Plyusnina, I.Z., Oskina, I.N., Trut, L.N., 1991. An analysis of fear and aggression during early development of behavior in silver foxes (*Vulpes vulpes*). *Appl. Anim. Behav. Sci.* 32, 253–268.
- Pongrácz, P., Miklósi, Á., Csányi, V., 2001a. Owners’ beliefs on the ability of their pet dogs to understand human verbal communication. A case of social understanding. *Curr. Psychol. Cogn.* 20, 87–107.
- Pongrácz, P., Miklósi, Á., Kubinyi, E., Gurobi, K., Topál, J., Csányi, V., 2001b. Social learning in dogs: the effect of a human demonstrator on the performance of dogs (*Canis familiaris*) in a detour task. *Anim. Behav.* 62, 1109–1117.

- Pongrácz, P., Miklósi, Á., Timár-Geng, K., Csányi, V., 2004. Verbal attention getting as a key factors in social learning between dog (*Canis familiaris*) and human. *J. Comp. Psychol.* 118, 375–383.
- Pongrácz, P., Miklósi, Á., Vida, V., Csányi, V., 2005a. The pet-dogs' ability for learning from a human demonstrator in a detour task is independent from the breed and age. *Appl. Anim. Behav. Sci.* 90, 309–323.
- Pongrácz, P., Miklósi, Á., Molnár, C., Csányi, V., 2005b. Human listeners are able to classify dog barks recorded in different situations. *J. Comp. Psychol.* 119, 136–144.
- Popova, N.K., Kulikov, A.V., Avgustinovich, D.F., Voitenko, N.N., Trut, L.N., 1997. Effect of domestication of the silver fox on the main enzymes of serotonin metabolism and serotonin receptors. *Genetika* 33, 370–374.
- Price, E.O., 2002. *Animal Domestication and Behavior*. CABI Publishing, Wallingford, United Kingdom, p.297.
- Rimbault, M., Ostrander, E.A., 2012. So many doggone traits: mapping genetics of multiple phenotypes in the domestic dog. *Hum. Mol. Genet.* 21 (R1), R52–R57.
- Rintala D.H., Matamoros R., Seitz L.L. 2008. Effects of assistance dogs on persons with mobility or hearing impairments: a pilot study. *45(4):489–504.*
- Robinson, G.E., Grozinger, C.M., Whitfield, C.W., 2005. Sociogenomics: social life in molecular terms. *Nat. Rev. Genet.* 6, 257–270.
- Robinson, G.E., Fernald, R.D., Clayton, D.F., 2008. Genes and social behavior. *Science* 322 (5903), 896–900.
- Rosengren Pielberg, G., Golovko, A., Sundström, E., Curik, I., Lennartsson, J., Seltenhammer, M.H., et al., 2008. A cis-acting regulatory mutation causes premature hair graying and susceptibility to melanoma in the horse. *Nat. Genet.* 40 (8), 1004–1009, Aug.
- Rubtsov N.B. (1998) The fox gene map. *ILAR Journal* 39(2/3). <http://dels-old.nas.edu/ilar_n/ilarjournal/39_2_3/39_2_3Fox.shtml>.
- Sablin, M.V., Khlopachev, G.A., 2002. The earliest Ice Age dogs: evidence from Eliseevichi I. *Curr. Anthropol.* 43, 795–799.
- Saetre, P., Strandberg, E., Sundgren, P.E., Pettersson, U., Jazin, E., Bergström, T.F., 2006. The genetic contribution to canine personality. *Genes. Brain. Behav.* 5 (3), 240–248, Apr.
- Sargan, D.R., Aguirre-Hernandez, J., Galibert, F., Ostrander, E.A., 2007. An extended microsatellite set for linkage mapping in the domestic dog. *J. Hered.* 98, 221–231.
- Savolainen, P., Zhang, Y.P., Luo, J., Lundeberg, J., Leitner, T., 2002. Genetic evidence for an East Asian origin of domestic dogs. *Science* 298, 1610–1613.
- Savolainen, P., Leitner, T., Wilton, A.N., Matisoo-Smith, E., Lundeberg, J., 2004. A detailed picture of the origin of the Australian dingo, obtained from the study of mitochondrial DNA. *Proc. Natl. Acad. Sci. U.S.A.* 101 (33), 12387–12390.
- Schoenebeck, J.J., Hutchinson, S.A., Byers, A., Beale, H.C., Carrington, B., Faden, D.L., et al., 2012. Variation of BMP3 contributes to dog breed skull diversity. *PLoS Genet.* 8 (8), e1002849. [10.1371/journal.pgen.1002849](https://doi.org/10.1371/journal.pgen.1002849).
- Scott, J.P., Fuller, J.L., 1965. *Genetics and the Social Behavior of the Dog*. The University of Chicago Press, Chicago, Illinois.
- Serpell, J.A., 2004. Factors influencing human attitudes to animals and their welfare. *Anim. Welf.* 13, S145–S151.
- Serpell, J.A., Hsu, Y., 2001. Development and validation of a novel method for evaluating behavior and temperament in guide dogs. *Appl. Anim. Behav. Sci.* 72 (4), 347–364, Jun 1.
- Shipman, P., 2010. The animal connection and human evolution author. *Curr. Anthropol.* 51 (4), 519–538.

- Skoglund, P., Götherström, A., Jakobsson, M., 2011. Estimation of population divergence times from non-overlapping genomic sequences: examples from dogs and wolves. *Mol. Biol. Evol.* 28 (4), 1505–1517, Apr.
- Statham, M.J., Trut, L.N., Sacks, B.N., Kharlamova, A.V., Oskina, I.N., Gulevich, R.G., et al., 2011. On the origin of a domesticated species: identifying the parent population of Russian silver foxes (*Vulpes vulpes*). *Biol. J. Linn. Soc. Lond.* 103, 168–175.
- Sutter, N.B., Bustamante, C.D., Chase, K., Gray, M.M., Zhao, K., Zhu, L., et al., 2007. A single IGF1 allele is a major determinant of small size in dogs. *Science* 316 (5821), 112–115.
- Svartberg, K., Forkman, B., 2002. Personality traits in the domestic dog (*Canis familiaris*). *Appl. Anim. Behav. Sci.* 79 (2), 133–155.
- Svartberg, K., Tapper, I., Temrin, H., Radesäter, T., Thorman, S., 2005. Consistency of personality traits in dogs. *Anim. Behav.* 69 (2), 283–291.
- Takeuchi, Y., Hashizume, C., Arata, S., Inoue-Murayama, M., Maki, T., Hart, B.L., et al., 2009a. An approach to canine behavioural genetics employing guide dogs for the blind. *Anim. Genet.* 40, 217–224.
- Takeuchi, Y., Kaneko, F., Hashizume, C., Masuda, K., Ogata, N., Maki, T., et al., 2009b. Association analysis between canine behavioural traits and genetic polymorphisms in the Shiba Inu breed. *Anim. Genet.* 40, 616–622.
- Tchernov, E., Valla, F.F., 1997. Two new dogs, and other Natufian dogs, from the Southern Levant. *J. Archaeol. Sci.* 24, 65–95.
- Topál, J., Miklósi, Á., Csányi, V., 1998. Attachment behaviour in dogs: a new application of Ainsworth's (1969) Strange Situation Test. *J. Comp. Psychol.* 112, 219–229.
- Topál, J., Gácsi, M., Miklósi, Á., Virányi, Z., Kubinyi, E., Csányi, V., 2005. Attachment to humans: a comparative study on hand-reared wolves and differently socialized dog puppies. *Anim. Behav.* 70, 1367–1375.
- Trut L.N., 1980a. The genetics and phenogenetics of domestic behaviour. In: *Problems in General Genetics (Proceeding of the 14th International Congress of Genetics)*, vol. 2, book 2, pp. 123–136.
- Trut L.N., 1980b. The role of behavior in domestication-associated changes in animals as revealed with the example of silver fox. Doctoral (Biol.) Dissertation, Novosibirsk: Inst. Cytol. Genet.
- Trut, L.N., 1988. The variable rates of evolutionary transformation and their parallelism in terms of destabilizing selection. *J. Anim. Breed. Genet.* 105, 81–90.
- Trut, L.N., 1999. Early Canid domestication: the Farm Fox Experiment. *Am. Sci.* 87, 160–169.
- Trut, L.N., 2001. Experimental studies of early Canid domestication. In: Ruvinsky, A., Sampson, J. (Eds.), *The Genetics of the Dog*. CABI, New York, pp. 15–43.
- Trut, L.N., Oskina, I.N., 1985. Age-related changes in blood corticosteroids in foxes differing in behavior. *Dokl. Akad. Nauk SSSR* 281 (4), 1010–1014.
- Trut, L.N., Dzerzhinskii, F.Y., Nikol'skii, V.S., 1991. Intracranial Allometry and Craniological Measurements in Silver Fox during Domestication. *Genetika (Moscow)* 27 (9), 1605–1612.
- Trut, L.N., Plusnina, I.Z., Oskina, I.N., 2004. An experiment on fox domestication and debatable issues of evolution of the dog. *Genetika (Russ.)* 40, 794–807.
- Trut, L., Oskina, I., Kharlamova, A., 2009. Animal evolution during domestication: the domesticated fox as a model. *Bioessays* 31 (3), 349–360.
- Turcsán, B., Kubinyi, E., Miklósi, Á., 2011. Trainability and boldness traits differ between dog breed clusters based on conventional breed categories and genetic relatedness. *Appl. Anim. Behav. Sci.* 132, 61–70.

- Udell, M.A.R., Dorey, N.R., Wynne, C.D.L., 2008. Wolves outperform dogs in following human social cues. *Anim. Behav.* 76, 1767–1773.
- Våge, J., Wade, C., Biagi, T., Fatjó, J., Amat, M., Lindblad-Toh, K., et al., 2010. Association of dopamine- and serotonin-related genes with canine aggression. *Genes. Brain. Behav.* 9, 372–378.
- Vas, J., Topál, J., Péch, É., Miklósi, Á., 2007. Measuring attention deficit and activity in dogs: a new application and validation of a human ADHD questionnaire. *Appl. Anim. Behav. Sci.* 103, 105–117.
- Vasileva, L.L., Trut, L.N., 1990. The use of the method of principal components for phenogenetic analysis of the integral domestication trait. *Genetika* 26, 516–524.
- Vilà, C., Savolainen, P., Maldonado, J.E., et al., 1997. Multiple and ancient origins of the domestic dog. *Science* 276, 1687–1689.
- Vilà, C., Wayne, R.K., 1999. Hybridization between wolves and dogs. *Conserv. Biol.* 13 (1), 195–198.
- Vilà, C., Maldonado, J.E., Wayne, R.K., 1999. Phylogenetic relationships, evolution, and genetic diversity of the domestic dog. *J. Hered.* 90 (1), 71–77.
- Vilà, C., Walker, C., Sundqvist, A., et al., 2003. Combined use of maternal, paternal and bi-parental genetic markers for the identification of wolf-dog hybrids. *Heredity* 90 (1), 17–24.
- Virányi, Z., Topál, J., Gácsi, M., Miklósi, Á., Csányi, V., 2004. Dogs respond appropriately to cues of humans' attentional focus. *Behav. Processes* 66, 161–172.
- Virányi, Z., Gácsi, M., Kubinyi, E., Topál, J., Belényi, B., Ujfalussy, D., et al., 2008. Comprehension of human pointing gestures in young human-reared wolves (*Canis lupus*) and dogs (*Canis familiaris*). *Anim. Cogn.* 11, 373–387.
- vonHoldt, B.M., Pollinger, J.P., Lohmueller, K.E., Han, E., Parker, H.G., Quignon, P., et al., 2010. Genome-wide SNP and haplotype analyses reveal a rich history underlying dog domestication. *Nature* 464 (7290), 898–902, 8.
- Wayne, R.K., 1986. Cranial morphology of domestic and wild canids: the influence of development on morphological change. *Evolution* 40, 243–259.
- Wayne, R.K., vonHoldt, B.M., 2012. Evolutionary genomics of dog domestication. *Mamm. Genome*. 23 (1–2), 3–18.
- Westwood, R.E., 1989. Early fur-farming in Utah. *Utah. Hist. Q.* 57, 320–339.
- Willis, M.B., 1999. Genetic aspects of dog behaviour with particular reference to working ability. In: Serpell, J. (Ed.), *The Domestic Dog*. Cambridge University Press, Cambridge, pp. 52–64.
- Wong, A.K., Ruhe, A.L., Dumont, B.L., Robertson, K.R., Guerrero, G., Shull, S.M., et al., 2010. A comprehensive linkage map of the dog genome. *Genetics* 184, 595–605.
- Yang, F., O'Brien, P.C., Milne, B.S., Graphodatsky, A.S., Solanky, N., Trifonov, V., et al., 1999. A complete comparative chromosome map for the dog, red fox, and human and its integration with canine genetic maps. *Genomics* 62 (2), 189–202, Dec 1.
- Zedda, M., Manca, P., Chisu, V., Gadau, S., Lepore, G., Genovese, A., et al., 2006. Ancient pompeian dogs—morphological and morphometric evidence for different canine populations. *Anat. Histol. Embryol.* 35 (5), 319–324, Oct.
- Zeuner, F.E., 1963. *A History of Domesticated Animals*. Harper and Row, NY.

Citations 5





References 163

All F1 pedigrees were produced in reciprocal manner with respect to parental gender and population of origin. Behavior of F2 individuals was tested, videotaped and scored from video records with a set of 98 traits [7, 12, 25]. Principal component (PC) analysis was used to define main axes of fox behavior as previously described [12].

Genotyping-By-Sequencing (GBS) Detects Genetic Structure and Confirms Behavioral QTL in Tame and Aggressive Foxes (*Vulpes vulpes*)

[\[Show abstract\]](#)

Article · Jun 2015

 Jennifer Johnson  Helena Wittgenstein  Sharon Mitchell [+1 more author...](#)  Katie E Hyma

[Read](#)

Genetics of Canine Behavior

[\[Show abstract\]](#)

 Full-text · Article · Sep 2007

 Katherine A Houpt

[Read full-text](#)

The Case Against Fur Factory Farming

 Full-text · Technical Report · Jan 2015 · Acta Veterinaria Brno

 Heather Pickett  Stephen Harris

[Read full-text](#)

The case against fur factory farming: A scientific review of animal welfare standards and 'WelFur'

 Full-text · Technical Report · Sep 2015 · Acta Veterinaria Brno

 Heather Pickett  Stephen Harris

[Read full-text](#)

The case against fur factory farming: A scientific review of animal welfare standards and 'WelFur'

 Heather Pickett  Stephen Harris

[Read](#)


Recommended publications

[Discover more publications, questions and projects in Foxes](#)

Data

Additional file 2

October 2011


 Anna V Kukekova  Jennifer L Johnson  Clotilde Teiling +13 more authors...  Gregory M Acland

[Read more](#)

Data

Additional file 7

October 2011


 Anna V Kukekova  Jennifer L Johnson  Clotilde Teiling +13 more authors...  Gregory M Acland

[Read more](#)

Data

Additional file 1

October 2011

 Anna V Kukekova  Jennifer L Johnson  Clotilde Teiling +13 more authors...  Gregory M Acland

[Read more](#)

Article

Genetics of behavior in the silver fox

November 2011 · Mammalian Genome · Impact Factor: 3.07

 Anna V Kukekova  Svetlana V Temnykh  Jennifer Johnson +1 more author...  Gregory M Acland

[Read more](#)

[Discover more](#)

Data provided are for informational purposes only. Although carefully collected, accuracy cannot be guaranteed. Publisher conditions are provided by RoMEO. Differing provisions from the publisher's actual policy or licence agreement may be applicable.

This publication is from a journal that may support self archiving. [Learn more](#)