Genetics and animal domestication: new windows on an elusive process

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Abstract

Domesticated animals are universally familiar. How, when, where and why they became domesticated is less well understood. The genetic revolution of the past few decades has facilitated novel insights into a field that previously was principally the domain of archaeozoologists. Although some of the conclusions drawn from genetic data have proved to be contentious, many studies have significantly altered or refined our understanding of past human animal relationships. This review seeks not only to discuss the wider concerns and ramifications of genetic approaches to the study of animal domestication but also to provide a broader theoretical framework for understanding the process itself. More specifically, we discuss issues related to the terminology associated with domestication, the possibility of domestication genes, and the promise and problems of genetics to answer the fundamental questions associated with domestication.

Introduction

Over the past 10 000 years, human history has been wholly transformed by the domestication of plants and animals. Although the term 'domestic animal' has universal meaning, fundamental questions regarding the basic definitions and processes underlying domestication remain largely unanswered. Within the last decade, however, new genetic techniques have moved rapidly to a point where they are becoming increasingly key components in understanding and, in some cases, re-evaluating our knowledge of perhaps one of the most important events in human prehistory: the shift from hunting wild animals to herding and hunting with domestic ones.

Recent reviews have focused on genetic research in the major domestic mammals (Bruford, Bradley & Luikart, 2003) as well as broader aspects of genetics and adaptation (Mignon-Grasteau et al., 2005). This review attempts to provide a background to the problem of defining domestication, followed by a discussion of how current theories regarding specific morphological changes associated with domestication might affect hypotheses related to a genetic approach. A broader theoretical framework for animal domestication follows based on tentative answers to some of the basic questions surrounding domestication, including when, where, how many times and which species were involved. Lastly, we explore possible future directions in terms of both empirical data and theoretical structures that can shed new light on our understanding of domestication.

Defining domestication

Terminology typically used in domestication studies, including the word 'domestication' itself, is often confusing and poorly defined. The primary reason for this stems from the inherent difficulty in assigning static terms to a process involving long-term and continuous change. An analysis of the linguistics of domestication offers an insight into these issues.

The field of lexical semantics recognizes two major kinds of opposites: complementaries and antonyms. Complementaries are opposites, which, between the two words, 'exhaustively divide some conceptual domains into two mutually exclusive compartments, so that what does not fall into one of the compartments must necessarily fall into the other' (Cruse, 1986, p. 197). Because no gradability exists between pairs of complementaries (e.g. true/false, dead/alive, open/shut), the negation of one term necessarily implies the other. By contrast, antonyms are defined as pairs of opposites that are readily gradable. These pairs (e.g. long/short, fast/slow, good/bad and hot/cold) are scaled over a continuum and are therefore only relevant in context. Antonyms also fail the negation test – something that is not hot or long is not necessarily cold or short (Cruse, 1986, p. 204). Often in domestication studies, the terms wild and domestic have been interpreted as complementaries and not as antonyms, despite the fact that 'wild' and 'domestic' represent the extremes of a process and not a simple dichotomy.

A vast range of human–animal relationships has existed throughout history, and the animals involved in many of

these relationships cannot be easily categorized as strictly wild or strictly domestic. Urban domestic pigs, for example, have often been allowed to wander freely through towns and forage for themselves, returning to their owners each evening. This practice was widespread as late as the early 20th century in Britain and continues to exist in other parts of the world (Albarella, Dobney & Rowley-Conwy, 2006). Among the Etoro of New Guinea, domestic female pigs are allowed to roam freely within villages before straying into the surrounding forests to breed with wild/feral males, thus blurring any superficial boundaries that may exist between wild and domestic animals (Rosman & Rubel, 1989). The fluid nature of these relationships has led some authors to question whether the term 'domestication', at least in its traditional definition, is completely relevant for animals such as pigs (Jarman, 1976; Zvelebil, 1995).

Any paradigm that relies on a strict wild/domestic dichotomy firstly prevents a deeper appreciation of those animals whose lives are spent somewhere in between. More importantly, because this sort of dichotomous perspective rules out long-term evolutionary change as an explanation for the process of domestication, it therefore (however unintentionally) both obscures the existence of transitional forms and prevents any real understanding of the domestication process.

Shared characteristics and the possibility of domestication genes

In his pioneering studies of domesticated mammals, Darwin (1868) noticed that virtually all domestic animals had undergone similar morphological and physiological changes relative to their wild counterparts (Table 1).

When thinking about the molecular basis of domestication, it is tempting to consider each of these traits independently and to therefore search for genes specifically responsible for each trait. This approach has already yielded significant insights into several genes (e.g. *MC1R*, *POMC*, *Agouti* and *TYRP1*) underlying differing coat and plumage patterns present in pigs, horses and chickens (Andersson, 2003), as well as specific genes (*IGF2*) involved in fat

Table 1 Similarities of traits in domesticated mammals

Trait	Domestic animals
Appearance of dwarf and giant varieties	All
Piebald coat colour	All
Wavy or curly hair	Sheep, poodles, donkeys, horses, pigs, goats, mice, guinea pigs
Rolled tails	Dogs, pigs
Shortened tails, fewer vertebrae	Dogs, cats, sheep
Floppy ears	Dogs, cats, pigs, horses, sheep, goats, cattle, rabbits
Changes in reproductive cycle	All

Adapted from Trut (1999).

deposition and muscle mass in pigs (Van Laere *et al.*, 2003). Although the field of functional genomics will no doubt identify additional genes underlying the phenotypic characteristics that differentiate wild and domestic animals, any research programme that remains rooted in the single trait–single gene model may be unconsciously ignoring the possibility of a deeper molecular basis for domestication.

Before considering an alternative, it is worth briefly discussing the traditional adaptationist explanation for the presence of the commonly shared traits found in domestic animals (see Table 1). Although speculation regarding the origin of traits found in domestic animals has often invoked purposeful selection on the part of prehistoric hunters, this type of explanation has been roundly criticized both in general (e.g. Gould & Lewontin, 1979) and when specifically applied to domestication (Morey, 1994).

This adaptationist style of argument has also been marshalled to explain the origin of domestication itself. Francis Galton (1907) suggested that the origin of dogs must have developed from the purposeful capturing and nurturing of wolf puppies. He based his idea on a large volume of ethnographic research indicating that pet keeping was common [and continues to be (Guppy, 1958)] among numerous hunter-gatherers. Although prehistoric hunters may have reared wolf puppies, Serpell (1989, p. 21) argues that 'on its own, Galton's theory cannot be used to explain why animal domestication occurred when and where it did'.

The origins of both domestic animals and the traits associated with them are certainly less straightforward than the 'desire it–produce it' model suggests. An alternative explanation that the traits associated with domestic animals were not individually selected for, but are part of an interconnected suite of traits that emerge during the process of domestication provided the foundation on which Dmitry Belyaev initiated the Fox-Farm experiment in 1959. Belyaev & Trut (1975) believed that physiology, morphology and behaviour were intrinsically connected, and that inducing a selection pressure on one attribute of an organism might have a significant (although unintended) impact on other characteristics. The methodology of this experiment involved subjecting a population of silver foxes (an animal never previously domesticated) to a rigorous selection pressure for a single behavioural trait: tameness.

By selecting solely against aggression, Belyaev hypothesized that he was also selecting for 'changes in the systems that govern the body's hormones and neurochemicals' (Trut, 1999). Belyaev believed that the genes controlling the balance of these hormones and neurochemicals existed on a high plain within the hierarchy of the genome and, thus, even tiny alterations within these regulatory regions could also significantly alter both the phenotypic and behavioural constitution of foxes (Trut, 1999).

Forty years of determined selection in over 45 000 foxes produced a sizeable population of tamed foxes. As Balyaev predicted, a host of additional changes never deliberately selected for also appeared. They included piebald coat colour, drooping ears, shorter, occasionally upturned tails, shortened snouts and shifts in the developmental timing of

various other characteristics. As they aged, many of the fox pups began behaving in a manner similar to domestic dogs by barking, whining and licking their handlers. A small percentage of the vixens even began mating twice a year (Trut, 1999).

The Fox-Farm experiment conclusively demonstrated that consistent and prolonged selection for a single behavioural trait can radically alter not only the behaviour and developmental characteristics of an animal, but its physical constitution as well. The tame foxes, with regard to nearly every affected trait, demonstrate a 'stretching' of those characteristics associated with the early stages of ontogeny, as well as an extension of juvenile traits into adulthood. These paedomorphic effects appear to act in concert across the entire animal spanning multiple behavioural and physical characteristics.

On the basis of these results, it is tempting to imagine a master suite of genes present in all animals and responsible for the shared, domestic characteristics listed in Table 1. The notion of a domestication gene has been explored by a handful of authors (e.g. Stricklin, 2001), although the practicalities of identifying those genes are daunting. Even if domestication is the result of only a few changes in upstream regulator or master genes, the host of behavioural and morphological changes evident between wild and domestic animals must be the result not just of the individual gene products but also of countless additional pleiotropic interactions over the course of development. The cascade initiated by those few genes is likely to be so complex that identifying the highest level 'domestication genes' becomes, at best, highly problematic.

Endocrine system

The first step in identifying what the molecular basis of domestication may be is to ascertain the physiological changes that result from paedomorphosis, and correlate those with the effects of changes in other systems. A recent study (Crockford, 2002) identified numerous similarities between traits associated with domestication and those indicative of hypothyroidism. This correlation highlighted the endocrine system (and more specifically the amount of thyroid hormone present early in development) as the likely culprit underlying domestication. Citing studies that demonstrate the importance of thyroid hormone in embryonic and postnatal growth, stress response behaviour, skeletal growth, 'brain development, hair production, adrenal gland function, skin and hair pigmentation production and the development and function of the gonads', Crockford (2002, p. 134) concludes that thyroid hormone metabolism is the essential factor in vertebrate heterochrony and thus the key to domestication.

The production of thyroid hormone constitutes a middle step along a complex cascade and feedback system that originates within the superchaismatic nuclei (SCN), a small region of the brain. Genes expressed within the SCN affect the amount of timing of hormones released from the pineal gland, and the hypothalamus (Reppert & Weaver, 2001).

The hypothalamus releases a hormone to the pituitary, which in turn releases a hormone signalling the thyroid gland to begin secreting thyroid hormone. The thyroid gland converts iodine into two different kinds of thyroid hormone: triiodothyronine (T3) and thyroxine (T4). These hormones are then released into the bloodstream, where they regulate the metabolism of every cell in the body (Crockford, 2002).

Studies on variations in thyroid hormones in lab rats show that not only do domesticated rats have smaller thyroid glands than wild rats but also this smaller gland reduces escape readiness and escape distance within domestic laboratory rats (Mosier & Richter, 1967). Additionally, domestic rats reach fertility earlier, end it later and have more offspring per pregnancy. Domestic rats are smaller overall, possess a diminished cerebellum (Clark & Price, 1981) and all of these changes have taken place in the last 100 years of well-documented rat domestication. Most strikingly, in an article on the effect of thyroid hormone on growth and development (Legrand, 1986), a figure is presented showing two rats: a normal 18-day-old rat next to a rat of the same age made hypothyroidic in the womb. The hypothyroidic rat is clearly smaller in size and, in sharp contrast to the upright ears of its normal neighbour, possesses floppy ears characteristic of many domestic animals (Fig. 1).

Although circumstantial, this evidence seems to suggest a link (however tenuous) between changes in the endocrine system and the process of domestication, although establishing what these changes might be remains extremely difficult. The reasons for this are twofold. Firstly, the sheer complexity of the endocrine system makes identifying a single step within the cascade tricky. Shifts in the amount of timing of

Figure 1 Two rats pictured 18 days after birth. The top rat was untreated and the bottom rat was made hypothyroidic with propylthioracil on the 18th day of foetal life. Several phenotypic traits obvious in the hypothyroid rat, including smaller overall size, shorter muzzle and, most noticeably, floppy ears, are superficially similar to traits shared by all domestic animals but absent in their wild ancestors. This correlation suggests a possible role for thyroid hormone during the process of domestication (Legrand, 1986, p. 506. Copyright 1986 From (Thyroid Hormone Metabolism) by G. Henneman, Ed. Reproduced by permission of Routledge/Taylor & Francis Group, LLC).

the release of thyroid hormone could occur because of changes in the myriad of genes regulating the production of hormones and hormone receptors in the SCN, the hypothalamus, the pituitary gland or the thyroid itself. Secondly, because the thyroid hormone plays such a vital role in virtually every aspect of development, changes in the production of thyroid hormone are not likely to be a result of functional changes in hormone genes, but are more likely to be changes in gene expression patterns, which would more likely have a molecular basis either in the promoter regions or in other transcription factor genes involved in expression. In either case, mutations in the non-coding elements of hormone genes or in transcription factors would allow the hormones to function normally, but the relative concentrations of those hormones in the bloodstream would be altered enough to affect large-scale change across the behaviour and morphology of the organism in question.

A recent paper exploring the pattern of gene expression in the brains of dogs, wolves and coyotes found significant differences in the amount of a host of genes expressed in the hypothalamus, suggesting that domestication has had a substantial effect on gene regulation in dog brains (Saetre *et al.*, 2004). Studies on plants have also revealed the importance of both upstream regions of genes affecting phenotypic change (e.g. *tb1* in maize) (Wang *et al.*, 1999). The crucial role played by transcription factors in shaping overall plant structure (Doebley & Lukens, 1998) and in the process of domestication (Vigouroux *et al.*, 2002) has also begun to be elucidated.

These results suggest not only the possibility that domestication is the result of a relatively small number of regulatory genes operating early in development and affecting the entirety of the organism but also that the molecular changes in those genes are unlikely to be found in the coding portions of the genes themselves. The challenge for developmental and molecular biologists is to identify what those genes might be and to shed light on the process of domestication by describing the complex genetic pathways underlying the differences between domestic and wild animals.

Genetics and the fundamentals of domestication

Where and how many times?

Virtually all of the molecularly based studies of domestication use datasets consisting of neutral genetic markers, and the vast majority of these use the control region of mitochondrial DNA. The observed differences between the molecular sequences of wild and domestic samples therefore are not a result of the process of domestication *per se*, but rather reflect (1) the variation already present in wild lineages before domestication began and (2) the secondary effects of isolation resulting from the isolation of wild and domestic populations.

In order to best identify the number of times and primary regions where domestication took place using genetic data, the ideal dataset would include not only DNA samples from modern wild and domestic taxa but also DNA samples from definitive wild and domestic representatives from archaeological sites representing as many geographical and temporal contexts as possible. Not only is a dataset of this calibre practically unfeasible, even if it was, the conclusions drawn from the data would not necessarily be unequivocal. The reasons for this are due to the strength of the phylogeographic signal among modern wild taxa from whose ancestors modern domestic animals are derived. A strong correlation between geographic location and genetic signature allows for straightforward identification of the geographic origins of the modern ancestor, as well as identification of the specific regions of domestication and even human movement of domesticates through time using ancient DNA. A weak correlation necessitates the use of more subtle statistical and phylogenetic methods that are more open to a variety of interpretations.

The odds of establishing a strong phylogeographic correlation are not good for several reasons. Firstly, the five stages of domestication outlined by Zeuner (1963) conclude with the 'persecution/extermination of wild ancestors' and, unfortunately, this fate has befallen the wild ancestors of the modern-day horse (Jansen *et al.*, 2002), cow (Troy *et al.*, 2001) and dromedary camel (Stanley, Kadwell & Wheeler, 1994). Establishing the phylogenetic pattern of modern-day wild animals is difficult when they no longer exist. Secondly, in the cases where wild animals are not extinct, the phylogenetic signal has sometimes proved to be extremely weak. This is especially true of wolves where one haplotype was shown to exist in Turkey, Sweden and Portugal and another in Saudi Arabia, Mongolia and China (Savolainen *et al.*, 2002). Lastly, recent and historic human-mediated dispersal of domestic and wild animals will have further blurred the correlation between genotype and geography, thus weakening any underlying signal.

Despite these difficulties, modern wild boar have recently been shown to have a robust phylogenetic signal, thus allowing straightforward conclusions to be drawn, not only regarding their origins and radiation, but also of the number and specific locations of regions where local wild boar have contributed DNA to modern domestic stock (Larson *et al.*, 2005). Specifically, this study identified six distinct regions of independent domestication that, when combined with the known archaeological centre of Eastern Turkey, brings the total number of locations of pig domestication (thus far) to seven. Over the past decade, every new published result that incorporates individuals sampled from a new region has seemingly increased the number of new centres of domestication. This is especially true for goats and pigs where a multitude of new haplotypes were found when samples from previously excluded regions were added to existing datasets (see Table 2). Given the number of regions as yet unsampled, these figures are likely to climb higher still as additional, regionally diverse samples are collected.

The primary conclusion drawn from this trend must be that animal domestication, far from being an isolated or unusual event in a relatively few limited and discrete

Table 2 Number of genetic lineages incorporated into domestic stocks (read roughly as domestication events) within a variety of domestic mammals

Taxa	Number	References
Pig *Sus domesticus*	7	Larson *et al.* (2005)
Dog *Canis familiaris*	Many	Vila *et al.* (1997), Savolainen *et al.* (2002)
Horse *Equus caballus*	Many	Vila *et al.* (2001), Jansen *et al.* (2002)
Goat *Capra hircus*	5	Luikart *et al.* (2001), Sultana, Mannen & Tsuji (2003), Joshi *et al.* (2004)
Cow *Bos taurus* and *B. indicus*	4	Troy *et al.* (2001), Mannen *et al.* (2004)
Sheep *Ovis aries*	2	Hiendleder *et al.* (2002)
Donkey *Equus asinus*	2	Beja-Pereira *et al.* (2004)
Water buffalo *Bubalus bubalus*	1–2?	Kierstein *et al.* (2004)

locations, was a much more common phenomenon, a view that appears to contradict the traditional view of early animal domestication.

When?

From a morphological perspective, animals undergoing the initial process of domestication (however the term is defined) would not have been significantly different from their wild ancestors. As a result, the primary zooarchaeological record is likely to provide little or no evidence for the existence of these early affected individuals. Thus, dates deriving from zooarchaeological remains that show clear morphological differentiation between wild and possibly domestic animals must necessarily be underestimates, at least with regard to the first interactions among humans and animals.

The domestication trajectory can theoretically be divided into phases during which differing selection pressures vary in intensity and subsequently allow for separate selective pressures to begin asserting themselves. Understanding other naturally occurring and mutually beneficial/altering relationships that exist between other organisms described as symbiotic, mutualistic, commensal or even parasitic is perhaps more useful in elucidating the first stage. During the initial phase of domestication (probably not readily visible in the archaeological record), humans probably played little or no direct role. Instead, the changing nature of the relationship between humans and, for example, wolves – as each population adjusted to the pressures exerted upon it by the other – likely predisposed them to eventual full domestication. As tamer wolves ventured closer to human settlements, physiologic and phenotypic changes would already have begun, but it was not until humans purposefully enhanced the selection pressure upon that behaviour that true dogs would become permanent members of human settlements and more readily recognizable in the archaeological record.

This scenario has been purported for the origins of pig domestication. At the early Neolithic site of Çayönü Tepesi (Eastern Anatolia), a unique zooarchaeological record spanning the 9–7th millennium BP provides some tantalizing evidence of 'staged' morphological change in the various proportions of the teeth and postcranial skeleton of *Sus*

scrofa (Ervynck *et al.*, 2002). Because a decrease in pig body size appears to occur later than the gradual decrease observed in the dentition (only becoming obvious in the latest phases of occupation at Çayönü), it has been argued that two separate (but related) stages are represented: (1) an earlier change in the rooting behaviour of pigs – unconsciously mediated by humans, and (2) a later demographic shift towards females – perhaps reflecting early husbandry (Zeder, 2001). The processes associated with stage 1 resulted in an 'intermediary' population upon which some indirect human influence was exerted, for example, by the conscious or unconscious supplying of food.

Shortening of the dental row may also have been linked with general morphological changes of the skull, which could reflect differences in the structure and behaviour of the brain, correlated with changes in the behaviour of the animals. Such differences have been well documented between domestic species and their wild 'ancestral' forms, and a reduction in brain size (in comparison with the overall body size) has been postulated as part of the process of domestication (Kruska, 1988). It is also possible that a change in brain size and function could have occurred in pigs of an intermediary status as a result of shifting selective pressures, and not just in animals that were being 'actively domesticated' by humans.

What is absolutely clear from research on the pigs from Neolithic Çayönü is that it reflects a single population under a gradual and slow process of change and not a sudden domestication event. The data are more in accordance with a population living initially in some sort of intermediary relationship with humans, gaining in intensity through time, and gradually resulting in characteristics that eventually discriminate them from the original wild population. How early the proposed mutual relationship began, and how long it lasted before the animal's skeletal morphology began to change, has, thus far, been impossible to assess.

Given its reliance on fairly crude phenotypic change, the zooarchaeological record has not been able to contribute to the debate as to whether there may have been an extended period of time during which various morphological change associated with domestication had yet to occur. If during this period, domestic animals and their wild progenitors were isolated from one another, and if the isolation lasted long enough for novel genotypes to accumulate, then

molecular data derived from wild and domestic animals could provide the clearest answer and an independent means to date the earliest stages of domestication.

Given the bias of the archaeological record, earlier dates for domestication derived from genetic sequences are to be expected. What was not expected, however, was the degree to which molecularly derived dates and archaeological dates disagree (see Table 3). One explanation for the discrepancy (mentioned in the majority of the references given in Table 3) is that the dates are accurate, but they do not reflect changes since domestication. Instead, the dates indicate the points of dichotomy between multiple lineages, all (or most) of which have subsequently been incorporated into modern domestic lineages. If true, this would point to either a greater number of domestication events, or limited numbers of events from highly genetically differentiated populations.

The consistent pattern of dissimilarity between date estimates may also reflect a more fundamental methodological bias within molecular clock estimates. To understand what that bias might be, it is worth discussing the basic methods used to estimate dates based on molecular data. After accumulating sequences of a relatively fast-moving gene (typically the control region of mtDNA) among a large number of domestic and wild individuals, the average pairwise distance between the domestic and wild individuals is calculated. A similar figure is then calculated between the wild individuals and a distantly related cousin used as an outgroup to root the phylogenetic tree. With these distances in hand, a rate of sequence evolution is calculated by dividing a date of the split between the outgroup and the wild individuals (usually derived from the fossil record) by the percentage sequence difference between the two. The 'domestication date' can then be found by dividing the distance between the domestics and the wilds by the calculated rate.

In the most well-known example, a biomolecularly derived date for the domestication of dogs was estimated to be *c*. 135 000 years ago, 10 times older than the archaeological evidence had previously indicated (Vila *et al*., 1997). The values used in this paper were: percentage difference between wolves and coyotes – 7.5%; date of phylogenetic split between wolves and coyotes – 1 million years; rate of mitochondrial clock – 1%/135 000 years; average divergence between dogs and wolves – 1%; date of domestication – 135 000 years. Since then, the majority of genetics-based

domestication papers have used this technique, often with slight adjustments to the way in which the genetic distances are calculated.

The most significant element of all these date calculations is the lack of reporting of error surrounding the estimates. The first potential source of error is the calibration point between the outgroup and the wild ancestor. Dates taken from the fossil record are not point estimates, but are instead ranges that often differ by more than a million years. In the case of coyotes and wolves, for example, Kurtén (1974) placed the split between 1.5 and 4.5 million years ago. Applying the deepest date within the methodology mentioned above would produce an estimate of dog domestication over half a million years ago.

Additional sources of error only widen the confidence interval surrounding the final estimate. Firstly, the power of the estimate is based partly on the number of base pairs used to derive the molecular rate. Studies that base their rate estimates on smaller sequence alignments will have proportionally larger 95% confidence intervals surrounding the molecular rate. These errors can be easily calculated assuming a Poisson distribution (Cooper, Grassly & Rambaut, 2001). More qualitatively, numerous models of evolution can be used to measure genetic distances, each of which may give different results. The lack of certainty as to which model is the most appropriate is another source of error. Lastly, a recent paper (Ho *et al*., 2005) argues that rates of sequence evolution are heavily dependent on the time depth of relationships within the dataset used to derive the rate. Datasets comprising closely related individuals produce relatively fast rates (likely akin to a mutation rate) when compared with datasets comprising different species (which reflect a substitution rate). Thus, when rates derived between species (e.g. coyote–wolf) are used to date splits within species (e.g. dogs), the resulting date will be artificially deep. [This issue, and its relevance to domestication, is discussed in greater detail in Ho & Larson (2006).]

The combination of all these sources of error arguably leads to a point where the summed error bars are wider than the value of the original estimate. It is tempting to presume that very early dates derived from molecular data suggest that the archaeological dates are significant underestimates and that domestication has been taking place for tens of thousands of years. The more likely explanation is that molecular clocks often do not have the resolution to date

Table 3 Disparity between archaeologically derived dates and molecular dates for domestication among a variety of animals

Animal	Approximate date BP	Range of molecular dates
Pig *Sus domesticus*	9000 – A	58 000 – B – 500 000 – C
Sheep *Ovis aries*	12 000 – A	84 000 – M – (375 000 – 750 000) – D
Dog *Canis familiaris*	14 000 – E 12 000 – F	(15 000 – 40 000) – H –135 000 – G
Cattle *Bos taurus* and *B. indicus*	8000 – A	10 100 – 37 600 – I
Donkey *Equus asinus*	5500 – A	303 000 –910 000 – J
Horse *Equus caballus*	6000 – A and K	320 000 – 630 000 – L

A, Reitz & Wing (1999); B, Kim *et al*. (2002); C, Giuffra *et al*. (2000); D, Hiendleder *et al*. (1998); E, Benecke (1987); F, Clutton-Brock (1995); G, Vila *et al*. (1997); H, Savolainen *et al*. (2002); I, Troy *et al*. (2001); J, Beja-Pereira *et al*. (2004); K, Clutton-Brock (1999); L, Vila *et al*. (2001); M, Guo *et al*. (2005).

very recent events (such as domestication), and that the error bars surrounding the molecular estimates actually envelope the archaeological dates, resulting in no discrepancy between the two. The lack of a statistically significant difference between the two estimates therefore removes the necessity to invent novel and far-fetched implausible justifications for the perceived inconsistency (e.g. Raisor, 2005).

Which wild species were involved?

The identity of the wild progenitor (or progenitors) of most domestic mammals remains unclear for two main reasons: Firstly, the potential wild progenitors of each domesticate are often able to interbreed and produce fertile offspring. This hybridization capability is not inconsistent with the 'biological species concept' (Mayr, 1963, p. 26; Rundle *et al.*, 2001), and although it has historically played a role in the sometimes confused identification of individual candidate ancestors, there has been recent clarification on the taxonomic front (Gentry, Clutton-Brock & Groves, 2004). Secondly, many domestic animals (including dogs, cats and cows) can produce viable offspring with a host of wild, closely related sister taxa (Adams, Leonard & Waits, 2003; Pierpaoli *et al.*, 2003; Verkaar *et al.*, 2004). Two conclusions can be drawn from this rampant interfertility. Firstly, the intuitive notion that each modern domestic animal (when discussed as a global population) is descended solely from a single wild species is almost certainly incorrect. As a result, the genetic ancestry of domestics is therefore likely to be relatively complex and thus not easily deduced from a single gene.

A brief example of this complexity can be found within the canid family. Not only has it been suggested that the red wolf *Canis rufus* is a hybrid between the grey wolf *Canis lupus* and coyotes *Canis latrans* (Wayne, Roy & Gittleman, 1998), a recent study isolated definitive dog mitochondrial haplotypes in a population of American coyotes, indicating that coyotes and dogs *Canis familiaris* occasionally mate and produce viable offspring (Adams *et al.*, 2003). Although it is generally thought that domestic dogs are descended solely from the grey wolf, these observations suggest that coyotes (and therefore possibly other canids) have contributed genetic material to various dog populations during or after their initial domestication. Domestic dogs, therefore, can be viewed not simply as designer wolves, but as a chimeric species possessing DNA from several ancestral sources.

Canids are not exceptional. Most domestic animals can produce viable hybrid offspring with a range of supposed wild ancestors, including those listed as potential ancestral species in Table 4. Because modern domesticates can easily breed across species barriers, the possibility that a series of early (intentional or unintentional) hybridization events between wild, closely related sister taxa were involved in the creation of domestic animals should be taken into consideration, especially when analysing genetic data. The failure to question the assumption of a non-hybrid origin can significantly alter the conclusions of a genetic study, especially those based on a single genetic locus.

The most striking example of the pitfalls of extrapolating evolutionary and domestic histories from a single gene is evident from studies of African cattle. Virtually all African cattle possess a European (taurine) mitochondrial signal but an Asian (indicine) Y-chromosome signature (Nijman *et al.*, 1999; Hanotte *et al.*, 2000; Hanotte *et al.*, 2002). The motley genome of these cattle indicates that the vast majority of African breeds are hybrids, and suggests that this could be a deliberate breeding strategy by African pastoralists. Other studies have demonstrated that fertile hybrids between various bovids, including bison, yak, banteng and gaur, occur with regularity (Verkaar *et al.*, 2004).

If large datasets incorporate domesticates derived from more than one ancestral species, the use of phylogenetic trees to elucidate and date the origins of domestic animals quickly becomes problematic. The best strategy would be (at least in cases where hypothesized ancestors remain extant) to determine the potential contributions of modern wild species to domestic stock by sampling multiple nuclear and mitochondrial loci. This exercise would also be an important component in a wider reappraisal of the underlying (occasionally unquestioned) assumptions regarding domestication.

Ways forward

Given its role as a novel and independent data source, biomolecular research is set to make a highly significant

Table 4 Short list of potential ancestors of modern domestic animals (Groves, 1981; Jordana, Pares & Sanchez, 1995; Vila, Maldonado & Wayne, 1999; Bruford *et al.*, 2003; Pierpaoli *et al.*, 2003; Verkaar *et al.*, 2004)

Domestic species	Partial list of potential wild progenitors
Sheep *Ovis aries*	*O. musimon/O. orientalis, O. ammon, O. vignei*
Goat *Capra hircus*	*C. aegagrus, C. falconeri*
Pig *Sus domesticus*	*S. scrofa, S. celebensis, S. barbatus*
Dog *Canis familiaris*	*C. lupus, C. latrans, C. aureus*
Cat *Felis catus*	*F. silvestris, F. chaus, F. manul*
Cattle *Bos taurus* and *B. indicus*	*B. primigenius, B. namadicus, B. grunniens, B. frontalis, B. javanicus, B. sauveli, B. bison, B. bonasus*
Horse *Equus caballus*	*E. przewalski, E. gmelini, E. silvaticus, E. robustus*

In the case of cattle, *B. taurus* and *B. indicus* have been primarily derived from the now extinct *B. primigenius* and *B. namadicus*, respectively. The other bovids listed in the table are known to have contributed DNA to domestic cattle in various regions.

contribution to the broader picture of animal domestication that will hopefully include insights not only into the makeup of modern domesticates but also the complex processes that have driven the domestication process itself.

Unfortunately, the early key centres of domestication took place in relatively low latitudes where hot summers and cold winters speed the degradation of biological remains. The often poor preservation of ancient bones and teeth excavated from key archaeological sites has effectively prevented large-scale ancient DNA analyses. A recent paper focusing on cattle domestication was only able to successfully amplify mitochondrial DNA from 12 of 101 ancient bone samples from 13 archaeological sites (Edwards *et al.*, 2004). This low rate of success does not bode well for future studies on other domestic mammals first domesticated in the near and middle east.

When successful, however, ancient DNA analyses could shed important light on numerous facets of animal domestication. Recent advances in phylogenetic methodology (Shapiro *et al.*, 2004) allow the use of multiple carbon-dated sequences within a phylogenetic tree to better estimate evolutionary rates. This internal calibration significantly reduces the errors that have continually plagued estimates derived from palaeontologic calibration points (see above).

Genome surveys and evolutionary development studies are slowly but consistently revealing new genes that are responsible for the distinct phenotypic differences between domestic and wild animals, including coat colour and muscle growth genes mentioned earlier (Andersson, 2003; Van Laere *et al.*, 2003). Because specific phenotypes can now be correlated with individual base pair differences in these loci, short-distance primer pairs spanning only those nucleotides of interest can be designed, thus allowing for the potential of diagnostic SNPs to be retrieved from ancient material. This type of research has already been successfully applied to maize domestication in Central America (Jaenicke-Despres *et al.*, 2003). By amplifying three nuclear genes controlling the specific phenotypic traits associated with domestication, this research was able to trace the allelic diversity and thus the signal of increasing artificial selection on maize over the last 4400 years.

Recovery of ancient DNA can only be undertaken on suitable material, the paucity of which remains frustrating. Cave sites or deeply stratified/waterlogged sites in temperate northern Europe, or even archaeological sites now buried by lakes or seas, may possess the suitably cold and stable environments required for long-term DNA preservation. Museum collections are another significant source of ancient DNA. Although often less than a century old, the numerous specimens kept in museums offer an opportunity to combine population-level surveys of genetic variation with phenotypic characters such as skull and tooth measurements. Ancient DNA will no doubt continue to provide important insights into the history and process of domestication, both on its own and in concert with independent datasets.

Thus far, virtually all genetic studies into domestication have generated large datasets of mtDNA sequences. The rapid and neutral rate of evolution (at least in the control region) means that sequence differences appear fast enough for changes to have occurred within the last 10 000 years. The high copy number of this region means that it is significantly more likely to survive relatively intact in ancient material, and thus it is an ideal choice for use in both modern and ancient DNA studies. Despite these benefits, mtDNA also possesses its own limitations and biases (including its maternal inheritance pattern).

Future studies will no doubt continue to sequence and analyse additional neutral markers such as microsatellite loci, but they will also increasingly focus on genetic variation between wild and domestic animals in non-neutral nuclear genes. In addition to the developmental genes mentioned above, nuclear genes not explicitly involved in domestication may also further our understanding of the origin of domestic animals. So-called speciation genes (Noor, 2003), including both those instrumental in bringing about speciation and those that possess marked variation between species, but very little within species, may allow us to determine definitively not only how many, but exactly which lineages of, for example, bovid, suid, equid or canid contributed DNA to modern cows, sheep/goats, pigs, horses and dogs.

Although the efforts of genome-oriented biologists will be enormously beneficial to the understanding of the genetic underpinnings to domestication, they have thus far been focused almost exclusively on unearthing single genes with a demonstrable phenotypic effect. As discussed previously, this type of approach is limited in its ability to reveal higher order genes that may, however convolutedly, control a wide range of behavioural, physiologic and phenotypic changes. In order to understand the origins of the kinds of organism-wide variation consistently revealed by the process of domestication, we may need to alter the way in which we think about the relationship between genes and domestication.

Although still in its infancy, the ideas associated with the concept of 'evolvability' may provide the foundations for a different approach. Originally coined by Richard Dawkins (1989), evolvability has had many definitions, the most appropriate in this context being 'the genome's ability to produce adaptive variants when acted on by the genetic system' (Wagner & Altenberg, 1996). Specific genes within bacterial lineages have been identified that appear to increase their rate of mutation when faced with environmental stress, thus generating greater diversity when it is most beneficial (e.g. Moxon *et al.*, 1994). This same kind of response has been demonstrated in eukaryotic organisms as well, although the mechanisms are slightly different (Poole, Phillips & Penny, 2003). With this in mind, the results of domestication are potentially the expression of an increase in phenotypic, behavioural and physiologic variability, brought on by genetic mechanisms under the stress of a new environmental factor: living in close proximity to human beings. The mechanisms involved in this process (which seem to increase genetic and phenotypic flexibility) may also confer upon domesticates the ability to mate with

closely related sister taxa and to produce fertile offspring. Investigating evolvability in other systems (e.g. biotic and computer model based) may provide a deeper understanding not only of the potential of genomes to generate diversity, but also the mechanisms they use to do so.

Genetics has already vastly expanded our understanding of domestication, for example in revealing numerous additional centres of domestication for the majority of modern domestic mammals. Molecular data have provided us with a new and more robust interpretative framework from which further models and hypotheses can be built and tested, and it has forced us to consider more deeply the process of domestication, especially within the context of evolutionary theory and the effects on the underlying genome.

There is no doubt that the development of genetics in archaeology will continue to revolutionize our view of the past, perhaps on a par with the development of radiocarbon dating during the second half of the 20th century. With regard to specific questions associated with animal domestication, however, it must not be forgotten that a vast amount of work has already highlighted morphometric and demographic signals associated with the process. Techniques such as geometric morphometric analysis, newly applied within the field of zooarchaeology, are also now beginning to help refine the 'signatures' of phenotypic change potentially associated with the early domestication process. Molecularly derived insights, however powerful, still represent a single line of evidence that is meaningful only when multiple independent modes of inquiry are fully explored and then integrated. This process of integration is just beginning and, although the limitations are obvious, the potential is huge.

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