



# Origin and domestication of the domestic goat (*Capra aegagrus hircus*): a synthesis

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**Abstract.** This mini-review synthesizes current archaeological, zooarchaeological, and genomic evidence regarding the origin and domestication of the domestic goat (*Capra aegagrus hircus*). Data consistently indicate that domestic goats derive primarily from the wild bezoar goat (*Capra aegagrus*) within a broad Near Eastern region encompassing eastern Anatolia, the Zagros Mountains, and the Iranian Plateau. Domestication began approximately 10,000-11,000 years ago and likely followed a two-stage process, involving prolonged pre-domestication management of wild populations followed by effective domestication capturing extensive genetic diversity. Mitochondrial DNA analyses reveal multiple maternal haplogroups (A, B, C, D, F, G), with haplogroup A dominating modern populations, reflecting strong demographic expansion during the Neolithic. The geographic spread of goats across Eurasia and Africa was rapid and accompanied by regionally structured genetic diversity shaped by migration, exchange, and environmental barriers. Genomic studies further demonstrate that domestication and subsequent artificial selection targeted genes associated with behavior, immunity, reproduction, and production traits, sometimes influenced by introgression from other wild *Capra* species. Overall, goat domestication emerges as a complex, multi-regional, and genetically diverse process closely linked to the development and expansion of early agricultural societies.

**Key Words:** *Capra aegagrus*, *Capra hircus*, domestication process, Fertile Crescent, goat domestication, genetic diversity, genomics, haplogroups, livestock evolution, mitochondrial DNA, Neolithic, zooarchaeology.

**Introduction.** Early humans, drawn by the rich and savory taste of wild game, were gradually motivated to tame and manage animals, marking the first steps toward domestication (Ştefan et al 2005; Adhikari 2023). Goats were among the very first livestock domesticated by humans, playing a central role in the emergence of Neolithic farming societies (Teletchea 2019; Liu et al 2024). Archaeology, zooarchaeology, and genetics together show that domestic goats derive primarily from the wild bezoar goat (*Capra aegagrus*) in the broader Fertile Crescent, with a complex, regionally structured domestication process (Legge 1996; Crepaldi et al 2024).

The aim of this study is to synthesize and critically integrate archaeological, genetic, and genomic evidence in order to clarify the origin, domestication process, and early dispersal of the domestic goat (*Capra aegagrus hircus*), with particular emphasis on identifying key domestication centers, understanding genetic diversity patterns, and elucidating the evolutionary mechanisms underlying domestication and subsequent breed development.

**Archaeological and geographic origins.** Initial domestication is documented around 10,000 years ago in the Zagros Mountains of western Iran, where age-sex patterns in bones show a clear shift from hunting to managed herding, especially selective culling of young males (Zeder & Hesse 2000). Zooarchaeological and genetic evidence together place key early domestication zones in eastern Anatolia, the Northern and Central Zagros, and the Central Iranian Plateau, with pre-domestication management of wild herds likely in southern Zagros and central Iran (Naderi 2007; Naderi et al 2008; Vahidi et al 2014). Goats

then spread rapidly across the Old World, reaching the Iberian Peninsula by about 7000 years before present and southern Africa by about 2000 years before present (Amills et al 2017) (Table 1).

Table 1  
Main early domestication regions of goats (summarized by Consensus 2026)

<i>Region / Area</i>	<i>Evidence type</i>	<i>Role in domestication</i>	<i>Citations</i>
Eastern Anatolia and Northern Zagros	Archaeology + mtDNA	Major center; source of most modern domestic goats.	(Zeder & Hesse 2000; Naderi 2007; Naderi et al 2008; Colli et al 2015)
Southern Zagros and Central Iranian Plateau	mtDNA, genetic diversity	Early management/pre-domestication, minor contribution.	(Naderi 2007; Naderi et al 2008; Vahidi et al 2014)
Southern Levant	Archaeology, microwear, management signals	Experimental early herding, diverse husbandry regimes.	(MacHugh & Bradley 2001; Sergio et al 2023)

**Wild ancestor, genetic lineages, and demographic history.** Multiple genetic lines show that bezoar (*Capra aegagrus*) is the primary and likely sole wild ancestor of domestic goats (Naderi 2007; Naderi et al 2008; Colli et al 2015; Amills et al 2017; Jordan et al 2025). Mitochondrial analyses reveal several maternal haplogroups (A, B, C, D, F, G), with haplogroup A now carried by more than 90% of domestic goats worldwide (Nomura et al 2013; Colli et al 2015; Amills et al 2017; Kadowaki et al 2017; Sadia et al 2023). Most domestic mitochondrial lineages are nested within bezoar lineages, indicating direct descent (Naderi 2007; Naderi et al 2008; Colli et al 2015; Jordan et al 2025). Coalescent analyses date the most recent common ancestor of domestic goat mtDNA to roughly 460,000 years ago, with major expansions beginning around 12-10 thousand years ago, at the Epipaleolithic-Neolithic transition (Nomura et al 2013; Colli et al 2015). These expansions reflect both natural population growth and human-mediated dispersal of early herds.

Importantly, large-scale comparisons of wild and domestic mtDNA and nuclear polymorphisms suggest a two-step process: a pre-domestication phase of long-term wild herd management across a broad area, followed by effective domestication capturing a wide array of wild haplotypes (Naderi 2007; Naderi et al 2008). This pattern contrasts with the classic "narrow bottleneck" domestication model; goats retained high genetic diversity, and early domestic stocks did not undergo an extreme genetic contraction (Naderi 2007; Naderi et al 2008; Vahidi et al 2014; Hermes et al 2020).

**Spread, regional diversity, and multiple domestication foci.** As goats spread from the Fertile Crescent, their genetic diversity structured regionally. Iranian goats today show high nuclear diversity and clustering into northern, central, and western groups, with western breeds remaining relatively distinct because of the Zagros barrier (Vahidi et al 2014). Some breeds in central and southern Iran occupy regions where mtDNA signals suggest early management and lie on basal branches of genetic trees, consistent with proximity to original domestication areas (Vahidi et al 2014).

Across Eurasia and adjacent regions, mitochondrial surveys reveal complex patterns. Inner Asian and Central Kazakh Bronze and Iron Age goats show unexpectedly high mtDNA diversity, carrying the dominant A lineage alongside rarer C and D lineages, likely reflecting repeated exchanges with source populations on the Iranian Plateau (Hermes et al 2020). In contrast, goats of the Northern Eurasian Steppe mostly show haplogroup A alone, suggesting a more restricted founder population (Hermes et al 2020). Ancient and modern goats from the southern Caucasus also predominantly carry haplogroup A, consistent with influx from Near Eastern domestication centers rather than local wild populations (Kadowaki et al 2017). Pakistani breeds display A and B lineages, again pointing to contributions from multiple wild *Capra* strains, including *C. aegagrus*

(Sadia et al 2023). More recent mitogenome work in Türkiye and Iraq confirms widespread dominance of haplotype A but also presence of G, supporting Türkiye’s role as an important genetic center linked to the Fertile Crescent (Teber et al 2025) (Table 2).

Table 2

Global maternal lineages in domestic goats/major mitochondrial haplogroups and their roles (summarized by Consensus 2026)

<i>Haplogroup</i>	<i>Approximate frequency, distribution, and significance</i>	<i>Citations</i>
A	> 90% of modern goats; Near Eastern origin; strong expansion with domestication.	(Nomura et al 2013; Colli et al 2015; Amills et al 2017; Kadowaki et al 2017)
B	~5% globally; more Asia-linked; higher $\omega$ suggests different selection history.	(Nomura et al 2013; Amills et al 2017; Sadia et al 2023)
C, D, G	Rare; present in Near East, Asia, and ancient lineages; reflect additional wild source populations and possibly secondary domestication events.	(Naderi et al 2008; Colli et al 2015; Amills et al 2017; Hermes et al 2020)

Note:  $\omega$  (omega) represents the ratio of nonsynonymous to synonymous substitution rates (dN/dS), commonly used as an indicator of selective pressure acting on genes. Values of  $\omega < 1$  indicate purifying selection,  $\omega = 1$  neutral evolution, and  $\omega > 1$  positive selection.

**Genomic signatures of domestication and later selection.** Whole-genome and high-density marker analyses clarify how domestication and subsequent breeding reshaped goat genomes. Comparisons of wild bezoar and domestic breeds identify numerous copy-number variants and rapidly evolving genes linked to behavior, coat color, immunity, and production traits (Dong et al 2015; Amills et al 2017; Zhang et al 2018; Signer-Hasler et al 2022; Taheri et al 2023). One set of domestication genes comes from an ancient introgression from a West Caucasian tur-like species into the ancestors of domestic goats, including a strongly selected MUC6 haplotype that enhances resistance to gastrointestinal pathogens and a separate locus probably related to behavior; these alleles rose to high frequency 7,200-8,100 years ago, paralleling the rise of haplogroup A (Zheng et al 2020). Other candidate domestication genes involve reproduction, seasonality (e.g., TSHR), and possibly body size or milk yield (Signer-Hasler et al 2022; Taheri et al 2023).

Genome-wide scans in modern Swiss breeds detect “runs of homozygosity” islands enriched for genes affected both by early domestication and later breed-specific selection, confirming that traits such as coat color (via ASIP) and reproductive timing have been repeatedly targeted (Dong et al 2015; Signer-Hasler et al 2022). Broader surveys across elite dairy, cashmere, and meat breeds demonstrate that intensive human selection further refined growth, hair, and lactation traits on top of the original domestication background (Zhang et al 2018).

**Conclusions.** Current archaeological and genetic evidence indicates that domestic goats descend primarily from the wild bezoar (*Capra aegagrus*), with effective domestication beginning about 10,000-11,000 years ago in a broad Near Eastern zone centered on eastern Anatolia and the Zagros-Iranian Plateau. This process likely involved an initial phase of long-term management of wild herds, followed by domestication that captured substantial wild genetic diversity rather than a narrow bottleneck. Mitochondrial lineages, dominated today by haplogroup A but including several rarer haplogroups, trace back to multiple regional wild populations and reveal complex routes of dispersal across Eurasia, Africa, and beyond. Whole-genome studies show that domestication and later breeding reshaped genes controlling behavior, immunity, coat color, reproduction, and productivity, sometimes augmented by introgression from other wild *Capra* species. Together, these lines of evidence portray goat domestication as an extended, regionally diverse, and genetically rich process tightly intertwined with the rise and spread of early farming societies.

**Conflict of interest.** The authors declare that there is no conflict of interest.

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