Selection signatures in the rabbit genome: domestic vs. wild populations

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Abstract. The domestication of the European rabbit (*Oryctolagus cuniculus*) represents a well-documented model for investigating genomic signatures of selection associated with recent and rapid evolutionary change. This mini-review synthesizes current knowledge on the origin, demographic history, and genomic consequences of domestication by comparing domestic and wild rabbit populations. Evidence indicates a single domestication event in western Europe, most likely in France approximately 1,400–1,500 years ago, followed by population bottlenecks and extensive human-mediated dispersal. Genomic analyses reveal a clear differentiation between wild and domestic populations, accompanied by reduced genetic diversity in domestic rabbits and varying degrees of admixture. Selection signatures associated with domestication exhibit a predominantly polygenic architecture, characterized by shifts in allele frequencies across numerous loci rather than fixation of single mutations. These signatures are enriched in regulatory regions and genes involved in neuronal development, supporting the hypothesis that behavioral traits such as tameness are central to the domestication process. Additional targets of selection include genes related to coat color, body size, and metabolic adaptation to controlled feeding regimes. Subsequent artificial selection during breed formation has further shaped the genome, generating breed-specific phenotypic diversity layered upon earlier domestication changes. Feral rabbit populations provide important insights into the reversibility of domestication, as selection in natural environments tends to counteract maladaptive domestication alleles while allowing some variants to persist. Beyond evolutionary implications, the dual role of rabbits as valuable livestock and invasive species highlights the importance of integrating genomic knowledge into both breeding strategies and ecological management. Overall, the rabbit genome illustrates domestication as a dynamic and ongoing process driven by polygenic adaptation, regulatory evolution, and continuous interaction between natural and artificial selection.

Key Words: artificial selection, feralization, genetic diversity, *Oryctolagus cuniculus*, polygenic adaptation, population genomics, rabbit domestication, regulatory evolution, selection signatures, wild vs domestic populations.

Introduction. Domestication of the European rabbit has left detectable "signatures of selection" in the genome when domestic animals are compared with wild populations. These signatures highlight loci and pathways involved in tameness, morphology, coat color, metabolism and adaptation back to wild conditions.

The aim of this mini-review is to synthesize and critically evaluate current genomic evidence on selection signatures in the rabbit genome, with a focus on differences between domestic and wild populations, in order to clarify the genetic architecture of domestication, identify key functional targets of selection, and highlight the evolutionary and applied implications of these processes.

Rabbits Tamed: Where and When Was *Oryctolagus cuniculus* Domesticated? The domestic rabbit descends from the European rabbit, originally restricted to the Iberian Peninsula and southern France, where the genus *Oryctolagus* emerged and diversified during the Pleistocene in response to climatic oscillations and geographic barriers (Ferrand & Branco 2007; Pelletier 2025). Two main wild subspecies formed, *O. c. algirus* in southwestern Iberia and *O. c. cuniculus* in northeastern Iberia and southern France, with the latter becoming the sole source of domestic stocks (Ferrand & Branco 2007; Carneiro et al 2011; Dorożyńska & Maj 2020).

Genetic and protein polymorphism studies show that wild populations from France and northern Spain (*O. c. cuniculus*) are the direct ancestors of all domestic rabbits, while southwestern Iberian populations (*O. c. algirus*) did not contribute directly to domestication (Carneiro et al 2011; Ferrand & Branco 2007). Mitochondrial DNA analyses identify two geographically separated maternal lineages and indicate northern Spain and possibly southern France as Late Glacial refugia for ancestral populations (Monnerot et al 1994; Hardy et al 1994a). Ancient DNA from Bronze Age and Roman period bones on the Mediterranean island of Zembra links those early translocated rabbits to modern populations from northern Spain and southern France, confirming long distance human transport of *O. c. cuniculus* well before full domestication (Hardy et al 1994b).

Molecular demographic modelling and historical sources converge on a single domestication event in western Europe, centered on southern or central France. Coalescent simulations, calibrated to post glacial expansions, place the onset of domestication roughly 1400–1500 years ago, with an initial founding population under about 1200 individuals, likely in French monastic contexts (Ferrand 2008; Carneiro et al 2011; Somerville & Sugiyama 2021). Subsequent trade and human mediated dispersal spread domestic rabbits across Europe and, later, worldwide, with modern genomic data tracing Chinese and Kenyan domestic rabbits back to European, especially French, *O. c. cuniculus* ancestors introduced within the last 800–1500 years (Long et al 2003; Owuor et al 2019; Xie et al 2024).

Genomic Patterns and Demographic Background. Domestic rabbits derive mainly from wild *O. c. cuniculus* in France, with a domestication origin about 800–1500 years ago (Ferrand & Branco 2007; Carneiro et al 2011; Carneiro et al 2014; Xie et al 2024). Domestic populations retain only ~60% of the nucleotide diversity found in French wild rabbits, reflecting two bottlenecks during domestication (Carneiro et al 2011). Whole genome sequencing confirms clear separation of wild and domestic clusters, but also admixture, especially in France, Hungary and introduced regions such as Australia (Iannella et al 2018; Andrade et al 2024; Fekete et al 2025).

Polygenic Basis and Functional Targets of Selection. Genome wide comparisons identify over 100 domestic specific selective sweeps, but few fixed SNPs; instead, domestication involved shifts in allele frequencies at many loci, particularly conserved noncoding regulatory sites (Carneiro et al 2014). Selected regions are enriched for genes affecting brain and neuronal development, supporting a polygenic basis for tameness and behavioral change (Carneiro et al 2014; Andrade et al 2024; Xie et al 2024). Additional sweeps in domestic populations affect starch digestion and fat metabolism, consistent with adaptation to high starch diets and managed feeding (Xie et al 2024) (Table 1).

Table 1

Examples of selected traits in domestic breeds vs. wild rabbits (summarized by Consensus, 2026)

Trait category	*Key genes/regions highlighted*	*Citations*
Behavior/brain	Enriched neuronal development genes; NTRK2 in meat vs. other breeds	(Carneiro et al 2014; Ballan et al 2022; Xie et al 2024)
Coat color & pattern	ASIP, MC1R, KIT, KITLG, MITF, OCA2, TYR, TYRP1	(Ballan et al 2022; Li et al 2022; Ballan et al 2023; Xie et al 2024)
Body size & morphology	LCORL/NCAPG, HMGA2, COL11A1, COL2A1, HOXD, KIF16B	(Ballan et al 2022; Li et al 2022; Ballan et al 2023)
Metabolism/diet	Starch and fat metabolism loci in Chinese domestic rabbits	(Xie et al 2024)

Selection Signatures within Domestic Breeds and Across the Wild–Domestic Divide. High density SNP scans in fancy and meat breeds reveal thousands of genomic regions with selection signatures, many overlapping pigmentation and body size genes that explain breed specific phenotypes layered on top of older domestication changes (Ballan et al 2022; Li et al 2022; Ballan et al 2023). Whole genome studies of wild vs. domestic animals detect numerous variants fixed in one group or the other, and regions under selection enriched in transcription factor binding sites, indicating a central role of regulatory evolution (Carneiro et al 2014; Fekete et al 2025). Some strongly selected regions lie in intergenic DNA, suggesting yet uncharacterized regulatory elements important for domestication (Carneiro et al 2014; Fekete et al 2025).

Introduced feral populations show mixed wild - domestic ancestry. Alleles that rose during domestication tend to be selected against when rabbits re adapt to natural environments, especially those with strongly maladaptive effects, whereas milder domestication alleles (for example, coat color dilution) can persist at appreciable frequencies (Andrade et al 2024). Parallel selection in independent feral populations again targets genes linked to neuronal and brain function, mirroring domestication signatures in reverse (Carneiro et al 2014; Andrade et al 2024).

The Domestic European Rabbit as a Farm Animal, not a Wild Release. *Oryctolagus cuniculus* has become an important domestic livestock species due to its outstanding zootechnical advantages in meat and fur production. At the same time, when released outside farms, both wild and feral rabbits are widely documented as invasive herbivores that can severely disrupt native ecosystems, especially on islands and in sensitive habitats (Oroian et al 2014; Petrescu-Mag 2018; Petrescu-Mag et al 2019).

Domestic rabbits originate from the European rabbit and include numerous breeds selected for rapid growth, high prolificacy, early maturity, efficient feed conversion, and the ability to use forages and fibrous by products, making them highly suitable for intensive and small-scale farming systems (Gidenne et al 2017; Bharathy et al 2021; Luchyn 2022; Ali et al 2022; Paladan 2022; Pustova & Pustova 2023; Bertine et al 2025). Rabbit meat provides high quality protein with low fat and cholesterol and can help address meat and protein shortages, particularly in developing countries (Gidenne et al 2017; Bharathy et al 2021; Ali et al 2022; Lopez 2022; Paladan 2022; Zotte & Cullere 2024; Bertine et al 2025). Modern intensive systems and genetic improvement have steadily improved feed efficiency and reduced environmental burdens per unit of product, reinforcing their value as farm animals kept under controlled conditions (Gidenne et al 2017; Luchyn 2022; Pustova & Pustova 2023; Magaña-Valencia et al 2025).

However, introducing or allowing domestic or wild *O. cuniculus* to establish in the wild frequently leads to serious ecological imbalances. On Mediterranean and Macaronesian islands, rabbits reduce arthropod diversity, depress recruitment, growth and flowering of endemic and threatened plants, increase bare soil, and promote erosion, with only partial recovery after removal (Parada-Díaz et al 2022; Kossoff et al 2024). In Australia and Mexico, invasive rabbits drive long term degradation of native pastures, change plant communities, compete with native herbivores, and contribute to declines in ecosystem integrity and biodiversity (Mutze et al 2016; Lurgi et al 2018; Halecki & López-Hernández 2023). Peri urban feral domestic rabbits rapidly form self-sustaining populations, expand their range, affect predator–prey dynamics, and become difficult to manage socially and ecologically (Sogliani et al 2021). Localized introductions for tourism have led to population explosions, vegetation loss, soil erosion, and damage to cultural assets, requiring costly control programs (Aslan et al 2025). Globally, the same species is a conservation paradox: beneficial and even keystone within parts of its native range, but a major invasive alien elsewhere (Lees & Bell 2008; Lurgi et al 2018; Bobadilla et al 2021).

These contrasting roles support the view that *O. cuniculus* should be managed as a domestic farm animal, with its place in controlled production systems rather than being released into the wild, where it often generates significant ecological disturbance.

Conclusions. Across multiple genomic scales, comparison of domestic and wild rabbits reveals a complex, polygenic architecture of domestication. Selection signatures are concentrated in regulatory regions and genes affecting the brain, pigmentation, morphology and metabolism, with relatively few hard sweeps to fixation. Subsequent breed formation and feralization have added further layers of selection, refining or reversing domestication alleles against the background of the ancestral wild genome.

Building on these observations, the evidence synthesized in this work underscores that rabbit domestication represents a paradigmatic case of gradual, genome-wide modulation rather than rapid fixation of single major-effect mutations. The predominance of allele frequency shifts at numerous loci—particularly within conserved noncoding elements—highlights the central role of regulatory evolution in shaping phenotypic diversity. This finding aligns with broader domestication theory, suggesting that behavioral traits such as tameness are primarily governed by subtle changes in gene expression networks, especially those involved in neurodevelopment and synaptic function.

Moreover, the demographic history of the European rabbit reinforces the importance of historical contingencies in shaping present-day genomic variation. The relatively recent domestication event, combined with identifiable bottlenecks and subsequent global dispersal, has produced a genomic landscape characterized by reduced diversity in domestic populations, yet persistent signals of admixture with wild gene pools. Such introgression, particularly in regions where domestic and wild populations coexist, complicates the distinction between natural and artificial selection and contributes to ongoing evolutionary dynamics.

The stratification of selection signatures across hierarchical levels—from the wild–domestic divide to breed-specific differentiation—further illustrates how initial domestication laid a genomic foundation upon which later artificial selection acted. Traits such as coat color, body size, and production efficiency reflect more recent, targeted selection pressures, superimposed on earlier changes related to behavior and adaptation to captivity. This layered structure of selection emphasizes that domestication is not a singular event but a continuous evolutionary process.

Equally significant is the insight provided by feral populations, which serve as natural experiments in reverse evolution. The observed selection against certain domestication alleles in wild environments demonstrates that many traits favored under human management are maladaptive in natural ecosystems. At the same time, the persistence of some alleles indicates that not all domestication-related variation is detrimental outside controlled conditions. These patterns reveal a dynamic balance between selection pressures and provide a deeper understanding of evolutionary reversibility and constraint.

From an applied perspective, these genomic insights carry important implications for both animal breeding and conservation biology. In livestock systems, understanding the polygenic and regulatory basis of key traits can inform more precise selection strategies, potentially improving productivity, robustness, and welfare. Conversely, recognizing the ecological risks associated with feral and invasive rabbit populations highlights the need for informed management practices that integrate genetic knowledge with ecological considerations.

In conclusion, the study of selection signatures in the rabbit genome offers a comprehensive view of domestication as a multifaceted evolutionary process shaped by demographic history, polygenic adaptation, and ongoing gene flow. Future research integrating functional genomics, epigenetics, and environmental data will be essential to fully elucidate the mechanisms underlying these patterns and to translate genomic knowledge into sustainable management and breeding strategies.

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

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