

DNA Methylation, Speciation and Domestication

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Commentary

More than 150 years after Mendel published his observations on the fundamental laws of inheritance and nearly 65 years after Avery provided unambiguous evidence that the hereditary material is DNA, unraveling the molecular basis underlying phenotypic plasticity and diversity is still a hot topic in genetics. Natural selection counteracts DNA sequence variation, yet losing genetic variation renders populations more vulnerable to changes in environmental conditions. This apparent contradiction can be resolved if adaptation is primarily dependent on altered gene regulation rather than on altered protein structures. Epigenetic modifications, which can effectively be maintained during cell division even across several generations, but at the same time are generally transient and as such, can flexibly be rearranged upon, e.g. environmental stimuli, offer an ideal solution to this inherent problem. In concert with these theoretical considerations, an increasing body of evidence demonstrates that evolutionary processes go hand in hand with shifts in epigenetic patterns, at least with regard to DNA methylation marks.

In fact, observations on natural darter populations [1] imply that divergence in methylomes not only precedes speciation, but is possibly also its major driver. Results on wild versus domesticated chicken strains show that adaptive changes in behavior are accompanied by heritable changes in gene expression and promoter methylation patterns [2] and inter-strain variance in genetic pathogen resistance also seems to be related to differential DNA methylation at corresponding regions [3]. Comparative studies on a long non-coding RNA, which presumably regulates growth and muscle development, detected strain-specific differences in expression and methylation levels in wild boars and domesticated pigs [4]. Evidence also suggests that domestication-related changes in songbird vocal patterns can be induced by alterations in methylation states [5]. Larger-scale evolutionary events wear the signature of epigenetic alterations as well. Human and chimp methylomes exhibit characteristic differences in sperm [6], brain [7] and non-brain tissues [8] that in several cases were also shown to correspond to gene expression pattern differences.

At present, one of the most investigated taxa with regard to population-related DNA methylation characteristics is canids. This is not by pure chance: the domestic dog (1) has got several phylogenetically close wild relatives, including its ancestor the gray wolf, (2) as a species it exhibits extraordinary phenotypic variation, and (3) it includes several breeds, each representing a separate and limited gene pool, making the dog an ideal model for comparative genetic and epigenetic analyses. Population-characteristic epigenetic patterns have been described both on the single gene and on the whole methylome level. In the brain, promoter methylation of a gene important in neuromodulation and neurotransmission was found to differ by breeds and also to correlate with transcription rates [9]. A genome-wise dog-wolf comparative study revealed the existence of

species-specific methylation patterns at several sites [10]. Results also implicated that species assignment could be possible based on solely DNA methylation data, although cluster formation varied with analysis method. Investigations on offspring of wolf-coyote crosses demonstrated that inter-specific hybridization resulted in site-specific methylation patterns, presumably influencing hybrid genome functioning [11]. Our group found that wolf and dog, as well as certain dog breeds can unambiguously be distinguished from each other on a DNA methylation pattern basis even with relatively few markers used, at least in the case of specific selected regions [12]. More research is needed before further interpretation can be made, however, these data might hold the key to understanding some curious phenomena related to domestication and speciation; for example why similar morphological and physiological changes can appear in distinct species when selecting for tameability [13], how and why such complex traits as human-directed social behavioral features can be highly heritable in dogs [14] or why could it be more important from the temperamental aspect whether a dog comes from a (relatively recently established) show or work line, instead of what function its breed historically fulfilled [15].

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