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Gene expression under human self-domestication: an in silico exploration of modern human high-frequency variants

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Abstract

Domesticated animals and modern humans show a set of behavioral and molecular changes that converge on shared genetic targets. There is evidence that these changes disproportionately target neurotransmission, in particular the glutamatergic signaling system. This has led to proposals that attenuation of glutamatergic signaling may be crucial for the downregulation of the stress response in both modern humans and domesticates and the potentiation of exploratory motor output in our species. Here, we use a deep learning method (ExPecto) to predict gene expression in silico of *H. sapiens*-specific (relative to the closest extinct human species, Neanderthals and Denisovans) variants of genes involved in glutamatergic signaling. This approach allows us to hone hypotheses about the functional implications of genetic changes in our species' recent evolution, including proposals as to the neurobiological substrates of *H. sapiens* so called 'self-domestication hypothesis'.