

Domestication of Salmon and Sheep: Contrasting Patterns of Genomic Diversity and Signatures of Selection

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Abstract

Domestication has radically reshaped animal physiology and behaviour, leaving behind signature patterns of genomic variation. In this study, we identify and characterise selection sweeps in two species with dramatically contrasting domestication histories. First, genome sequence from 43 diverse sheep breeds was used to identify selection sweeps in a species domesticated approximately 10,000 years ago. The consequence is the impact of domestication and subsequent selection can be difficult to dissect. Secondly, genome data was used to identify sweeps in Atlantic salmon which were first domesticated less than 50 years ago. This offers the opportunity to explore the earliest impacts of moving animals under reproductive control and into a captive environment. In each study species, convincing evidence is presented for genomic regions and genes that are likely to have been involved in domestication and/or positive selection. Importantly, we extend these findings using functional genomics which seeks to identify a genome wide collection of gene regulatory elements and assess their putative involvement in the development of the domestication phenotype. For sheep, we demonstrate that proximal regulatory elements have played a key role. In the case of salmon, preliminary data is presented which begins to characterise genomic features beyond only protein coding genes. Through the consideration of multiple species with divergent population histories, the study deepens our understanding of the evolutionary processes of animal domestication and opens new avenues for improved genetic improvement.

Introduction

A growing number of studies are successfully documenting the evolutionary consequences of domestication and positive selection through assessing patterns of genetic variability. Selection sweeps are characterised by low diversity surrounding beneficial alleles driven to high population frequency. This means simple approaches that measure nucleotide diversity and allele frequency differences can be used to identify the genes that are likely to have contributed to selection. The power of such studies has been dramatically increased through the availability of genome sequencing, and we apply these methods here to two species with contrasting population histories.

Results

The study utilised whole genome sequencing of sheep from 43 globally representative breeds and 17 Asiatic Mouflon, their wild counterpart. Sequencing to an average of 11 fold coverage per animal identified 28.1 M SNP which were used to search for sweep regions. Domestic sheep genomes were searched for shared regions of both low nucleotide diversity and high divergence from wild sheep. We identified 635 regions containing genes involved in weight, milk production and reproduction. Next, we used human ENCODE and Epigenome data to predict regulatory features such as promoters and enhancers within the sheep genome. Our predictions were tested against histone modification mark data (H3K4me3, H3K27ac) collected from sheep adipose tissue, confirming human epigenetic data does capture sheep regulatory elements. Importantly, co-analysis revealed the 635 sweep regions were significantly enriched for proximal regulatory elements, strongly suggesting that remodelled gene expression has contributed to the evolution of the domestication phenotype. We applied the same methodology in Atlantic salmon, by collecting whole genome sequence from domestic animals and comparing the patterns of genome variation to wild populations. We identified approximately 5 M SNP and fewer genome regions that displayed convincing evidence of selection in domesticated fish (71). These contained genes involved in sexual reproduction, olfactory systems, neuronal development and cholesterol homeostasis. It is not currently possible to assess if regulatory elements are implicated, due to the paucity of epigenome data for teleost fish. In response, we have commenced production of RNA-seq, ATAC-seq and methylation data generation and preliminary results are presented that begin to characterise the salmon regulome.

Discussion

Livestock present a wonderful model with which to better understand the rapid evolutionary changes that underpin the domestication phenotype. This study implicates key gene players, and sets the stage for the next phase of experimentation which seeks to isolate the functional mutations involved.