SOX10 regulates multiple genes to direct eumelanin vs. pheomelanin production in domestic rock pigeon

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ABSTRACT

The domesticated rock pigeon (Columba livia) has been bred for hundreds of years to display an immense variety of ornamental attributes such as feather color and color patterns. Color is influenced by multiple loci, which impact the type and amount of melanin deposited on the feathers. Pigeons homozygous for the “recessive red” mutation, which causes downregulation of Sox10, display brilliant red feathers instead of blue/black feathers. Sox10 encodes a transcription factor important for melanocyte differentiation and function, but the genes that mediate its promotion of black vs. red pigment are unknown. Here, we present a transcriptomic comparison of regenerative feathers from wild-type and recessive red pigeons to identify candidate SOX10 targets. Our results identify both known and novel targets, including many genes not previously implicated in pigmentation. Collectively, the data suggest that downregulation of multiple genes may ultimately be responsible for the shift from eumelanin to pheomelanin synthesis in recessive red pigeons. These data highlight the value of using novel, emerging model organisms to gain insight into the genetic basis of pigment variation.

RESULTS

Transcriptomic comparisons identify differentially-expressed genes between wild-type (n = 4) and recessive red (n = 3) pigeons. Dotted line indicates \( P \)-value cutoff of adjusted \( P < 0.05 \). Genes implicated in pigment production indicated by name and highlighted in red. Enrichment was identified for GO Term Biological Process “pigment” \( P = 6.57 \times 10^{-10} \).

These data support the hypothesis that DE gene comparisons between wild-type and recessive red feathers accurately captures transcriptional differences relevant to their different melanin phenotypes.

Fig. 1. Transcriptomic analysis of differentially expressed (DE) genes in recessive red feathers identifies enrichment for pigment genes

Fig. 2. qRT-PCR validates transcriptomic comparisons of wild-type and recessive red feathers

Fig. 3. DE genes are enriched for SOX10 binding motifs

Fig. 4. Many DE genes are near SOX10-occupied loci in mouse melanocytes

Fig. 5. Comparison of DE genes in recessive red pigeons and Sox10\(^{+/−}\) mice

Because melanocyte development is abrogated in Sox10\(^{+/−}\) mice, previous research identified DE genes between wild-type and Sox10\(^{−/−}\) mouse melanocytes. Surprisingly, only 4 genes (Pmel, Papss1, Gpr137c, Poppa)1 were downregulated in both recessive red pigeons and Sox10\(^{+/−}\) mice. These data support the hypothesis that substantial differences in the transcriptional targets of SOX10 have evolved between mouse and pigeon.

SUMMARY

• Transcriptomic comparisons of wild-type and recessive red feathers identifies putative SOX10 targets.
• Pheomelanin of recessive red birds does not appear to be due to downregulation of Mc1r or Tyr.
• Sox10 may promote eumelanism by regulating multiple target genes.
• Substantial differences in SOX10 targets may exist between mouse and pigeon.

FUTURE DIRECTIONS

• Sequencing of additional biological replicates to improve statistical confidence.
• Derivation of pigeon melanocytes in vitro.
• Mutagenesis of DE genes to evaluate roles in pigment formation.

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REFERENCES