Author's Accepted Manuscript

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ww.elsevier.com/locate/developmentalbiology

 PII:
 S0012-1606(17)30458-X

 DOI:
 https://doi.org/10.1016/j.ydbio.2017.12.013

 Reference:
 YDBIO7651

To appear in: Developmental Biology

Received date: 30 June 2017 Revised date: 5 December 2017 Accepted date: 18 December 2017

Cite this article as: Jialiang S. Wang, Carlos R. Infante, Sungdae Park and Douglas B. Menke, PITX1 Promotes Chondrogenesis and Myogenesis in Mouse Hindlimbs Through Conserved Regulatory Targets, *Developmental Biology*, https://doi.org/10.1016/j.ydbio.2017.12.013

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ABSTRACT

The PITX1 transcription factor is expressed during hindlimb development, where it plays a critical role in directing hindlimb growth and the specification of hindlimb morphology. While it is known that PITX1 regulates hindlimb formation, in part, through activation of the *Tbx4* gene, other transcriptional targets remain to be elucidated. We have used a combination of ChIP-seq and RNA-seq to investigate enhancer regions and target genes that are directly regulated by PITX1 in embryonic mouse hindlimbs. In addition, we have analyzed PITX1 binding sites in hindlimbs of Anolis lizards to identify ancient PITX1 regulatory targets. We find that PITX1-bound regions in both mouse and Anolis hindlimbs are strongly associated with genes implicated in limb and skeletal system development. Gene expression analyses reveal a large number of misexpressed genes in the hindlimbs of *Pitx1-/-* mouse embryos. By intersecting misexpressed genes with genes that have neighboring mouse PITX1 binding sites, we identified 440 candidate targets of PITX1. Of these candidates, 68 exhibit ultraconserved PITX1 binding events that are shared between mouse and Anolis hindlimbs. Among the ancient targets of PITX1 are important regulators of cartilage and skeletal muscle development, including Sox9 and Six1. Our data suggest that PITX1 promotes chondrogenesis and myogenesis in the hindlimb by direct regulation of several key members of the cartilage and muscle transcriptional networks.

Keywords:

PITX1, Hindlimb, *Anolis*, Mouse, Chondrogenesis, Myogenesis 1. Introduction

The *Pitx1* gene encodes a bicoid-class homeodomain transcription factor that plays a central role in growth and patterning of the vertebrate hindlimb (Lanctôt et al., 1999; Szeto et al., 1999). The complete ablation of *Pitx1* function in mice results in reduced

1

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