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REVIEW
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Importance of Long Non-coding RNAs in the Development and Disease of Skeletal Muscle and Cardiovascular Lineages

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The early mammalian embryo is characterized by the presence of three germ layers-the outer ectoderm, middle mesoderm and inner endoderm. The mesoderm is organized into paraxial, intermediate and lateral plate mesoderm. The musculature, vasculature and heart of the adult body are the major derivatives of mesoderm. Tracing back the developmental process to generate these specialized tissues has sparked much interest in the field of regenerative medicine focusing on generating specialized tissues to treat patients with degenerative diseases. Several Long Non-Coding RNAs (lncRNAs) have been identified as regulators of development, proliferation and differentiation of various tissues of mesodermal origin. A better understanding of lncRNAs that can regulate the development of these tissues will open potential avenues for their therapeutic utility and enhance our knowledge about disease progression and development. In this review, we aim to summarize the functions and mechanisms of lncRNAs regulating the early mesoderm differentiation, development and homeostasis of skeletal muscle and cardiovascular system with an emphasis on their therapeutic potential.

Keywords: non-coding RNA, skeletal muscle, endothelial cell, vascular smooth muscle cell (VSMC), differentiation, mesoderm, myogenesis, cardiovascular diseases

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INTRODUCTION

Gastrulation results in the formation of the three germ layers - ectoderm, mesoderm and endoderm. The mesoderm is a middle layer between the innermost, endoderm and the outer ectoderm. The transition from epithelial cells to mesenchymal cells marks the formation of mesoderm which is further organized into the paraxial, intermediate and lateral mesoderm (Nakaya and Sheng, 2008; Evseenko et al., 2010). The three parts of the mesoderm are acted upon by several lineage commitment programs and differentiate into the progenitor cells that give rise to musculoskeletal, urogenital and cardiovascular structures of the body (Doss et al., 2012). Cells of these organs have the same genome, but the differences in transcriptionally active and inactive regions of genome guide the precursor cells toward different cell fates (Iwafuchi-Doi and Zaret, 2016). The differences in genomic organization, followed by activation or silencing of genes, are the result of complex gene regulatory networks (GRNs) (Materna and Davidson, 2007). For many years these GRNs were thought to be controlled exclusively by protein coding genes until the discovery