



Category: Animal genomics

Micro-RNA and epigenetic factors regulatory network during Myelopoiesis

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Abstract

Mammalian hematopoiesis is a hierarchal developmental process, which starts with Hematopoietic Stem Cells (HSCs) in bone marrow and through progressive stages of lineage commitment and differentiation gives rise to different mature blood cell types. These blood types can be classified into myeloid and lymphoid lineages. Epigenetic factors (EFs) are a class of gene regulators that modulate chromatin signatures and also work in concert with other classes of regulators like transcription factors (TFs) and non-coding RNAs (ncRNAs), in regulating normal development process. Perturbations in the expression of these regulators have been linked to various developmental defects and diseases progression including hematopoiesis. We are interested in understanding the cross-talk among these crucial regulators during myeloid cell development and acute myeloid leukemia. Towards this, we have analyzed the mRNA expression profile during each stage of myeloid cell development. The differentially expressed EFs during each stage of development were integrated with a network formed using curated gene regulations from different databases and a potentially active EF sub-network for each stage of development was extracted. These active stage specific sub-networks were further analyzed to obtain the unexplored potential regulatory relationship between EFs and miRNAs in a stage specific manner. The stage specific regulatory network generation will provide a framework for further understanding and targeting crucial EFs in hematopoiesis or blood cell development, perturbation in which leads to leukemia.

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