Abstract

To improve modern therapeutic and diagnostic methods, it is crucial to understand the development of the cardiac sympathetic system and to identify the genes involved in its regulation. Neural crest cells give rise to the sympathetic precursors that migrate towards the dorsal aorta. This migration is regulated by the NRP1/SEMA3A and neuregulin/ERBB signaling. The differentiation towards the sympathetic phenotype is regulated by transcriptional factor networks, including ASCL1, PHOX2A/B, GATA3, HAND2, HIF1A and ISL1. Next, neurons migrate to the final paravertebral position, which is regulated by the BDNF/TRKB signaling. The final step in the development of cardiac sympathetic neurons is the axon growth and guidance towards the heart. This is regulated by the NGF/TRKA and NRP1/SEMA3A signaling. This thesis aims to map current knowledge of different regulation pathways involved in the cardiac sympathetic development (especially in the mouse model) with emphasis on transcriptional factors. This type of information should help us better understand the pathophysiology of some cardiovascular diseases associated with the dysfunctional sympathetic system, such as arrhythmias, congestive heart failure or myocardial infarction, which remain to be main causes of death worldwide.