N-Myc-mediated epigenetic reprogramming drives lineage plasticity in advanced prostate cancer

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Abstract

Despite recent advances in the development of highly effective androgen receptor (AR)-directed therapies for the treatment of prostate cancer, nearly 37% of patients develop resistance. A further third of these patients progress to develop aggressive neuroendocrine prostate cancer (NEPC) for which no effective therapies exist. Lineage plasticity, a process by which differentiated cells lose their identity and acquire an alternative lineage phenotype, has recently been proposed as a mechanism of resistance to targeted therapies in several cancer types, such as leukemias and epithelial tumors (including prostate cancer). However, the molecular programs underlying this lineage plasticity are poorly understood. Previously, we observed that the majority of NEPC and 20% of castration-resistant prostate cancer (CRPC) aberrantly overexpress the transcription factor MYCN (N-Myc). In spite of this frequent occurrence, the role of N-Myc in driving lineage plasticity and the epigenetic mechanisms which regulate disease progression remain to be elucidated. To address this, we analyzed overall survival and whole transcriptome data from a cohort of over 200 prostate cancer patients, including the largest-to-date population of NEPC patients. We also analyzed epigenetic modifications along with the N-Myc transcriptome, cistrome and chromatin-bound interactome by performing ChIP-seq, RNA-seq and RIME in a combination of mouse models, human prostate cancer cell lines, and NEPC patient-derived organoids. We found that the expression of MYCN in CRPC and NEPC patients correlates with reduced overall survival. NEPC tumors are significantly enriched for stem cell genes associated with normal neuroendocrine cell precursors and embryonic stem cells as well as for neural lineage-defining genes from activated neural stem cells. The integration of next-generation sequencing data revealed that the N-Myc cistrome is and rogen-dependent and drives a transcriptional program leading to epithelial plasticity and the acquisition of clinically relevant neuronal lineage markers. Interestingly, histone marks specifically associated with lineage-defining genes are epigenetically reprogrammed by N-Myc. Finally, we demonstrated that N-Mycinduced gene expression and epigenetic changes can accurately classify our patient cohort. In summary, here we describe a novel role for N-Myc in prostate cancer, characterized by changes in the N-Myc cistrome and interacting cofactors, as well as reprogramming of the epigenome in an androgen context-dependent manner. This reprogramming is associated with an induction of a lineage plastic state and a switch towards a neural identity that favors the development of AR independence and NEPC.

Conflicts of Interests

The authors declare no conflicts of interests.

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