

Urbanucci A., Braadland P.

Institute for Cancer Research, Dept. of Tumor Biology, Oslo, Norway

Tumor evolution is based on the ability to constantly mutate and activate different pathways under the selective pressure of targeted therapies. Epigenetic alterations including those of the chromatin structure are associated with tumor initiation, progression and drug resistance. Many cancers, including prostate cancer, present enlarged nuclei, and chromatin appears altered and irregular. These phenotypic changes are likely to result from epigenetic dysregulation. High-throughput sequencing applied to bulk samples and now to single cells has made it possible to study these processes in unprecedented detail. It is therefore timely to review the impact of chromatin relaxation and increased DNA accessibility on prostate cancer growth and drug resistance, and their effects on gene expression. In particular, we focus on the contribution of chromatin-associated proteins such as the bromodomain-containing proteins to chromatin relaxation. We discuss the consequence of this for androgen receptor transcriptional activity and briefly summarize wider gain-of-function effects on other oncogenic transcription factors and implications for more effective prostate cancer treatment.