Therapeutic opportunities in transcriptional regulation of breast cancer

Forskningsleder Rasmus Siersbæk

Gruppens kerneforskningsområder

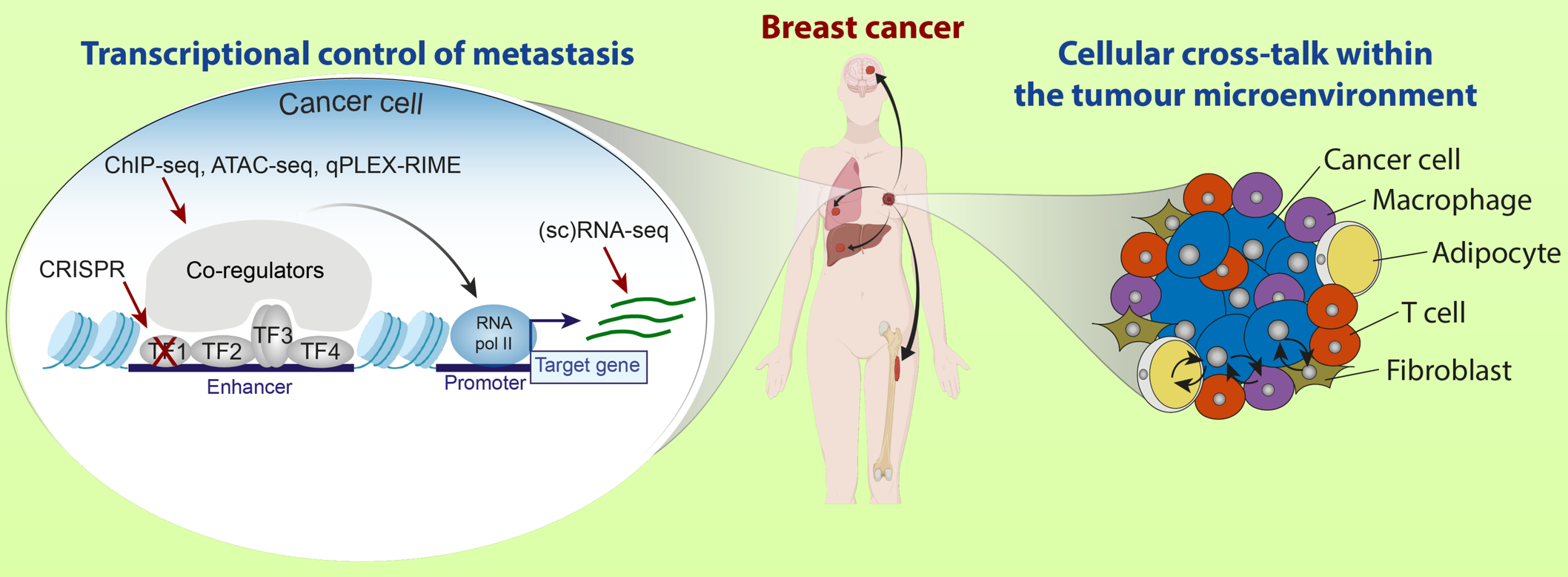
Cancer cells develop from normal cells due to accumulation of multiple oncogenic mutations that ultimately lead to uncontrolled growth. The resulting primary tumour can then further spread to other distant organs in the body (e.g. lung, liver and brain) to form secondary tumours through a process termed metastasis. The development of these secondary tumours is the main cause of death for most cancer patients, yet we know remarkably little about this process.

We are specifically interested in understanding the biology of breast cancer, which is the most common type of cancer affecting women. Specifically, we focus on how breast tumours metastasise (i.e. spread) to other parts of the body to try to identify therapeutic opportunities, where we can block this process. Our research is centered around the transcription factors and co-regulatory proteins that drive this metastatic process by controlling the activity of our genes. Our overall goal is to provide fundamental insight into how breast cancer cells operate at the genomic level and use this information to identify new therapeutic opportunities to inhibit cancer progression. We use a variety of technologies and model systems to investigate these regulatory mechanisms including

1. global analyses of the genome and proteome, e.g next-generation sequencing.
2. genome editing approaches
3. single-cell analyses
4. cell lines, mouse models and patient samples

Taken together, our research is focused on understanding the transcriptional mechanisms controlling breast cancer metastasis with the aim to provide clinically relevant information on treatment opportunities.

Er du interesseret i at skrive projekt i gruppen, så kontakt : siersbaek@bmb.sdu.dk



Projekter	Beskrivelse
Transcriptional regulation of triple negative breast cancer metastasis.	Triple negative breast cancer is a particularly aggressive and metastatic subtype of breast cancer with limited treatment options. In this project, we aim to understand how this subtype is controlled at the transcriptional level to identify potential new treatment opportunities.
Transcriptional regulation within the tumour microenvironment at the single-cell level.	It is now clear that cancer cells are very heterogenous and respond differently to treatment. Furthermore, the tumour microenvironment, i.e. the cells surrounding the tumour, plays and important role in controlling the phenotype of the cancer cells. In this project, we investigate the heterogeneity of breast cancer cells and try to understand how other cell types impact the phenotype and treatment responses of the tumour.