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Dissecting the contribution of tumour-infiltrating myeloid cells in dictating tumour epigenetic reprogramming

Summary

About 80% of breast cancers (BCs) are hormone dependent. Accordingly, anti-hormonal therapy remains a mainstay of treatment, however, a considerable fraction of these patients ultimately progress with advanced cancer. Genomic alterations are enriched in advanced BCs and proposed to be the cause of the generation of therapy-resistant relapsed cancer clones. This model is very simplistic since it ignores the interconnections occurring between tumour cells and the surrounding microenvironment. The BC microenvironment is highly infiltrated by immature myeloid cells (IMCs). Whether these cells can contribute to the observed genomic alterations remains unexplored. My project is based on the hypothesis that IMCs infiltrating BCs have the capacity to induce cancer-relevant genomic alterations in the tumour cells, driven by epigenetic reprogramming. The results of such research will challenge the concept that clonal evolution is only driven by cell-autonomous mechanisms, by expanding the importance of myeloid cells in contributing to therapy response and relapse.