Delineating the different states of the epithelial/mesenchymal spectrum in breast cancer

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Epithelial-to-mesenchymal transition (EMT) is associated with the generation of heterogeneous cancer cell phenotypes, which endorses the adaptation to the diverse microenvironmental changes during tumour progression. However, the functional characteristics and molecular features of cells in different states of the epithelial/mesenchymal spectrum are largely unrevealed yet. We have recently established partial and full EMT lineage tracing systems in a mouse model of metastatic breast cancer and revealed that cancer cells that have ever undergone a partial EMT, but not a full EMT, contributes to metastasis formation. We further set up a flow cytometry sorting strategy based on the combinatorial expression of the epithelial cell marker EpCAM and our lineage tracing systems identifying partial or full EMT states. Transplantation of the sorted EMT-lineage subpopulations revealed that distinct subpopulations have different capabilities of tumour-propagation and metastatic lung colonization. Employing next generation RNA sequencing of 5-cell pools we currently aim at identifying the transcriptomic features of the various subpopulations of the EMT spectrum in our mouse models.