Adjustment of dendritic cells to the breast-cancer microenvironment is subset specific

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The functions and transcriptional profiles of dendritic cells (DCs) result from the interplay between ontogeny and tissue imprinting. How tumors shape human DCs is unknown. Here we used RNA-based next-generation sequencing to systematically analyze the transcriptomes of plasmacytoid pre-DCs (pDCs), cell populations enriched for type 1 conventional DCs (cDC1s), type 2 conventional DCs (cDC2s), CD14+ DCs and monocytes-macrophages from human primary luminal breast cancer (LBC) and triple-negative breast cancer (TNBC). By comparing tumor tissue with non-invaded tissue from the same patient, we found that 85% of the genes up-regulated in DCs in LBC were specific to each DC subset. However, all DC subsets in TNBC commonly showed enrichment for the interferon pathway, but those in LBC did not. Finally, we defined transcriptional signatures specific for tumor DC subsets with a prognostic effect on their respective breast-cancer subtype. We conclude that the adjustment of DCs to the tumor microenvironment is subset specific and can be used to predict disease outcome. Our work also provides a resource for the identification of potential targets and biomarkers that might improve anti-tumor therapies.

Keywords : Dendritic cell subsets, breast cancer, transcriptomics, RNA-seq,
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