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M1-M2 macrophages and their bone marrow-derived progenitors in breast tumor microenvironment

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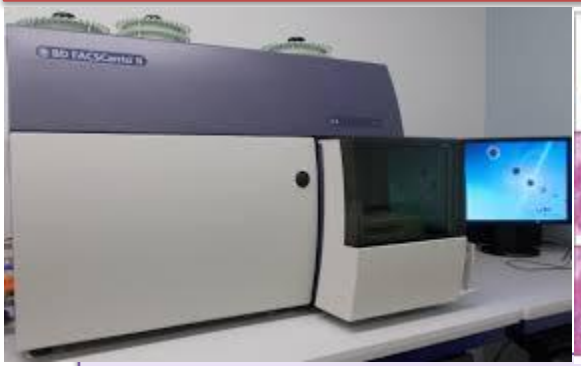
Background: Tumor-infiltrating lymphocytes (TILs) have been shown to provide prognostic and potentially predictive value in early triple-negative and Her2-overexpressing, but not in luminal A and B breast cancer (International TILs Working Group 2014). In the ME, macrophages are differentiated both from monocytes and tumor-recruited bone marrow cells. M1 macrophages harbor antitumoral activity, whereas M2 macrophages support tumor progression.

Methods: Tumor cell suspension was stained anti-CD34-PerCP/Cy5.5, anti-CD11b-PE, anti-CD45-PE-Cy7 (Abcam, USA) and analyzed by flow cytometer FACS Canto II (BD, USA). The ME (n=3) was isolated by laser microdissection (PALM, CarlZeiss, Germany). Total RNA was isolated by RNeasy Micro Kit (Qiagen, USA), and transcriptome amplification was performed using QuantiTect WTA Kit (Qiagen, USA). Macrophage-related (M1 and M2) gene expression was analyzed by RT-PCR (CXCL11, CD206, CHID1, CHI3L2, TGFB1, IL10, IL12). Gene expression values were normalized gene ACTB and normal tissue.

Results: The number of bone marrow progenitor cells (CD34+CD45+CD11b+) amounted to 0.99 (0.72-2.03)% in breast tumors. The ME was represented either M1 or M2 macrophages or simultaneously two subpopulations in combination with the expression of key cytokines that provide their functional activity.

Objectives: The study included 16 patients with luminal A and B IC NST, T1-4N0-3M0, 29 to 70 years old.



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