

The Role of Lipid Metabolism in Breast Cancer Progression and Treatment Resistance

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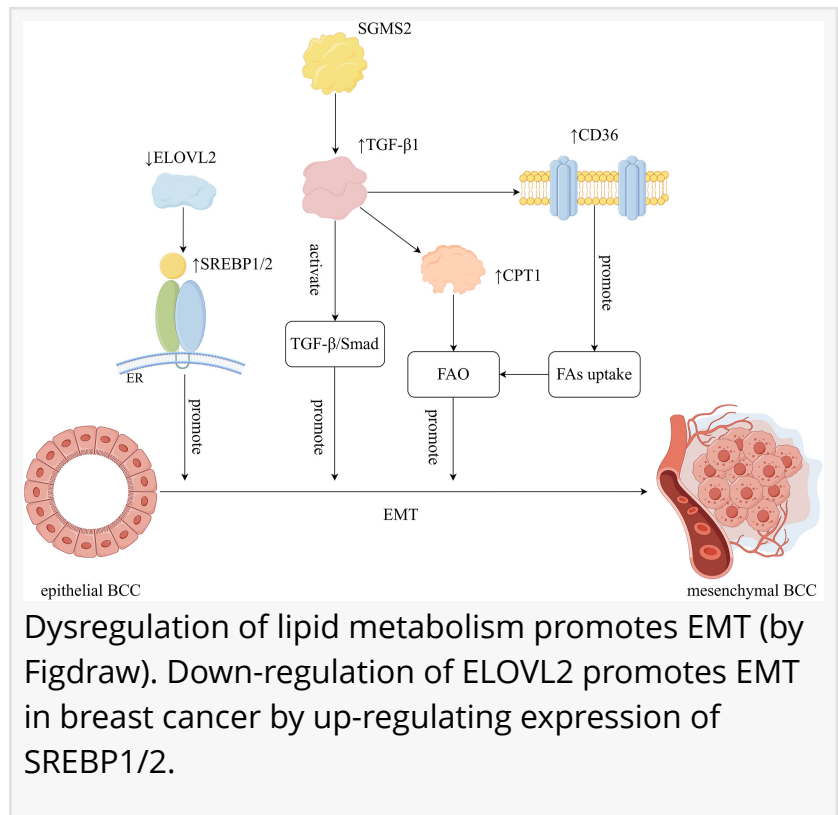
Lipid metabolism has emerged as a central player in the progression and therapy resistance of breast cancer, particularly the aggressive subtype known as triple-negative breast cancer (TNBC). This review article highlights how disruptions in lipid regulation can significantly influence the behavior of breast cancer cells, impacting their growth, metastasis, and response to treatment.

Alterations in the metabolism of fatty acids, cholesterol, sphingolipids, and glycolipids are profoundly intertwined with breast cancer cell survival and invasiveness. The uptake and

biosynthesis of fatty acids are notably upregulated in tumor cells, which not only fuels cellular energy demands but also supports membrane synthesis and intracellular signaling. Key enzymes and transporters, such as CD36, FASN, and FABP4, are instrumental in facilitating this metabolic shift, thereby enhancing tumor proliferation and metastatic potential.

In cholesterol metabolism, the focus falls on how elevated cholesterol synthesis and its potent metabolite 27-hydroxycholesterol (27HC) accelerate tumor progression and interfere with immune responses. Proteins such as SREBP2, NSDHL, and STARD4 further contribute to this dysregulation, reinforcing cancer cell survival and dissemination. The interplay of 27HC with estrogen receptors and immune-modulatory pathways further complicates therapeutic strategies, particularly in hormone-sensitive and resistant tumors.

The dual nature of sphingolipid metabolism, especially the contrasting roles of ceramide and its glycosylated derivatives, underscores a complex metabolic paradox. While ceramide accumulation exhibits tumor-suppressive effects, including enhanced apoptosis and



chemotherapy sensitization, glycosylated forms such as Globo-H ceramide and GD2 are linked to tumorigenesis, angiogenesis, and cancer stem cell maintenance.

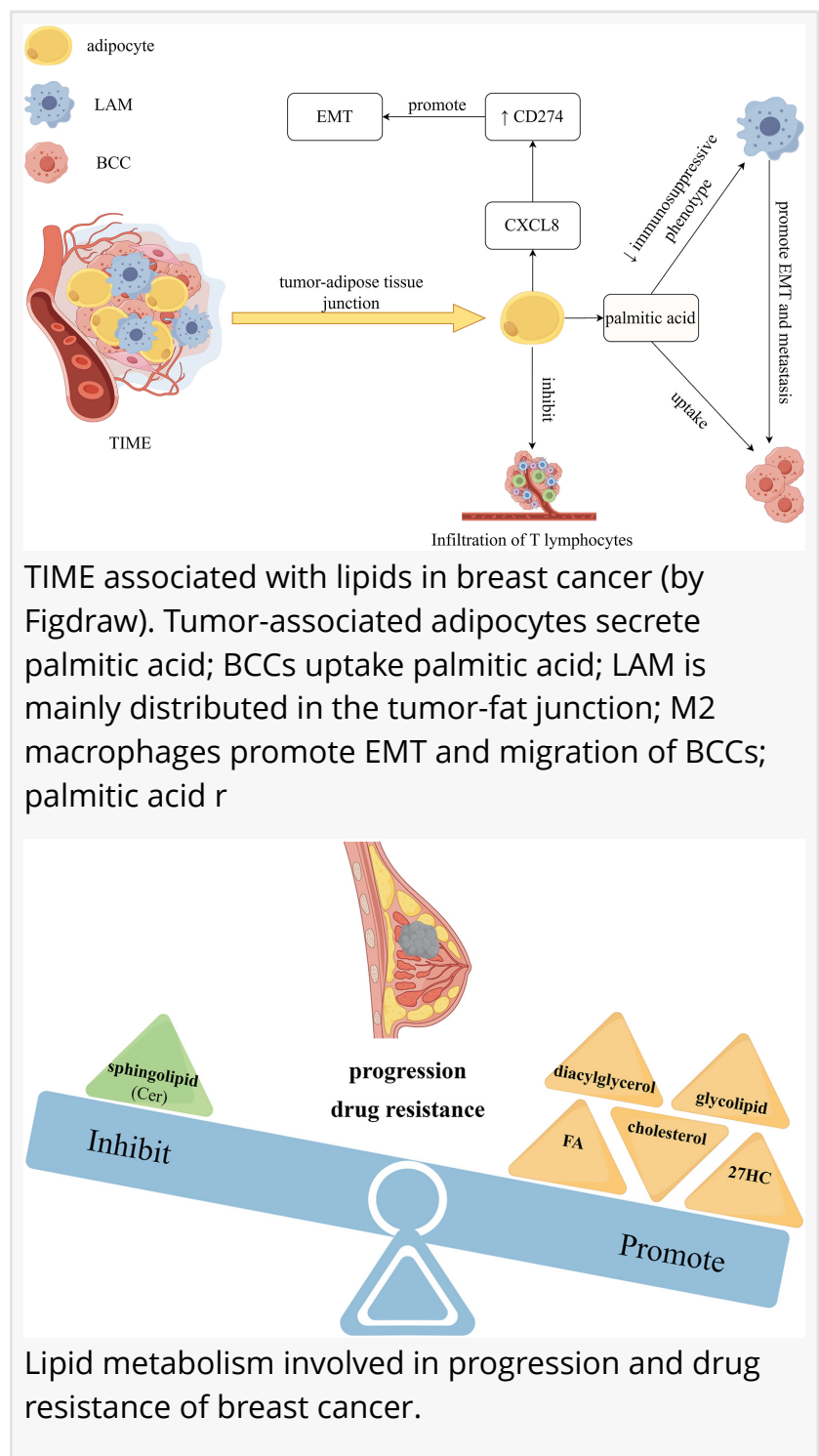
A crucial outcome of lipid reprogramming is its role in promoting epithelial-mesenchymal transition (EMT), a process associated with enhanced migratory ability and drug resistance. Factors like ELOVL2, SGMS2, and CXCL8 modulate EMT through intricate signaling cascades, including TGF- β , PI3K/AKT, and SREBP1/2 axes.

Beyond intrinsic cancer cell metabolism, the surrounding tumor immune microenvironment (TIME) also adapts in response to lipid cues. M2 macrophages, cancer-associated fibroblasts, and CD8⁺ T cells exhibit lipid-driven phenotypic shifts that support tumor evasion and therapy failure.

Resistance to standard treatments—including chemotherapy, endocrine therapy, HER2-targeted therapy, and immune checkpoint inhibitors—is intimately linked to lipid metabolic rewiring. Upregulation of CD36, FASN, CPT1, and GPR120 exemplifies how tumor cells exploit lipid pathways to avoid apoptosis, reduce drug accumulation, and sustain stemness.

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Reference

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