Journal of Molecular Pathophysiology, 2024
VOL 13, NO. 1, PAGE 01-02

COMMENTARY

Open Access

Immune Evasion Strategies and the Role of Checkpoint Molecules in Metastatis

Branwen Lee*
Department of Oncology and Metastasis Research, Johns Hopkins University, Maryland, USA

ARTICLE HISTORY
Received: 22-Dec-2023, Manuscript No. JMOLPAT-24-126698;
Editor assigned: 25-Dec-2023, PreQC No. JMOLPAT-24-126698 (PQ);
Reviewed: 09-Jan-2024, QC No. JMOLPAT-24-126698;
Revised: 16-Jan-2024, Manuscript No. JMOLPAT-24-126698 (R);
Published: 24-Jan-2024

About the Study

Metastasis is a complex and multifaceted process that plays a pivotal role in the progression of cancer. It represents the spread of cancer cells from the primary tumor to distant organs or tissues, leading to the formation of secondary tumors. At the heart of metastasis lies a series of intricate molecular events that enable cancer cells to invade surrounding tissues, enter the bloodstream or lymphatic system, and establish new colonies in distant sites. Several cellular and molecular components interact delicately during this process, which is mediated by numerous signaling channels and genetic changes.

The process of metastatic cells begins with local invasion, where cancer cells acquire the ability to penetrate the surrounding Extra Cellular Matrix (ECM) and basement membrane. This step is facilitated by changes in cell adhesion molecules, such as integrins, which mediate the interaction between cancer cells and the ECM. Additionally, the secretion of enzymes like Matrix Metallo Proteinases (MMPs) enables the degradation of ECM components, creating pathways for cancer cells to move beyond the confines of the primary tumor. After cancer cells are able to pass through local barriers, they start the process of intravasation, which allows them to enter lymphatic or blood vessels. This phase requires the cancer cells to undergo Epithelial Mesenchymal Transition (EMT), a phenotypic switch characterized by the loss of epithelial characteristics and the acquisition of a more migratory and invasive mesenchymal phenotype.

In the bloodstream or lymphatic system, cancer cells face numerous challenges, including shear forces, immune surveillance, and interactions with platelets. These challenges shape the survival and fate of Circulating Tumor Cells (CTCs). Platelets play a crucial role in protecting CTCs from immune recognition and facilitating their adhesion to endothelial cells, promoting extravasation into distant tissues. The immune system can recognize and eliminate CTCs through mechanisms involving Natural Killer (NK) cells and Cytotoxic T Lymphocytes (CTLs). Successful metastatic cells are known for their ability to elude immune monitoring, which is frequently accomplished by down regulating antigens and expressing immune checkpoint molecules. Extravasation marks the next critical step in the metastatic cascade, where cancer cells exit the bloodstream or lymphatic vessels and infiltrate distant tissues. This process involves interactions between cancer cells and the endothelial cells lining the blood vessels, mediated by adhesion molecules like selectins and integrins.

Angiogenesis, the formation of new blood vessels, is a crucial aspect of metastatic colonization, ensuring a sufficient supply of nutrients and oxygen for the growing secondary tumor. Vascular Endothelial Growth Factor (VEGF) and other pro-angiogenic factors play a central role in coordinating the process of angiogenesis. Moreover, the immune microenvironment of the metastatic place undergoes changes that facilitate immune evasion. Metastatic cells are protected from the host immune system by their acquisition of immunosuppressive cells, such as regulatory T cells and myeloid-derived suppressor cells, which provide an immunosuppressive milieu.

Metastatic cells and the extracellular matrix involve in a reciprocal and dynamic interaction. The Extra Cellular Matrix (ECM) affects the behavior of metastatic cells and can be altered by cancer cells to form a favorable environment. These interactions are bidirectional and impact cell migration, proliferation, and survival. They are mediated by integrins and other cell surface receptors. The

Contact: Branwen Lee, Email: Lbranwen123@yahoo.com

metastatic microenvironment is further formed by the changed expression of remodeling enzymes and ECM components.

The molecular changes linked to metastasis are primarily driven by changes in the expression of certain genes and epigenetic modifications. The acquisition of metastatic traits often involves mutations in key *oncogenes* and *tumor suppressor* genes. For example, mutations in the *TP53* gene, a well-known tumor suppressor, are frequently observed in metastatic cancers. Technological developments in molecular profiling, including next-generation sequencing, have provided important new information about the genomic structure of metastatic cancers. The identification of driver mutations, amplifications, and other genetic changes unique to metastatic lesions could be beneficial for the creation of customized treatments. By customizing treatment plans based on the distinct genetic characteristics of each patient's metastatic tumor, precision medicine techniques aim to maximize therapeutic benefit while reducing side effects.