

Investigation of FoxM1 Gene Expression in Breast Cancer and Its Relationship with miR-216B-5p Expression Level

Authors : Ramin Mehdiabadi

Abstract : Background: Breast cancer remains the most prevalent cancer diagnosis and the leading cause of cancer death among women globally, representing 11.7% of new cases and 6.9% of deaths. While the incidence and mortality of major cancers are declining in developed regions like the United States and Western Europe, underdeveloped and developing countries exhibit an increasing trend, attributed to lifestyle factors such as smoking, physical inactivity, and high-calorie diets. Objective: This study explores the intricate relationship between the mammalian transcription factor forkhead box (FoxM1) and the microRNA miR-216b-5p in various subtypes of breast cancer, aiming to deepen the understanding of their roles in tumorigenesis, metastasis, and drug resistance. Methods: Breast cancer subtypes were categorized based on key biomarkers: estrogen receptors, progesterone receptors, and human epidermal growth factor receptor 2. These include luminal A, luminal B, HER2 enriched, triple-negative, and normal-like subtypes. We focused on analyzing the expression levels of FoxM1 and miR-216b-5p, given the known role of FoxM1 in cell proliferation and its implications in cancer pathologies such as lung, gastric, and breast cancers. Concurrently, miR-216b-5p's function as a tumor suppressor was evaluated to ascertain its regulatory effects on FoxM1. Results: Preliminary data indicate a nuanced interplay between FoxM1 and miR-216b-5p, suggesting a potential inverse relationship that varies across breast cancer subtypes. This relationship underscores the dual role of these biomarkers in modulating cancer progression and response to treatments. Conclusion: The findings advocate for the potential of miR-216b-5p to serve as a prognostic biomarker and a therapeutic target, particularly in subtypes where FoxM1 is prominently expressed. Understanding these molecular interactions provides crucial insights into the personalized treatment strategies and could lead to more effective therapeutic interventions in breast cancer management. Implications: The study highlights the importance of molecular profiling in breast cancer treatment and emphasizes the need for targeted therapeutic approaches in managing diverse cancer subtypes, particularly in varying global contexts where lifestyle factors significantly impact cancer dynamics.

Keywords : breast cancer, gene expression, FoxM1, microRNA

Conference Title : ICCST 2024 : International Conference on Cancer Science and Therapy

Conference Location : Quebec City, Canada

Conference Dates : December 23-24, 2024