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Update on Epithelial Ovarian Cancer (EOC), Types, Origin, Molecular Pathogenesis, and Biomarkers

Authors : Salina Yahya Saddick

Abstract : Ovarian cancer remains the most lethal gynecological malignancy due to the lack of highly sensitive and specific screening tools for detection of early-stage disease. The OSE provides the progenitor cells for 90% of human ovarian cancers. Recent morphologic, immunohistochemical and molecular genetic studies have led to the development of a new paradigm for the pathogenesis and origin of epithelial ovarian cancer (EOC) based on a ualistic model of carcinogenesis that divides EOC into two broad categories designated Types I and II which are characterized by specific mutations, including KRAS, BRAF, ERBB2, CTNNB1, PTEN PIK3CA, ARID1A, and PPPR1A, which target specific cell signaling pathways. Type 1 tumors rarely harbor TP53. type I tumors are relatively genetically stable and typically display a variety of somatic sequence mutations that include KRAS, BRAF, PTEN, PIK3CA CTNNB1 (the gene encoding beta catenin), ARID1A and PPP2R1A but very rarely TP53 . The cancer stem cell (CSC) hypothesis postulates that the tumorigenic potential of CSCs is confined to a very small subset of tumor cells and is defined by their ability to self-renew and differentiate leading to the formation of a tumor mass. Potential protein biomarker miRNA, are promising biomarkers as they are remarkably stable to allow isolation and analysis from tissues and from blood in which they can be found as free circulating nucleic acids and in mononuclear cells. Recently, genomic anaylsis have identified biomarkers and potential therapeutic targets for ovarian cancer namely, FGF18 which plays an active role in controlling migration, invasion, and tumorigenicity of ovarian cancer cells through NF-κB activation, which increased the production of oncogenic cytokines and chemokines. This review summarizes update information on epithelial ovarian cancers and point out to the most recent ongoing research.

Keywords : epithelial ovarian cancers, somatic sequence mutations, cancer stem cell (CSC), potential protein, biomarker, genomic analysis, FGF18 biomarker
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