

Differential Regulatory Gene Expression at the Proteomic Level in Subtypes of Human Ovarian Cancer Cell-Lines

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Ovarian carcinoma is the most lethal neoplasm and the fifth leading cause of mortality in women. Among the different subtypes, widely heterogeneous high-grade serous ovarian cancer (HGSOC) poses a great challenge to modern chemotherapy due to its high recurrence rate and resistance to standard treatments. Recent studies suggest that survival time-line and disease recurrence are linked to the variable expression of biomarkers in cancer cells. Therefore, using Western blot analyses, we assessed the expression of a host of regulatory gene protein products at the whole-cell level in extracts from both three HGSOC and five non-HGSOC cell lines. Some of our most distinctive findings from those analyses were that: 1) Nrf2, a key factor in the anti-oxidant response element system, is expressed as a series of protein bands of variable molecular weight in all but the Kuramochi (HGSOC) cell line; 2) Estrogen receptor alpha is expressed in all but the OVSAHO (HGSOC) cell line; and 3) the AUF-1, p120-catenin, and NFkB-p50 proteins are expressed in both HGSOC and non-HGSOC cell types. We will next follow up those findings conducted at the whole-cell level with assessments at the individual cell and subcellular level using immunohistochemical analyses.