Analysis of Potential Protein Biomarkers in Epithelial Ovarian Cancer Using the Gene Expression Omnibus Database

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Introduction:

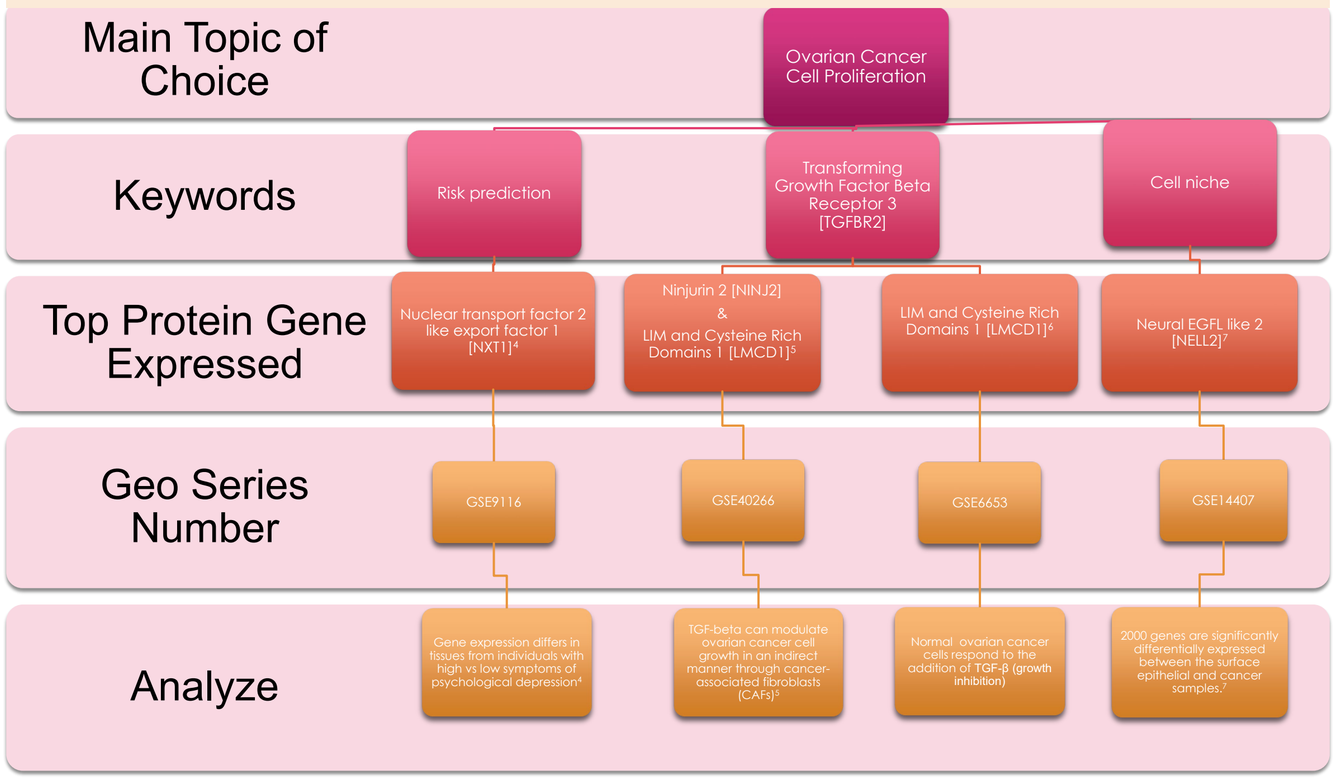
Human epithelial ovarian cancer (EOC) is the most lethal of the gynecological malignancies of the female reproductive system[1-2]

- It is imperative to find a detection or therapeutic strategy that is specific and sensitive enough to accurately detect early-staged ovarian cancer cells when the cancer cell is still small and confined to the ovary
- The current standard diagnostic approved by the US FDA is the CA-125 test coupled with the transvaginal ultrasound[2-3]
- The CA-125 test cannot be categorized as a screening assay for cancer detection in the general population
- The CA-125 test cannot be used as a single diagnostic test to clinically confirm EOC because an increase in CA-125 can be seen in other conditions such as endometriosis and ovarian cysts[3]
  - When the CA-125 test is combined with the transvaginal ultrasound (TVU), a predictive value (PPD) of 40% was obtained. A high PPD was achieved in patients with advanced stage EOC, where three out of the four tumors displayed in early-stage cancer came back with a normal prognosis[9]
- Using the GEO2R Gene Expression Omnibus database, data analysis compared samples with differential genes expression under the conditions of risk prediction, depression, Transforming Growth Factor Beta (TGFβ) Receptor 3 signaling disruption, in addition to the cell niche under various experimental conditions

Research Goals:

- A comparison of the dominant key genes using GEO2R that are transformed in ovarian cancer promoting epithelium cell proliferation and cell differentiation
- Using the Gene Expression Omnibus database (GEO), identify four genes that are associated with common factors of epithelial ovarian cancer and compare them with the ”Gold-standard,” CA125 (MUC16)

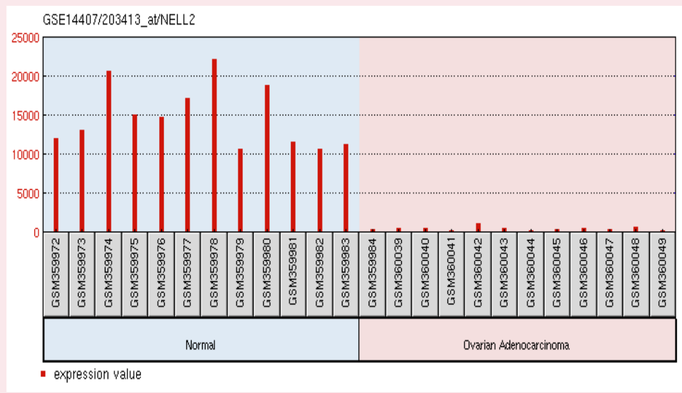
Study Design: GEO Database Search



Conclusion:

- Experimental data analysis using GEO allows the discovery of other than MUC16 that are expressed in association with EOC
- These four revealed genes are not addressed in the literature and require further investigation and recognition due to their significant differential expression levels in sample comparison studies
- Depression, TGFBR2 signaling disruption, and the cell niche are potential confounding factors in epithelial ovarian cancer proliferation
- Molecular mechanisms for each EOC factor are significantly expressed through four genes

Study Design: Gene Information Chart

Top Gene Expression	How Genes Alter Cell Behavior and Cell Function
Nuclear transport factor 2 like export factor 1 [NXT1][4]	• Risk factors such as depression can effect the Neuroendocrine system, which effects the activity of tumor cells[4] • Patients with depressive symptoms show an increase in transcription factors, such as NXT1, which also showed an elevation in norepinephrine[4]
Ninjurin 2 [NINJ2][5]	• Transforming Growth Factor Beta Receptor 3 [TGFBR2] influences ovarian cancer metastasis by the way of cancer-associated fibroblasts (CAFs)[5] • Transcriptional profiling of normal ovarian cell tissues treated with TGF-β have shown a key CAF gene expression, versican (VCAN)[5]
LIM and Cysteine Rich Domains 1 [LMCD1][6]	• When TGF-β is activated, LMCD1 was one of the identified transcriptional factors containing SMAD4 in promoter regions[6] • Increases in LMCD1 regulates cancer cell invasion and metastasis[8]
Neural EGFL like 2 [NELL2][7]	• Expression differs greatly between normal ovarian tissues and cancer tissues • Nell2 is significantly upregulated in normal ovarian tissues • Nell2 downregulation indicates an ovarian adenocarcinoma 

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