Introduction:

Human epithelial ovarian cancer (EOC) is the most lethal of the gynecological malignancies of the female reproductive system1-2.

- It is imperative to find a detection or therapeutic strategy that is specific and sensitive enough to accurately detect early-stage 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 ultrasound3-5.
- 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 cysts5.

When the CA-125 test is combined with the transvaginal ultrasound (TVU), a predictive value (PPV) of 40% was obtained. A high PPV 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 prognosis6.

- 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 (TGF-β) 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 expressed through four genes.
- 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:

Main Topic of Choice: Nuclear transport factor 2 like export factor 1

Keywords: LIM and Cysteine Rich Domains 1; Ninjurin 2; Neural EGFL like 2; Nuclear transport factor 2 like export factor 1 [NXT1]; Neuroendocrine system; Transforming Growth Factor Beta Receptor 3 [TGFBR2]; Ovarian Cancer Cell Proliferation; Cell niche; Normal  ovarian cancer tissues; Cysteine Rich Domains 1 [LMCD1]; Transforming Growth Factor-β (TGF-β) signaling.

Top Protein Gene Expressed:

- Nell2 is downregulated in EOC.
- Nell2 is significantly upregulated in normal ovarian tissues.
- Ninjurin 2 downregulation indicates an ovarian adenocarcinoma.

S1 table:

<table>
<thead>
<tr>
<th>Gene Expression</th>
<th>How Genes Alter Cell Behavior and Cell Function</th>
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<tbody>
<tr>
<td>Nuclear transport factor 2 like export factor 1 [NXT1]</td>
<td>- Risk factors such as depression can effect the Neuroendocrine system, which affects the activity of tumor cells6.</td>
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<tr>
<td>LIM and Cysteine Rich Domains 1 [LMCD1]</td>
<td>- Transcriptional profiling of normal ovarian cell tissues treated with TGF-β have shown a key CAF gene expression, versican (VCAN8).</td>
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<tr>
<td>Neural EGFL like 2 [NELL2]</td>
<td>- When TGF-β is activated, LMD1 was one of the identified transcriptional factors containing SMAD4 in promoter regions9.</td>
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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.

References: