Pancreatic adenocarcinoma has no cure. Historically, specific leukocyte populations, including macrophages and T-cells, are thought to play a role in resistance to standard therapies. Some tumors are more fibrotic than others, while some have a greater leukocyte population than others. Historically, specific leukocyte populations, including macrophages and T-cells, are thought to hinder tumor infiltration of the opposite cell population. Both tumor fibrosis and leukocyte infiltration are thought to play a role in resistance to standard therapies.

**Experimental Model**

- LSL-Kras<sup>12D2</sup> Pdx<sup>-1</sup> Cre<sup>+</sup> (KPC mice)
- LSL-Trp53<sup>177H</sup> Pdx<sup>-1</sup> Cre<sup>+</sup> (KPC tumors, spontaneous)
- KPC tumor cell line (implantable)

**Hypothesis**

<table>
<thead>
<tr>
<th>Collagen Promoting Genes</th>
<th>Matrix Metalloproteinase Genes</th>
<th>Collagen Promoting Genes</th>
<th>Matrix Metalloproteinase Genes</th>
</tr>
</thead>
<tbody>
<tr>
<td>CTGF</td>
<td>+++</td>
<td>Mmp-8</td>
<td>+++</td>
</tr>
<tr>
<td>IL-4</td>
<td>+++</td>
<td>Mmp-13</td>
<td>+++</td>
</tr>
<tr>
<td>PDGF</td>
<td>+++</td>
<td>Mmp-14</td>
<td>+++</td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th>Macrophage Attracting Genes</th>
<th>T cell Attracting Genes</th>
</tr>
</thead>
<tbody>
<tr>
<td>CCL2</td>
<td>++</td>
</tr>
<tr>
<td>Csf1</td>
<td>++</td>
</tr>
<tr>
<td>VEGFA</td>
<td>++</td>
</tr>
</tbody>
</table>

**Results**

Figure 1. The heterogeneity of pancreatic cancer tumors. Left: Tumor sections were stained for leukocytes (brown) and nuclei (blue). Right: Tumor sections were stained for collagen content (blue) and tumor cells (red).

**Methods**

**Primer design**: Gene sequences were found using the UCSC Genome Browser, primers were designed using Primer 3 and synthesized by IDT DNA, and resuspended in H2O.

**RNA isolation**: Tumors were minced in TRIzol and extraction was performed using a Qiagen RNeasy kit. RNA was quantified using the Qubit system.

**cDNA synthesis**: cDNA was synthesized using Multiscribe Reverse Transcriptase with random hexamers (Applied Biosystems) and diluted 1:10 in H2O.

**qRT-PCR**: Gene expression was determined using Sybr Green technology and expression levels were calculated relative to β-actin.

**Statistics**: Statistics were calculated by ANOVA with Graphpad Prism.

**Conclusions**

- **Collagen Promoting Genes**
  - CTGF
  - IL-4
  - PDGF

- **Matrix Metalloproteinase Genes**
  - Mmp-8
  - Mmp-13
  - Mmp-14

- **Macrophage Attracting Genes**
  - CCL2
  - Csf1
  - VEGFA

- **T cell Attracting Genes**
  - Foxm1
  - mki67
  - Plk1

**References**


**Acknowledgements**

We would like to acknowledge Dr. Kristen Long for her guidance and our collaborators at the University of Pennsylvania, in the laboratory of Dr. Gregory Beatty, for supplying us with tumors.