Prostate cancer (PCa) is the most common cancer in American males aside from cutaneous malignancies. It is also the second leading cause of cancer deaths in American men behind lung cancer. Despite the high incidence and mortality associated with PCa, routine genetic testing has lagged behind despite widely available genetic testing. Availability and coverage of germline genetic testing (GGT) has been increasing in utilization for men with (or at risk of) PCa. The genetic landscape of PCa is being explored in different populations and disease characteristics. The Risk Assessment Program (RAP) at Fox Chase Cancer Center (FCCC) (Philadelphia, PA) was established and has been ongoing since 1991. In 1996 the more specific Prostate Risk Assessment Program (PRAP) was established as well. Participants in the RAP/PRAP were considered to have increased risk of PCa due to family history or ethnicity. These Risk Assessment Programs have been early adopters of germline genetic testing for men with or at risk of PCa. Here, we describe the genetic, clinical and tumor characteristics of PCa patients found to harbor Pathogenic (Pa) or Likely Pathogenic (LPa) mutations after GGT at a single institution.

Medical chart reviews were conducted for all patients with a diagnosis of PCa who had GGT performed at a single institution from 1991-2021. 251 patients were included in the study. Specific genes, nucleotides and amino acid substitutions were recorded for all patients with clinically significant mutations. Various clinical and tumor characteristics were analyzed as shown below. Treatments pursued for each patient were reviewed as well.

### Results

- Twenty one percent (21.1% 53/251) of patients were found to have at least 1 pathogenic (Pa) or likely pathogenic (LPa) mutation.
- These mutations were present in the following genes: BRCA1, BRCA2, CHEK2, MSH2, MSH3, RECQL4, PALB2, MUTYH, ATM, CFTR, NBN, APC, NTHL1, FH and PMS2.
- The most prevalent mutations occurred in the BRCA2 gene followed by BRCA1 and then CHEK2.
- More than 50% (63.3%, 31/49) of mutation carriers had Gleason scores ≤ 7.
- The percentage of various other clinical/tumor characteristics present in our cohort are displayed below.

### Clinical Characteristics

<table>
<thead>
<tr>
<th>Clinical Characteristics</th>
<th>Tumor Characteristics</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age at Diagnosis</td>
<td>Type of Cancer</td>
</tr>
<tr>
<td>Ethnicity</td>
<td>Stage</td>
</tr>
<tr>
<td>Race</td>
<td>Gleason Score</td>
</tr>
<tr>
<td>Ashkenazi Jewish Heritage</td>
<td>PSA at Diagnosis</td>
</tr>
<tr>
<td>Performance Status</td>
<td>Progression to Advanced Disease</td>
</tr>
<tr>
<td>Family Hx of Cancer</td>
<td>Locally Advanced Cancer</td>
</tr>
<tr>
<td>Smoking Status</td>
<td>Metastatic Disease</td>
</tr>
</tbody>
</table>

### Future Directions

Having conducted chart reviews and gathered data regarding clinical characteristics, tumor characteristics and treatment strategies, we can evaluate for trends associated with specific Pa or LPa mutations.

### References