WHOLE EXOME SEQUENCING OF PERITONEAL AND PLEURAL MALIGNANT MESOTHELIOMA

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## Cohort Characteristics:

- **Number of cases = 10**

<table>
<thead>
<tr>
<th></th>
<th>Pleural Malignant Mesothelioma</th>
<th>Peritoneal Malignant Mesothelioma</th>
</tr>
</thead>
<tbody>
<tr>
<td># of cases</td>
<td>4</td>
<td>6</td>
</tr>
<tr>
<td>Gender</td>
<td>Male: 2, Female: 2</td>
<td>Male: 4, Female: 2</td>
</tr>
<tr>
<td>Asbestos Exposure</td>
<td>Yes: 3, No: 1</td>
<td>Yes: 1, No: 4, 1: Unknown</td>
</tr>
<tr>
<td>Histological Type</td>
<td>Epithelial or Epithelioid</td>
<td>Epithelial or Epithelioid</td>
</tr>
<tr>
<td>History of Smoking</td>
<td>Yes: 1, No: 3</td>
<td>Yes: 3, No: 3</td>
</tr>
<tr>
<td>Vital Status</td>
<td>Dead: 4</td>
<td>Alive: 2, Dead: 4</td>
</tr>
<tr>
<td>Median Survival</td>
<td>17.5 months</td>
<td>22.5 months</td>
</tr>
</tbody>
</table>
Whole Exome Sequencing Pipeline

Quality Control and Mapping
- Raw Reads (SOLiDS)
- Quality Control
- Mapping by Life Technologies (LifeScope)

Pre-processing
- GATK
- Indel Realignment
- Base Recalibration

Variant Calling & Annotation
- MuTect
- VarScan
- SNPs and Indel
- Annotation on Maftools
- Additional Filtering
MAF ONCOPLOT: PLEURAL MESOTHELIOMA:

Altered in 4 (100%) of 4 samples.
MAF ONCOPLOT: PERITONEAL MESOTHELIOMA:

Altered in 6 (100%) of 6 samples:
- MUC8
- FAM47C
- QOLGA6L2
- APRBP2
- KCNJ12
- MUC17
- MYO19
- TAS2R43
- TNF112
- ZNF156
- ABCA1
- ASB3
- AHIHAK
- AKAP13
- ANAPC4
- ANO3
- ANO10
- ANO2
- ANO5
- ARMCX1
- ATP6V0A2
- BAZ2B
- BLACE
- BRCA2
- C10orf11B
- C10orf88
- CACPD1
- CASK2
- CDDC41
- C6orf78
- CEP1
- CHEX2
- CRYX
- CCDC20
- CPVL
- CRYAB
- CTC2-2419N.1
- CWC27
- DOCK7
- EPH41
- LMBT3
- LHX2
- CPH3B
- OR1C5
- PLEKH4A7
- PWP2
- RSP9
- SLC45A2

Type
- Peritoniad
- Missense_Mutation
- Nonstop_Mutation
- Nonsense_Mutation
- Multi_Hit
- Frame_Shift_Ins
- Splice_Site
- Translation_Start_Site

Altered in 5 (83.33%) of 6 samples:
- APPBP2
- TAS2R43
- ATP6V0A2
- FERD3L
- HSD17B13
- MCA
- OBP2B

Type
- Peritoniad
- Missense_Mutation
- In_Frame_Ins
- Frame_Shift_Del
CONCLUSION:

- Identified increased number of mutation in pleural vs peritoneal mesothelioma samples.
- BAP-1 Mutation has found in 2 of the pleural samples.
- MUC6 seems to be variant in both pleural and peritoneal but it is a big gene; however literature shows that it’s involved in many abdominal cancers. Therefore, is it possible that it is significant in mesothelioma even though it is a big gene and can accumulate passenger mutation?
- Is this a significant finding?
- We are looking at TCGA variant and RNA Seq data to validate the MUC6 variant frequency and gene expression
  - Pittsburgh Genome Resource Repository (PGRR) – a local infrastructure for all TCGA protected and public data hosted at the Pittsburgh Supercomputing Center (PSC).
  
MUC6 Protein Expression Overview

BAP-1 Protein Expression Overview
RELATED WORK:

- Whole exome sequencing of peritoneal mesothelioma has shown BAP-1, NF2, SETD2, CDKN2A and LSAT2 mutations.
- The number of samples are analyzed ranges from 2-13.

REFERENCE:


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THANK YOU