Background

- Malignant pleural mesothelioma (MPM) is a rare form of thoracic cancer associated with exposure to asbestos.
- Patients with MPM have a dismal prognosis with a short overall survival.[1]
- Cytokine and chemokine presence within the tumor microenvironment (TME) is reflective of the type of immune response and the permissiveness of the tumor to immune infiltration.

Methods

- Twelve MPM tissue resections snap frozen in liquid nitrogen were lysed using two different detergents:
  - T-PER Tissue Protein Extraction Reagent
  - RIPA buffer
- Assessment of total protein concentration in each sample was tested in duplicate on three colorimetric assays—a Lowry-based assay, a Bradford reagent-based assay, and a BCA protein assay
- Presence of 79 cell signaling factors was assessed in duplicate using a Luminex-based approach.
- Optimal protein concentration for detection was assessed by comparing read quality of 0.5 mg/mL and 1 mg/mL sample concentration.
- Results were compared with gene expression profiling using the Nanostring tumor signaling 360 panel of RNA extracted from the same tumor tissue.

Results

- Total protein concentration was found most consistently using a BCA protein assay
- T-PER reagent samples showed higher read quality
- One mg/mL total sample protein concentration demonstrated high resolution while minimizing sample used
- Presence of Eotaxin and MIP-3α was found to be significantly higher in tumor tissue as compared to tumor-associated normal tissue
- Presence of MCP-1 and CTLA4 was found to be significantly lower in tumor tissue as compared to tumor-associated normal tissue
- No correlation has yet been detected between protein isolation and RNA expression data.

Conclusions

- Detection of proteins within primary tumor tissue using a Luminex system was optimized.
- Immune-related proteins possibly associated with tumor tissue as compared to tumor-associated normal tissue were identified.
- More samples are required to determine significant differences in presence of additional cell signaling molecules.
- Analysis is ongoing to determine associations with cytokine presence and tumor thickness as well as correlations with gene expression data.

References