Abstract #11606

• Background
  - Immune therapies such as checkpoint inhibitors, CAR T cells, NK cells, and therapeutic vaccines are revolutionizing cancer medicine with remarkable responses in some patients.
  - Current clinical immunotherapy strategies include targeting tumor associated antigens (TAAs) such as HER2 (trastuzumab) or targeting immune cell checkpoints (ipilimumab, nivolumab)
  - Many patients fail to respond with these drugs suggesting a lack of specific immune cells or insufficient amounts of the TAAs.

- We analyzed whole genome sequencing (WGS) and RNA sequencing (RNAseq) data from The Cancer Genome Atlas (TCGA) to identify neoepitopes (tumor-specific antigens derived from mutations in cancer) that could be exploited to develop next-generation, patient-specific cancer immunotherapies.

• Methods
  - TCGA WGS and RNAseq data were obtained from the University of California, Santa Cruz (UCSC) Cancer Genomics Hub (https://cghub.ucsc.edu).
  - Neoepitopes were identified by creating all possible permutations of either 9-mer or 15-mer amino acid strings derived from single nucleotide variants (SNVs) or insertions/deletions (indels).
  - All neoepitopes were filtered against all possible 9-mer and 15-mer amino acid sequences from every known human gene along with alignments to the IMGT/HLA database.
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• Results
  - Neoepitope Counts
  - High Neoepitope Burden Gives Rise to More Expressed Neoepitopes
  - Tissue Typing and Predicting MHC Presentation from Whole Genome and RNA Sequencing Data

• Conclusions
  - Most identified neoepitopes are patient-specific.
  - Neoepitope-MHC interactions restrict commonly more shared mutations.
  - Development of personalized immunotherapies is dependent on accurate DNA and RNA sequencing.

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