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Genomic and Evolutionary Classification of Lung Cancers in Never Smokers from the Sherlock-Lung Study

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Lung cancer in never smokers (LCINS): 2

- Accounts for 15-25% of all lung cancer cases worldwide
- ▶ Is the 7th cause of cancer mortality in the US
- > Has predominant adenocarcinoma subtype
- Only a few risk factors are known, accounting for a small proportion of the cases

The Sherlock-Lung study

To use tumor genomic changes as "footprints" to infer etiological processes and evolutionary trajectories of LCINS tumorigenesis



Sherlock-Lung

To mine large electronic health records (EHR) to uncover associations of LCINS with other medical conditions or long-term medication use



Special exposures population (n~300)

Design





General population (n~1700) 4

(n~1700)

2000 tumor samples/ 2000 blood samples

Whole genome sequencing

Mutational Signatures Mutational burden Driver genes Telomere length Neoepitopes Viral remnants Copy numbers Structural variants Germline variants

Aim 1

Characterize the genomic and evolutionary landscape of LCINS

1000 tumor samples/ 1000 normal lung tissues

RNA seq + methylation arrays

Gene expression Inferred mutations Fusions Structural changes Methylation patterns CIMP Methylation signatures Immune cell subtypes 16S RNA – microbiome <u>Aim 2</u>: Develop an integrated molecular, histological and radiological classification of lung cancer in never smokers

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Molecular landscape









Zhang et al., Nature Genetics 2021 (in press)

Tumor mutational burden across cancer types



Telomere length across cancer types



Landscape of copy number alterations







Genomic features by subtype

Mutational signatures



Signature contribution



Timing tumors' evolutionary history







Timing tumors' evolutionary history

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Molecular age: median age of the appearance of the most recent common ancestor (MRCA)



Timing tumors' evolutionary history

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Molecular age: median age of the appearance of the most recent common ancestor (MRCA)



Timing tumors' evolutionary history by subtype



Piano tumor features vs. other subtypes 19





1 KRAS UBA1, RET, NKX2-1, ARID1A only in piano mutually exclusive



Slow growth rate

Stem cells?



Development score: SOX2, SOX9, HMGA2

Sherlock-Lung



TCGA-LUAD



Lineage infidelity: TP63 expression

Sherlock-Lung



Pilot studies to verify cell-oforigin and evolutionary trajectories:

- snRNA-seq
- Single molecule DNA-seq

Piano tumor stem cell-like features



KRAS UBA1, RET, NKX2, ARID1A



Slow growth rate

cells?

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Stem



Number of cases with T/N WGS, RNA seq and methylation by sex, ethnicity and tobacco smoking ²³



Aim 2: tumor classification

Molecular landscape



CLINICAL IMPLICATIONS

2,430 scanne 875 subj Use of CT-scans or biopsy slides to predict genomic features/TME of the corresponding lesions and provide crucial information for clinical decision-making

ned images nalyzed

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Analyses by SCNA-subtypes, driver genes, smoking status, ethnicity, sex...

TME by H&E, immunofluorescence, RNA-seq, methylation, deep learning

Collaborators

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