Detect Early-Stage Cancers From the Blood T cell Repertoire

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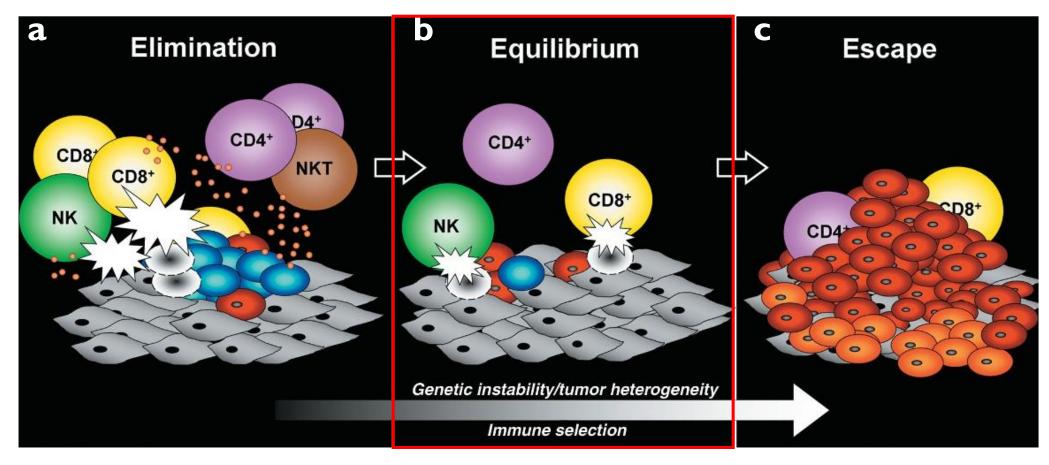
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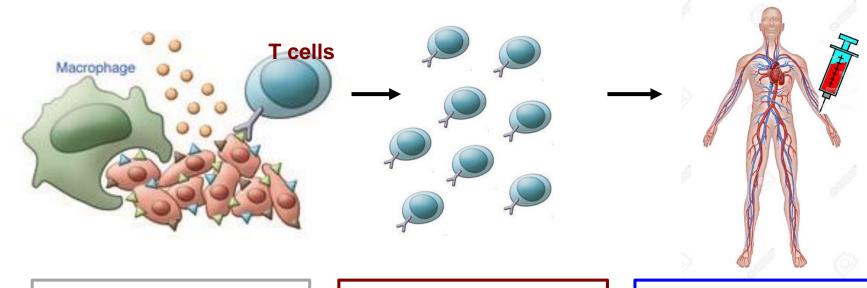
UT Southwestern Medical Center

Basis of using the adaptive immune system as an early cancer reporter

Immunoediting: Sustained caner-specific immune responses since early-stage



T cell proliferation upon cancer-specific recognition



Cancer sensing

T cells sensing the early-stage cancer cells

More T cells made

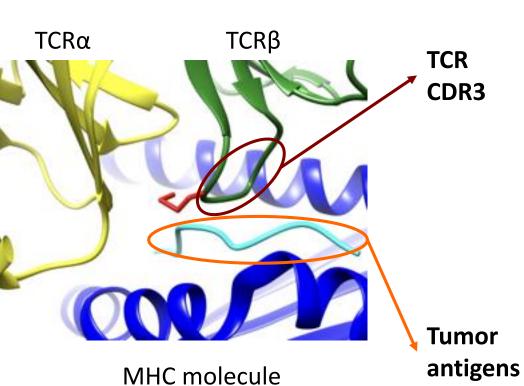
Many copies are made of the T cells that recognize cancer cells

Altered T cells now in the blood

T cells that recognize cancer cells can be detected in blood sample

A major challenge: To recognize cancer-associated TCRs

in the blood repertoire



CASSLKLAGPDTQYF CASSLGSGTAQGYEQYF CASTLGQTPKTQYF CASSLGTGIRTDTQYF CASSLGTSLGQETQYF



Somatic mutations Frameshift indels **Tissue-restricted genes** De novo ORF Post-translational modification Translated 'non-coding' genes

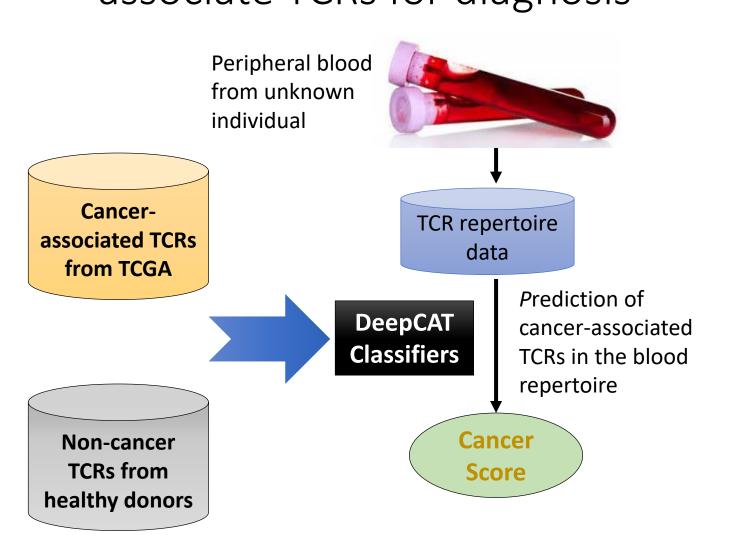
T cell repertoire with over 100M clones

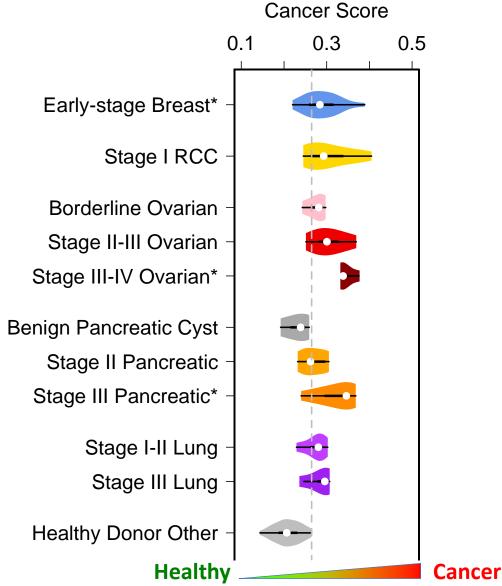
CASSYSENEQFF **CASRSYVASSNEOFF CASTOWYGGGTPPYF CASSLTTGVFSQPQHF CATSPYSVTTFANTIYF** CAGMTVTEAFF

CASSLKLAGPDTQYF CASSLGSGTAQGYEQYF CASTLGQTPKTQYF **CASSLGTGIRTDTQYF** CASSLGTSLGQETQYF

CASSQALLAPSTDTQYF CASSEGGIGELFF **CASSQDTDGRMFF** CASSEAPGTSVGGLFF CASTTGDGLGAFF **CASSQDIGNFEQFF CASSGTGGYSGANVLTF**

DeepCAT: A potential solution to de novo detect cancerassociate TCRs for diagnosis





Advantages of TCR-based detection method

- Non-invasive
 - Blood TCR repertoire is easy to obtain
- Sensitive early detection
 - T cell proliferation at early stage amplifies cancer signals
- Low cost
 - Targeted TCR repertoire sequencing is cheap (~\$100 sequencing cost per sample)
- Easy to combine with most of methods based on liquid biopsies
 - Use of PBMCs instead of plasma

Potential caveats of TCR-based detection method

- Difficult to detect cancer localization
 - TCRs are not linked to cancer types due to unknown antigens
- Unknown confounders of other immunologic conditions
 - Autoimmune disorders, chronic infections, pregnancy, etc may change the immune repertoire and affect the predictions
- Potentially longer assessment time
 - Library + Next generation sequencing may take 1-2 weeks
- Requirement of exclusive computational analysis
 - TCR repertoire is very difficult to analyze. Our effort remains one of the very few attempts in this field.

Future directions

Collection of more TCR-seq samples from cancer patients and healthy individuals

- Improve the performance of DeepCAT for better prediction accuaracy (current AUC=0.95, aim to increase it to 0.99)
- Develop new computational methods to distinguish cancer localizations with blood TCR repertoire
- Conduct a prospective clinical study to evaluate cancer score as a novel diagnostic marker

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