Immunophenotyping to Differentiate Responder and Non-Responder Patients in Cancer Immunotherapy

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Confronting the Clinical, Economic and Human Toll of Cancer

Cancer (2017): New Diagnoses 1.68 million; Deaths: 600,920

Projected Increase in Incidence of 20% by 2020 and 30% by 2030
The Promise of Cancer Immunotherapy

- immune checkpoint modulation
- adoptive T cell therapy and T cell engineering
- antibodies and antibody drug conjugates
  - fractionated radiation
- cancer vaccines
- oncolytic viruses
- combination therapies
Realizing the Promise of Cancer Immunotherapy

• wide variation in Rx response rates
  - only 20-40% positive responses even in most responsive malignancies
  - even lower percentage of clinically durable responses (KM-“long tail”)

• improve response rates across all malignancies
• management of serious AEs (CRS, autoimmune risk)
• will I/O combination regimens increase response rates?
• rationale for selection of combination regimens
• improved preclinical models for new I/O agent discovery and combination testing

Urgent need for multi-parameter immunophenotyping to reliably predict responder vs non-responder patients (immunoscore : immunopredictor : immune response index)
Cancer as a Complex Adaptive System

The Requirement for Holistic, Systems-Based Approaches to Improve Patient Selection for Immunotherapy and Optimize Therapeutic Outcomes and Cost-Effectiveness
Mapping the Complex Spatio-Temporal Dynamics of Adaptive Co-evolution in the Tumor-Immune Ecosystem

- innate and adaptive immune phenotype(s)
- tumor (sub)clonal diversity
- germline genetics
- local and systemic
- microbiome
- predisposition alleles
- HLA genetics
- inter-patient/ intra-patient
- mutagen burden and neoantigen profile
- immuno-editing
- intrinsic and acquired Rx resistance
- Rx
Cancer as a Complex Adaptive System

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- germline genetics
- microbiome
- local and systemic
- Rx

ill-defined systemic factors affecting disease risk, progression and Rx responses

- age
- gender
- ethnicity
- environmental risk factors/lifestyle
- adiposity
- comorbidities
- chronic, subclinical inflammation
- selection pressure of prior Rx regimen(s)
General Classes of Tumor-Immune Microenvironments (TIME)

- **Infiltrated-excluded**
- **Infiltrated-inflamed**
- **Infiltrated-TLS**

Adapted from: M. Binnewies et al. (2018) Nature Med. 24, 541
Tumor Immunophenotypes Associated With Responsiveness to Immune Checkpoint Blockade

“Hot”, “Inflamed”, “Immunogenic”

- high tumor mutation burden
- high tumor-infiltrating CD8⁺ cytotoxic cells
- activation of tissue-resident T cells (Tres)
- long lived memory T cells (Tem)
- high Th1 and T17 helper cells
- CD21⁺DCs
- high expression of Th1 stimulating cytokines
- higher expression of TIL checkpoint receptors
- M1 phenotype tumor-associated macrophages (TAM)
- low Tregs, MDSCs, low TGF-β
Formation of Ectopic/Tertiary Lymphoid Intra-tumoral and Peri-tumoral Structures (TLS) and Lymphoid Cell Aggregates and Better Patient Survival

- detected in CRC, ovary, lung tumors (plus autoimmune diseases and chronic inflammation)
- proliferation of B and T cells
- CD21+ dendritic cells in germinal centers
- 12 gene cytokine gene expression involved in T cell homing and TLS development
  - CCL3, 4, 5, 8, 18 and CXCL 9, 10, 11, 13, 19, 21
  - no expression of CCL1, 20 and 22 involved in recruitment of Tregs
Tumor Immunophenotypes Associated With Non-Responsiveness to Immune Checkpoint Blockade

“Cold”: “Non-Inflamed”, “Non-Immunogenic”, “Immune Desert”

- low mutational and neoantigen burdens
- low CD8+ effector cells
- high Tregs and MDSCs, low Th1
- immunoediting and loss/down-regulation of neoantigens
- impaired antigen presentation
  - loss/downregulation of MHC
  - JAK 1/2 and β2 microglobin mutations in MHC1
- increased levels of immunosuppressive cytokines
  - PTEN loss and increased CCL2, VEGF and reduced T cell infiltration
  - β-catenin/Wnt mutations and reduced CCL4 chemokine production and dendritic cell recruitment
- CCR2/CCL2 and M2 phenotype TAMs
- IPRES (innate PD-1 resistance) gene signature
  - immunosuppressive cytokines, EMT-TFs and pro-angiogenic factors
Shifts of Intratumoral Immune Cell Populations to Immunosuppressive Phenotypes with Tumor Progression

Blue = enrichment
Yellow = depletion

The Publish and Vanish Syndrome

- low success rates in the clinical validation of cancer biomarkers

The Cancer Biomarker Challenge

Tumor Mutational Burden and Response to Immune Checkpoint Blockade

From: M. Yarchoan et al. (2017) NEJM 377, 2501
Immune Profiling Across 19 Solid Cancers Sorted by Mutational Load, Adaptive and Innate Immune Subpopulations and Clinical Outcomes

Adapted from: Charoentong et al., 2017, Cell Reports 18, 248–262
Neoantigen Burden and Prediction of Responsiveness to Immune Checkpoint Blockade (ICB)

Enhanced neoantigen expression

- Tumor Mutational Burden (TMB)
- Defective DNA Mismatch Repair (dMMR) and methylation status
- Microsatellite Instability (MSI)

Association with responsiveness to ICB

Non-synonymous single nucleotide variants versus indel/frameshift mutations
Mismatch Repair Deficiency Predicts Response of Solid Tumors to PD-1 Blockade

Mismatch repair deficiency in 12,019 samples across 24 tumor types

From: D. T. Lee et al. (2017) Science 357, 409
MSI-H/dMMR as ‘Cancer Agnostic’ Marker for Patient Stratification for anti-PD-1 Therapy
TMB Profiling

- limitations on tissue and/or poor quality of extracted DNA
  - Hellman et al (2018) NEJM 378, 2093 only 1004/1739 pts suitable

- sample
  - FNA biopsy or resection?

- multiple TMB test protocols
  - WES or targeted sequencing panels
  - depth of sequencing
  - lack of concordance between NGS panels of different sizes
  - different cut-off points
  - subtraction of clonal hematopoiesis mutations

- TAT and cost
## Tumor Mutational Burden (TMB)

<table>
<thead>
<tr>
<th>Workflow</th>
<th>Step 1: In silico analysis</th>
<th>Step 2: Empirical analysis</th>
<th>Step 3: Clinical analysis</th>
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<tr>
<td>Samples</td>
<td>Publicly available TCGA data</td>
<td>Cells derived from human tumors</td>
<td>Clinical Samples</td>
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<tr>
<td>Goals</td>
<td>Identify sources of variability between TMB calculated using whole exome sequencing (WES) &amp; various targeted panels used in the clinic</td>
<td>Agree upon creation of a universal reference standard using WES Identify sources of variability after alignment of TMB scores from targeted panels to the reference standard</td>
<td>Conduct a retrospective analysis using patient outcome data to assess the variability around clinically meaningful cut-off values and inform clinical use.</td>
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<td>Timeframe</td>
<td>May 2018</td>
<td>Fall 2018</td>
<td>Winter 2018/Spring 2019</td>
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Analysis of Tissue and Blood-Based Tumor Mutational Burden in NSCLC

259 patient samples:
OAK and POPLAR trials
Spearman correlation = 0.64

Genome Doubling in 9,692 Cancers and Association with Worse OS Outcomes

- 28.2% prevalence, second only to TP53 mutations
- arose exclusively in MSI-stable tumors
- evolution of sub-tetraploid CNAs and (sub)clonal diversification?

From: C.M. Bielski et al. (2018) Nature Genetics 0165-1
Copy Number Loss (>2000) as a Potential Resistance Phenotype for Double Non-Responders to Sequential CTLA-4 and PD-L1 Blockade and Loss of Tumor Suppressor Genes

From: W. Roh et al. (2017) Sci. Trans. Med. 9, eaah3560
Neoantigen Expression and Detection in Prediction of Responsiveness to Immune Checkpoint Blockade (ICB)

- antigen loss/reduced expression
- impaired immune recognition and antigen processing

- loss of mutations encoding neoantigens
  - clonal immuno-editing
  - chromosomal deletion(s)

- HLA genotype and loss of HLA heterozygosity

- pathway mutations in antigen processing
  - JAK 1, 2
  - β2M, TAP1
  - IFN-γ

intrinsic and acquired resistance to ICB
Tumor Neoantigen Landscape Is Diverse and Sparse

- 8243 samples from 20 solid tumor types
- 1 petabyte of genomic data → 50 gigabytes of structured immunogenomic data
- Number of neoantigens correlated with mutational load
- 933,954 expressed nsSNV neoantigens (911,548 unique) originating from 893,960 somatic point mutations
- < 10% derived from driver genes and bulk from passenger genes
- Only 24 of the 911,548 unique antigens were shared in at least 5% patients or more than one cancer type
Tumor-Specific Neoantigen Burden Across 19 Cancer Types

Adapted from: S. Turajlic et al. (2017) Lancet Oncology 18, 1009
Splice-Site Mutations Across Genes and 8656 TCGA Tumor Types

- predicted higher MHC binding affinities (Net MHC4, NetMHCpan-3.0) for splice variants
- higher number of neoantigens (2-3x) in splice variants than nsSNV neoantigens
- elevated expression of PD-1, PD-L-1 in tumors with higher splice burden

Adapted from: R. E. Jayasinghe et al. (2018) Cell Reports 23, 270
Mapping of Tumor Neoantigen Affinities for MHC Binding

- strong-binding neopeptides with MHC-I affinities <500nM associated with better response rates to ICB in NSCLC and melanoma
- differential agretopicity index (DAI= difference in binding affinities of wt/mutated peptides) as a potentially superior index of peptide immunogenicity than standard single neopeptide-MHC affinity profiling?

HLA Loss of Heterozygosity in Lung Adenocarcinoma and Lung Squamous Cell Carcinoma

- HLA loss of heterozygosity and failure to recognize antigenic peptides no longer presented on the lost allele
- enrichment of neoantigens predicted to bind with high affinity to lost vs retained HLA alleles
- higher frequency of LOH in subclones at metastatic sites
  - role of immune microenvironment(s) as a selective force in shaping branched clonal evolution?

The Need for Systems-Level Characterization of Immune-Response Networks in Different Cancer Types, Different Metastases and Different I/O Regimens

New Analytical Platforms for Increased Granularity for Classification of Immune Cell Subsets, Tumor (Sub)Clonality and Cellular ‘State Spaces’
System-Level Characterization of Immune-Centric Networks in Disease

- High dimensional phenotyping on an unprecedented scale
  - From multiOmics profiling to stringent clinical annotation
  - Standards: pre-analytical processing, assays, data formats
- Daunting level of theoretical ‘large N’ combinatorial interactions
  - Tumor (sub)clonal heterogeneity, diversity of immune cell subsets, signaling molecules and intracellular pathways
- Linear and non-linear effects in input:output interactions and biological outcomes
- Massive data
  - Design of experimental protocols to integrate diverse datasets
  - Data standards and format for data exchange and meta-analysis
Patient-Paired Sample Congruence (or Lack of!) in Two Commercial Liquid Biopsy Tests for Prostate Cancer

- G. Torga and K.J. Pienta (2018) JAMA Oncol. 4, 868
- blood sample cfDNA profiling by Guardant and Personal Genome Diagnostics Inc. (40 pts)
- concordance achieved in only 35% samples
The Immune Landscape of Cancer

- 33 TCGA cancer types (30 solid tumor types)
- 11,180 samples
- Patient age range 10-90 years (median 60)
- 22 immune cell subsets
- 166 immune expression signatures
  - 83 cancer context
  - 77 general validity for immune response
- 6 expression cluster groups
  - N = 2416, 2591, 2397, 1157, 385, 180

Distribution of Six Co-Clustered Immune Expression Signatures that Span Anatomic Location and Tumor Type in Analysis of 30 TCGA Tumor Subtypes (N=11,180)

- top third includes cancers most responsive to ICB
  - lung AD, SC; melanoma; kidney (clear and papillary); head-neck; bladder
  - uveal melanoma and adrenocortical carcinoma lowest lymphoid fraction (LF)
  - glioma subtypes greatest LF range (related to microglia content ?)

From: V. Thorsson et al. (2018) Immunity, 48, 812
Multi-Attractor Landscapes, State Space Occupancies and Co-Evolutionary Pathways in Complex Adaptive Systems

- Gene-regulatory networks
- Functional pathways, modules and signaling network architectures
Multi–Attractor Landscapes, State Space Occupancies and Co-Evolutionary Pathways in Complex Adaptive Systems

Rx-induced shift(s) in landscape topologies

Gene-regulatory networks

Functional pathways, modules and signaling network architectures

State spaces

Immune cell subsets

Tumor (sub) clones
Understanding the (Pre) Exhaustion T Cell Phenotypes Induced by Upregulation of Immune Checkpoint Molecules and Chronic TCR Stimulation

Identification of T Cell ‘State Spaces’ and Responsiveness to Reinvigoration by ICB (and other I/O Rx)
t-SNE Clusters (7) of Single T Cell Subsets in NSCLC

Single Cell Analysis of CD8+ Cell State Transitions in NSCLC

Adapted from X. Guo et al. (2018) Nat. Med. 24, 479
Integration of scRNA Seq and Spatial Transcriptomic in the Analysis of Immune Cell Subsets in Pancreatic Ductal Carcinoma

Adapted from: R. Moncada et al. (2018) bioRxiv254375
Spatial Transcriptomics

- microdissection and microfluidics capture of double/triplet cells to define state spaces generated by physical interactions
- profiling from tissue sections
- new automated imaging methods with high (40) multiplex immunofluorescence analysis of frequency of cell type adjacencies and protein expression

G. Gut et al. (2018) Science 361, 468
System-Level Sankey Plot of Inter-cellular Cytokine-Immune Cell Subset Interactions Derived from Large Scale Literature Analysis (immunoXpresso)

Deep Phenotyping and ID of Genetic Contributions to Individual Variation in Cytokine Responses

O.B. Bakker et al. (2018) Nature Immunology 19, 776

• 91 cytokine-stimulus pairs in 534 individuals elicited by 20 pathogens
• 70% heritability
Deep Phenotyping and ID of Genetic Contributions to Individual Variation in Cytokine Responses

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- 70% heritability

Do germ line variants in lymphokine/cytokine affect responsiveness to I/O therapy and AE risk (cytokine release syndrome)?
A Conceptual Framework for Efficacy of ICB Therapy

Adapted from A.C. Huang et al. (2017) Nature 545, 60

HIGH

strong reinvigoration
but clinical failure

• immuno-editing and
  immune-escape (sub)clones
• impaired antigen presentation

red = NR
green = R

LOW

T cell Reinvigoration

Antigen Load/Disease Burden

large tumors
strong reinvigoration

• activated signature

large tumors
low/intermediate reinvigoration

• high suppressive TME
• severe exhaustion

small tumors
strong reinvigoration

small tumors
weak reinvigoration

• activated signature
• poor priming
• poor immunogenicity

small tumors
weak reinvigoration

large tumors
strong reinvigoration

• activated signature

T cell Reinvigoration

HIGH

LOW
Need for New Minimally-Invasive Assays for Monitoring Patient Responses to Immunotherapy

- handicap of ‘static’ snapshot of immune profile in resected tissue lesions/biopsies versus longitudinal monitoring of dynamic changes in tumor progression/Rx responses
- how far do blood-based (liquid biopsy) assays mirror intra-tumoral events in anatomically dispersed metastases?
  - ctDNA and mutanome profiling?
  - immune cell subsets and trafficking?
  - cytokine signaling networks?
  - exosome species?
Exosomes and Modulation of Immune Functions

Tumor-Derived Exosomes as a Potential Molecular Profiling Platform to Assess Variation in Immunotherapy Efficacy?
Immune Stimulation by Cancer-Derived Exosomes

- direct activation of effector T cells by MHC class I and II complexes on vesicle membrane
  - T cell priming required
  - B cell-derived exosomes stimulate primed CD4+ T cells but not naïve T cells
- transfer of tumor neoantigens to dendritic cells (DCs) and stimulation of naïve CD4+ T cells
- stimulation of pro-inflammatory M1 phenotype in macrophages
Immune Suppression by Cancer-Derived Exosomes

- exosomal PD-L1 suppression of CD8+ T cells
- decreased production of immunostimulatory molecules
  - IL-2, IL-17 and IFN-γ
- increased levels of immune inhibitory proteins
  - TGF-β, IL-10, COX-2
- miR212 induction of reduced MHC II expression
- miR222, miR494 and M1 to M2 shift in tumor associated macrophages
- immunosuppression of B cells by exosome membrane-associated CD39 and CD73 via production of extracellular adenosine
- impaired differentiation of DCs from bone marrow precursors
- enhanced survival of MDSC via activation of STAT3
- inhibition of NK cells by exosome surface MICA/MICB liquids, TGF-LAG and induction of inhibitory TGF-β
Blood-based Exosome Profiling


- $10^{12}$ exosomes/ml
- proprietary aptamer oligonucleotide library for capture of diverse exosome species based on surface ligands
  - unbiased target identification
  - NGS readout of selective binding
- identify cell-of-origin
- quantitative and qualitative disease-associated changes in membrane proteins and internal cargo
Tumor-Derived Exosomes as a Potential Molecular Profiling Platform to Assess Immunotherapy Efficacy

- assessment of \( \text{Exo}^{\text{stim}} \) and \( \text{Exo}^{\text{supp}} \) ratio in tumor progression and therapeutic efficacy
  - baseline before immunotherapy
  - effect of prior Rx on baseline
  - measure dynamic changes in ratio during immunotherapy (and other therapies)
  - patterns and ratio in R and NR cohorts and/or adverse events
The Need for Standards in Immuno-Profiling, Data Curation, Annotation and Inter-operable Database Design

- recognition in development of nearly 40 Minimum Information for Biomedical Investigations (MIBBI)
  - https://fairsharing.org/collection/MIBBI
- evolving framework for immune datasets
  - Minimal Information for Adaptive Immune Receptor Repertoire
    F. Rubelt et al. (2017) Nat. Immunol. 18, 1274
- journals have different (or no) policies to standardize nomenclature and access to raw data/analytical computer code(s)
Immunotherapy offers hope to some people with hard-to-treat cancers — but it can backfire.

**Cancer drugs may speed tumours in some people**
Influence of the Gut Microbiome on Immunotherapy Responses

- possible role of dysbiosis in creating chronic inflammation and immunosuppressive phenotype
- limited insight into the roles of diet and microbial metabolites on cancer risk, progression and I/O Rx response
- effect of oral antibiotics on I/O efficacy
Will Combination Regimens Increase Response Rates in Immuno-Oncology?

- within and across cancer types
- dramatic expansion in combination trials
  - biological rationale for MOAs of the selected agents
  - dosing and sequence, duration, toxicity profile
- limitations of preclinical models for new I/O agent discovery and evaluation of combination regimens
  - organoids, orthotopic human xenografts
Will Combination I/O Regimens Increase Pan-Cancer Response Rates

Targets of Anti-PD-1/PD-L1 Combination Clinical Trials

Numbers of trials using common combo strategies:

1. Anti-CTLA-4 agents: 251
2. Chemotherapies: 170
3. Radiotherapies: 64
4. Anti-VEGFA agents: 43
5. Chemoradiotherapy combos: 42

Now Comes the Really Hard Part!

- balancing hype versus hope
- realism of likely time frame (and cost) of major gains in next-generation I/O therapies
  - efficacy within and across malignancies
  - combination Rx (current agents)
  - 2/3rd generation I/O agents

- societal (cost) and individual (futile Rx) implications of unrestricted use of first-generation I/O absent predictive markers to stratify responder and non-responder cohorts
DTC Saturation Advertising Campaigns

A Delicate Ethical Balance: Come and Be Cured by Us: (Go Elsewhere at Your Peril)!

We see through cancer's disguise.

Who will crack the cancer code?

Attacking cancer is now personal.

We can now see cancer so precisely, we can predict its future.

We are coming at cancer in ways cancer doesn't see coming.

We're not just fighting cancer. Now we're outsmarting it.
Immunotherapy: Hype and Hope

- deserved recognition of ICB as major therapeutic advance
- media hype, scale of corporate DTC and AMC advertising campaigns emphasizing responders
  - distorts public awareness that NR>R
  - unrealistic patient expectations of successful outcome
  - potential for serious toxicities
  - cost of futile therapy in NR patients/toxicity risk
- patient demands for immunotherapy despite no evidence of efficacy in their specific malignancy
Cancer Treatment Cost

Value Frameworks for Oncology
Is the Bar in the ASCO Value Frameworks Too High in Assessing Long-Term Benefits in I/O Therapy?

- JAMA Oncology (2018) 4,326
  - analysis of approved I/O agents (2011 to 8/17)
- 23 indications for 6 I/O agents for metastatic solid tumors
- only 3 gained durable survival bonus points under ASCO framework
Performance-Based Contracts and Pricing: The Inevitable Future Landscape for Immunotherapy?

- robust prediction of responders and non-responders
- companion diagnostics and labeling requirements
- performance-based outcomes and premium pricing

Integration of R:NR immunophenotypes into clinical trials and registration dossier

Risk sharing
The Urgent Clinical and Economic Imperatives for Predictive Markers to Differentiate Responder and Non-Responder Patients in Different I/O Regimens

- single most important opportunity for the (bio)pharmaceutical industry in advancing rational immunotherapy?
- increased payer pressure for performance-based outcomes and premium pricing?
- proactive industry engagement or reactive response to payer imposition?