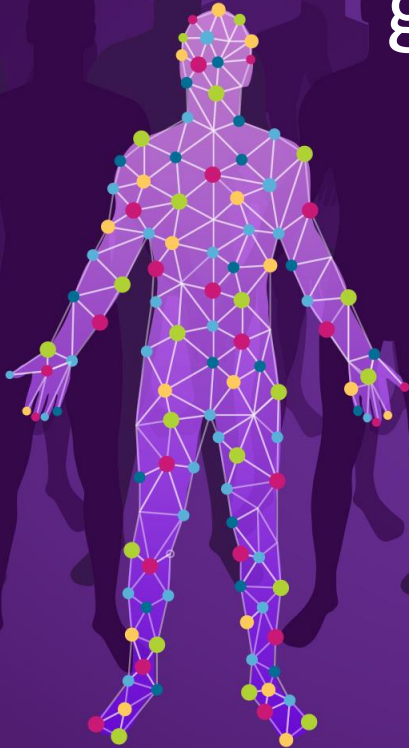


Biomarkers to assess risk and guide immunosuppression in kidney transplantation

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New York , NY



CUTTING EDGE of **TRANSPLANTATION**

TRANSPLANT SUMMIT 2019

***NO SIZE FITS ALL:** Uncovering the
Potential of Personalized Transplantation*

Disclosure

Faculty: Peter Heeger

Relationships with commercial interests:

Grants/Research Support: Alexion Pharmaceuticals

Speakers Bureau/Honoraria: None

Consulting Fees: None

Other: None

Learning Objectives

To differentiate a biomarker from a surrogate endpoint

To explain the clinical utility of urinary CXCL9 testing among other biomarkers to diagnose kidney transplant rejection during CNJ withdrawal

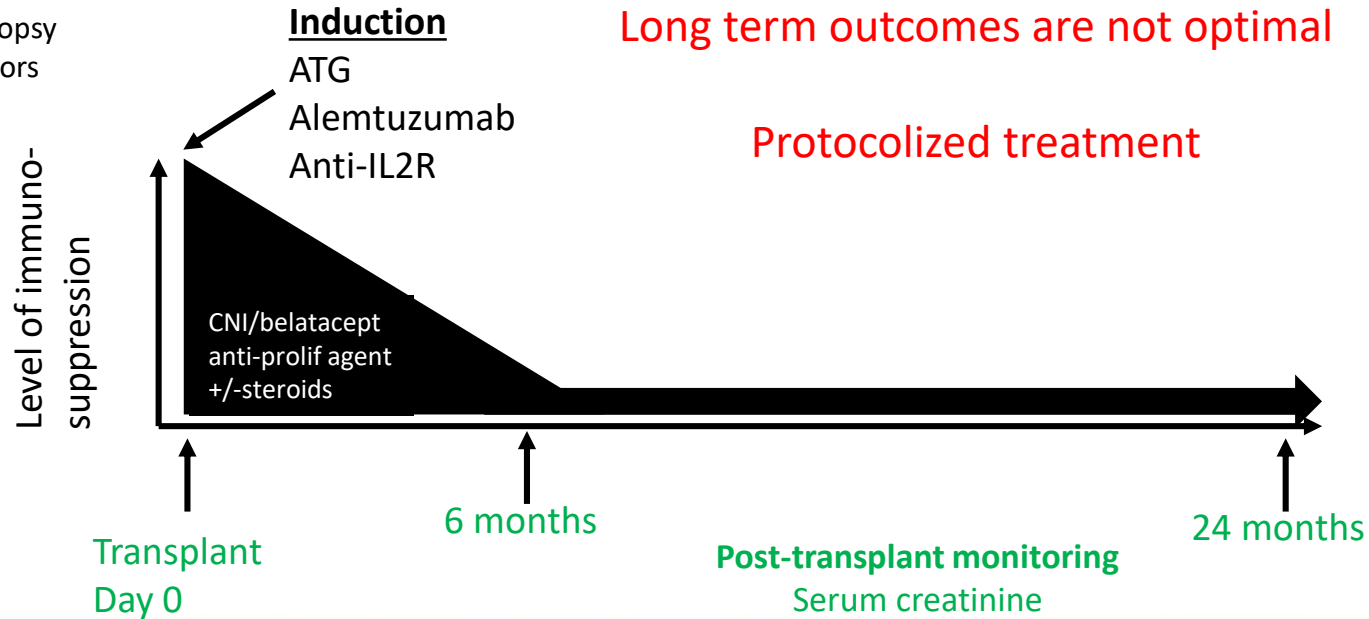
To explain the utility of pretransplant biomarkers as risk assessment tools for guiding CNJ withdrawal post transplant

Definitions

- **Biomarkers** are anatomic, physiologic, biochemical, or molecular parameters that indicate, or are associated with an alteration in physiology and are of clinical significance (this doesn't necessarily mean they are clinically useful)
- **Surrogate Markers** can be defined as biomarkers that have established clinical utility
- **Surrogate Endpoints** are biomarkers used (in clinical trials) to evaluate the safety or effectiveness of a therapy and serve as alternatives to traditional endpoints.

The need for biomarkers in transplantation

**Pre-transplant
Risk assessment**
HLA typing
Cross matching
Implantation biopsy
Clinical risk factors



Biomarkers-potential uses

- Surrogate endpoints for clinical trials
- Risk assessment for post transplant outcomes
 - who is most likely to do badly (rejection/graft loss) and might require more/different immunosuppression
 - who is most likely to tolerate decreasing immunosuppression?
- Noninvasive diagnosis graft injury
 - Prevent morbidity of biopsy
 - Detect subclinical or incipient injury and or fibrosis
 - safety net for drug withdrawal studies
 - long term monitoring to detect changes in status
- Predict DGF
- Detect Immune tolerance

Biomarkers can support drug development & approval

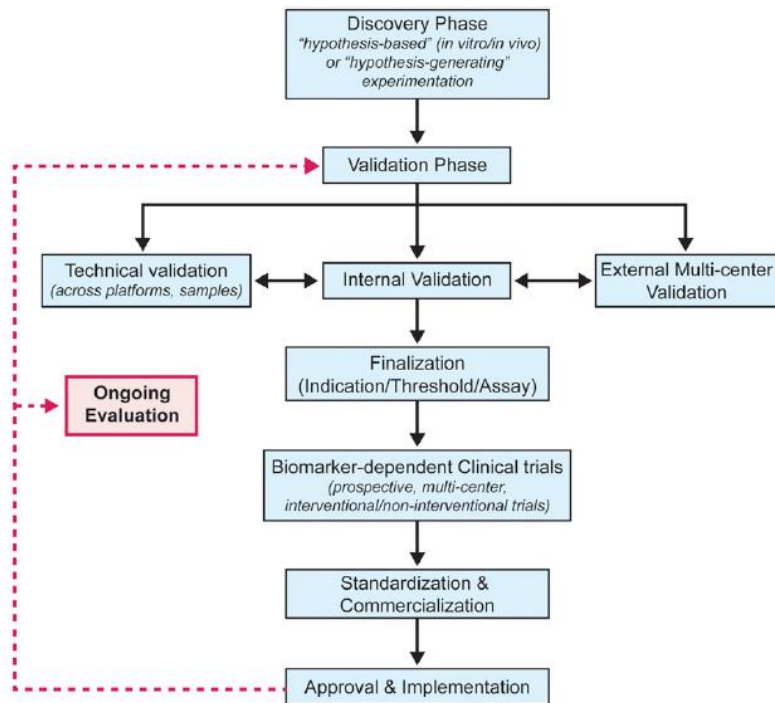
- Trials cannot be done using hard endpoints of graft or patient survival because they would take too long, so we need surrogates of these hard endpoints
- AR is the only approved surrogate endpoint but
 - a) it occurs relatively infrequently and
 - b) graft failure occurs in the absence of AR
- Are there viable alternatives?

Candidate surrogate endpoints

- De novo class II DSA
- Changes in eGFR during the first 2 years (kidney transplant)
- iBOX score (kidney transplant)
- IVUS measurements of cardiac vasculopathy (heart transplant)
- others

Beyond clinical trials

Moving Biomarkers Toward Clinical Implementation in Transplantation



Menon, Murphy, Heeger, JASN 2017

Multicenter validation and assay standardization are crucial

American Journal of Transplantation 2013; 13: 1859–1870
Wiley Periodicals Inc.

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Brief Communication

doi: 10.1002/ajt.12287

Comprehensive Assessment and Standardization of Solid Phase Multiplex-Bead Arrays for the Detection of Antibodies to HLA

E. F. Reed^{1,*}, P. Rao¹, Z. Zhang¹, H. Gebel²,
R. A. Bray², I. Guleria³, J. Lunz⁴,
T. Mohanakumar⁵, P. Nickerson⁶,
A. R. Tambur⁷, A. Zeevi⁴, P. S. Heeger⁸
and D. Gjertson¹

¹Department of Pathology and Laboratory Medicine

facturers (AUC > 0.9) and suggested optimal cutoffs from 1000 to 1500 MFI. Global normalization further reduced MFI variation to levels near 20%. Standardization and normalization of solid phase HLA antibody tests will enable comparison of data across laboratories for clinical trials and diagnostic testing.

²Department of Immunology and Transplantation Medicine

- Representative example of CTOT biomarker standardization
- Rigorous analytical validation is critical
- Inter-laboratory reproducibility important

Pre-transplant biomarkers for risk stratification in transplantation

- Are there biomarkers that can be measured pre-transplant that can predict risk of post transplant rejection and/or graft function (beyond DSA)?
- If yes, one implication is that treatment strategies for high vs low risk patients could be individualized prior to transplant to optimize outcomes
- Yesterday we heard about pre transplant gene expression/non HLA mismatches
 - Sarwal, UCSF
 - Murphy, Mount Sinai

Donor-reactive Memory T cells and transplant outcome

- Memory cells are resistant to most immunosuppressant meds, are present at high frequency, have high functional avidity and respond rapidly to antigenic challenge
- Hypothesis: high frequencies of memory T cells reactive to donor HLA negatively impact transplant outcomes

Pre-transplant donor-reactive T cells and post-transplant outcome

IFN γ ELISPOT

Pre-transplant donor reactive ELISPOT			
Variable	Negative ($<25/300$ K)	Positive ($> 25/300$ K)	p value
Acute cellular rejection	17%	50%	.036
GFR (MDRD) 12 months	55 ± 20 ml/min/1.73 m ²	37 ± 16 ml/min/1.73 m ²	.006
DGF	23%	31%	NS

Validation sets

- Other independent validation:
- Donor reactive IFN γ ELISPOT assays pre- and post-transplant correlate strongly with AR and 1 y eGFR
 - Berlin group (Volk, Reinke)
 - Barcelona (Grinyo, Bestard)
 - Results from multicenter CTOT-01 study

*American Journal of Transplantation 2015; 15: 3166–3173
Wiley Periodicals Inc.*

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and the American Society of Transplant Surgeons*

doi: 10.1111/ajt.13401

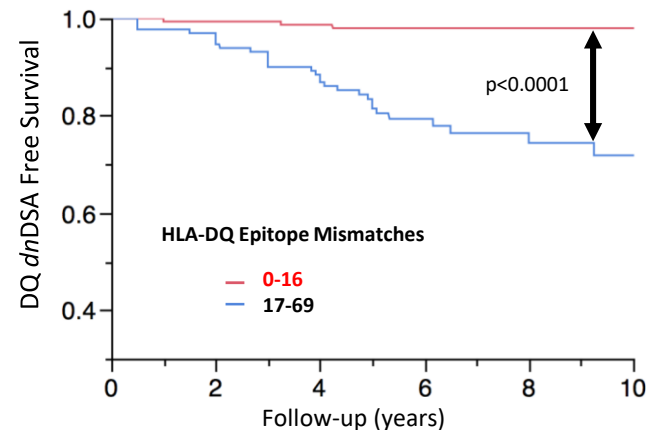
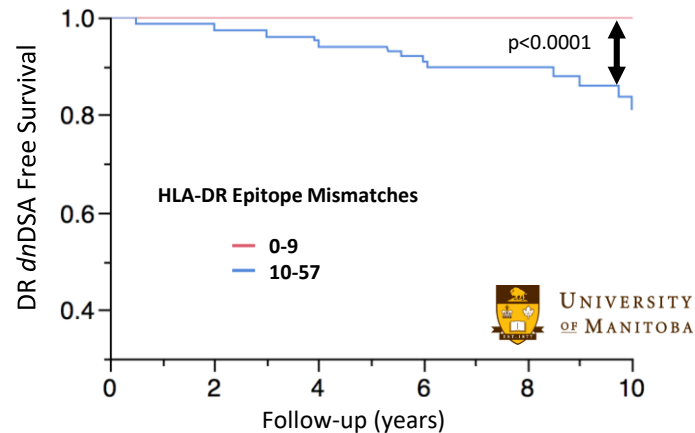
**Interferon Gamma ELISPOT Testing as a
Risk-Stratifying Biomarker for Kidney Transplant
Injury: Results From the CTOT-01 Multicenter Study**

Status: Pre-transplant donor-reactive IFN γ ELISPOT as a biomarker for post-transplant outcome

- Tested and validated by multiple groups
- Utility of using marker to guide therapy unknown
- Complex assay
- Requires customization (donor reactive)
- Some commercial interest

HLA EPITOPE Analysis (molecular mismatch) as a biomarker for developing DSA

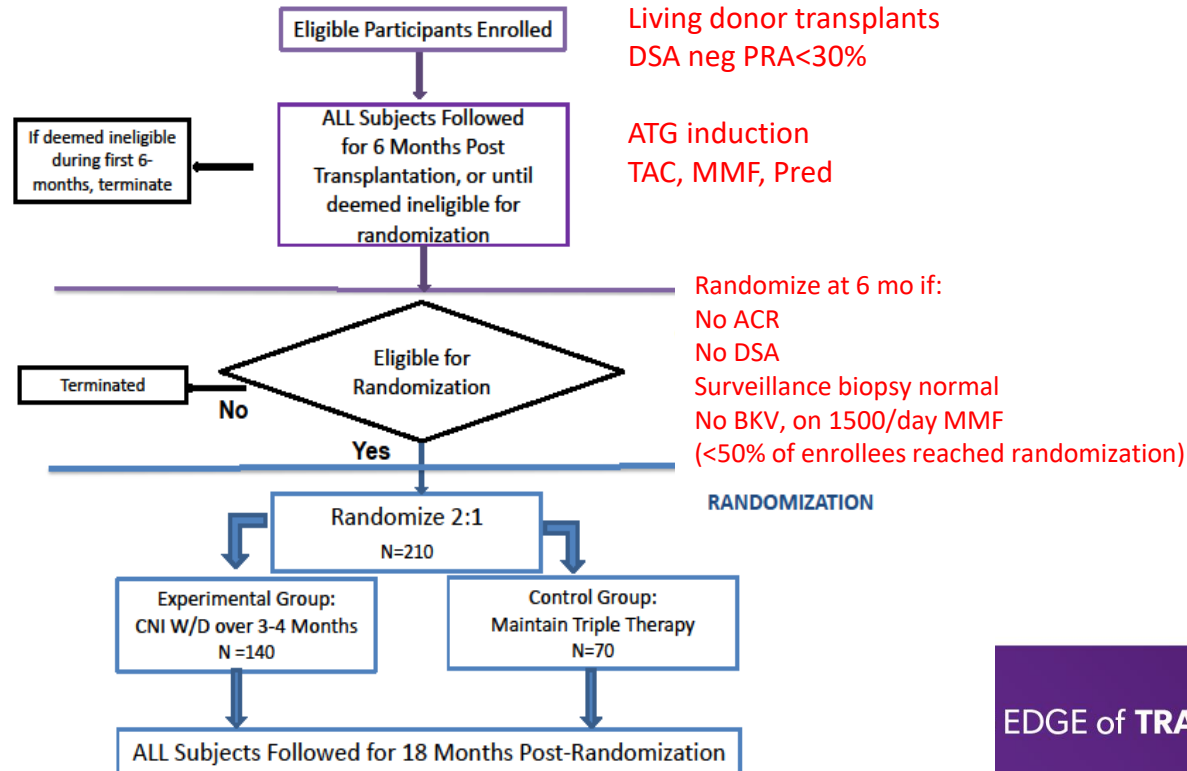
Epitope MM Load associated with
de novo DR or DQ Donor specific
antibody (DSA)



Can pre-transplant biomarkers
predict those at highest risk for
poor outcomes during changes
in immunosuppression?

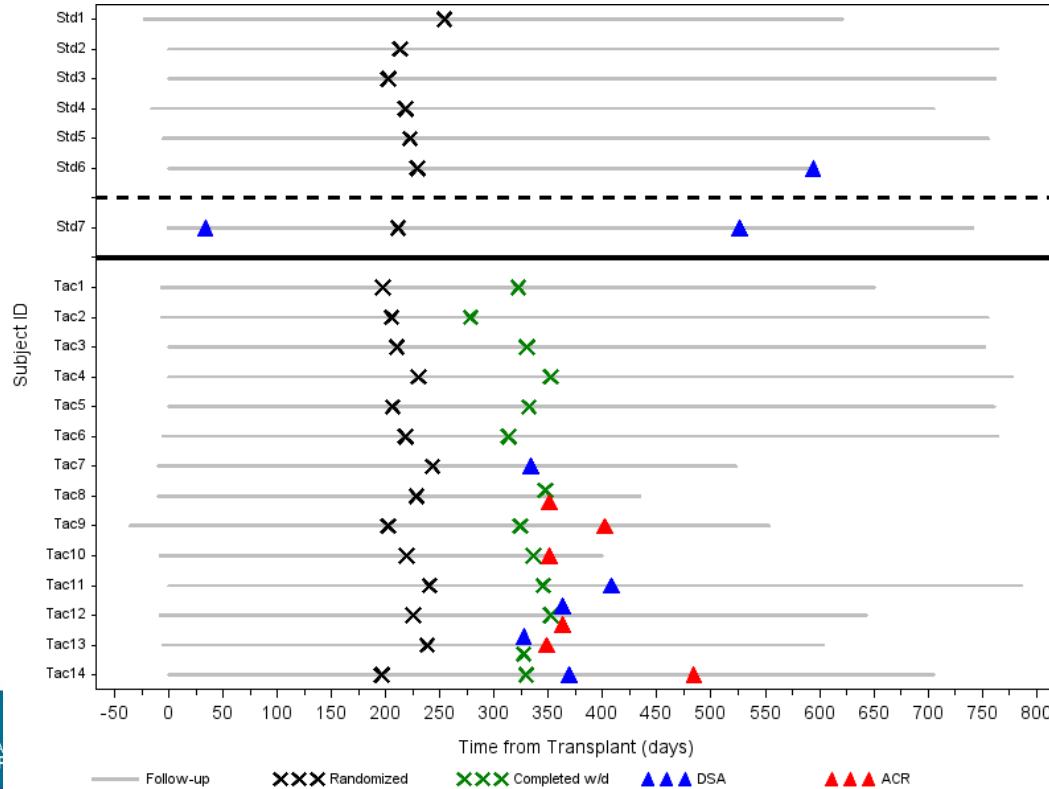
CTOT09

TAC withdrawal in low risk, stable recipients of first living donor kidneys



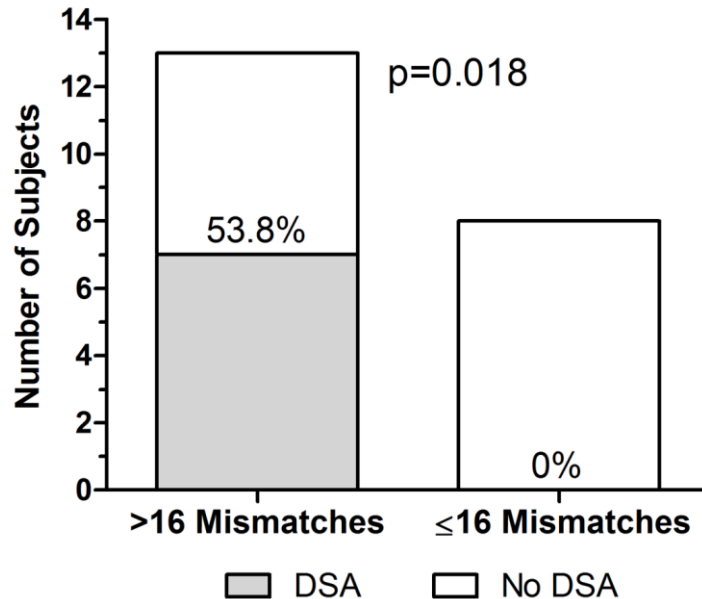
Study terminated due to absence of equipoise

Confirms standard clinical risk assessment is inadequate!



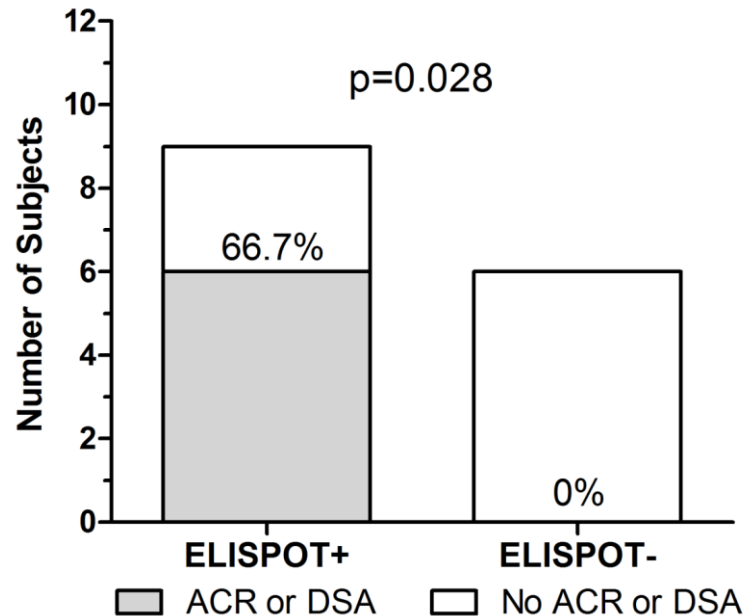
Pre-transplant risk assessment

High epitope load associates with development of de novo DQ DSA in the CTOT09 cohort

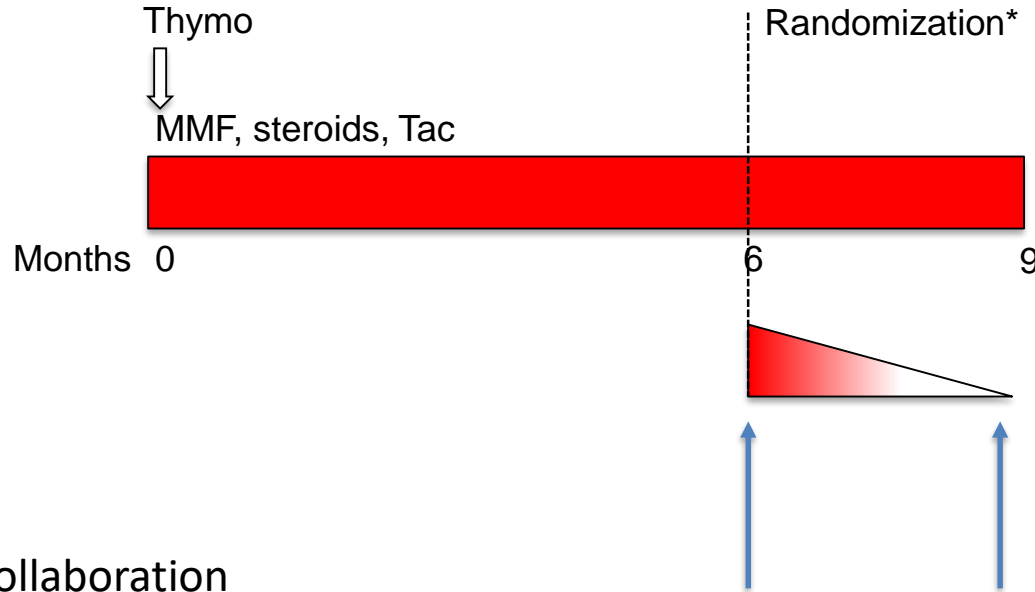


Pre transplant risk assessment

ACR/DSA upon withdrawal associated with high pre-transplant anti-donor IFN γ ELISPOTs in the CTOT-09 cohort



Do peripheral blood gene expression profiles obtained before and after withdrawal provide insight?

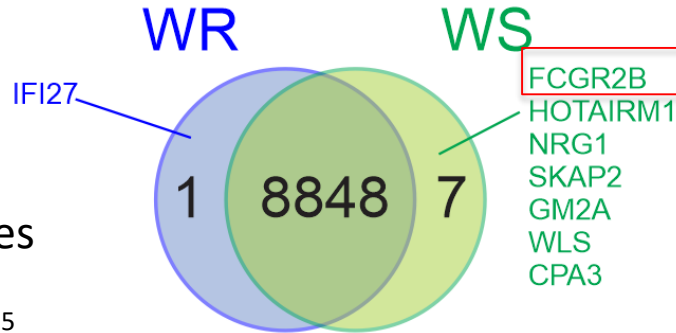
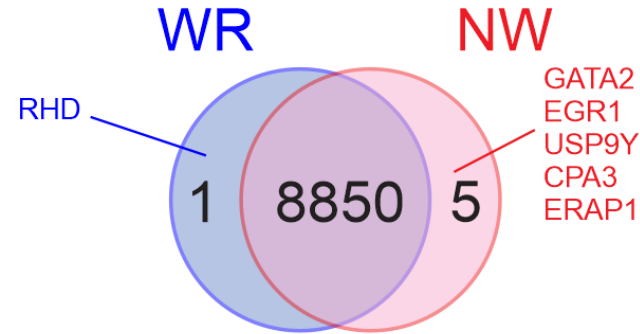
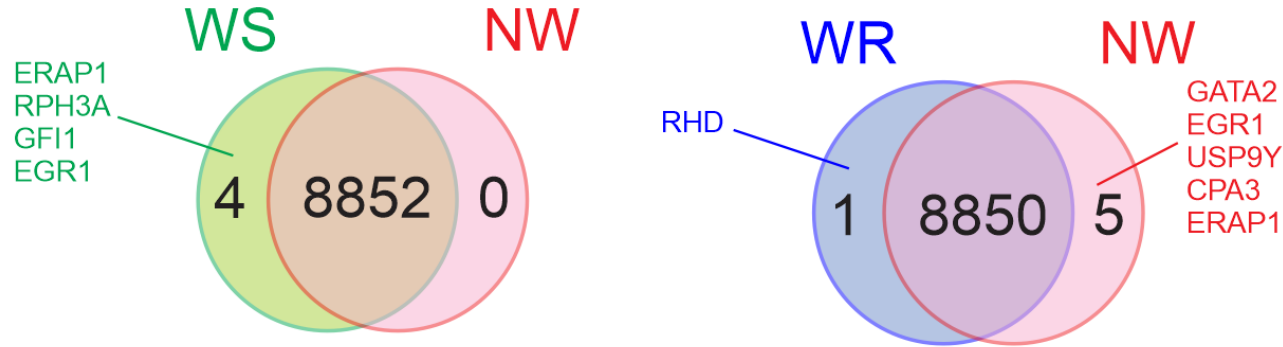


Work done in collaboration
with Dan Salomon, Scripps

PBMC RNA Affimetryx Array analysis

Few Differences in Transcriptional Programs at Baseline (before randomization)

Differential Gene Expression

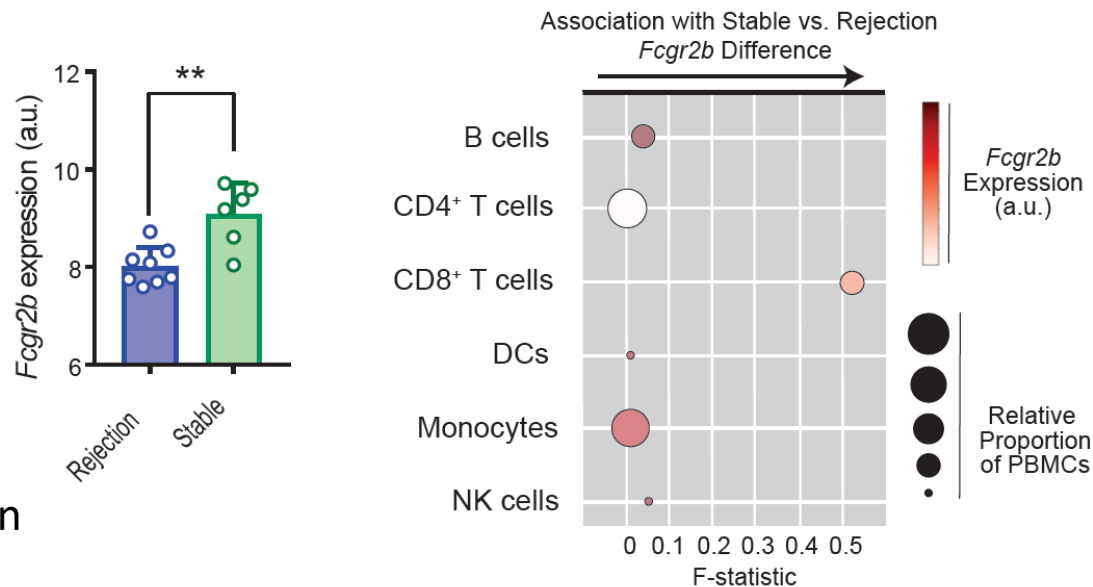


NW: No withdrawal (n=4)
WR: Withdrawal AR (n=8)
WS: Withdrawal stable (n=6)

N = 8856 genes

Upregulation logFC > 1.5
Downregulation logFC < -1
p < 0.001 (no adjustment)

FcγR2b has coinhibitory functions on CD8⁺ T cells

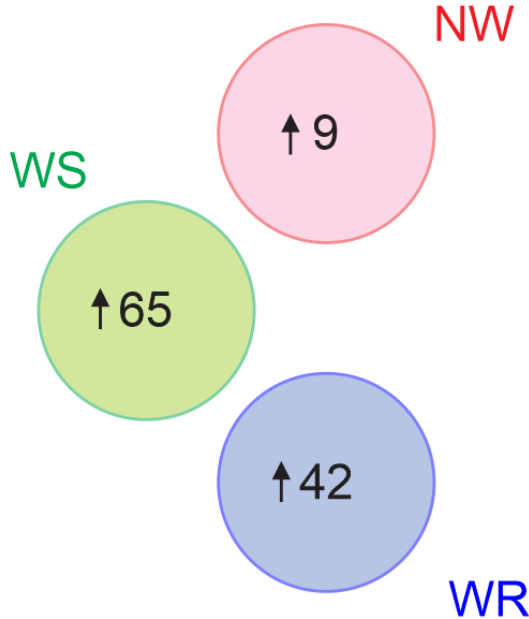


Work done in collaboration
with Mandy Ford, Emory

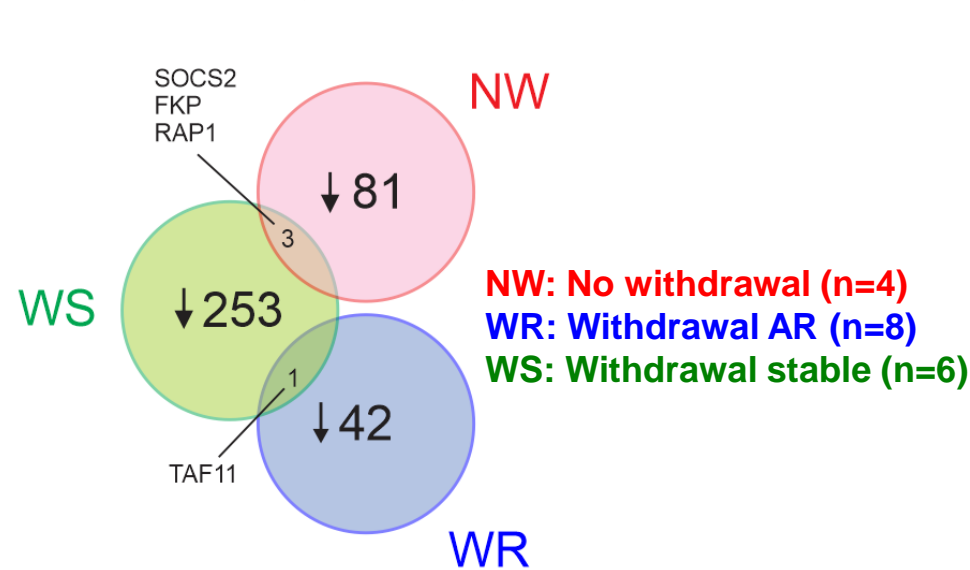
Evolution of the transcriptional program between 0 and 3 months post-randomization

- The three groups have distinct upregulated transcriptional programs.
- The Withdrawal Stable group is characterized by a large downregulatory transcriptional program.

Upregulated genes



Downregulated genes



Evolution of the transcriptional program between 0 and 3 months post-randomization

Upregulated genes

Downregulated genes

NW

No enrichment

↑ 9

WS

↑ 65

Cell Death
Apoptosis

↑ 42

MAPK cascade activation
Activation of Protein
Kinase Activity

WR

NW

No enrichment

↓ 81

SOCS2
FKP
RAP1

3

WS

↓ 253

TAF11

1

No enrichment

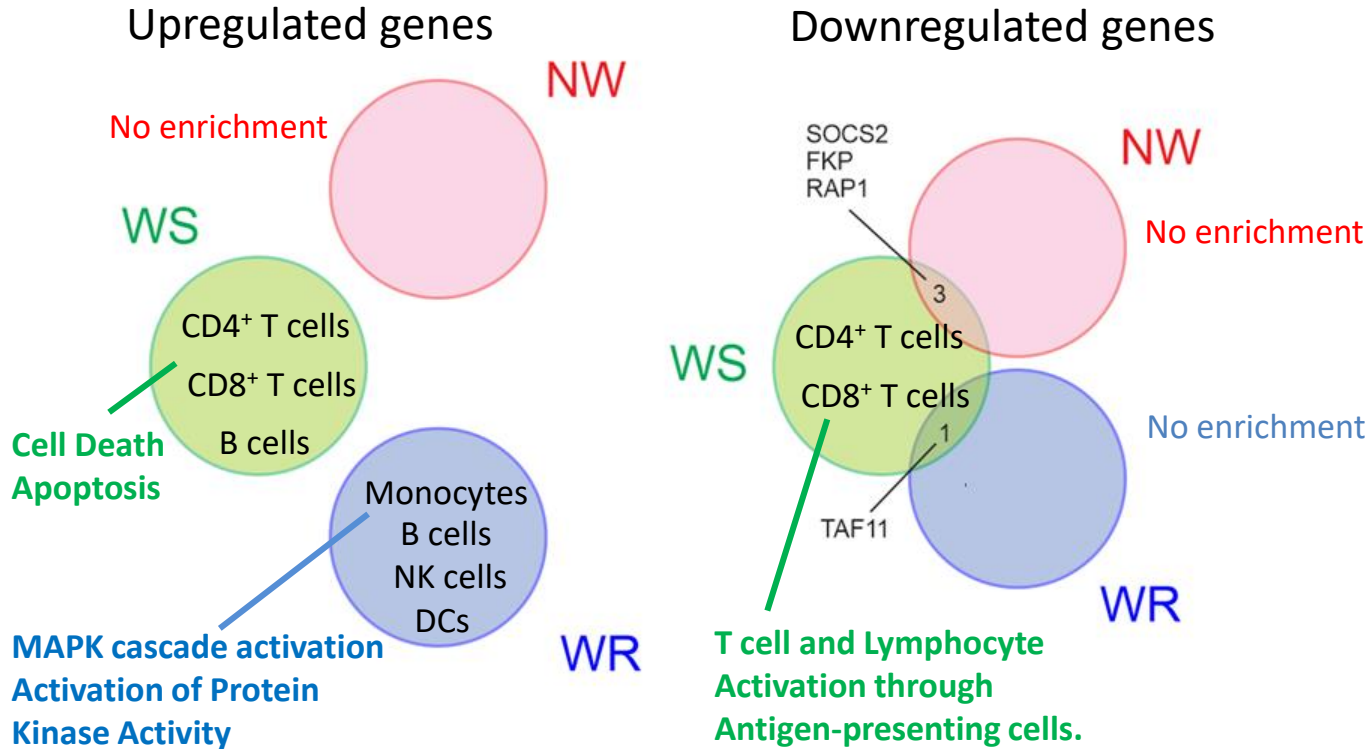
↓ 42

WR

T cell and Lymphocyte
Activation through
Antigen-presenting cells.

Evolution of the transcriptional program between 0 and 3 months post-randomization

CellCODE analysis (SPV estimation + interaction model + GO term enrichment)



Gene expression profiling prior to and during Tac withdrawal has potential to guide decision-making

Post transplant biomarkers

The NEW ENGLAND JOURNAL of MEDICINE

- Urine

- Gene expression (PCR/nanostring)
- cfDNA
- Protein (chemokines)

- Blood

- Gene expression patterns
- cfDNA
- others

Identification of Common Blood Gene Signatures for the Diagnosis of Renal and Cardiac Acute Allograft Rejection

Li Li^{1,3}, Kiran Khush^{2,3}, Szu-Chuan Hsieh^{1,3}, Lihua Ying¹, Helen Luikart², Tara Sigdel^{1,3}, Silke Roedder^{1,3}, Andrew Yang², Hannah Valentine^{2,3}, Minnie M. Sarwal^{1,3*}

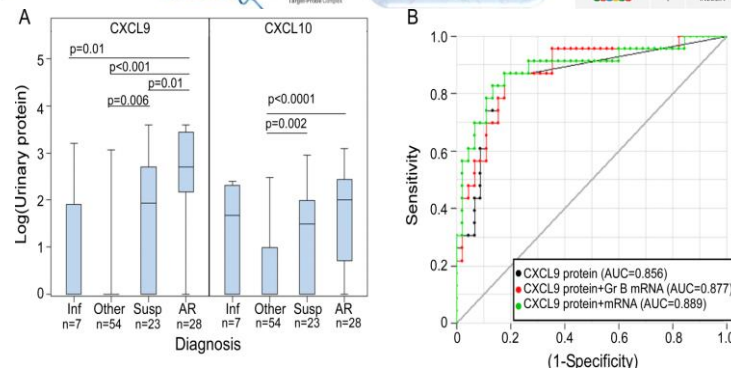
1 Department of Pediatrics, Stanford University, Palo Alto, California, United States of America, 2 Division of Cardiovascular Medicine, Department of Medicine, Stanford University, Palo Alto, California, United States of America, 3 California Pacific Medical Center Research Institute, San Francisco, California, United States of America

Development and clinical validity of a novel blood-based molecular biomarker for subclinical acute rejection following kidney transplant

John J. Friedewald¹ | Sunil M. Kurian² | Raymond L. Heilman³ | Thomas C. Whisenand⁴ | Emilio D. Poggio⁵ | Christopher Marsh² | Prabhakar Baliga⁶ | Jonah Odum⁷ | Merideth M. Brown⁷ | David N. Ikle⁸ | Brian D. Armstrong⁸ | Jane L. Charette¹ | Susan S. Brietgam¹ | Nedjema Sustento-Reodica¹ | Lihui Zhao¹ | Manoj Kandpal¹ | Daniel R. Salomon^{2,7} | Michael M. Abecassis¹ | for the Clinical Trials in Organ Transplantation 08 (CTOT-08)

ORIGINAL ARTICLE

Urinary-Cell mRNA Profile and Acute Cellular Rejection in Kidney Allografts

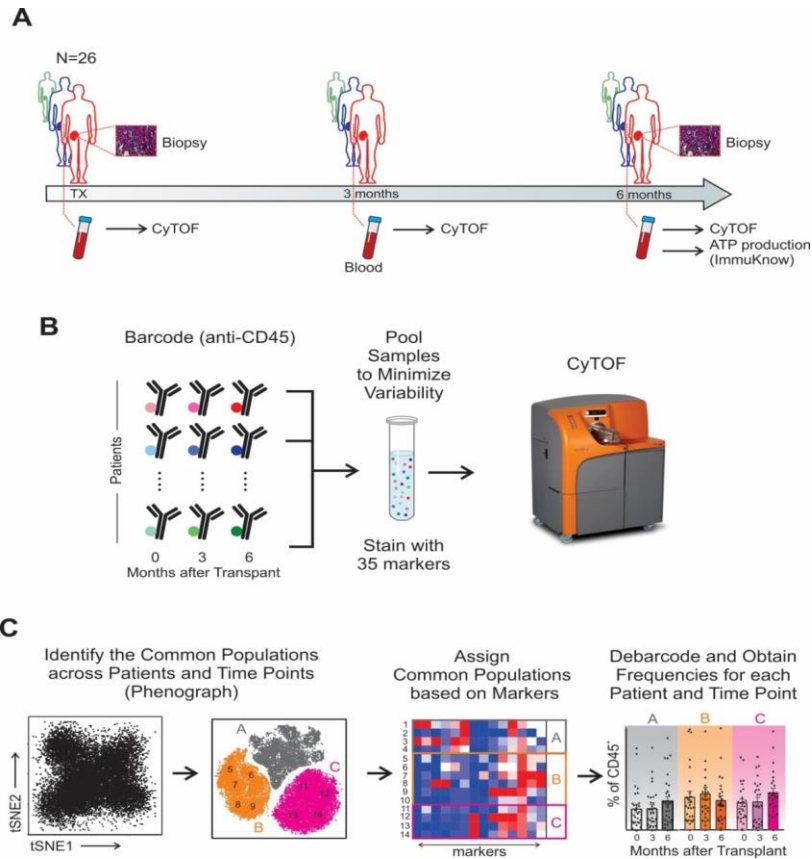


Peripheral blood T cell exhaustion as a biomarker for posttransplant outcome

- A differentiation state that prevents immunopathology in situations of persistently high antigen load and inflammation
- Exploited by pathogens and tumors to dampen or silence potentially protective immunity
- Associated with PD1 expression (target of checkpoint blockade)
- Functionally: progressively decreased proliferative capacity and interleukin-2 (IL-2) production followed by a reduced ability to secrete tumor necrosis factor α (TNF α) and interferon γ (IFN γ)
- Role in transplantation is unclear but more exhaustion is hypothesized to be associated with better outcomes (opposite of tumors)

Exhaustion and kidney transplant outcomes

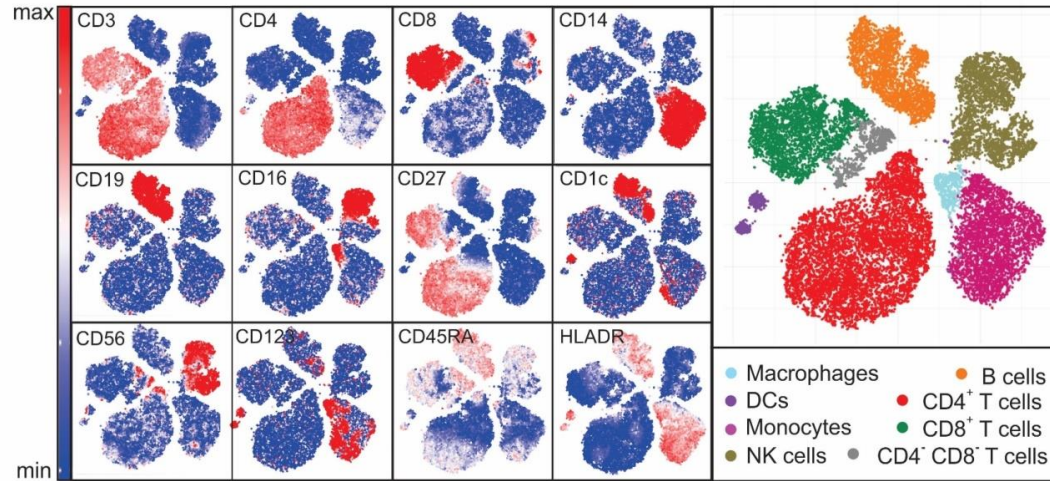
Paolo Cravedi and Miguel Fribourg



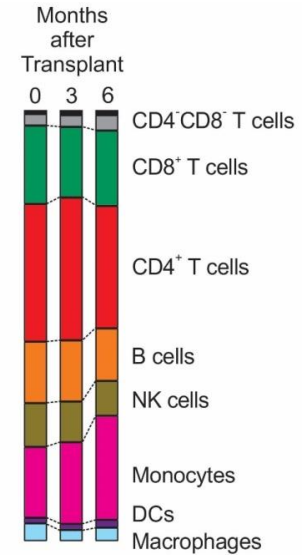
Kidney International 2019, in press

26 CTOT01 subject samples (frozen) studied at 0, 3 and 6 mo post-transplant

A



B



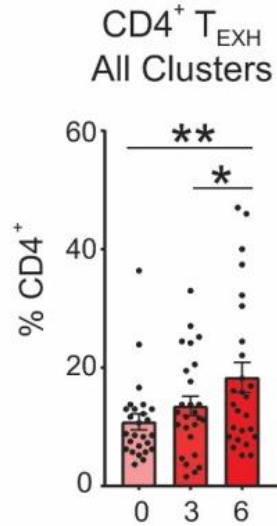
Kidney International
2019, in press



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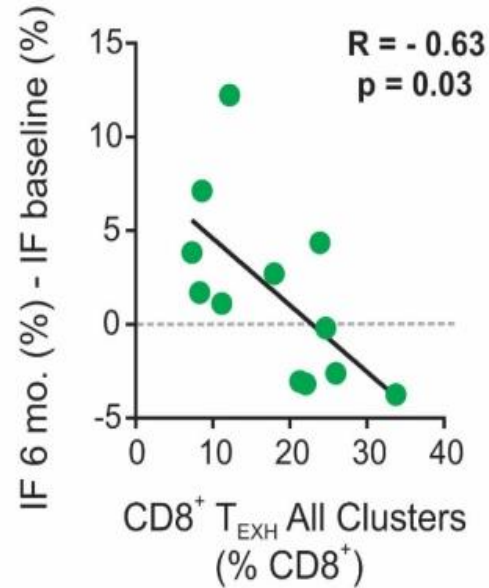
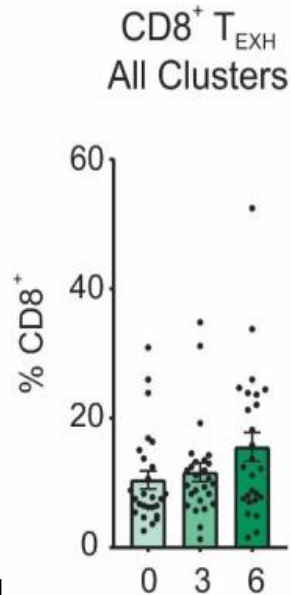
Increased CD4⁺ T_{EXH} cells post-transplant, inverse correlation with ATP production and association with graft fibrosis

A



Kidney International 2019, in press

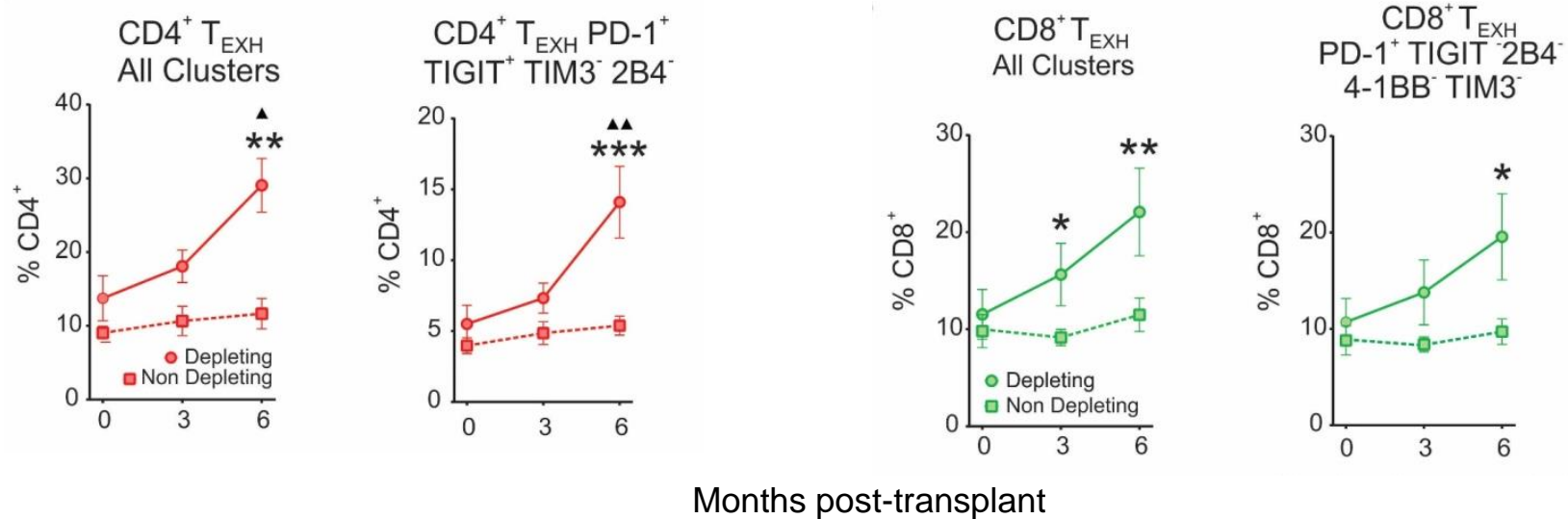
26 CTOT01 subject samples (frozen) studied at 0, 3 and 6 mo post transplant: CD8⁺ T cell subsets



Kidney International
2019, in press

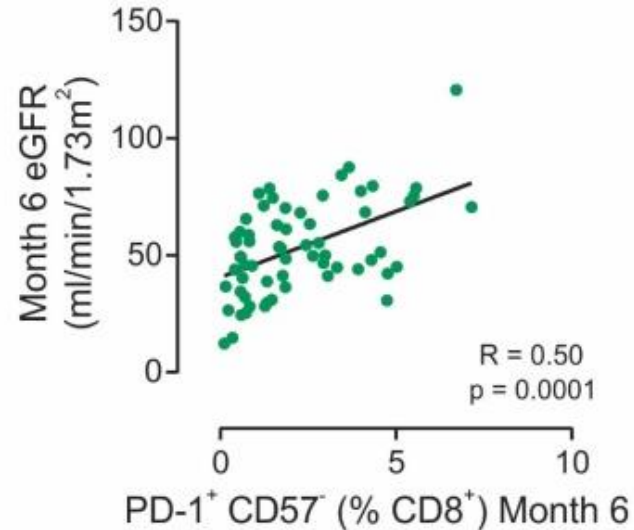
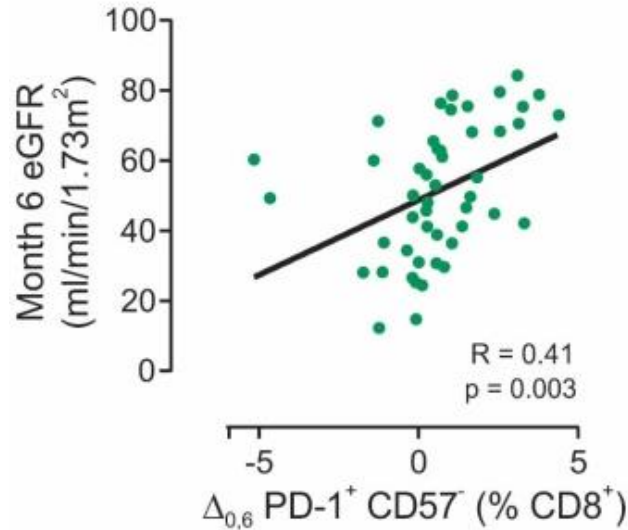
T cell exhaustion phenotype associates with ATG induction

CTOT01 was an observational study and ATG given at discretion of investigator



Kidney International 2019, in press

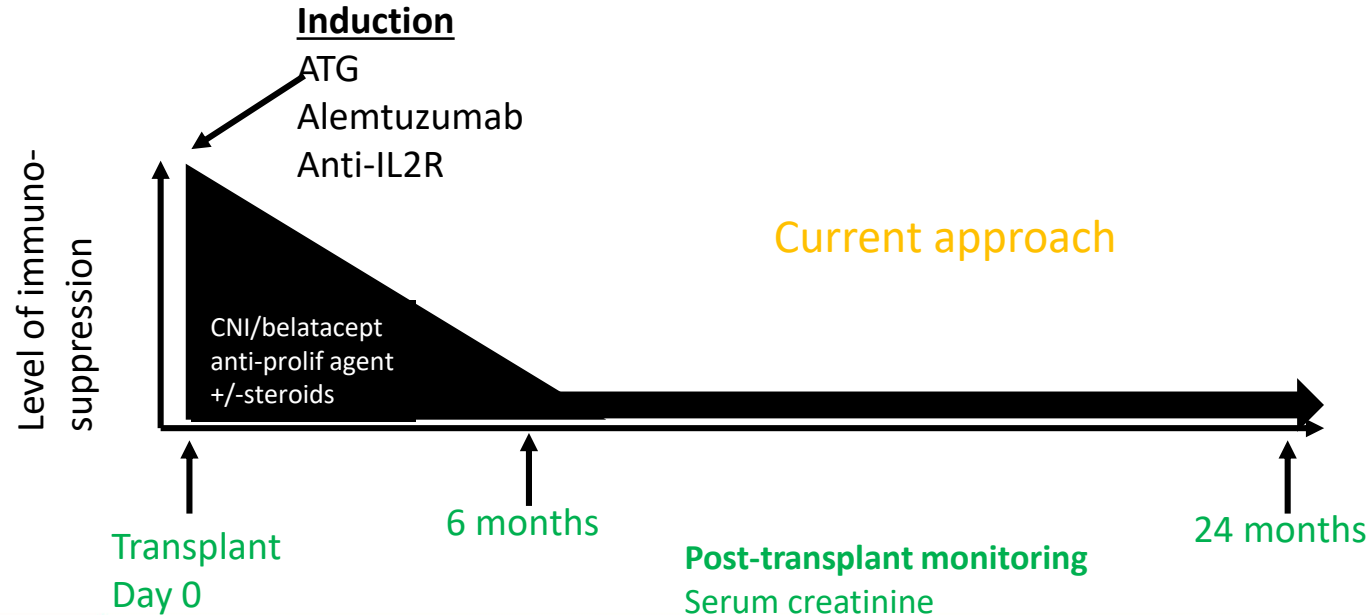
50 CTOT19 subjects: flow cytometry using PD1 and CD57 Texh at 6 mo associates with better eGFR



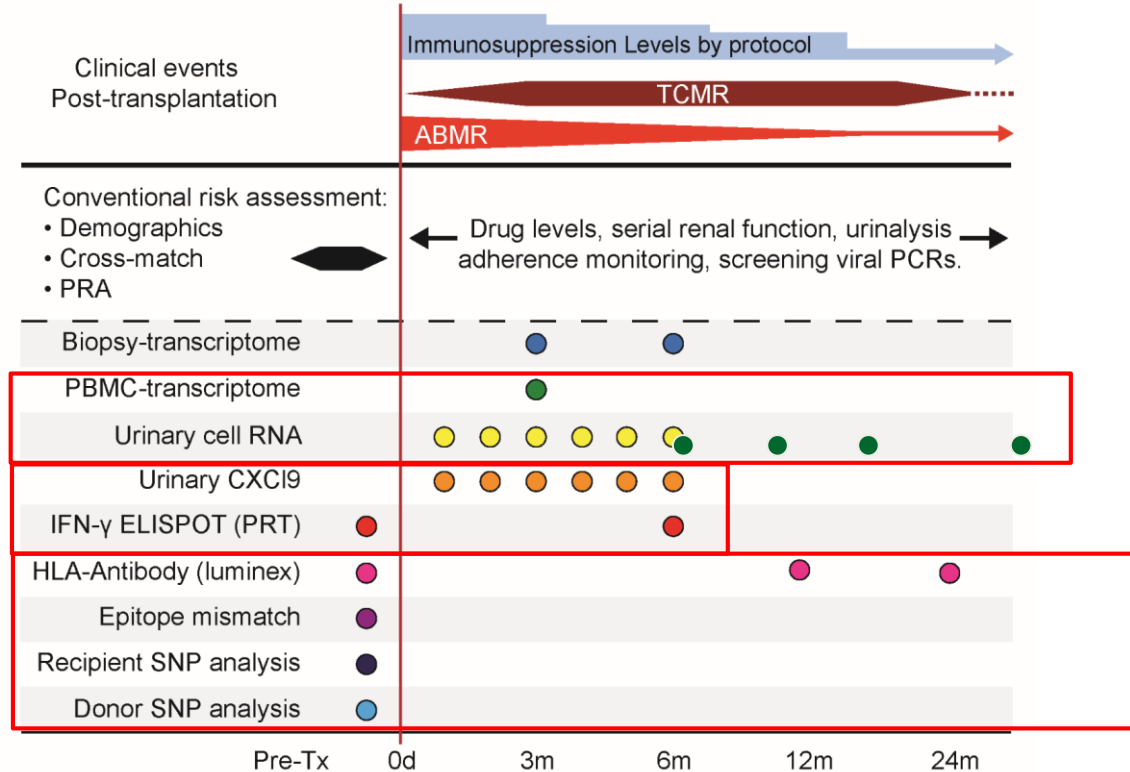
Kidney International 2019, in press

Pre-transplant
Risk assessment
HLA typing
Cross matching
Implantation biopsy
Clinical risk factors

What do we do now?



Precision/Individualized Care



Need to perform controlled trials to assess utility of biomarker-directed changes in therapy

- Incorporate validated biomarkers into clinical trial designs
 - Test whether biomarker based changes in therapy including during drug withdrawal detect subclinical injury and improve outcomes
 - Randomized controlled trials
 - One arm standard of care
 - One arm treat based on biomarker status
 - Is outcome better in the biomarker guided group?

Heeger Consortium CTOT Collaborators

Donald Hricik -- University Hospital Case Medical Center	<i>Cleveland, United States</i>
N Bridges-- National Institutes of Health	<i>Bethesda, United States</i>
Richard Formica -- Yale University	<i>New Haven, United States</i>
R Fairchild, E Poggio -- Cleveland Clinic	<i>Cleveland, United States</i>
K Tinckam -- Toronto General Hospital	<i>Toronto, Canada</i>
D Rush, I Gibson, P Nickerson, C Wiebe -- University of Manitoba	<i>Winnipeg, Canada</i>
D Ikle, PhD, B Armstrong, K Spain-- Rho	<i>Chapel Hill, United States</i>
M Samaniego -- University of Michigan	<i>Ann Arbor, United States</i>
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S Bunnapradist, E Reed, -- University California Los Angeles	<i>Los Angeles, United States</i>
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F Shihab—U Utah	<i>Salt Lake City, United States</i>
J Goebel-Cincinnati Children's	<i>Cincinnati, United States</i>
D Brennan Wash U	<i>St Louis, United States</i>
F Vincenti, UCSF	<i>San Francisco, United States</i>
D Foley, U Wisc	<i>Madison, United States</i>
R Mannon, UAB	
J Bromberg, UMD	

Thank you



Birmingham, United States