

Evaluation of Activation and Homing Markers on Regulatory T cells using the 12-Color BD FACSLytic™ Flow Cytometer

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Introduction

Deeper understanding of regulatory T cell (T_{reg}) biology is critical for the successful development of therapeutic and diagnostic applications. T_{reg} heterogeneity in terms of phenotype, function, and distribution is widely documented, thereby making a more detailed characterization of these cells critical for downstream applications. Several reports have identified distinct T_{reg} immunophenotypic signatures correlating with different biological functions including activation and tissue homing¹⁻⁹. Furthermore, others have combined high parameter mass cytometry approaches with high dimensional data analysis tools to reveal additional heterogeneity within the human T_{reg} compartment^{10,11}. Here, we report the development and utility of a more conventional flow cytometry based assay to explore T_{reg} heterogeneity. We developed an 8-color backbone plus 4-color drop-in modular flow cytometry assay to identify and characterize T_{reg} subsets in greater depth. Specifically, we developed two different T_{reg} characterization drop-in panels to explore two critical facets of T_{reg} biology:

- Homing (CD31, CD183, CD194 and CD196)
- Activation (PI16, CD39, CD147 and HLA-DR)

The 8-color backbone panel enabled clear identification of CD3⁺CD4⁺CD127^{low/neg}CD25⁺FoxP3⁺ T_{reg} cells, and further categorized as CD45RA⁺ (naïve) and CD45RA⁻ (effector) subsets. The inclusion of CD15s and CD161 in the backbone panel enabled identification of functionally suppressive effector¹ and/or pro-inflammatory cytokine-secreting^{2,3} T_{reg} cells within the heterogeneous CD45RA⁻ population, respectively.

The markers in the homing drop-in panel helped us identify recent thymic emigrants within the naïve T_{reg} cell population, and T_{reg} effector-like T_{reg} subsets based on a gating strategy that has been shown previously⁴. Simultaneous assessment of the markers in the activation panel enabled us to study the correlation between them. Our 12-color activation panel recapitulates some of the earlier observations and more importantly expands the knowledge of the interplay of activation markers with the inclusion of CD15s and PI-16.

Overall, our results highlight an interesting interplay between different T_{reg} markers, their putative biological function, and the underlying heterogeneity within the T_{reg} population. Altogether, this modular 12-color flow cytometry assay presents a new approach to enable deeper and more comprehensive analysis of different aspects of T_{reg} biology in a simplified workflow.

Methods

Fresh whole blood from healthy donors was used for peripheral blood mononuclear cell (PBMC) preparation. The PBMCs were surface stained using BD Horizon™ Brilliant Stain Buffer (Cat. No. 659611) with the antibodies listed below. For intracellular (IC) staining of FoxP3, BD Pharmin™ Transcription Factor (TF) Buffer Set (Cat. No. 562574) was used. Samples were analyzed on a 12-color BD FACSLytic™ flow cytometer, and data analysis was performed using BD FACSuite™ software.

8-Color Backbone Panel

| Fluorochrome | Target Antigens |
|--------------|-----------------|
| 1. BV421 | CD25 |
| 2. BV510 | CD15s |
| 3. FITC | CD4 |
| 4. PE | CD161 |
| 5. BB700 | CD127 |
| 6. PE-Cy7 | CD45RA |
| 7. AF647 | FoxP3 |
| 8. APC-H7 | CD3 |

4-Color Homing Drop-In Panel

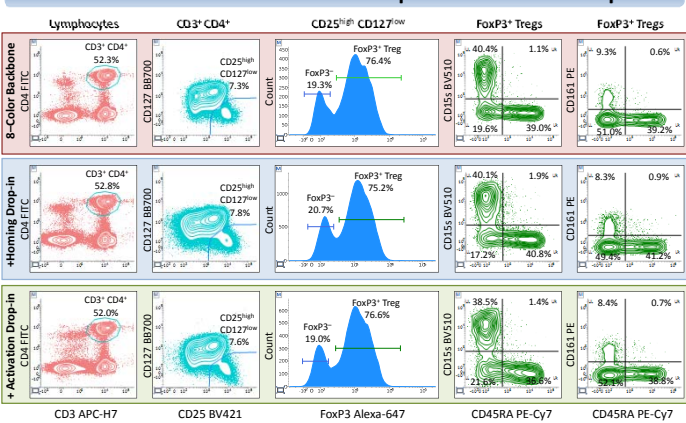
| Fluorochrome | Target Antigens |
|--------------|-----------------|
| 1. BV605 | CD31 |
| 2. BV711 | CD183 |
| 3. BV786 | CD194 |
| 4. APC-R700 | CD196 |

4-Color Activation Drop-In Panel

| Fluorochrome | Target Antigens |
|--------------|-----------------|
| 1. BV605 | PI16 |
| 2. BV711 | CD39 |
| 3. BV786 | CD147 |
| 4. APC-R700 | HLA-DR |

12-color modular flow cytometry panel for T_{reg} identification (8-color backbone panel) and characterization (4-color activation/homing drop-in panels)

Results 1. Resolution of the 8-color plus 4-color modular panel



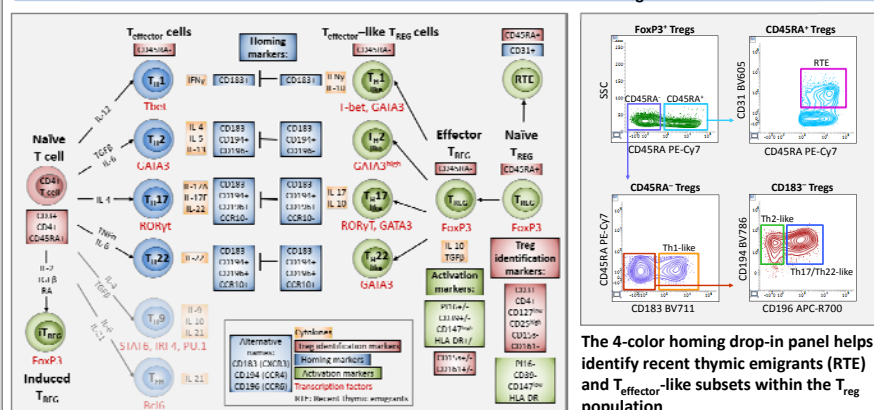
Resolution of the 8-color backbone panel for T_{reg} identification was not impacted by the addition of 4-color T_{reg} homing or activation drop-in panels significantly:

The 8-color backbone panel helps identify T_{reg} cells as CD3⁺CD4⁺CD127^{low/neg}CD25⁺FoxP3⁺ cells, and further characterize them as naïve (CD45RA⁺), effector suppressive (CD45RA⁻CD15s⁺) or pro-inflammatory cytokine secreting (CD45RA⁻CD161⁺) T_{reg} cell subsets^{1,3}. There is minimal impact in resolution and population percentage of major T_{reg} subsets upon addition of 4-color homing or activation drop ins.

References

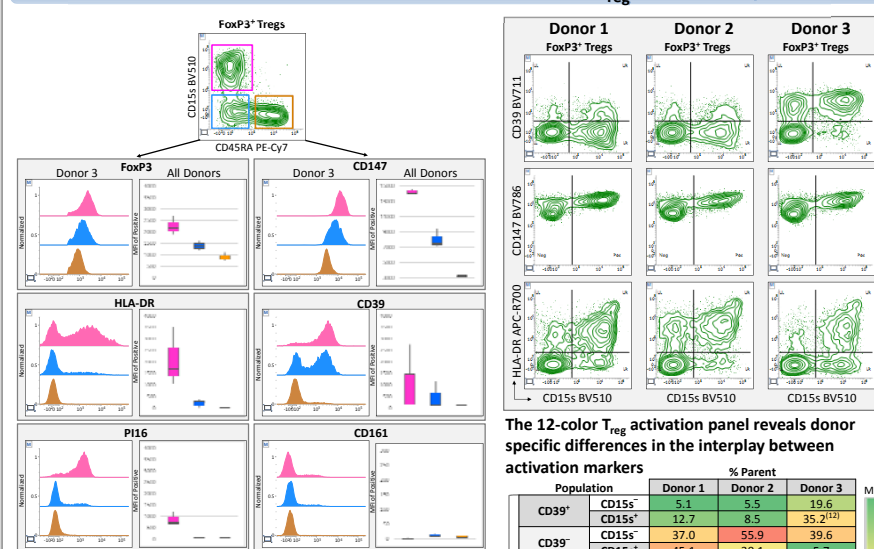
- Warne M, Clayton T, Sapp J, Baghdasari D, Neillaker B, Boonyi D, Gian L, Higgins B, Salazar S, Roberts J, Warner K, Cheever A, Valvano D, Kenton S, Scully S, Amador J, Gnanapavan S, Sanyal S (2015) Identifies highly differentiated and most suppressive CD4⁺ regulatory T cells in humans. *PLoS One* 10(12):e0187225-226.
- Preissner AM, Bending D, Ueno S, Wu D, Nisida K, Weidrumen LK, CD151 defines the subset of FoxP3⁺ cells capable of producing immunomodulatory cytokines. *Blood* 2013 Apr 10; 121(15):2847-2858.
- Ahali S, Mitchell-Petrucci E, Foster GA, Dowling D, Demerutis L, Walter G, Carraro JL, Scotti C, Minion B, Chanu P, Khawari W, Koroloff S, Heck S, Gronowicz B, Traut T, Cooper M, Thimm D, Lehrer H, John S, Lombardi C (2015) Expression characteristics of a subpopulation of human regulatory T cells that produces IL-35 in a Th17-independent manner. *Cell Immunol* 2015; 316:193-204.
- Dubin T, Dubin B, Lapanowicz A, Salazar S, Campbell D. Functionally distinct subsets of human FOXP3⁺ Treg cells that phenotypically mirror effector Th cells. *Blood* 2012 May 16; 119(10):4454-4465.
- Nicolaisen M, Morganelli L, Biffi D, Bristol-Lowery M, Gough J, Gough S, Gough M, Hill D, Milano G, Santoni T, To S, Zola H, Barry SC, Kivimaki P. FHL3 is expressed by a subset of human memory Treg with enhanced migration to CD11c and CD135. *Cell Immunol* 2012 Jun; 269:121-128.
- Salazar T, Banks SL, Lapanowicz A, Landt M, Thayer B, Taitan K, Torngren RM, CD147 (B220/SLAMF7) identifies FOXP3⁺CD4⁺CD127^{low/neg} activated human regulatory T cells. *Blood* 2012 Nov 15; 120(23):4751-4757.
- Bastarache A, Wolf E, Miller DM. HNF1C class I expression identifies functionally distinct human regulatory T cells. *J Immunol* 2006 Apr 15; 176(8):4622-4631.
- Schier M, Santoni M, Schmitt E, Reuter A, Fugère F, Chen M, Saxena S. CD161⁺CD45RA⁻ Treg subsets potentially affect the suppressive activity of the total Treg pool in renal transplant patients. *PLoS One* 2012; 7(1): e34208.
- Bonnafant-Espitalier M, Di Mitri D, Storch J, Djavanmardi A, Giannetti R, Högner S, Costanzo D, Bernardi G, Dotti-Francia M, Rosini PM, Battistoni M, Molinelli O, Laik O. Expression of endonucleolytic CD39 by FoxP3⁺ Treg cells: hypothesis of extracellular ATP and immune suppression. *Blood* 2007 Aug 13; 110(18):3225-32.
- Mason GM, Lewis K, Mitchell R, Ellis R, Al-Khatib J, Freeman M, Mack S, Lombardi G, Traut T. Phenotypic complexity of the human regulatory T cell compartment revealed by mass cytometry. *J Immunol* 2010 Sep 1; 185(9):5057-5077.
- Kornel M, Simons S, Baral S, Geppert T, DeLotto P. Analysis of mass cytometry data with tSNE reveals phenotypic heterogeneity within human Tregs. *J Immunol Methods* 2014; 412:13 Supplement:02-22. [Erratum in 2016].
- Risau A, Baumann J, Caspi A, Mahtani A, Koliter M, Anik PC, Dodge-Rubiani A, Mittrecker WM, Koch-Nolte J, Haeg F, Tolosa E. The expression of CD39 on regulatory T cells is genetically encoded and further upregulated at sites of inflammation. *J Autoimmun* 2015; Apr; 58:12-20. doi: 10.1016/j.jaut.2014.12.007. Epub 2015 Jan 29.

Results 2. Evaluation of the modular 12-color T_{reg} homing panel



The 4-color homing drop-in panel helps identify recent thymic emigrants (RTE) and T_{reg} effector-like subsets within the T_{reg} population

Results 3. Evaluation of the modular 12-color T_{reg} activation panel



Correlation between CD15s expression and other markers: The results indicate a correlation between high levels of CD15s and FoxP3, and activation markers HLA-DR, PI16, CD147 and CD39. No correlation with CD15s was seen for CD161.

The 12-color T_{reg} activation panel reveals donor specific differences in the interplay between activation markers

| Population | % Parent | | | |
|---------------------|--------------------|---------|---------|----------------------|
| | Donor 1 | Donor 2 | Donor 3 | |
| CD39 ⁺ | CD15s ⁺ | 5.1 | 5.5 | 19.6 |
| | CD15s ⁻ | 12.7 | 8.5 | 35.2 ⁽¹²⁾ |
| CD39 ⁻ | CD15s ⁺ | 37.0 | 55.9 | 39.6 |
| | CD15s ⁻ | 45.1 | 30.1 | 5.7 |
| CD147 ⁺ | CD15s ⁺ | 43.2 | 62.3 | 59.9 |
| | CD15s ⁻ | 56.8 | 37.7 | 40.1 |
| HLA-DR ⁺ | CD15s ⁺ | 12.1 | 15.5 | 6.2 |
| | CD15s ⁻ | 47.0 | 32.1 | 26.6 |
| HLA-DR ⁻ | CD15s ⁺ | 31.0 | 46.6 | 53.6 |
| | CD15s ⁻ | 9.9 | 5.8 | 13.7 |

Conclusions

- The 8-color backbone panel reported here enables high resolution identification of the T_{reg} compartment and subpopulations therein.
- Supplementation of the backbone with 4-color drop-in panel(s) for activation or homing markers enables deeper characterization of T_{reg} subsets without any significant impact on the resolution of parent populations.
- Addition of the 4-color homing drop-in panel enabled identification of recent thymic emigrant T_{reg} cells within the naïve T_{reg} population as well as T-effector like subsets within the effector T_{reg} population as reported previously⁴.
- Addition of the 4-color activation drop-in panel enabled identification of a previously reported highly immunosuppressive subpopulation expressing high levels of CD15s, HLA-DR, PI-16, CD147 and CD39 within CD45RA⁻ effector T_{reg} population^{1-3, 5, 9}. Furthermore, our 12-color assay was able to pick up variations in donor-specific counts of T_{reg} subsets.
- Overall, by combining multiple markers in a single tube this 12-color modular flow cytometry assay on BD FACSLytic system enables researchers to study different facets of T_{reg} biology, such as homing, activation, proliferation, maturation, stability in the context of a workflow optimized for ease of use (time and cost).