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Flow Cytometric Analysis of B, NK and T cell Subpopulations in Whole Blood **Samples from Non-Human Primate**

Iohann Boulay, Selly Hau Yee Hung, Vanessa Plouffe, Karine Blouin, Daniela Andreeva, Julie Mercier, Frédéric Bouchard and Karine Dumaresg-Doiron







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Flow Cytometric Analysis of B, NK and T cell Subpopulations in Whole Blood Samples from **Non-Human Primate**

Iohann Boulay, Selly Hau Yee Hung, Vanessa Plouffe, Karine Blouin, Daniela Andreeva, Julie Mercier, Frédéric Bouchard and Karine Dumaresg-Doiron Immunology Department, CiToxLAB North America, Laval, Quebec, Canada

PURPOSE

While comprehensive assessment of the immune system health often involves the evaluation of major lymphocyte cell lineages (B, NK and T cells), the advent of modern flow cytometry now also allows more in-depth analysis of these cell subsets. In support of toxicology studies, two staining panels were developed and qualified to monitor naïve (TN), effector memory (TEM) and central memory (TCM) T cytotoxic and helper cells, as well as B and NK cells, in Non-Human Primate peripheral whole blood.

MATERIAL AND METHODS

Table 1. Material and Methods

	Cynomolgus Monkey Panel	Rhesus Monkey Panel							
Procedure	Whole blood samples stained with the Lyse/Wash procedu								
Anticoagulant	Sodium Heparin Lithium Heparin								
Antibodies	Anti-CD3 PE-Cy7	Anti-CD3 Alexa Fluor 488							
	Anti-CD4 PerCP-Cy5.5	Anti-CD4 APC-eFluor 780							
	Anti-CD8 APC	Anti-CD8 APC							
	Anti-CD16 PE	Anti-CD16 PE							
	Anti-CD28 BV421	Anti-CD28 V450							
	Anti-CD95 BB515	Anti-CD95 PE-Cy7							
	Anti-CD20 BV510	Anti-CD45 BV510							
Viability Stain	Fixable Viability Dye eFluor 780 Annexin V PerCP-Cy								
Acquisition Setting	Acquisition Stop set at 20 000 lymphocytes								
Instrument	BD Biosciences FACSVerse	with integrated flow sensor							

Fluorochrome selection was based on instrument configuration as well as surface marker expression to minimize spillover and maximize resolution. The use of the built-in flow sensor allowed the establishment of absolute cell counts in a simplified single-platform manner, avoiding the use of counting beads with the samples.

Table 2. Lymphocyte Subsets Phenotype

Lymphocyte Subset	Abbreviation	Phenotype
B cells (Cynomolgus monkey only)	В	CD20+ CD3-
NK cells	NK	CD16+ CD3-
NK CD8+ cells	CD8+ NK	CD16+ CD3- CD8+
T cells	Т	CD3+ CD16-
Cytotoxic T cells	Te	CD3+ CD16- CD8+ CD4-
Naïve Cytotoxic T cells	Tc N	CD3+ CD16- CD8+ CD4- CD28+ CD95-
Central Memory Cytotoxic T cells	Te CM	CD3+ CD16- CD8+ CD4- CD28+ CD95+
Effector Memory Cytotoxic T cells	Tc EM	CD3+ CD16- CD8+ CD4- CD28- CD95low/neg
Helper T cells	Th	CD3+ CD16- CD4+ CD8-
Naïve Helper T cells	Th N	CD3+ CD16- CD4+ CD8- CD28+ CD95-
Central Memory Helper T cells	Th CM	CD3+ CD16- CD4+ CD8- CD28+ CD95+
Effector Memory Helper T cells	Th EM	CD3+ CD16- CD4+ CD8- CD28- CD95 ^{low/neg}

Lymphocytes were identified by their size and granularity. Dead cells and doublets were excluded from analysis. When used in the combo, CD45 negative events were also excluded from analysis.



ASSAY QUALIFICATION

Interaction Between Reagents: Because the selected reagents are used in combination, verification that an antibody recognizes the same cells, in the same proportion, whether it is used alone or in combination was performed.

Table 3. Cynomolgus Monkey Panel: Interaction Between Reagents

	1		Proportion in Lymphocytes (%gated in lymphocytes)								
					In	d. 1	.s (/ogateu a	i i j in piloc j te		Ind. 2	Ind. 3
		CD16+	CD4+	CD3+	CD8+	FVD-	CD28+	CD20+		CD95+	
Alone	Mean (n=2)	33.7	29.7	59.6	56.3	98.0	46.8	3.08	16.0	21.5	19.5
Combination	Mean (n=5)	36.6	27.4	58.1	58.7	96.7	45.8	3.39	13.7	20.3	16.4
	% Difference	8.4	-7.7	-2.4	4.3	-1.4	-2.1	9.6	-14.9	-5.7	-17.3
					Abs	olute Cell Co	unt (x10 ⁶ cel	ls/L)			
					Inc	d. 1				Ind. 2	Ind. 3
		CD16+	CD4+	CD3+	CD8+	FVD-	CD28+	CD20+		CD95+	
Alone	Mean (n=2)	1425	962	2335	2241	3509	1918	114.9	644.4	816.3	871.6
Combination	Mean (n=5)	1341	1003	2127	2149	3537	1678	124.5	503.5	766.7	702.3
	% Difference	-6.1	4.3	-9.3	-4.2	0.8	-13.4	8.0	-24.6	-6.3	-21.5

Table 4. Rhesus Monkey Panel: Interaction Between Reagents

	(, Burn (, Burn (, Burn) , Burn)											
		Ind. 1										
	CD16+	CD4+	CD3+	CD8+	Annexin V-	CD28+	CD45+	CD95+				
Mean (n=2)	10.9	43.5	72.6	44.9	98.9	63.2	99.8	73.8				
Mean (n=5)	10.5	44.4	73.3	44.3	97.7	64.1	99.7	76.6				
% Difference	-3.4	2.0	1.0	-1.3	-1.2	1.4	-0.1	3.8				
		Absolute Cell Count (x10 ⁶ cells/L)										
				In	d. 1							
	CD16+	CD4+	CD3+	CD8+	FVD-	CD28+	CD20+	CD95+				
Mean (n=2)	620.7	2615	4126	2685	5591	3791	5548	4155				
Mean (n=5)	532.2	2236	3697	2231	4924	3231	5024	3861				
% Difference	-15.3	-15.6	-11.0	-18.5	-12.7	-15.9	-9.9	-7.3				
	Mean (n=2) Mean (n=5) % Difference Mean (n=2) Mean (n=5) % Difference	CD16+ Mean (n=2) 10.9 Mean (n=5) 10.5 % Difference -3.4 CD16+ Mean (n=2) 620.7 Mean (n=5) 532.2 % Difference -15.3	CD16+ CD4+ Mean (n=2) 10.9 43.5 Mean (n=5) 10.5 44.4 % Difference -3.4 2.0 CD16+ CD16+ CD4+ Mean (n=2) 620.7 2615 Mean (n=5) 532.2 2236 % Difference -15.6 -15.6	CD16+ CD3+ CD3+ Mean (n=2) 10.9 43.5 72.6 Mean (n=5) 10.5 44.4 73.3 % Difference -3.4 2.0 1.0	In CD16+ CD3+ CD3+ Mean (n=2) 10.9 43.5 72.6 44.9 Mean (n=5) 10.5 44.4 73.3 44.3 % Difference -3.4 2.0 1.0 -1.3 Mean (n=5) 620.7 2615 4126 2685 Mean (n=2) 620.7 2615 4126 2685 Mean (n=5) 532.2 2236 3697 2231 Mean (n=7) -18.5 -18.5 -18.5	$\begin{tabular}{ c c c c c c c c c c c c c c c c c c c$	$\begin{tabular}{ c c c c c c c c c c c c c c c c c c c$	$\begin{tabular}{ c c c c c c c c c c c c c c c c c c c$				

Minimal interaction between the different antibodies and the viability dyes were detected. The CD95+ cell counts in the Cynomolgus Monkey panel is slightly underestimated in the combo staining yet, not in all individuals tested.

Precision: To evaluate precision, 5 independent multicolor staining replicates were performed and the closeness of the individual measures was evaluated.

Table 5. Cynomolgus Monkey Panel: Inter-tube Precision Results

	Proportion in Lymphocytes (%gated in lymphocytes)												
	Live	B	NK	CD8+ NK	Т	Te	Te N	Te CM	Te EM	Th	Th N	Th CM	Th EM
Mean (n=5)	96.4	2.14	35.2	25.4	54.7	22.9	10.1	2.35	6.59	25.3	11.4	9.79	0.348
St. Dev.	1.6	0.36	0.7	0.6	1.4	0.9	0.8	0.09	0.56	0.6	0.9	0.30	0.058
% CV	1.6	17.0	2.0	2.4	2.5	3.8	8.1	3.9	8.6	2.3	8.2	3.1	16.7
						Absolute C	ell Count (x	10 ⁶ cells/L)					
	Live	B	NK	CD8+NK	Т	Te	Te N	Te CM	Tc EM	Th	Th N	Th CM	Th EM
Mean (n=5)	3583	79.85	1310	944.5	2034	849.3	373.7	87.33	244.8	942.4	424.4	364.0	12.90
St. Dev.	172	16.97	71	57.0	91	36.9	25.1	5.78	15.8	49.6	32.0	20.4	2.20
% CV	4.8	21.2	5.4	6.0	4.5	4.3	6.7	6.6	6.5	5.3	7.5	5.6	16.9

Table 6. Rhesus Monkey Panel: Inter-tube Precision Results

	Proportion in Lymphocytes (%gated in lymphocytes)												
	Live	CD45+	NK	CD8+ NK	Т	Te	Tc N	Te CM	Tc EM	Th	Th N	Th CM	Th EM
Mean (n=5)	96.8	99.6	8.97	8.84	73.5	26.7	13.1	4.93	8.55	41.7	34.3	7.13	0.169
St. Dev.	0.5	0.1	0.41	0.40	0.5	0.2	0.3	0.14	0.19	0.4	0.5	0.18	0.016
% CV	0.5	0.1	4.5	4.5	0.7	0.6	2.0	2.9	2.2	1.0	1.4	2.5	9.5
	Absolute Cell Count (x10 ⁶ cells/L)												
	Live	B	NK	CD8+ NK	Т	Te	Tc N	Te CM	Te EM	Th	Th N	Th CM	Th EM
Mean (n=5)	5216	4833	434.8	427.9	3564	1297	635.4	238.8	414.6	2023	1666	354.7	8.20
St. Dev.	401	223	10.3	10.8	178	57.6	28.9	12.0	22.5	108	94	32.9	0.80
% CV	7.7	4.6	2.4	2.5	5.0	4.4	4.6	5.0	5.4	5.3	5.6	9.3	9.8

The method presented excellent precision except for some cell populations of small size. The variation between the measurements for B cells and Th EM cells were slightly higher in the Cynomolgus Monkey panel, yet acceptable.

Sample Stability: Sample stability was assessed by subjecting whole blood samples to various storage time period. Upon collection, whole blood samples were stored at room temperature with orbital shaking. Upon staining procedure, stained samples were stored at room temperature and protected from light. Acceptable sample stability was observed as follow.

Condition	Cynomolgous Monkey Panel (n=3)	Rhesus Monkey Panel (n=3)
Upon Blood Collection	Up to 1 hour	Up to 24 hours
Upon Staining Procedure	Up to 3 hours	Up to 1 hour

Upon storage, the recovery of the CD4+ TEM cells was relatively high compared to the fresh sample, yet considered acceptable due to its small population size.

REFERENCES

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RESULTS

To further characterize the performance of the assay, whole blood samples were obtained from immunocompromised (Thymoglobulin (ATG)-treated) Cynomolgus monkeys or immunocompromised and myeloablated Rhesus monkeys. The various cell populations were monitored to assess the extent of immunosuppression and recovery profiles.

The Immunosuppresive Model in Cynomolgus Monkey: While a single ATG administration did not have a profound effect on the various cell populations, T cell populations, especially the Th EM and Tc EM populations, seemed to be most affected by the ATG treatment.

All T cell populations were able to recover to baseline population size during the course of the study.

The Immunosuppresive and **Mveloablative Model in Rhesus** Monkey: Extensive decrease was observed in the size of the various

populations after myeloablation. The dual treatment of the myeloablation and immunosuppression further exacerbated the decrease. Only T cells were able to recover fully from the myeloablative treatment even after an observation period of 30 days. The recovery observed in T cell population was mainly driven by the over-recovery of Tc cells, more specifically Tc EM cells. Yet, it is also interesting to note the important recovery of the central memory T cells, in contrast to the naïve T cells compartment.

CONCLUSION

Overall, the flow cytometry methodology described herein was found to be suitable for the exploration of the population kinetics of various T cell subsets, as well as NK and B cells. The current panels allow characterization of the major contributors in the depletion/recovery phase of the lymphocyte population in more depth. The methodology is a single-platform without the need of counting beads. Furthermore, it possesses potential precision improvements over other single-platform methods requiring the spiking of counting beads and two-platform methods requiring a second analysis of the sample to obtain absolute count measurements.

