Program Number: 236

Human B-cell development is a regulated process characterized by the ordered differential expression of numerous cell surface and intra-cytoplasmic antigens, immunoglobulin gene rearrangements, and ultimately class switching. This process originates from self-renewing hematopoletic stem cells in the fetal liver and postnatal bone marrow and ends with the ultimate export of mature naive B-cells from the marrow into the peripheral blood circulation.

B-cell precursors have been extensively studied in mouse and human systems and there is general agreement that CD34 and CD36 help identify early B-cell progenitors. However, the relative order of CD19 and CD10 up-regulation is not well established, with numerous conflicting published reports.

Recently, a new type of modeling program has been developed that allows a detailed objective analysis of the relative order of antigen up-and down-regulation for highdimensional cytometry data. In this study, Probability State Modeling was used to determina the relative order of CD38, CD19 and CD10 up-regulation for a number of uninvolved bore marrow specimens. It also provided detailed correlated information on other cytometric features such as forward angle light scatter (PSC), bids scatter (SC), CD2, CD9, and CD41.

Introduction

Early development of human B-cells occurs in distinct steps or stages in the bone marrow (BM). Many of here stages are defined by changes in the varrangement status of immunojacobilin (lg) heavy (H) and lght chains (L), the expression of transcription fastors, well as specific phenotypic changes on the cell staffee. Although much is toxed of the surfaces and cytoplasmic proteins that appear and disappear any approximation of these cells develop remain unknow. Also, the literature contains a number of conflicting reports on the progression of many of these phenotypic changes. The exact timing of these cellular changes are important to document since may balac science suddles are based on purification methods that use specific marker protein combinations. Also, many these normal stages of differentiations.

This study examines very early tymphold and B-cell phenotypic changes by the technique of Probability State Modeling (PSM). PSM uses an retaively objective and accurate modeling approach that orders events along a progression axis. Once ordered, the correlated changes of other cell features can also be studied. The cellular features examined are CD34, CD38, CD19, CD19, CD45, CD81, forward angle scatter (FS), and alde scatter (FS).



In ten of the thinteen samples, CD10 and CD13 apparently up-regulated nearly together (black arrows); whereas, in three samples, CD10 seemed up-regulates alightly before CD19 (black open clicities). Obstant partitions to bearvations were that PSC was highest in the PI stage. CD34, CD45, and SSC stepped down through the HSC, PI, CLP, and IS stages for many of the files.

Probability State Modeling Analysis of CD38, CD10, and CD19 Up-regulation in Early Human B-Cell Development

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3

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 CD10 CD19 CD19 Positions

 File: CD19 CD10 DIF
 CD100 CD10 DIF
 CD100 CD100 DIF
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B_BM00010	69.65	64.55	5.11	CD10,19,20,34,38,45,K,L,FS,SC (11,528/632,595)
B_BM00011	64.38	58.69	5.69	CD10,19,20,34,38,45,K,L,FS,SC (14,590/742,320)
B_BM00012	\$3.60	82.59	1.01	CD10,19,20,34,38,45,K,L,FS,SC (6,787/522,838)
B_BM00013	26.79	26.20	0.59	CD9,10,19,20,34,38,45,FS,SC (2,230/171,218)
B_BM00014	53.04	53.04	0.00	CD9, 10, 19, 20, 34, 38, 45, FS, SC (5, 526/359, 633)
B_BM00015	76.34	77.01	-0.67	CD9,10,19,20,34,38,45,FS,SC (14,914/321,185)
B_BM00016	83.97	86.53	-2.56	CD9,10,19,20,34,38,45,FS,SC (6,069/290,688)
B_BM00017	71,49	56.67	14.82	CD9,10,19,20,34,38,45,FS,SC (16,347/371,037)
B_BM00018	27.06	25.78	1.28	CD9,10,19,20,34,38,45,FS,SC (7,269/415,403)
H ₀ : Diff = 0; t=0.48; since t _{0.05[2],12} = 2.18, H ₀ could not be rejected. Positive Sign Test for Diff; P(X>=8), n=13 is >0.26, no proclivity for CD10				

up-regulating before CD19 can be deduced.

The above tails unmanifest by Arabien similary of CDD and CDD sequelations for this above, This units as its Arguments creates, Ter and the above tails unmanifest by Arabien similary of CDD and CDD sequelations for this above. The units as its Arguments creates, Ter and the above the sequelation of CDD and CDD sequelations that above tails are able to the additional and and the additional additional and the additional and the additional and the additional and the additional additional additional additional additional additional additional and the additional additional and the additional additionad addited additional additional additional additionad addit



Phobability Rate Modeling is a cold that scientification are to lowering a single isomer nation (hogh) to deduce a neurith more complies progression (bottom). This nation relation in this scample is the howering that neuritary isolated by forators. Charling in the An Utari bas single nation is it possible to uncreat a very complex progression involving many learness (bottom). No to ely can be system determine a deter but it can produce a single graph that shows the order and percentagion of all the intermediation stage threatmee Overlay, middle effect and a the dimensional contextual surface plots that appropriately blend colors from defined stages (bottom right). For more details see poster PR, program number 121



The above Hi-Lo progression plots show the modulation of CD20, CD3, and CD81 for a number of Satmode Files. The low-boundary in these plot was set to a 0.5 fraction, which is the median of all the events in each progression state along the axis. The high-boundary was set to 0.95 to show the upper 95% limit of the data.

When hoch CD10 and CD12 are expressed, CD20 is expressed on many of the events (fire 3 row). Sense files showed relatively high CD0 expression any bit het HSC sage (free), When CD15 is expressed, monty of the events express high levels of CD2, but here is a significant fraction that don't express CD2. For the one file that had CDB1 (last row), it seems to be up-regulated slightly when CD10 and CD19 are upregulated.



Probability State Modeling (PBI) analyses serve parformation 11 bigh-dimensional literatoria filts from clinical samples obtained by literative of Wanaphone 10 portune Liboratory. Doily wave progenitors and a sample focal serve satisfactor for analysis (CDA), gained on COMSIS (DepArtil) in his study. The only information provides to the model was that COM, cont COM sup-registrate, and progenitor argongenism. The analysis wave single contraction of the contract server that the comparison of the comparison as a divide information provides to the match (CDA) and CDM superimentation provides to the progenitor progenitor. The only information provides to the model was that COM supergravity and without a verse that the verscoles - in the comparison track service progenitor state (CL), gravy) and and when CDM supergravity. The only information gain clinicity (Comparison and the CDM supergravity. The third progenitor states (CL), gravy) and and when CDM supergravity. The only information gain clinicity (Comparison and the CDM supergravity. The third progenitor states (CL), gravy) and and when CDM supergravity. The only information gain clinicity (Comparison and the (CDM supergravity. The Comparison states (CL) on the (CL) supergravity. The comparison states (CL) on the (CL) supergravity and the comparison state states (CL) and the CDM supergravity. The comparison state (CL) and the CDM supergravity and the CDM supergravity. The comparison state (CL) and the CDM supergravity and the CDM supergravity. The comparison state (CL) and the CDM supergravity and the comparison states and the comparison states and the comparison states (CL) on the CDM supergravity. The comparison state states and the comparison stat

Summary

8

The results of these analyses show that CD38 is up-regulated well before CD19 and CD10. There does not seem to be statistically significant proclivity of cells to express CD10 before CD19, suggesting that either the CLP phenotype of CD34, CD38, CD19, CD19- may be too small to measure for many bone marrow specimens or that it does not exist as a real intermediate lymphoid progenitor stage. A more consistent conclusion from this data is that CD19 and CD19 are commonly co-expressed.

Other observations from this study are that FSC is very high once CD38 is expressed and then drops after CD10 is expressed. CD34, CD45, and SSC commonly drop in intensity in a step-wise manner until the B1 or PrOB stage. After CD10 and CD19 are expressed; CD20, CD9, and CD81 are up-regulated for many events.

After CD19 was up-regulated, many events showed variable degrees of positivity for CD20. Some samples showed high CD9 expression in the HSC stage. In P1 and CLP stages, CD9 expression dropped to intermediate levels. Most events showed positive CD9 expression after CD19 was up-regulated, but a significant number of events remained negative.