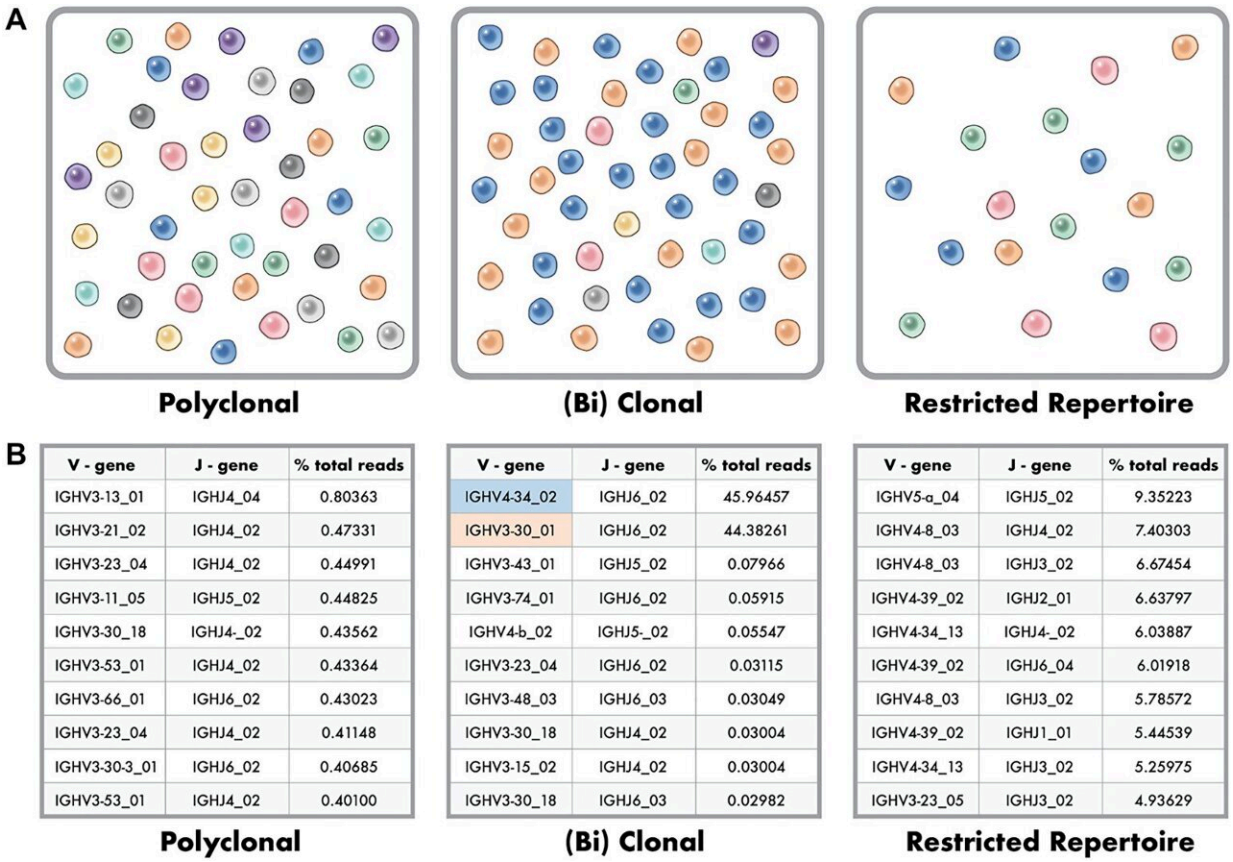
Automated, accurate reporting for NGS-based clonality testing

May 16 2023



V - gene	J - gene	% total reads
IGHV3-13_01	IGHJ4_04	0.80363
IGHV3-21_02	IGHJ4_02	0.47331
IGHV3-23_04	IGHJ4_02	0.44991
IGHV3-11_05	IGHJ5_02	0.44825
IGHV3-30_18	IGHJ4-_02	0.43562
IGHV3-53_01	IGHJ4_02	0.43364
IGHV3-66_01	IGHJ6_02	0.43023
IGHV3-23_04	IGHJ4_02	0.41148
IGHV3-30-3_01	IGHJ6_02	0.40685
IGHV3-53_01	IGHJ4_02	0.40100

Polyclonal

V - gene	J - gene	% total reads
IGHV4-34_02	IGHJ6_02	45.96457
IGHV3-30_01	IGHJ6_02	44.38261
IGHV3-43_01	IGHJ5_02	0.07966
IGHV3-74_01	IGHJ6_02	0.05915
IGHV4-b_02	IGHJ5-_02	0.05547
IGHV3-23_04	IGHJ6_02	0.03115
IGHV3-48_03	IGHJ6_03	0.03049
IGHV3-30_18	IGHJ4_02	0.03004
IGHV3-15_02	IGHJ4_02	0.03004
IGHV3-30_18	IGHJ6_03	0.02982

(Bi) Clonal

V - gene	J - gene	% total reads
IGHV5-a_04	IGHJ5_02	9.35223
IGHV4-8_03	IGHJ4_02	7.40303
IGHV4-8_03	IGHJ3_02	6.67454
IGHV4-39_02	IGHJ2_01	6.63797
IGHV4-34_13	IGHJ4-_02	6.03887
IGHV4-39_02	IGHJ6_04	6.01918
IGHV4-8_03	IGHJ3_02	5.78572
IGHV4-39_02	IGHJ1_01	5.44539
IGHV4-34_13	IGHJ3_02	5.25975
IGHV3-23_05	IGHJ3_02	4.93629

Restricted Repertoire

Polyclonal, Clonal and Restricted Repertoire Phenotypes in Clonality Testing. Credit: *Oncotarget* (2023). DOI: 10.18632/oncotarget.28429

A new research paper titled "Development and implementation of an automated and highly accurate reporting process for NGS-based

clonality testing" has been published in *Oncotarget*.

B and T cells undergo random recombination of the VH/DH/JH portions of the immunoglobulin loci (B cell) and T-cell receptors before becoming functional cells. When one V-J rearrangement is over-represented in a population of B or T cells indicating an origin from a single cell, this indicates a clonal process. Clonality aids in the diagnosis and monitoring of lymphoproliferative disorders and evaluation of disease recurrence.

In a new study, researchers Sean T. Glenn, Phillip M. Galbo Jr., Jesse D. Luce, Kiersten Marie Miles, Prashant K. Singh, Manuel J. Glynias, and Carl Morrison from Roswell Park Comprehensive Cancer Center aimed to develop objective criteria that could be automated to classify B and T cell clonality results as positive (clonal), no evidence of clonality, or invalid (failed).

"Using clinical samples with 'gold standard' clonality data obtained using PCR/CE testing, we ran NGS-based amplicon clonality assays and developed our own model for clonality reporting," the researchers explain.

To assess the performance of their model, the researchers analyzed the NGS results across other published models. Their model for clonality calling using NGS-based technology increases the assay's sensitivity, more accurately detecting clonality. In addition, they built a computational pipeline to use their model to objectively call clonality in an automated fashion.

"Collectively, the results outlined below will have a direct clinical impact by expediting the review and sign-out process for concise clonality reporting," summarize the researchers.

More information: Sean T. Glenn et al, Development and implementation of an automated and highly accurate reporting process for NGS-based clonality testing, *Oncotarget* (2023). DOI: 10.18632/oncotarget.28429

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