
RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia.

Journal: Nat Genet

Publication Year: 2014

Authors: Elli Papaemmanuil, Inmaculada Rapado, Yilong Li, Nicola E Potter, David C Wedge, Jose Tubio, Ludmil B Alexandrov, Peter Van Loo, Susanna L Cooke, John Marshall, Inigo Martincorena, Jonathan Hinton, Gunes Gundem, Frederik W van Delft, Serena Nik-Zainal, David R Jones, Manasa Ramakrishna, Ian Tittley, Lucy Stebbings, Catherine Leroy, Andrew Menzies, John Gamble, Ben Robinson, Laura Mudie, Keiran Raine, Sarah O'Meara, Jon W Teague, Adam P Butler, Giovanni Cazzaniga, Andrea Biondi, Jan Zuna, Helena Kempinski, Markus Muschen, Anthony M Ford, Michael R Stratton, Mel Greaves, Peter J Campbell

PubMed link: 24413735

Funding Grants: Dual targeting of tyrosine kinase and BCL6 signaling for leukemia stem cell eradication

Public Summary:

The ETV6-RUNX1 fusion gene, found in 25% of childhood acute lymphoblastic leukemia (ALL) cases, is acquired in utero but requires additional somatic mutations for overt leukemia. We used exome and low-coverage whole-genome sequencing to characterize secondary events associated with leukemic transformation. RAG-mediated deletions emerge as the dominant mutational process, characterized by recombination signal sequence motifs near breakpoints, incorporation of non-templated sequence at junctions, approximately 30-fold enrichment at promoters and enhancers of genes actively transcribed in B cell development and an unexpectedly high ratio of recurrent to non-recurrent structural variants. Single-cell tracking shows that this mechanism is active throughout leukemic evolution, with evidence of localized clustering and reiterated deletions. Integration of data on point mutations and rearrangements identifies ATF7IP and MGA as two new tumor-suppressor genes in ALL. Thus, a remarkably parsimonious mutational process transforms ETV6-RUNX1-positive lymphoblasts, targeting the promoters, enhancers and first exons of genes that normally regulate B cell differentiation.

Scientific Abstract:

The ETV6-RUNX1 fusion gene, found in 25% of childhood acute lymphoblastic leukemia (ALL) cases, is acquired in utero but requires additional somatic mutations for overt leukemia. We used exome and low-coverage whole-genome sequencing to characterize secondary events associated with leukemic transformation. RAG-mediated deletions emerge as the dominant mutational process, characterized by recombination signal sequence motifs near breakpoints, incorporation of non-templated sequence at junctions, approximately 30-fold enrichment at promoters and enhancers of genes actively transcribed in B cell development and an unexpectedly high ratio of recurrent to non-recurrent structural variants. Single-cell tracking shows that this mechanism is active throughout leukemic evolution, with evidence of localized clustering and reiterated deletions. Integration of data on point mutations and rearrangements identifies ATF7IP and MGA as two new tumor-suppressor genes in ALL. Thus, a remarkably parsimonious mutational process transforms ETV6-RUNX1-positive lymphoblasts, targeting the promoters, enhancers and first exons of genes that normally regulate B cell differentiation.

Source URL: <https://www.cirm.ca.gov/about-cirm/publications/rag-mediated-recombination-predominant-driver-oncogenic-rearrangement-etv6>