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Leukemia translocations

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Chromosomal translocations involving the mixed-lineage leukemia gene (*MLL/ALL1*) define a subset of human acute leukemias with poor prognosis. In the Advanced Online Publication of Nature Genetics, Armstrong *et al.* describe a gene-expression profile analysis of leukemic cells with *MLL* translocations (DOI:10.1038/ng765). They compared the expression profiles of over 12,000 genes in B-precursor acute lymphoblastic leukemia (ALL) cells from patients with or without a rearranged *MLL* gene. The MLL samples had a distinct profile, with about 1,000 genes underexpressed and 200 highly expressed. The gene expression pattern was characteristic of maturational arrest at an early lymphoid progenitor stage; several *HOX* genes were highly expressed in MLL compared to other ALL samples. Armstrong *et al.* used principal component analysis (PCA) to cluster the MLL, ALL (acute lymphoblastic leukemia) and AML (acute myelogenous leukemia) expression profiles. They found that MLL profiles were distinct from ALL and AML samples, and defined a set of 100 genes that could distinguish MLL from the other leukemic classes. Such studies may lead to the development of translocation-specific therapies for MLL patients.

References

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