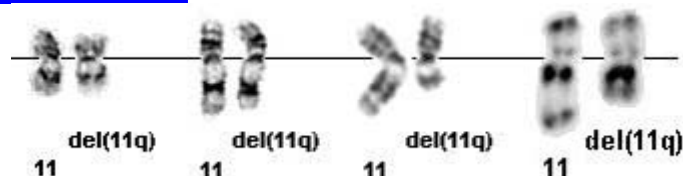


del(11q) in non-Hodgkin's lymphoma (NHL)

Identity



del(11q) G- banding (the 3 left partial karyotypes) - Courtesy Diane H. Norback, Eric B. Johnson, Sara Morrison-Delap Cytogenetics at the Waisman Center; R-banding (right) - Editor

Clinics and Pathology

- Disease** the overall incidence in NHL is 4-5%, the highest incidence having been reported in [mantle cell lymphoma](#), where up to 70% of the cases studied by FISH may harbour a cryptic deletion in association with the classical [t\(11;14\)](#) translocation; FISH detects an approximate 10% incidence of 11q deletion among other histologic subsets of B-NHL; among [diffuse large B-cell lymphoma](#) the 11q- chromosome shows a preferential association with the immunoblastic variant; sensitive molecular cytogenetic methods may show 50-70% of [T-cell prolymphocytic leukemia](#) to carry an 11q deletion involving the ATM gene
- Prognosis** a possible association between 11q-/ATM- and poor prognosis in B-cell NHL was reported

Cytogenetics

Cytogenetics the chromosome 11q deletion occurring in NHL most frequently affects Morphological the q22-23 bands; the 11q- anomaly occurs as a secondary change in the majority of cases

Cytogenetics because the size of the deleted segment may be beyond the resolution Molecular power of conventional banding analysis, many cases can only be detected by interphase FISH or other genetic methods using probes targeting the 11q22.3-q23.1 region

Genes involved and Proteins

Note the region of minimal deletion was narrowed down to a 2-3 Mb pair segment where the ataxia teleangiectasia ([ATM](#)) gene is located; sequencing studies showed mutation in the remaining ATM allele in a significant fraction of cases

External links

Other database [del\(11q\) in non-Hodgkin's lymphoma \(NHL\)](#) [Mitelman database \(CGAP - NCBI\)](#)

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