

Classical Hodgkin's lymphoma shows epigenetic features of abortive plasma cell differentiation.

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Source

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Abstract

BACKGROUND: Epigenetic changes are involved in the extinction of the B-cell gene expression program of classical Hodgkin's lymphoma. However, little is known regarding epigenetic similarities between cells of classical Hodgkin's lymphoma and plasma cell myeloma, both of which share extinction of the gene expression program of mature B cells.

DESIGN AND METHODS: Global histone H3 acetylation patterns were determined in cell lines derived from classical Hodgkin's lymphoma, plasma cell myeloma and B-cell lymphoma by chromatin immunoprecipitation and subsequent hybridization onto promoter tiling arrays. H3K27 trimethylation was analyzed by chromatin immunoprecipitation and real-time DNA polymerase chain reaction for selected genes. Epigenetic modifications were compared to gene expression data.

RESULTS: Characteristic B-cell genes were hypoacetylated in classical Hodgkin's lymphoma and plasma cell myeloma cell lines as demonstrated by comparison of their histone H3 acetylation patterns to those of B-cell lines. However, the number of genes jointly hyperacetylated and expressed in classical Hodgkin' lymphoma and plasma cell myeloma cell lines, such as IRF4/MUM1 and RYBP, is limited. Moreover, H3K27 trimethylation for selected characteristic B-cell genes revealed that this additional epigenetic silencing is much more prevalent in classical Hodgkin's lymphoma than in plasma cell myeloma.

CONCLUSIONS: Our epigenetic data support the view that classical Hodgkin's lymphoma is characterized by abortive plasma cell differentiation with a down-regulation of characteristic B-cell genes but without activation of most genes typical of plasma cells.

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