Oncogenes MYC, MAX, and MNT upregulate branched chain amino acid metabolism in peripheral T cell lymphoma

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Peripheral T cell lymphoma (PTCL) is an aggressive non-Hodgkin lymphoma arising in T lymphocytes. Overexpression of the oncogenes *MYC*, *MAX*, and *MNT* is implicated in non-Hodgkin lymphomas where these genes control growth and proliferation by regulating the expression of metabolic genes. The mitochondrial branched-chain aminotransferase (*BCAT2*) and ketoacid dehydrogenase (*BCKDHA*, and *DBT*) genes encode for enzymes that breakdown branched-chain amino acids (BCAAs). BCAAs are a source of energy and metabolites for lymphoma cells. We aimed to investigate whether the expression of *MYC*, *MAX* and *MNT* correlate with that of *BCAT2*, *BCKDHA*, and *DBT* and to understand whether overexpression of *BCAT2, BCKDHA* and *DBT* in PTCL patients correlates with lower cancer survival.
The genomics analysis and visualization platform (R2) was used to access information about the overall survival and gene expression of 193 specimens from newly diagnosed PTCL patients. Kaplan Meier survival curves were downloaded from the platform along with the 2log expression values of each gene of interest. Pearson's correlation coefficient (R) was used to measure the strength and direction of the relationship between the oncogenes and the metabolic genes.

Results indicated a positive and statistically significant correlation between *BCAT2* and *MYC, BCKDHA* and *MYC/MAX*, and *DBT* and *MAX/MNT.* Overexpression of *BCAT2, BCKDHA,* and *DBT* correlated with significantly lower PTCL survival. The findings suggested that the oncogenes upregulate the BCAA metabolic genes in PTCL. While the molecular mechanism of these correlations needs to be addressed experimentally, the findings may serve as a basis for future pharmacotherapy for PTCL patients.