Prognostic value of DNA Damage Inducible Transcript 4 gene (DDIT4) in various Cancers: In silico evaluation

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BACKGROUND: *DDIT4* gene encodes a protein whose main action is to inhibit mTOR. We have previously described that the expression of this gene is an independent prognosis factor for triple negative breast cancer resistant to neoadjuvante chemotherapy. **HYPOTHESIS:** *DDIT4* gene has influence in the outcome of several malignant tumors. **METHODS:** The influence of *DDIT4* expression in the outcome of patients of several cancer types was evaluated in terms of disease free survival (DFS), progression free survival (PFS) or overall survival (OS). We performed an *in silico* study of public datasets obtained and analyzed in the KM Plotter platform. Also, two datasets were downloaded from the TCGA project. Meta-analysis was performed in SurvExpress datasets using Review Manager 5.3. The structural alterations in DDIT4 were explored in several genomic projects using cBioPortal platform. **RESULTS:** Meta-analysis revealed that high DDIT4 level was significantly associated with a worse prognosis in acute myeloid leukemia (HR=2.06, CI95%: 1.56-2.73); breast cancer (HR=1.31, CI95%: 1.11-1.54), being a prognosis factor in Luminal A, Luminal B and basal type; glioblastoma multiforme (HR=1.23, CI95%:1.09-1.39); lung cancer and colon cancer with a higher risk of recurrence as well as a higher risk of death. Also, DDIT4 expression was associated with the molecular risk in AML patients. In contrast, DDIT4 didn't show association with the outcome in ovarian cancer, prostate cancer and liver cancer. Furthermore, *DDIT4* had low structural alterations rates (5.1%) ; however, in breast tumors xenografts, gene amplification occurred in 17.4%. In summary, DDIT4 might be a potential candidate for the development of targeted therapy in several cancer types.