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PYURF and ZED9 Have a Prominent Role in Association with Molecular Pathways in Bortezomib in Myeloma Cells in Acute Myeloid Leukemia

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Abstract : Acute myeloid leukemia (AML) is the most typically diagnosed leukemia. In older adults, AML imposes a dismal outcome. AML originates with a dominant mutation, then adds collaborative, transformative mutations leading to myeloid transformation and clinical/biological heterogeneity. Several chemotherapeutic drugs are used for this cancer. These drugs are naturally associated with several side effects, and finding a more accurate molecular mechanism of these drugs can have a significant impact on the selection and better candidate of drugs for treatment. In this study, we evaluated bortezomibin myeloma cells using bioinformatics analysis and evaluation of RNA-Seq data. Then investigated the molecular pathways proteins- proteins interactions associated with this chemotherapy drug. A total of 658upregulated genes and 548 downregulated genes were sorted.AUF1 (hnRNP D0) binds and destabilizes mRNA, degradation of GLI2 by the proteasome, the role of GTSE1 in G2/M progression after G2 checkpoint, TCF dependent signaling in response to WNT demonstrated in upregulated genes. Besides insulin resistance, AKT phosphorylates targets in the nucleus, cytosine methylation, Longevity regulating pathway, and Signal Transduction of S1P Receptor were related to low expression genes. With respect to this results, HIST2H2AA3, RP11-96O20.4, ZED9, PRDX1, and DOK2, according to node degrees and betweenness elements candidates from upregulated genes. in the opposite side, PYURF, NRSN1, FGF23, UPK3BL, and STAG3 were a prominent role in downregulated genes. Sum up, Using in silico analysis in the present study, we conducted a precise study ofbortezomib molecular mechanisms in myeloma cells. so that we could take further evaluation to discovermolecular cancer therapy. Naturally, more additional experimental and clinical procedures are needed in this survey.

Keywords : myeloma cells, acute myeloid leukemia, bioinformatics analysis, bortezomib
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