SKIN CANCER (OTHER THAN MELANOMA)

# MOLECULAR PROFILING OF TOX-DEFICIENT NEOPLASTIC CELLS IN CUTANEOUS T CELL LYMPHOMA

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Background: Cutaneous T cell lymphoma (CTCL) is a rare but potentially devastating primary cutaneous lymphoma. CTCL is characterized by localization of neoplastic T lymphocytes to the skin, with mycosis fungoides (MF) and its leukemic form, Sézary syndrome (SS) being the most common variants. Thymocyte selection-associated high-mobility group box (TOX) gene has been found to be highly expressed in MF and SS which shows an additional diagnostic value. It is reported that higher expression levels of TOX in patients will increase risks of disease progression and poor prognosis. However, the molecular events leading to these abnormalities have not been well understood. Knockdown of TOX gene will induce differentially expressed genes (DEGs), Gene Ontology (GO) and DEGs pathways. However, the relationship between TOX expression and DEGs has not been studied yet.

Objectives: To better understand the molecular mechanism underlying TOX-mediated DEGs in CTCL, and to identify DEGs pathways triggered after knockdown of TOX gene in the CTCL cell line Hut78.

Methods: In this study we employed two shRNA-mediated lentivirus to knockdown TOX gene in the skin lymphoma cell line HuT78, and RNA sequencing (RNAseq) analysis was applied to analyze DEGs, DEGs GO and their corresponding pathways.

Conclusions: Knockdown of TOX can induce up-regulation of 547 genes and down-regulation of 649 genes, respectively. Most
DEGs are enriched in cancer, and relate to the Wnt and mTOR signaling pathways, and therefore, they can regulate cellular processes and induce different biological regulation. Transcriptome analysis of DEGs after knockdown of TOX in our study can provide novel insights leading to candidate targets for therapy for CTCL in the near future.