LncRNAs Influence on NK Cells: Potential Therapeutic Target for Neuroblastoma

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Neuroblastoma (NB) is the most common extracranial cancer diagnosed in children, accounting for 6% of all pediatric cancer cases and 15% of childhood cancer deaths. The disproportionate NB mortality rate is attributed to clinical heterogeneity, ranging from spontaneous regression to aggressive metastasis in high risk (HR) patients, who present with an overall survival (OS) rate of 50%. Due to the poor prognosis of HR patients, the goal of the present study was to investigate the genetic parameters that differentiate NB patients based on OS. The recent identification of long non-coding RNAs (lncRNAs) as master genetic regulators implicated in cancer dysregulation also led this study to identify a lncRNA associated with enhanced survival (i.e., OS > 5.0 years) and an anti-tumor immune response. A bulk RNA-seq dataset containing primary NB tumor samples (n = 152) from the TCGABioLinks database was separated into poor survival (n = 69) and good survival (n = 83) groups. A differential gene expression analysis determined lncRNA RP11-277P12.20 was upregulated in good survival candidates and a Kaplan-Meier survival analysis showed that a higher expression of RP11-277P12.20 was associated with longer survival. Gene expression, functional annotation, and NK cell receptor/ligand expression analyses revealed a potential role of RP11-277P12.20 in regulating natural killer (NK) cell activity and cytotoxicity, thus revealing a promising target for the first lncRNA-based therapy for NB. Therefore, further research should include in vitro studies to assess the role of lncRNA RP11-277P12.20 throughout NB progression.

Awards Won:
Third Award of $1,000