

This international effort represents the largest and most comprehensive molecular analysis of TETs conducted to date is expected to have important clinical and translational implications for this rare disease.

Keywords: TCGA, genomics; myasthenia gravis (MG)

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AB008. OS02.02. Identification of differentially expressed genes between thymoma and paraneoplastic thymic tissues

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Abstract: Thymoma represents the most common anterior mediastinal compartment neoplasm. Due to having different histological types, thymoma shows different clinical characteristics. Furthermore, thymoma is often associated with autoimmune disorders, such as myasthenia gravis (MG). Although tumorigenesis of thymoma still remains unknown, its carcinogenesis is characterized by the stepwise accumulation of genetic and molecular abnormalities after

carcinogen exposure. Our study tries to demonstrate the underlying genetic mechanisms of tumorigenesis of thymoma and understand the related features: association with MG, histologic variability, and heterogeneity of malignant behavior. We analyzed 31 thymoma (including 5 cases of type AB, 6 B1-type cases, 12 B2-type cases, 5 B2B3-type cases, 3 type-B3 cases; only 6 cases of thymoma were not associated with MG, 25 cases with MG) using CapitalBio mRNA microarray and preliminarily identified some differentially expressed genes after comparisons between thymoma and the thymus tissue around tumor. Among them, 292 genes increased more than 2-fold, 2 genes more than 5-fold; on the other hand, 596 genes were decreased more than 2-fold, 115 genes more than 5-fold, 21 genes more than 10-fold, 6 genes more than 20-fold. Among these genes upregulated or downregulated, 6 driver genes, such as FANCL, NCAPD3, NCAPG, OXCT1, EPHA1 and MCM2, were identified. We selected 2-fold upregulated and 2-fold downregulated genes to generate a supervised clustering heat map. Six distinct clusters were identified. In cluster 1, two were type B2 tumors; in cluster 6, three were type B2/B3 tumors. KEGG database analysis found that pathogenesis of thymoma might be associated with several signaling pathways, which provides important information for revealing genetic mechanisms of thymoma. By comparing with genetic differences of thymoma with MG and without, 4 genes (PNISR, NBPF14, PIK3IP1 and RTCA) were upregulated more than 2-fold, more than 30 genes were downregulated more than 2-fold, and 2 signaling pathways with more than 2-fold upregulated genes (TGF-beta signaling pathway and HTLV-I signaling pathway) were found. The study would shed light on molecular bases for selecting appropriate oncological management, predict prognosis and provide important information on the genetic background of thymoma for classification purposes. Confirmation of the data will be performed using immunohistochemical and multiplex quantitative RT-PCR methods.

Keywords: Thymoma; CapitalBio mRNA microarray; differentially expressed genes

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