AB021. PS01.03. Copy number alteration and gene expression analysis of surgically resected thymic epithelial tumors

Takao Nakanishi[1], Toshi Menju[2], Yosuke Fujii[3], Ryo Miyata[2], Hiroyuki Ishikawa[2], Shigeto Nihsikawa[2], Koji Takahashi[2], Masatsugu Hamaji[2], Makoto Sonobe[2], Naoki Nakajima[4], Akihiko Yoshizawa[4], Ryo Yamada[3], Hiroshi Date[2]

[1]Thoracic Surgery, Nishi-Kobe Medical Center, Kobe, Japan; [2]Department of Thoracic Surgery, Kyoto University Hospital, Kyoto, Japan; [3]Statistical Genetics, Center for Genomic Medicine, Kyoto University Graduate School of Medicine, Kyoto, Japan; [4]Department of Diagnostic Pathology, Kyoto University Hospital, Kyoto, Japan

Background: Thymic carcinoma is rare and a comparatively poor prognostic mediastinal tumor. Due to small number of cases, our knowledge of treatment and prognostic factor is limited. Previous report revealed few mutation rate, and inverse correlation of mutation and copy number alteration (CNA) was reported, so we hypothesized most thymic carcinomas originate from certain CNAs. To substantiate the hypothesis, we extracted CNA and gene expression data from surgical sample of thymic carcinomas and compared these of thymomas, then integrated them with clinical information.

Methods: Between January 2009 and December 2016, patients underwent surgery for thymic epithelial tumor (TET) in our institution were reviewed. Age, gender, tumor size, WHO histology, clinical and pathological Masaoka stage and recurrence and prognostic status were collected. RNA and DNA were extracted from FFPE operative sample, then gene expression data were obtained by GeneChip Human Transcriptome Array 2.0 (Affymetrix, Santa Clara, California, USA), and CNA were detected by OncoScan (Affymetrix, Santa Clara, California, USA). These results were analyzed using Transcriptome analysis console (Affymetrix, Santa Clara, California, USA), Nexus expression for OncoScan (BioDiscovery) and R.

Results: We had seven cases primary thymic squamous cell carcinoma. As comparison we had four cases of type A thymoma and five cases of type B2/3 thymoma. CNA data from thymic squamous cell carcinoma showed similar characteristics, chromosome 1q gain, 6 loss and 16q loss, while type A thymoma showed little CNA, corresponded with previous report. CNA profiles of TETs showed certain concordance with their pathology and prognosis, while gene expression profile predicted poor prognostic group more accurately.

Conclusions: We reported the result of genome wide gene expression and CNV analysis. These results support appropriateness of our hypothesis. Further analysis is going to extract prognostic biomarkers and druggable targets.

Keywords: Gene expression; copy number alteration (CNA)

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