日本電気泳動学会 電子メール通信 No. 60

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【Journal of Electrophoresis: 論文掲載のお知らせ】

日本電気泳動学会会員の皆様

本日，Journal of Electrophoresis Vol. 61(2017) No. 1 p1-15 (J-STAGE 電子版) に，以下の論文が掲載されましたのでお知らせ致します。

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J Electrophoresis.2017;61:1-7.

Title: Secretomics identifies follistatin as a predictive biomarker for response to treatment with tyrosine kinase inhibitors in synovial sarcoma

Authors: Zhiwei Qiao, Fusako Kito, Yoko Takai, Rieko Oyama, Tadashi Kondo

Abstract: Sarcoma is a rare malignancy with an aggressive clinical course. Tyrosine kinase inhibitors (TKIs) have emerged as effective drugs in targeted therapy for malignancies; in particular, pazopanib was recently approved for the treatment of sarcoma. However, as only a limited proportion of patients exhibit favorable response to treatment with TKIs, predictive biomarkers of response to these drugs are urgently needed. In this study, we attempted to identify predictive biomarkers for response to TKIs in synovial sarcoma. We performed a magnetic bead–based assay (Bio-Plex) using synovial sarcoma cell culture supernatant and validated the results by ELISA and western blotting. Cellular protein and mRNA expression levels of candidate biomarkers were evaluated by western blotting and RT-PCR. Gene expression profiling of candidate biomarkers was conducted by meta-analysis of publicly available gene expression data from 149 patients with synovial sarcoma. We found that follistatin (FST) was significantly highly expressed in TKI-resistant cells. Moreover, cell proliferation was decreased following gene silencing of FST. Meta-analysis revealed that the mRNA expression of FST varied among the 149 patients with synovial sarcoma, and that 23 genes were co-expressed with FST; these included genes encoding receptor tyrosine kinase-like orphan receptor 1, Sal-like protein 4, and signal transducer CD24. This study suggested that FST represents a candidate predictive biomarker for response to treatment with TKIs in synovial sarcoma. Secretomics is a promising approach for predictive biomarker exploration. The utility of FST as a predictive biomarker for response to treatment with TKIs in synovial sarcoma should be further validated using clinical samples.

J Electrophoresis.2017;61:9-15.

Title: Metastasis-associated gene signature in primary myxoid liposarcoma identified through a gene expression study

Authors: Zhiwei Qiao, Takashi Tajima, Fusako Kito, Yasuhito Arai, Akira Kawai, Tadashi Kondo

Abstract: Myxoid liposarcoma (MLS) is a rare mesenchymal malignancy with unique extrapulmonary metastatic potential. Although MLS has been associated with specific chromosomal translocations, the factors and pathways regulating metastasis in MLS remain unknown. To identify the molecular mechanisms underlying MLS metastasis, we compared global gene expression profiles of primary tumor tissues from MLS patients with different metastatic statuses using DNA microarray analysis. In total, 393 genes were differentially expressed between the tumors from four patients with metastasis and those from 11 patients without metastasis. Differentially expressed genes were functionally annotated based on Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis. Supervised classification based on the 393 genes clearly discriminated samples according to metastatic status. The pathways responsible for metastasis included “focal adhesion,” “pathways in cancer,” “ECM-receptor interaction,” and “tight junction.” The differential expression of alpha-synuclein was confirmed at the protein level; the protein was downregulated in metastatic MLS. Meta-analysis revealed that MLS could be discriminated from the other sarcomas based on the expression of the metastasis-associated genes. The metastasis-associated genes identified in this study are worthwhile further investigation to further our understanding of MLS and are expected to lead to novel clinical applications for MLS.

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