

MICRORNA EXPRESSION ABNORMALITIES IN PITUITARY ADENOMAS ARE ASSOCIATED WITH DISTINCTIVE PATHOLOGIC FEATURES AND MAY CONTRIBUTE TO TUMORIGENESIS

Zhi Rong Qian¹, Toshihito Tanahashi², Katsuhiko Yoshimoto³, Shozo Yamada⁴, Sakurako Katsuura², Kazuhito Rokutan² and Toshiaki Sano¹

¹ Department of Human Pathology, Institute of Health Biosciences, University of Tokushima Graduate School, Tokushima

² Department of Stress Science, Institute of Health Biosciences, University of Tokushima Graduate School, Tokushima

³ Department of Medical Pharmacology, Institute of Health Biosciences, University of Tokushima Graduate School, Tokushima

⁴ Department of Hypothalamic and Pituitary Surgery, Toranomon Hospital, Tokyo

PURPOSE: MicroRNAs are small noncoding RNAs that regulate gene expression by targeting specific mRNAs for degradation or translation inhibition. Recent evidence indicates that microRNAs can contribute to tumorigenesis and tumor progression and may have diagnostic and prognostic value in several human malignancies. We investigated the global microRNA expression patterns in normal human pituitary and adenomas to evaluate their involvement in tumorigenesis and clinicopathologic features of these tumor types.

MATERIALS AND METHODS: Using the most new microarray, we studied the global microRNA expression in 5 human adenohipophyses and 48 pituitary adenomas, including 14 somatotroph, 6 lactotroph, 13 corticotroph (8 associated with Cushing's disease and 5 silent), and 15 gonadotroph adenomas.

RESULTS: Our data showed that a common pattern of microRNA expression distinguishes any tumor type from normal pituitary tissues, suggesting that this set of microRNAs might be involved in pituitary tumorigenesis. In addition, some microRNAs expression can distinguish among each tumor type. Moreover, several of the identified miRNAs are involved in clinicopathologic features such as invasion and tumor size.

CONCLUSION: These results suggest that alteration in microRNA expression is related to pituitary tumorigenesis and tumor progression, and might prove useful in distinguishing tumors with different clinical behavior.