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이차성 부갑상샘항진증을 가진 만성신부전 환자의 부갑상샘조직에서 microRNA의 발현변화

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Differential MicroRNA Expression on Parathyroid Tissue in 2nd Hyperparathyroidectomy Patients

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Background: MicroRNAs (miRNAs) are important regulators of gene expression, which may have roles in 2nd hyperparathryoidism of ESRD patients. The molecular factors that control parathyroid hyperplasia and adenoma, are poorly understood. We studied the miRNA profile between normal parathyroid group, and 2nd hyperparathyroidism in ESRD patients group to find out the difference of miRNA expression.

Methods: Parathyroid tissue samples including clinical data were obtained for 7 patients (2 normal parathyroid gland by thyroid cancer patients, 5 2nd hyperparathyroidism ESRD patients). Total RNA was extracted from fresh frozen tissue. RNA was reverse transcribed and preamplified using Megaplex premier pools, and was run by TaqMan array MicroRNA Card A,B. Data analysis was performed using DataAssist soft ware v 3.01(applied Biosystems)

Results: miR-10a,15b,18a,103,145,148b,185,193a,301,425,532,532-3p,1274A,1275,1291 were up-regulated to 2 fold change, and miR-34a,139-5p were down regulated in ESRD patients. Clustering analysis was done.

Conclusions: Due to diversity and complexity of miRNAs in ESRD patients, there was a limitation of study in CKD patients. TaqMan low density array may have a merit by screening and semi-quantitive method for study. Various miRNAs may influence on development or aggravation in 2nd hyperparathyroism in ESRD patients. So further study may be needed to understand mechanisms of up- or down- regulated miRNAs in patients with 2nd hyperparathyroidism.

Key Words: 말기신부전, 이차성 부갑상선항진증, 마이크로알엔에이
ESRD, Secondary hyperparathyroidism, MicroRNA