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ESRP1 has a prognostic value in biochemical recurrence and cancer specific survival of prostate cancer

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The study was aimed to identify targetable genes in PC from The Cancer Genome Atlas (TCGA) and to validate the significance of the genes identified in clinical studies using immunohistochemistry in PC patients' prostatectomy microarray. Omics data and clinical data of 550 PC patients were obtained from TCGA. Several significant genes were identified from TCGA dataset having the most number of point mutation to exhibit significantly strong positive relationship in expression values with the most frequently mutated gene. Further validation of different expression values for the list of genes between tumor and normal lesions was performed to evaluate their prognostic significance using tissue microarray of 514 prostatectomy specimens by performing immunohistochemistry in clinical setting from a single cancer institution. Prognostic powers of these genes were investigated on the NCC dataset. Immunohistochemistry were performed on the genes associated with the most mutated gene. The gene markers' prognostic factors were analyzed using Cox proportional hazard analysis with a significant p-value<0.05. *FRG1B* gene was found lineage-specific mutation with *ESRP1, RAD51* and *CHEK2* genes in the TCGA dataset. The union of samples with these three up-regulated markers with *FRG1B* mutation showed significant differences in disease-free survival compared to the samples without expression of two combinational series ($p<0.05$). Analysis of the clinicopathological factors related to three markers suggested that expression of *ESRP1* was a significant risk factor for biochemical recurrence (BCR, HR 1.003) and cancer-specific survival (HR 1.048), even after adjusting for significant prognostic clinicopathological factors of BCR and CSS ($p<0.05$). On the other hand, *CHEK2* was not significant in any BCR and CSS. *RAD51* could not be evaluated because of its overall overexpressed in specimens. The study identified that *ESRP1* was a potentially significant target gene of survival prognoses in PC.

Biography

Sung Han Kim has completed his MD from Seoul National University of Medicine, Seoul, Korea and Postdoctoral studies from National Cancer Center, Goyang, Korea. He is working as Clinical Staff, Associate Researcher and Director of Jinsoo Chung, Prostate Cancer Center, Korea. He has published more than 30 papers in reputed journals.

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