97P TNFSF14overexpression and poor prognosis in early stages of non-small cell lung cancer prognosis: Immune-checkpoint inhibitor databases-based study

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INTRODUCTION

Genomics has a scarcity that compiles all immuno-oncology targets for translational research and drug discovery for early stages of cancers. 1-4Our study investigated a new gene model from recent immune checkpoint inhibitor databases (ICI) for the early stage of non-small cell lung cancer (NSCLC)

METHODS AND MATERIALS

We performed transcriptomic analysis from The Cancer Genome Atlas (TCGA) and matching ICI genes by two recent databases, IMPRES and CKTTD, to find a new specific ICI gene signature for early lung lung adenocarcinoma LUAD and squamous cell cancer diagnosis LUSC. Real-time PCR, and western blot were used for validation

RESULTS

The new signature gene has higher sensitivity with IMPRES genes in both early lung subtypes, AUC = 74% (LUAD) and AUC = 81% (LUSC), than the CKTTD database results in the same group of patients. The novel nomogram for survival prediction of TNFSF14 in LUAD and LUSC patients was used with both signatures showing significant Cox regression for overall survival with adjusted clinical variables. qPCR, PCR, and western blotting were used to test expression of TNFSF14 in RT qPCR (HBE vs H1703 or A549 P<0.001***). The risk score and immune cell infiltration immune cell subpopulation infiltration revealed a highly significant correlation with risk signature.

CONCLUSIONS

In addition to the novel signatures from recent ICI database ,future studies are necessary to test the clinical usefulness of TNFSF14 in individualized early NSCLC management with ICI drugs.

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