## P072

## Molecular characteristics Related To 18F-FDG Uptake in Intrahepatic Cholangiocarcinoma

Keun Soo AHN<sup>1</sup>, Koo Jeong KANG<sup>1</sup>, Yong Hoon KIM<sup>1</sup>, Tae-Seok KIM<sup>1</sup>, Kyoung Sook WON<sup>2</sup>

<sup>1</sup>Surgery, Keimyung University Dongsan Medical Center, Korea <sup>2</sup>Nuclear Medicine, Keimyung University Dongsan Medical Center, Korea

**Introduction** : In intrahepatic cholangiocarcinoma (iCCA), genetic characteristics on 18F-FDG-PET scans are not yet clarified. If they are evaluated, we can predict molecular features based on the FDG uptake. We analyzed RNA sequencing in iCCA patients to evaluate gene expression signatures associated with FDG uptake patterns.

**Methods** : We performed RNA sequencing of 22 cases iCCA who underwent preoperative 18F-FDG- PET, and analyzed the clinical and molecular features according to the maximum standard uptake value(SUVmax). Genes and biological pathway which are associated with SUVmax were analyzed.

**Results** : Patients with SUVmax higher than 9.0(n=9) had poorer disease-free survival than those with lower SUVmax(n=13, P=0.035). Genes related to glycolysis and gluconeogenesis, phosphorylation and cell cycle were significantly correlated with SUVmax ( $| r | \ge 0.5$ ). RRM2, which is related to the toxicity of Gemcitabin was positively correlated with SUVmax, and SLC27A2 which is associated with Cisplastin response was negatively correlated with SUVmax. Cell cycle, hypoxia and metabolism-related pathways were enriched in high SUVmax patients.

**Conclusions** : The genomic features of gene expression and pathways can be predicted by FDG uptake features in iCCA. Patients with high FDG uptake have enriched cell cycle, metabolism and hypoxic pathways, which may lead to a more rational targeted treatment approach.

Corresponding Author. : Keun Soo AHN ( ahnksmd@gmail.com )