세미나초록

<table>
<tr><td>발표주제</td><td colspan="2">Integrated invasive and non-invasive transcriptomic analyses
for personalized therapy in the patients with lung cancer</td></tr>
<tr><td>발표내용</td><td colspan="2">Lung cancer is the most common cause of cancer-related death in the world, and early diagnosis of lung cancer leads to higher cure rates. While low dose CT screening is an approved early detection modality, utilization remains low and there is an unmet need for new approaches. The resistance against chemo-/RT therapy has been suggested as a major player for the low cure rate, which directly affects survival rate of patients with lung cancer. Although a personalized chemotherapy has been widely used to treat lung cancer patients, it has never been addressed to utilize radiation therapy. To this end, we identified 232 consecutive patients with stage IA-IIIC NSCLC treated with chemoradiotherapy or stereotactic ablative radiotherapy (SABR), and found the mutations on KEAP1/NFE2L2 predict local recurrence. Functional evaluation of the KEAP1/NFE2L2 mutations on radiotherapy cohort using cell biology confirmed the predictive power of the mutations and found the inhibition of glutaminase pathway could overcome KEAP1/NFE2L2-driven radioresistance. Regarding this, the first part of this talk will focus on how Chemo-/RT can be personalized in lung cancer.
Tumor-derived nucleic acids provide unique molecular signature of cancers and represents an ideal biomarker for detecting cancers. Tumor cells continually release nucleic acids, including RNAs, into the circulation and these cell-free nucleic acids are promising biomarkers for measuring the presence of tumors in plasma. My previous group has previously developed a non-invasive method called Cancer Personalized Profiling by Deep Sequencing (CAPP-Seq) for detection of cfDNA. This approach involves capturing target regions followed by next generation sequencing with a lower limit of detection of ~0.002%. The latter part for the presentation will discuss the utility of cell free nucleic acids using Next Generation Sequencing method to detect cancer and to apply it into cancer biology.</td></tr>
<tr><td>발표자</td><td colspan="2">Young-Jun Jeon</td></tr>
<tr><td rowspan="2">학력
(학사이상)</td><td>연도</td><td>학력사항</td></tr>
<tr><td>2002
2005
2015</td><td>학사 - 성균관대학교 유전공학과
석사 – 광주과학기술원 생명과학과
박사- The Ohio State University School of Medicine</td></tr>
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주요약력	연도	내용
	2006 ~ 2008 2015 ~ 2016 2016 ~ 2020 2020 ~ 현재	석사 후 연구원 (서울대학교) 박사 후 연구원 (The Ohio State University) 박사 후 연구원 (Stanford University) 성균관대학교 융합생명공학과 조교수