

# “The role of myeloid cells to lung cancer development and treatment”

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**Date**                    **Friday, October 20, 2017**

**Time**                    **10:00 am - 11:00 am**

**Venue**                 **Biken Hall, RIMD Main Building 1F**

## ***Brief summary***

Tumor orchestrated changes in the immune cell composition in the microenvironment limits generation of sufficient anti-tumor immune responses. One of the most prominent features of Kras mutant lung tumors is their rich myeloid cell content. To study this systematically, we generated bi-transgenic mice expressing a conditional *IL-17A* allele along with conditional *Kras*<sup>G12D</sup> and performed immune phenotyping and survival analysis. Tumors in *IL-17:Kras*<sup>G12D</sup> mice grew more rapidly, resulting in a significantly shorter survival as compared to *Kras*<sup>G12D</sup>. *IL-6*, *G-CSF*, *MFG-E8*, and *CXCL1* were increased in the lungs of *IL17:Kras* mice. Time course analysis revealed that tumor-associated neutrophils (TANs) were significantly elevated, and lymphocyte recruitment was significantly reduced in *IL17:Kras*<sup>G12D</sup> mice as compared to *Kras*<sup>G12D</sup>. In therapeutic studies, PD-1 blockade was not effective in treating *IL-17:Kras*<sup>G12D</sup> tumors. In contrast, blocking *IL-6* or depleting neutrophils with an anti-Ly-6G antibody in the *IL17:Kras*<sup>G12D</sup> tumors resulted in a clinical response associated with T cell activation. Through RNA sequencing of sorted neutrophils, we identified arginase 1 as one of the highly induced genes in the tumor as compared to the normal lungs. Inhibition of arginase activity resulted in a similar therapeutic effect highlighting the importance of myeloid cell derived arginase as a biomarker of resistance to immune checkpoint blockade and a viable therapeutic target.

**Host**    Shohei Koyama (Department of Immunopathology, IFRcC/ Department of Respiratory Medicine and Clinical Immunology, Graduate School of Medicine, Osaka University)