

## AB043. P014. Genomic characterization of pancreatic cancer in Chinese population

Wentao Gao<sup>1,2</sup>, Kai Zhang<sup>1,2</sup>, Zipeng Lu<sup>1,2</sup>, Jishu Wei<sup>1,2</sup>, Junli Wu<sup>1,2</sup>, Feng Guo<sup>1,2</sup>, Jianmin Chen<sup>1,2</sup>, Chunhua Xi<sup>1,2</sup>, Min Tu<sup>1,2</sup>, Lei Tian<sup>1,2</sup>, Kuirong Jiang<sup>1,2</sup>, Yi Miao<sup>1,2</sup>

<sup>1</sup>Pancreas Center, the First Affiliated Hospital of Nanjing Medical University, <sup>2</sup>Institute of Pancreas, Nanjing Medical University, Nanjing 210029, China

**Background:** In pancreatic cancer (PC), pancreatic ductal adenocarcinoma (PDAC) is the most common type, accounting for >90% of all patients. PDAC is one of aggressive diseases that mostly presents at an advanced stage and have a poor prognosis with the 5-year survival rate is 8.2%. Researchers have identified a large number of mutations and copy number alterations (CNAs), including *KRAS*, *TP53*, *SMAD4*, and *CDKN2A*. But the genomic features of PC in Chinese population are still largely unknown. This study aims to expound the genomic characterization of PC in Chinese population by whole exome sequencing.

**Methods:** Patients of Han nation were recruited and consent obtained for researches from the Pancreas Biobank in

Pancreas Centre of the First Affiliated Hospital of Nanjing Medical University. Whole exome sequencing (WES) was performed on 64 primary PDAC specimens with criteria of neoplastic cellularity over 50% to an average depth of 97×, and compared to the germline from the blood samples (an average depth of 102×). Mutations and indels were detected by qSNP and Genome Analysis Toolkit (GATK).

**Results:** The mean age of our patients was 66.0±9.4 and there were 35 males and 29 females in these patients. Surgical procedures for these patients included distal pancreatectomy [14], segmental resection [1], (pylorus-preserving) Whipple's procedure [46], total pancreatectomy [3]. The results of WES revealed recurrent somatic mutations in *KRAS* (72%), *TP53* (50%), *SMAD4* (22%), *RNF43* (8%), *MUC5B* (8%), *U2AF1* (6%), and *FLG* (6%). We next investigated the mutation spectrum of PC and the result showed that the predominant substitution in PC was C to T and C to A.

**Conclusions:** Our study updated the genomic features of PDAC to help us know more about the initiation and progression in this deadly disease.

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