

# The National Lung Cancer Gene Library Alliance of China was launched

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The National Lung Cancer Gene Library Alliance of China was launched on 12<sup>th</sup> Oct. 2012 in Guangzhou, as initiated by State Key Laboratory of pulmonary diseases, the 1<sup>st</sup> Affiliated Hospital of Guangzhou Medical University and BGI Genomic Research Institution. More than 20 3A-hospitals from all over China joined in this alliance as the first members (Figure 1).

“The objective of this alliance is to prolong the overall survival of advanced stage lung cancer patients”, Prof. Jianxing He, one of the initiator of the alliance said, “The first approach is to find the sensitive gene target of chemotherapy and targeted therapy and make an individually effective strategy for each patient. Then we will focus on researches on finding out the cause of lung cancer genomically, which may control the incidence in the very beginning”.

“It is a new progress in China.” said Professor Jian Wang, dean of BGI Genomic Research Institute, “Although there have been 19 tissue banks established in China, none of them shares the same standard or allies with each other. Therefore they cannot share their precious data or tissues. The alliance is to connect all the hospitals which have the probability to collect and build up the tissue bank to share the data and tissues.”

“With more tissues and data being shared, it will surely improve the possibility to find out the genomic cause of lung cancer”. Professor Wang added.

However, we are just keeping up the pace, according to Prof. He, “National gene alliances have been established in many developed countries. China has the largest lung cancer population with which we would have achieved more. Those data are too precious treasures that it would be a big loss for lung cancer research if we just let it be there. Chinese medical personnel should also consider making contributions to the



**Figure 1.** The National Lung Cancer Gene Library Alliance of China was launched.

world’s medical and health career”.

The tissue collection is undergoing voluntarily among patients after gene sequencing. Tissues will be used to analyze the homogenesis of same kind and heterogenesis of different kind, which may describe the sketch of gene causes in lung cancer.

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