**METHODS**

A multicenter study in China was initiated from July 2013, and a total of 3279 NSCLC patients have been enrolled as of November 2016 from four medical centers in many different areas. They were screened by using a next-generation sequencing (NGS)-based gene panel assay for detecting EGFR-KDD.

**RESULTS**

Of this entire cohort, just one (0.07% EGFR+NSCLC) patient was identified with an EGFR-KDD in Chinese population. Here is a 63-year-old Chinese female with a left lung tumor (NSCLC T1N0M1, stage IV) and pleural metastasis. Histologic examination of the surgical specimens from the left lung tumor and pleural nodes revealed lung adenocarcinoma. Using a next generation sequencing assay, we found that the tumor had EGFR-KDD and the most common types of EGFR mutations were wild. The patient experienced a stable tumor response to icotinib. Considering this rare EGFR mutation and response to TKI treatment, we conclude that the incidence of rare EGFR gene mutations in NSCLC patients should be studied.

**CONCLUSIONS**

The frequency of EGFR-KDD in Chinese population with NSCLC is more than Caucasus population (0.07% vs 0.02%). This case facilitates an increase in the detection of uncommon EGFR gene mutations and enhances the evidence of a clinical response to EGFR inhibitors. The landscape of EGFR-TKI-responsive EGFR genotypes demonstrates that comprehensive molecular types are necessary to realize the identification of patients who would benefit from targeted therapy, especially EGFR-wild NSCLC patients.

**REFERENCES**

2. Cancer Discov. 2015, 5: 1155-1163