

EGFR

IDYLLA™ EGFR MUTATION DETECTION ON SOLID BIOPSY

BACKGROUND INFORMATION*

Lung cancer is the most common cancer worldwide, contributing for 13% of all cancer types. 85% of lung cancers are non-small cell lung cancers (NSCLC), of which histologically adenocarcinoma is the most prevalent.

EGFR mutations are mainly observed in lung cancer. *EGFR* mutation testing in exons 18-21 is recommended in all patients with advanced NSCLC of a non-squamous subtype. Activating mutations in the *EGFR* gene have been associated with sensitivity and resistance to a number of targeted anti-cancer therapeutics.^{11,17}

Exon 19 deletion and exon 21 (L858R, L861), exon 18 (G719X), and exon 20 (S768I) mutations are associated

with sensitivity to TKI's. Exon 20 insertion mutation may predict resistance to TKI's. EGFR T790M mutation is the main indicator of the patient's resistance to TKI therapy and has been reported in about 55% of patients with disease progression after initial response to 1st or 2nd generation TKI's.^{11,17}

The prevalence of *EGFR* mutations in NSCLC adenocarcinomas is 10-15% of Western and up to 50% of Asian patients. Sensitizing *EGFR* mutations are predictive for response to *EGFR* tyrosine kinase inhibitors.^{11,17,21}

*Idylla™ EGFR Mutation Test is validated for metastatic NSCLC

DIAGNOSTIC PRODUCT

Idylla™ EGFR Mutation Test (CE IVD)

EGFR

Diagnostic use

51 in exons
18,19,
20,21
mutations

approx. **150** min
sample-to-result
< **2** min
hands-on time



FFPE

Directly on 1 FFPE tissue section
(5 µm) from **metastatic
non-small-cell lung cancer**



**Qualitative genotype call
+ Cq values**



Mutation detection **for
treatment assessment**

“Today, EGFR testing is a cumbersome process and it often takes several weeks before results are analyzed. This may lead to the administration of anti-EGFR therapy as second-line agents, which is less efficient than their use in first-line therapy. The Idylla™ EGFR Mutation Test technology has the potential to change that: it is a cost-effective solution, ensuring reliable and fast detection of all relevant mutations”

*Prof Giancarlo Troncone
University of Napoli Federico II, Naples*