Precision Panel- 50 Genes

PATIENT	REPORT DATE	BOOKING ID
Megha Kalyan	17 July 2024	# 012407040113

Test Description

The MolQ Precision Panel includes 50 genes, involving hotspot regions and 3159 unique variants, applicable to a wide range of tumor types for detection of SNV (single and multiple nucleotide variation), Insertion-Deletion, Copy Number Variation (CNV), and gene Fusions. Fusion and splice variants are detected in RNA.

Patient Demographic

Name: Ms. Megha Kalyan
Sex: Female
Date of Birth/Age: 42 years
Disease: Lung Adenocarcinoma

Clinician

Clinician Name: Dr Amit Verma
Medical Facility: Dr AV Institute of Personalized Cancer Therapy and Research
Pathologist: Not Provided

Specimen

Booking ID: 012407040113
Sample Type: FFPE Block No. 11323/24 A2
Site: Lung
Tumor Content Percentage: 20-30%
Date of Collection: 04-07-2024
Date of Booking: 04-07-2024

CLINICAL SYNOPSIS

Megha Kalyan, is a known case of lung adenocarcinoma. She has been evaluated for pathogenic variations in the genes listed in Appendix 2.

RESULT SUMMARY

Variants detected as per NCCN Guidelines: Clinically relevant *EGFR* exon 19 deletion *EGFR* (p.Glu746_Ala750del, VAF= 20.91%) mutation is detected.

Other variants detected:

Not Applicable

Note: The average Base Coverage Depth achieved was 971X in this sample.

RESULTS

Variant in *EGFR* gene is detected.

RELEVANT BIOMARKERS

Gene/ Transcript (Locus)	Variant ID	Variant	Exon	Coverage	Allele Frequency	Variant Effect	*Relevant Therapies (In this cancer type)	*Relevant Therapies (In other cancer type)	Tier[1]
EGFR NM_005228.5 (chr7:55242465)	COSM6225	c.2236_2250delGAATTAAGAGAAGCA (p.Glu746_Ala750del)	19	837	20.91%	Non frame shift Deletion	Afatinib[i,ii] bevacizumab* + erlotinib[ii] dacomitinib[i,ii] erlotinib[i,ii] erlotinib + ramucirumab[i,ii] gefitinib*[i,ii] osimertinib [i,ii] osimertinib + chemotherapy[i] gefitinib + chemotherapy amivantamab + chemotherapy atezolizumab + bevacizumab + chemotherapy	None	Ia

* Public data sources included in relevant therapies: FDA[i], NCCN, EMA[ii], ESMO

[1]Li et al. Standards and Guidelines for the Interpretation and Reporting of Sequence Variants in Cancer: A Joint Consensus Recommendation of the Association for Molecular Pathology, American Society of Clinical Oncology, and College of American Pathologists. J Mol Diagn. 2017 Jan;19(1):4-23.

RELEVANT NON-SMALL CELL LUNG CANCER FINDINGS

Gene	Findings	Gene	Findings	Gene	Findings
ALK	None detected	*KRAS*	None detected	*NTRK3*	None detected
BRAF	None detected	*MET*	None detected	RET	None detected
EGFR	Exon 19 deletion	*NTRK1*	None detected	ROS1	None detected
ERBB2	None detected	*NTRK2*	None detected		

CLINICAL CORRELATION AND VARIANT INTERPRETATION

EGFR **p.Glu746_Ala750del (Exon 19 deletion)** **Coverage 837**

Gene description: The *EGFR* gene encodes the epidermal growth factor receptor (EGFR) tyrosine kinase, a member of the ERBB/human epidermal growth factor receptor (HER) family. In addition to EGFR/ERBB1/HER1, other members of the ERBB/HER family include ERBB2/HER2, ERBB3/HER3, and ERBB4/HER4[1]. EGFR ligand induced dimerization results in kinase activation and leads to stimulation of oncogenic signaling pathways including the PI3K/AKT/MTOR and RAS/RAF/MEK/ERK pathways. Activation of these pathways promote cell proliferation, differentiation, and survival[2,3].

Alterations and prevalence: Recurrent somatic mutations in the tyrosine kinase domain (TKD) of *EGFR* are observed in approximately 10-20% of lung adenocarcinoma, and at higher frequencies in never-smoker, female, and Asian populations[4-7]. The most common mutations occur near the ATP-binding pocket of the TKD and include short in-frame deletions in exon 19 (*EGFR* exon 19 deletion) and the L858R amino acid substitution in exon 21[8]. These mutations constitutively activate EGFR resulting in downstream signaling, and represent 80% of the *EGFR* mutations observed in lung cancer. A second group of less prevalent activating mutations include E709K, G719X, S768I, L861Q, and short in-frame insertion mutations in exon 20[9-12]. *EGFR* activating mutations in lung cancer tend to be mutually exclusive to *KRAS* activating mutations[13]. In contrast, a different set of recurrent activating *EGFR* mutations in the extracellular domain include R108K, A289V and G598V and are primarily observed in glioblastoma[8,14]. Amplification of EGFR is observed in several cancer types including 30% of glioblastoma, 12% of esophageal cancer, 10% of head and neck cancer, 5% of bladder cancer, and 5% of lung squamous cell carcinoma[4,5,7,14,15]. Deletion of exons 2-7, encoding the extracellular domain of *EGFR* (EGFRvIII), results in overexpression of a ligand-independent constitutively active protein and is observed in approximately 30% of glioblastoma[16-18].

Potential relevance: Approved first-generation EGFR tyrosine kinase inhibitors (TKIs) include erlotinib[19] (2004) and gefitinib[20] (2015), which block the activation of downstream signaling by reversible interaction with the ATP-binding site. Although initially approved for advanced lung cancer, the discovery that drug sensitivity was associated with exon 19 and exon 21 activating mutations allowed first-generation TKIs to become subsequently approved for front-line therapy in lung cancer tumors containing exon 19 or exon 21 activating mutations. Second-generation TKIs afatinib[21] (2013) and dacomitinib[22] (2018) bind EGFR and other ERBB/HER gene family members irreversibly and were subsequently approved. First- and second-generation TKIs afatinib, dacomitinib, erlotinib, and gefitinib are recommended for the treatment NSCLC harboring *EGFR* exon 19 insertions, exon 19 deletions, point mutations L861Q, L858R, S768I and codon 719 mutations, whereas most *EGFR* exon 20 insertions, except p.A763_Y764insFQEA, confer resistance to the same therapies[23-26]. However, in 2021, the irreversible tyrosine kinase inhibitor, mobocertinib[27] was FDA approved for the treatment of NSCLC with *EGFR* exon 20 insertion mutations. Additionally, in 2022, the FDA granted breakthrough therapy designation to the irreversible EGFR inhibitors, CLN-081 (TPC-064)[28] and sunvozertinib[29], for locally advanced or metastatic non-small cell lung cancer harboring *EGFR* exon 20 insertion mutations. In lung cancer containing *EGFR* exon 19 or 21 activating mutations, treatment with TKIs is eventually associated with the emergence of drug resistance[30]. The primary resistance mutation that emerges following treatment with first-generation

TKI is T790M, accounting for 50-60% of resistant cases[8]. Third generation TKIs were developed to maintain sensitivity in the presence of T790M. Osimertinib[31] (2015) is an irreversible inhibitor indicated for metastatic *EGFR* T790M positive lung cancer and for the first-line treatment of metastatic NSCLC containing *EGFR* exon 19 deletions or exon 21 L858R mutations. Like first-generation TKIs, treatment with osimertinib is associated with acquired resistance. In this case, resistance is associated with the C797S mutation and occurs in 22-44% of cases[30]. The T790M and C797S mutations may be each selected following sequential treatment with a first-generation TKI followed by a third-generation TKI or vice versa[32]. T790M and C797S can occur in either cis or trans allelic orientation[32]. If C797S is observed following progression after treatment with a third-generation TKI in the first-line setting, sensitivity may be retained to first-generation TKIs[32]. If C797S co-occurs in trans with T790M following sequential treatment with first- and third-generation TKIs, patients may exhibit sensitivity to combination first- and third-generation TKIs, but resistance to third-generation TKIs alone[32,33]. However, C797S occurring in *cis* conformation with T790M, confers resistance to first- and third-generation TKIs[32]. Fourth-generation TKIs are in development to overcome acquired C797S and T790M resistance mutations after osimertinib treatment. EGFR targeting antibodies including cetuximab (2004), panitumumab (2006), and necitumumab (2016) are under investigation in combination with EGFR-targeting TKIs for efficacy against *EGFR* mutations. The bispecific antibody, amivantamab[34], targeting EGFR and MET was approved (2021) NSCLC tumors harboring *EGFR* exon 20 insertion mutations. In 2024, a CNS penetrating small molecule, ERAS-801[35] received fast track designation for the treatment of adult patients with *EGFR* altered glioblastoma. HLX-42[36], an anti-EFGR-antibody-drug conjugate (ADC) consisting of an anti-EGFR monoclonal antibody conjugated with a novel high potency DNA topoisomerase I (topo I) inhibitor, received a fast-track designation (2024) for the treatment of patients with advanced or metastatic *EGFR*-mutated non-small cell lung cancer whose disease has progressed on a third-generation EGFR tyrosine kinase inhibitor. CPO301[37] received a fast-track designation (2023) from the FDA for EGFR mutations in patients with metastatic NSCLC who are relapsed/refractory or ineligible for EGFR targeting therapy such as 3rd-generation EGFR inhibitors including osimertinib. The Oncoprex immunogene therapy quaratusugene ozeplasmid[38] in combination with osimertinib received a fast-track designation from the FDA (2020) for NSCLC tumors harboring EGFR mutations that progressed on osimertinib alone. BDTX-189[39] was granted a fast-track designation (2020) for the treatment of solid tumors harboring an *EGFR* exon 20 insertion mutation.

RECOMMENDATIONS

- Validation of the variant(s) by Sanger sequencing is recommended to rule out false positives.
- Genetic counselling is advised for interpretation on the consequences of the variant(s).
- If results obtained do not match the clinical findings, additional testing should be considered as per referring clinician's recommendations.

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APPENDIX 1: TEST METHODOLOGY

Method

DNA and RNA were extracted from samples using the Qiagen FFPE DNA kit and Promega ReliaPrep FFPE Total RNA Miniprep system. Isolated DNA/RNA was directly loaded on Genexus Next Generation Sequencer and subjected to automated library preparation and template preparation followed by sequencing at average depth of ~4000X.
It utilizes unique molecular tags to enable high sensitivity detection of variants. Analysis is done using Ion Torrent Reporter Software (version 6.6.2.1), the data is visualized on Integrative Genomics Viewer (IGV, version 5.01 (0)) and analyzed. The final report is generated using Oncomine curated knowledgebase reporter and includes clinical trials information continuously being updated for the best of the patient management as per clinical guidelines.

DISCLAIMER

- This report was generated using the materials and methods as recommended which required the use of quality reagents, protocols, instruments, software, databases and other items, some of which were provided or made accessible by third parties. A defect or malfunction in any such reagents, protocols, instruments, software, databases and/or other items may compromise the quality or accuracy of the report.
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- Due to inherent technology limitations of the assay, not all bases of the exome can be covered by this test. Accordingly, variants in regions of insufficient coverage may not be identified and/or interpreted. Therefore, it is possible that certain variants are present in one or more of the genes analyzed, but have not been detected. The variants not detected by the assay that was performed may/ may not impact the phenotype.
- It is also possible that a pathogenic variant is present in a gene that was not selected for analysis and/or interpretation in cases where insufficient phenotypic information is available.
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LIMITATIONS

- Variants with very low allele frequency (<0.5%) present in the given specimen or lower copy number variation might not be detected. Similarly fusion variants with less read may not be detected. Variant detection is also based on release of tumor percentage and affected by tumor heterogeneity.
- The FFPE fixation issues and the age of the block also widely affects the genomic findings.

APPENDIX 2: GENES LIST

DNA Hotspots					
AKT1	*AKT2*	*AKT3*	*ALK*	*AR*	*ARAF*
BRAF	*CDK4*	*CDKN2A*	*CHEK2*	*CTNNB1*	*EGFR*
ERBB2	*ERBB3*	*ERBB4*	*ESR1*	*FGFR1*	*FGFR2*
FGFR3	*FGFR4*	*FLT3*	*GNA11*	*GNAQ*	*GNAS*
HRAS	*IDH1*	*IDH2*	*KIT*	*KRAS*	*MAPK1*
MAPK2	*MET*	*MTOR*	*NRAS*	*NTRK1*	*NTRK2*
NTRK3	*PDGFRA*	*PIK3CA*	*PTEN*	*RAF1*	*RET*
ROS1	*SMO*	*TP53*			
CNVs					
ALK	*AR*	*CD274*	*CDKN2A*	*EGFR*	*ERBB2*
ERBB3	*FGFR1*	*FGFR2*	*FGFR3*	*KRAS*	*MET*
PIK3CA	*PTEN*				
Inter-genetic Fusions					
ALK	BRAF	*ESR1*	*FGFR1*	*FGFR2*	*FGFR3*
MET	*NRG1*	*NTRK1*	*NTRK2*	*NTRK3*	*NUTM1*
RET	*ROS1*	*RSPO2*	*RSPO3*		
Intra-genetic Fusions					
AR	*EGFR*	*MET*			