Real-World ROS1 Testing in First-Line Non-Small Cell Lung Cancer

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Background

- Biomarker testing is critical for guiding oncology care, and tyrosine kinase inhibitors (TKIs) have transformed the treatment of non-small cell lung cancer (NSCLC) by targeting specific biomarkers (e.g., ROS1).
- With targeted therapy advancements and increased response durations, biomarker testing is even more important for guiding patient care.
- This study describes real-world patterns of *ROS1* testing in pts with metastatic NSCLC (mNSCLC), for which guidelines recommended RNA next-generation sequencing (NGS).

Methods

- Adults diagnosed with mNSCLC (N=12,540) on or after 01-Oct-2017 through 31-Aug-2025 were identified from the Integra PrecisionQ database, a fully de-identified oncology dataset comprising records of ~2.2 million pts with cancer across >500 US care sites.
- Metastatic status and biomarker information were verified through manual chart review of clinical notes and genomic/pathology reports, and *ROS1* abstraction captured the type of biomarker test and documentation of test result.
- Descriptive analyses examined testing status by patient demographics, Eastern Cooperative Oncology Group performance status (ECOG PS), recurrent vs de novo presentation, and treatment patterns.
- Exclusion criteria included patients with other primary cancers and those enrolled in clinical trials during the observation period.

Results

- Of 12,540 curated patients, 11,333 (90%) received a biomarker test and 10,124 (81%) were tested for *ROS1*.
- Mean age and race did not differ by *ROS1* testing status, but females were slightly more likely to be tested (Table 1).

Results

Table 1. Baseline Clinical and Demographic Characteristics of mNSCLC Patients by *ROS1* Test Status

	Received ROS1 test (n=10,124)	No ROS1 test (n=2416)	*P*
Median age, years [min-max]	70.0 [24.0-90.0]	70.0 [27.0-90.0]	0.09
Sex, n (%)	**n=10,085**	**n=2411**	
Female	5184 (51.4)	1163 (48.2)	<0.01
Male	4901 (48.6)	1248 (51.8)	
Unknown	*39*	*5*	
Payer, n (%)	**n=6553**	**n=1576**	
Commercial	1874 (28.6)	477 (30.3)	
Self-Pay	164 (2.5)	34 (2.2)	0.57
Medicare/Medicaid	4515 (68.9)	1065 (67.6)	
Unknown	*3571*	*840*	
Race, n (%)	**n=8816**	**n=2002**	
American Indian or Alaska Native	8 (0.1)	3 (0.1)	
Asian	240 (2.7)	31 (1.5)	
Black or African American	1113 (12.6)	280 (14.0)	0.14
Native Hawaiian/Other Pacific Islander	6 (0.1)	0 (0.0)	
White	7449 (84.5)	1688 (84.3)	
Unknown	*1308*	*414*	
Ethnicity, n (%)	**n=7884**	**n=1885**	
Hispanic or Latino	218 (2.8)	42 (2.2)	0.42
Not Hispanic or Latino	7666 (97.2)	1843 (97.8)	
Unknown	*2240*	*531*	
Smoking history, n (%)	**n=10,060**	**n=2400**	
Current Use – Active	2,944 (29.3)	815 (34.0)	
Never	1485 (14.8)	262 (10.9)	<0.01
Previous Use	5631 (56.0)	1323 (55.1)	
Unknown	*64*	*16*	
ECOG, n (%)	**n=7260**	**n=1483**	
ECOG 0	2574 (35.5)	458 (30.9)	
ECOG 1	3401 (46.8)	700 (47.2)	<0.01
ECOG 2+	1285 (17.7)	325 (21.9)	
Unknown	*2864*	*933*	
Diagnosis type, n (%)	**n=10,124**	**n=2416**	
De novo	5111 (50.5)	921 (38.1)	<0.01
Recurrence	5013 (49.5)	1495 (61.9)	
Unknown	*0*	0	

Table 2. Type of Genomic Panel Received by *ROS1*-Tested Patients

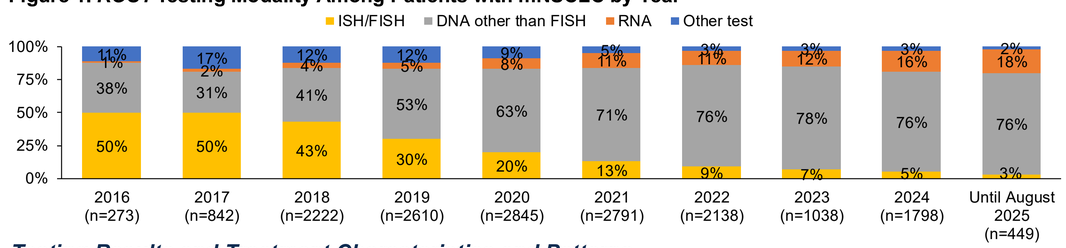
Type of Genomic Test	n	All Patients with *ROS1* Test* (n=10,124)	Total Number of Tests (n=13,611)
RNA	1461	14.4%	10.7%
ISH/FISH	3452	34.1%	25.4%
DNA other than FISH	7552	74.6%	55.5%
Other test	1146	11.3%	8.4%

*Patients may have had multiple tests.

Table 3. *ROS1* Testing Among mNSCLC Patients by Testing Category and Sample Type

	n	%
Testing Category		
Somatic	8523	98.0%
Germline	130	0.6%
Both	122	1.4%
Sample Type		
Solid Tumor Tissue	4686	47.6%
Blood	2312	23.5%
Both	2837	28.8%

Figure 1. *ROS1* Testing Modality Among Patients with mNSCLC by Year



Testing Results and Treatment Characteristics and Patterns

- Most *ROS1*-tested patients (n=7881; 78%) had a result before starting mNSCLC first-line therapy (m1L), and 141 (1.4%) were *ROS1*-positive.
- Of 141 *ROS1*-positive patients, 132 initiated m1L therapy and 109 of those patients (83%) began treatment after a confirmed positive result (median of 23 days from test result to treatment).
- ROS1 TKIs were used in m1L in 40% (44/109) of patients, primarily crizotinib (n=17) or entrectinib (n=11). The remaining 65 patients received chemotherapy, immunotherapy, or non-ROS1 TKIs, including 13 who utilized an EGFR TKI and had an identified EGFR co-mutation and 8 who received a ROS1 TKI in a later line of therapy.

Study Limitations

- The study uses secondary data collected from EHRs and curation of unstructured data and medical notes. As such, some degree of missingness may be present in the data that cannot be verified through patient re-contact.
- A data curation process was used to ascertain clinical and treatment characteristics and is limited to practices where EHR access is granted for manual abstraction. This leads to smaller study sample size that may affect study representativeness and precision of effect estimates. The ROS1-positive patients in this study likely includes those that do not have an actionable ROS1 alteration.
- No single testing method achieves 100% sensitivity for ROS1 fusions; therefore, the testing landscape of ROS1 is challenging due to limitations of available modalities.[1]

CONCLUSIONS

- Of all patients who had an identified test, 81% received a *ROS1* test; however, only 14% of patients received the gold-standard RNA test and only 40% of *ROS1*-positive mNSCLC patients utilized a ROS1-specific TKI in the metastatic 1L setting.

Reference:
1. Davies KD, Le AT, Sheren J et al. Comparison of Molecular Testing Modalities for Detection of ROS1 Rearrangements in a Cohort of Positive Patient Samples. *J Thorac Oncol*. 2018 Oct;13(10):1474-1482.