Coding Trends of Single Gene and Next Generation Sequencing Tests for Patients With Advanced Non-Small Cell Lung Cancer Using an Electronic Health Record (EHR)-Linked Claims Database

RWD35

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INTRODUCTION

- Studies of the prevalence and outcomes associated with genomic tests are difficult to conduct with claims data and, instead, tend to rely on EHR or chart abstraction.[1-3]
- Limitations of claims data include:
  - Lack of specific billing codes (until recently)
  - Coding systems not keeping up with rapid evolution of genomic testing
  - No unified coverage policies and/or billing guidelines
- Being able to accurately identify genomic tests in claims data would facilitate evaluation of:
  - Testing trends over time
  - Outcomes, including economic evaluation, for different testing modalities
  - Adherence/divergence from clinical guidelines

AIM

- This retrospective observational study explored how to identify single gene tests (SGT) and next generation sequencing (NGS) tests in claims data using the Flatiron Health nationwide longitudinal de-identified EHR-derived database linked with the Komodo Healthcare Map™ database.

Objective	Outcomes
Assess the proportion of genomic tests, both SGT and NGS, in the Flatiron Health database that have matching claims in the Komodo database within ± 30 days of the result date	• The proportion of SGT with matching claims within ± 30 days of the result date • The proportion of NGS tests with matching claims within ± 30 days of the result date
Understand the different coding methods by which NGS tests are billed	• The proportion of NGS tests identified by different coding algorithms

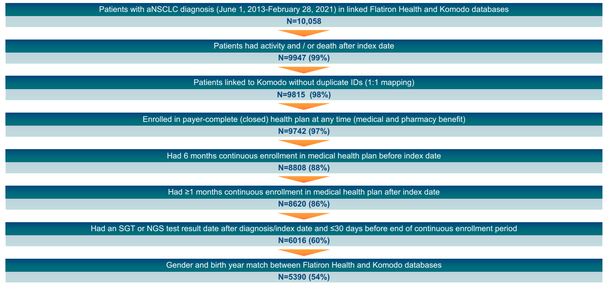
METHODS

Study design

Study population	• Adults with diagnosis of advanced (stage III or IV) non-small cell lung cancer (aNSCLC) in the Flatiron Health database linked 1:1 with the Komodo database – ≥ 2 documented visits within study period – Activity and death after index date – No duplicate IDs • Inclusion criteria listed in **Figure 1**
Databases	• The Flatiron Health database comprises patient-level structured and unstructured data, curated via technology-enabled abstraction. During the study period, the data originated from approximately 280 US cancer clinics (~800 sites of care).[4,5] • The Komodo Health Healthcare Map™ consists of proprietary real-time commercial claims activity data on 330 Million US patients and their interactions with the US healthcare system.
Selection period	aNSCLC diagnosis date documented June 1, 2013, through February 28, 2021
Index date	Date of aNSCLC diagnosis as documented in the Flatiron Health database
Matching claim	Any biomarker testing claim documented in Komodo that is within ± 30 days of a documented SGT or NGS test in Flatiron Health
Methods used to identify genomic tests	A comprehensive list of specific and non-specific laboratory and/or current procedural terminology (CPT) codes for identifying SGT and NGS tests (**Figure 2**)

Figure 1. Selection of Study Population

Figure 1: The study population of 5390 patients had 6770 SGT and 2873 NGS tests identified in their EHR.



RESULTS

Table 1. Study Population

Characteristic	Flatiron (N=5390)	Komodo (N=5390)
Age, mean (SD)		
	65.9 (9.2)	65.9 (9.2)
Gender, n (%)		
Female	2780 (51.6)	2780 (51.6)
Male	2610 (48.4)	2610 (48.4)
Race and ethnicity, n (%)		
White	3520 (65.3)	
Black or African American	529 (9.8)	
Asian	223 (4.1)	
Hispanic or Latino	4 (0.1)	
Other or unknown	1114 (20.7)	
Region, n (%)		
Northeast	1144 (21.2)	
South	1800 (33.4)	
Midwest	999 (18.5)	
West	696 (12.9)	
Other	28 (0.5)	
Not reported	723 (13.4)	
Practice type, n (%)		
Community	4746 (88.1)	
Academic	644 (11.9)	

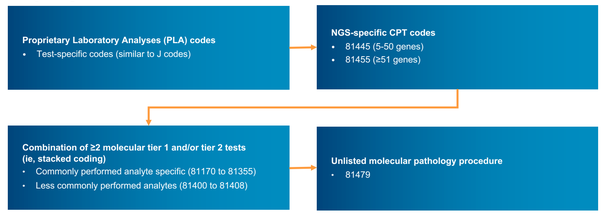
We ensured 1:1 linking of the Flatiron Health and Komodo databases by excluding any patients with discordant age and/or gender across both databases.

Developing Hierarchical Algorithm to Identify NGS tests

- To identify NGS tests in claims data, we implemented a hierarchical algorithm with strict criteria in which highly specific codes superseded less specific codes (**Figure 2A**).
- To increase matching yields, we implemented a modified algorithm with more lenient criteria (**Figure 2B**).

Figure 2. Hierarchical Algorithms to Identify NGS Tests in Claims

A. Original Algorithm With Strict Criteria



B. Modified Algorithm With Lenient Criteria

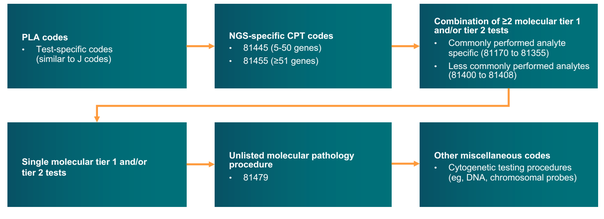
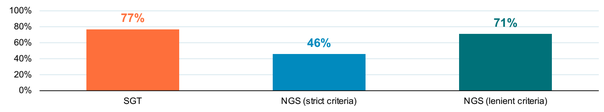


Figure 3. Percentage of Genomic Tests With Matching Claims

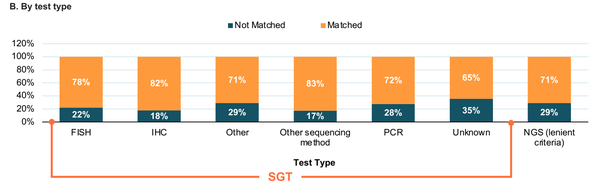
Interpretation (Figure 3)

Most genomic tests in the Flatiron Health database, including 71% of NGS tests had a matching claim identified using lenient criteria.

A. By general categories



B. By test type



FISH, fluorescence in situ hybridization; IHC, immunohistochemistry; PCR, polymerase chain reaction.

Figure 4. Matching Rates for SGT and NGS Tests Over Time

Interpretation (Figure 4)

- SGT had more matching claims than NGS tests identified by strict definition.
- Over time, the matching rates for SGT improved whereas those for NGS tests improved between 2014 and 2019 and were stagnant in 2020.
  - With only 2 months of data from 2021, we could not determine the trends in NGS test matching rates for the whole year.

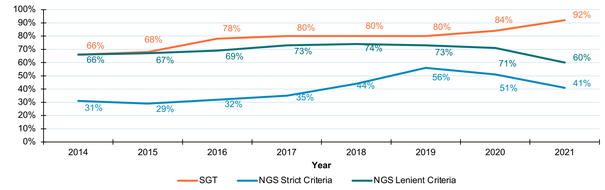
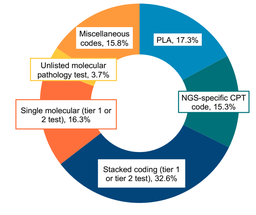


Figure 5. Matching Rates[a] for Components of NGS Coding Algorithm

Interpretation (Figure 5)

Stacked codes (32.6%) and PLA codes (17.3%) were the most used billing methods for NGS tests.



[a]Based on NGS coding categorization for matched tests after applying the hierarchical algorithm.

Table 2. Correlation Matrix of Different NGS Coding Systems

Interpretation (Table 2)

- The applied hierarchical algorithm masked the fact that the coding systems are not mutually exclusive. For example, patients with an NGS-specific CPT code might also have stacked codes, miscellaneous codes, etc.
- The most frequently used coding systems were miscellaneous codes, stacked tier 1 and/or tier 2 test, and unlisted molecular pathology test.

	PLA codes	NGS-specific CPT code	Stacked tier 1 and/or tier 2 test	Single molecular tier 1 or tier 2 test	Unlisted molecular pathology test	Miscellaneous codes	Total
PLA codes	1825	0	0	0	0	0	1825
NGS-specific CPT code	57	1622	0	0	0	0	1679
Stacked tier 1 and/or tier 2 test	246	312	3339	0	0	0	3897
Single molecular tier 1 or tier 2 test	96	167	0	1724	0	0	1987
Unlisted molecular pathology test	170	201	998	350	389	0	2108
Miscellaneous codes	1143	1418	2099	1122	389	1670	7841

LIMITATIONS

- Like other claims database studies, limitations of our study include:
  - Incomplete, inaccurate, and missing coding of data
  - Lack of specificity
  - Uncertain generalizability to other populations
- Due to the variability in coverage for NGS tests, we did not anticipate 100% matching claims as many NGS tests are paid for by patients rather than the payer.

CONCLUSIONS

- Matching rates for SGT were slightly higher than for NGS tests.
  - This is expected given that most payers cover SGTs, providing better access to these tests than to NGS tests.
- The matching rate for NGS tests is contingent on what coding algorithm is applied.
- Researchers need to weigh the tradeoff between specificity and sensitivity of different algorithms when identifying NGS tests.
- This work lays a foundation for future efforts to develop algorithms to identify genomic tests in claims data.

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DISCLOSURES

- IMA, TMT, DS, WW, RR, and SO are employed by Genentech, Inc.