

# Real-World Treatment Pathways of Lung Cancer Patients in Taiwan: A Common Data Model Analysis Using TMUCRD

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## Background

Lung cancer remains the leading cause of cancer-related mortality worldwide, accounting for approximately 1.8 million deaths and 18.7% of all cancer deaths in 2022 (1-3). The study of treatment pathways has emerged as a valuable method for characterizing real-world clinical practice beyond the constraints of randomized clinical trials (4, 5). In the context of lung cancer, these analyses offer critical insights into treatment patterns, including underuse, overtreatment, and therapeutic inertia (4, 6). Given the complexity and rapidly evolving landscape of lung cancer therapeutics, examining real-world treatment sequences presents an opportunity to bridge the gap between evidence-based recommendations and actual clinical practice, ultimately supporting more effective and personalized oncology care.

## **Objective**

To characterize real-world treatment pathways among patients with primary lung cancer by identifying prevailing therapeutic sequences and transitions across multiple lines of therapy by drug class.

## **Method**

This study was conducted using electronic health record (EHR) data from three affiliated institutions of Taipei Medical University: Taipei Medical University Hospital, Shuangho Hospital, and Wanfang Hospital (TMUCRD). The data were transformed into the Observational Medical Outcomes Partnership Common Data Model (OMOP-CDM) format, as standardized by the Observational Health Data Sciences and Informatics (OHDSI) collaborative, to facilitate analysis. Diagnosis and medication information for patients from 2005 to 2020 were extracted for observational research to obtain treatment pathways for lung cancer.

Adult patients (aged  $\geq 18$  years) who were diagnosed with and treated for primary lung cancer were included in the study. The index date was defined as the date of the patient's first exposure to any pharmacologic treatment. Treatment pathways were constructed to visualize the sequence of therapies received across different lines of treatment. Therapeutic exposures were categorized into the following groups: mono-chemotherapy, dual chemotherapy, EGFR inhibitors, fusion, HER2-targeted therapies, cell cycle inhibitors, other targeted therapies, and immune checkpoint inhibitors, including PD-1, PD-L1, CTLA-4, and hormonal therapies. Each pharmacologic treatment was defined at the ingredient level, and combination regimens containing these ingredients were included in the pathway analysis. Events were treated independently, and no minimum patient count threshold was applied for pathway inclusion. The treatment pathways were limited to the first five sequential steps per patient, and each treatment was recorded only once per pathway to avoid duplication. The analyses were performed using ATLAS, an open-source, web-based platform developed by the OHDSI; R (version 4.4.3) with the "TreatmentPatterns" package; and Python (version 3.9.6) (7, 8).

## **Result**

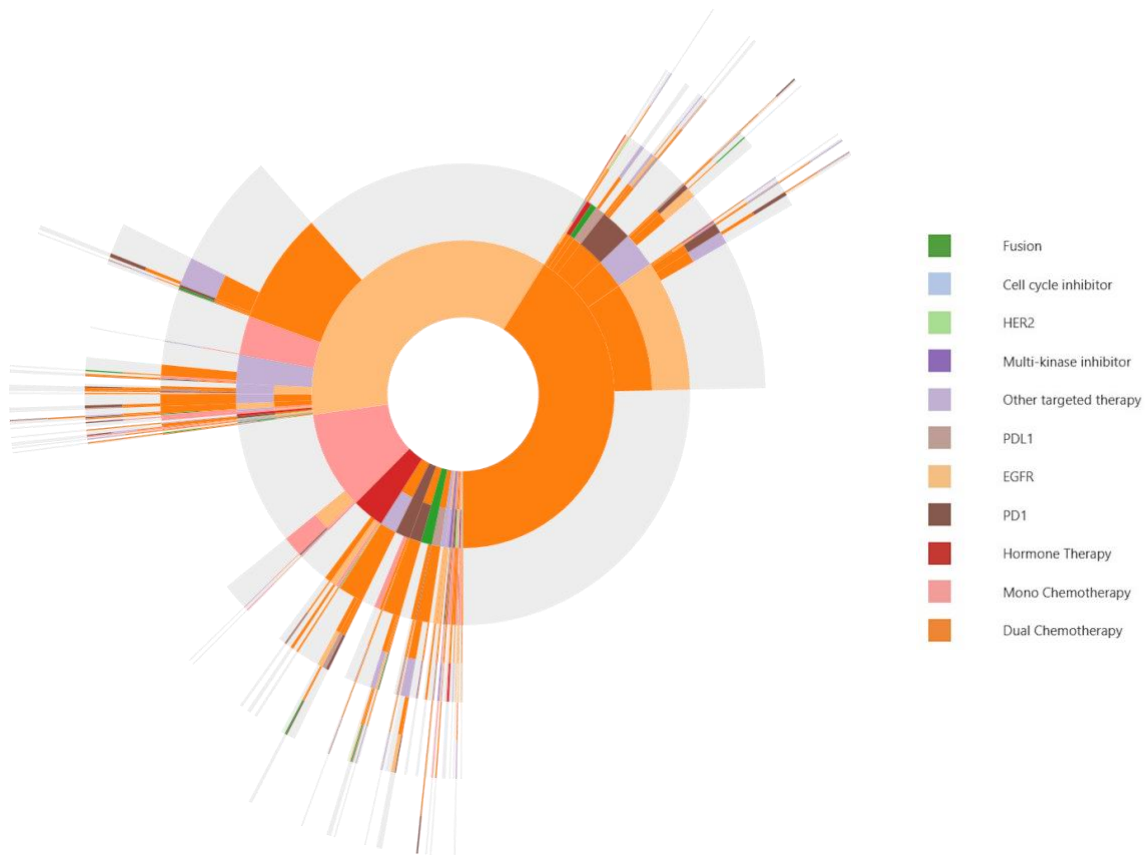
A total of 1,895 adult patients diagnosed and treated for primary lung cancer were included in the analysis. Most patients received only one to three lines of treatment. The most common first-line therapy was dual chemotherapy, administered to 480 patients (25.3%), followed by EGFR-targeted therapy ( $n = 391$ , 20.6%) and mono chemotherapy ( $n = 164$ , 8.6%).

Sequential treatment patterns showed that patients starting with dual chemotherapy frequently moved on to EGFR-based regimens, including combination therapies like “EGFR + dual chemotherapy”. Patients starting with EGFR inhibitors frequently received dual chemotherapy as a subsequent line of therapy, indicating therapeutic cycling based on disease progression. A smaller proportion of patients progressed to targeted combination regimens involving PD-1/PD-L1 inhibitors, fusion-targeted agents, or HER2-directed therapies, typically in third or later lines of treatment.

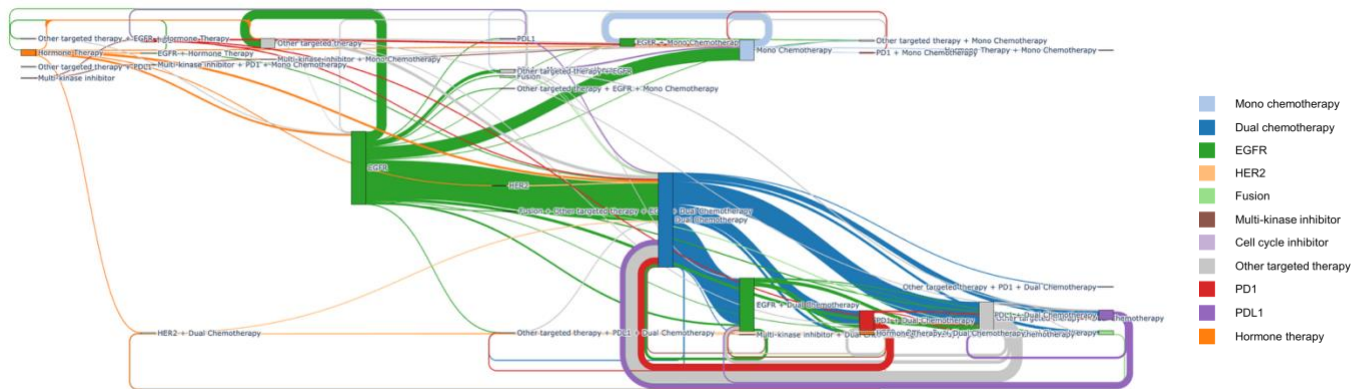
The sunburst and Sankey diagrams highlighted the diversity and complexity of real-world treatment sequences, with a substantial drop-off observed beyond the second-line, and wide heterogeneity in subsequent therapies. Pharmacologic regimens containing the same active ingredients were grouped and analyzed at the therapeutic class level to reflect treatment strategy rather than specific product usage.

## **Conclusion**

This study highlights the heterogeneous nature of real-world lung cancer treatment pathways, with chemotherapy and EGFR inhibitors as predominant first-line therapies and a gradual integration of targeted and immunotherapies in later lines. Mapping these sequences provides critical insights into treatment effectiveness, variation in care, and opportunities for optimization. To improve outcomes and promote equitable, evidence-based cancer care, further multinational and cross-disciplinary research is essential. Such efforts will enhance the global understanding of treatment patterns, support policy development, and bridge the gap between clinical guidelines and practice.



**Figure 1. Sunburst visualization of lung cancer treatment pathways by therapeutic categories and treatment sequence**



**Figure 2. Sankey diagram of lung cancer treatment sequences by therapeutic categories**

## References

1. Wu Z, Xia F, Lin R. Global burden of cancer and associated risk factors in 204 countries and territories, 1980–2021: a systematic analysis for the GBD 2021. *Journal of Hematology & Oncology*. 2024;17(1):119.
2. Zhou J, Xu Y, Liu J, Feng L, Yu J, Chen D. Global burden of lung cancer in 2022 and projections to 2050: Incidence and mortality estimates from GLOBOCAN. *Cancer Epidemiology*. 2024;93:102693.
3. Bray F, Laversanne M, Sung H, Ferlay J, Siegel RL, Soerjomataram I, et al. Global cancer statistics 2022: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. *CA: a cancer journal for clinicians*. 2024;74(3):229-63.
4. Pucci C, Martinelli C, Ciofani G. Innovative approaches for cancer treatment: Current perspectives and new challenges. *ecancermedicalscience*. 2019;13:961.
5. Sharma P, Jhawar V, Mathur P, Dutt R. Innovation in cancer therapeutics and regulatory perspectives. *Medical oncology*. 2022;39(5):76.
6. Dickson NR, Beauchamp KD, Perry TS, Roush A, Goldschmidt D, Edwards ML, et al. Impact of clinical pathways on treatment patterns and outcomes for patients with non-small-cell lung cancer: real-world evidence from a community oncology practice. *Journal of Comparative Effectiveness Research*. 2022;11(8):609-19.
7. Hripcsak G, Ryan PB, Duke JD, Shah NH, Park RW, Huser V, et al. Characterizing treatment pathways at scale using the OHDSI network. *Proceedings of the National Academy of Sciences*. 2016;113(27):7329-36.
8. Zhang X, Wang L, Miao S, Xu H, Yin Y, Zhu Y, et al. Analysis of treatment pathways for three chronic diseases using OMOP CDM. *Journal of medical systems*. 2018;42:1-12.