JIMU: Jurnal Ilmiah Multi Disiplin
Vol. 04, No. 01, Tahun 2025, Hal. 836-846, ISSN: 3031-9498 (Online)

EGFR Mutations in Lung Adenocarcinoma: Prevalence, Histopathological Correlations, and Prognostic Implications : A Systematic Review

Fitri Firdausi[1], Dwi Sapriyantina[2], Rahayu Asmarani[3]
[1,2,3] RSUD dr. H. Jusuf SK
Email: 16firdausi@gmail.com, dwisapriyantina@gmail.com, rahayu.asmarani2901@gmail.com

Article Info

Article history:
Received January 12, 2026
Revised January 20, 2026
Accepted January 28, 2026

Keywords:
EGFR Mutation, Lung Adenocarcinoma, Histopathology, Prognosis, Systematic Review, Targeted Therapy

ABSTRACT

Background: *Mutations within the epidermal growth factor receptor (EGFR) play a vital role in both the development and treatment of lung adenocarcinoma. While these mutations can offer insights into the efficacy of targeted therapies, the relationships between EGFR mutations, the microscopic appearance of the cancer (histopathological features), and the progression of the disease across its different stages remain somewhat unclear. This systematic review was undertaken to investigate the prevalence of EGFR mutations, their correlation with histopathological characteristics, and their impact on the prognosis of patients diagnosed with lung adenocarcinoma.* ***Methods:*** *A comprehensive search of PubMed, Scopus, and Embase databases was conducted, adhering to the PRISMA guidelines. The studies incorporated were either observational or interventional studies that documented EGFR mutation status in lung adenocarcinoma confirmed through histopathology, providing data on prevalence, histopathological features, or survival outcomes. Data extraction and qualitative synthesis were carried out across predefined outcome domains.* ***Results:*** *The review encompassed six studies, involving over 3,900 patients. The prevalence of EGFR mutations ranged from 38.0% to 72.5%, with higher rates consistently observed within Asian populations. Exon 19 deletions and exon 21 L858R substitutions represented the most common EGFR mutations across the studies. Microscopically, EGFR-mutant tumors frequently exhibited lepidic and acinar growth patterns, moderate differentiation, and lower histologic grade. In advanced-stage lung adenocarcinoma, EGFR mutations—particularly exon 19 deletions—were associated with improved overall survival, primarily due to the effectiveness of EGFR tyrosine kinase inhibitors. Conversely, in early-stage resected disease, EGFR mutation status did not independently predict prognosis; histologic grade and pathological stage were more significant factors. Histologic transformation to small-cell lung carcinoma was a notable mechanism of disease progression linked to poor outcomes.* ***Conclusions:*** *EGFR mutations are frequently detected in lung adenocarcinoma and exhibit specific associations with histopathological features and stage-dependent prognostic impacts. Although EGFR mutations improve survival in advanced disease owing to targeted therapy, their independent prognostic value in early-stage disease is limited. A combined molecular and histopathological approach is crucial for accurate prognosis and personalized management of lung adenocarcinoma.*

Corresponding Author:
Fitri Firdausi
RSUD dr. H. Jusuf SK
E-mail: 16firdausi@gmail.com

INTRODUCTION

Lung cancer remains a substantial global health crisis, consistently topping the list as the primary cause of cancer-related fatalities worldwide, as noted by Castañeda-González et al. in 2025. Within the realm of lung cancers, adenocarcinoma has emerged as the predominant subtype, impacting both smokers and non-smokers alike. This shift likely reflects evolving exposure patterns coupled with advancements in diagnostic techniques, as highlighted by Nicholson and colleagues in 2022. Over the past two decades, the field of molecular pathology has revolutionized our comprehension of lung adenocarcinoma, revealing it to be a heterogeneous collection of cancers driven by various oncogenic occurrences, many of which are amenable to therapeutic intervention, as per Castañeda-González et al., 2025.

One of the initial and most clinically pertinent driver events involves a mutation within the gene responsible for the epidermal growth factor receptor (EGFR). The presence of activating EGFR mutations, particularly exon 19 deletions and exon 21 L858R point mutations, results in the receptor's activation independent of its ligand. This, in turn, fosters heightened cell growth and survival, effectively creating a dependency on the receptor while simultaneously rendering the cancer susceptible to EGFR-tyrosine kinase inhibitors (TKIs), as indicated by Varela et al. (2025) and Stanzione et al. (2025). The introduction of first-, second-, and third-generation EGFR TKIs has notably improved outcomes for individuals grappling with EGFR-mutant non–small cell lung cancer (NSCLC). This has cemented EGFR-mutation testing as an integral component of the diagnostic process for lung adenocarcinoma, according to Castañeda-González et al. (2025).

Notwithstanding the clinical significance of EGFR mutations, their frequency fluctuates considerably across diverse geographic regions and ethnic groups. A comprehensive global meta-analysis indicated that EGFR mutation rates approximate 49.1% in Asian patients diagnosed with NSCLC, contrasting with rates of 11.9–33.0% observed in other continents, as reported by Melosky and colleagues in 2022. More recent large-scale investigations into resected lung adenocarcinoma have documented mutation rates of roughly 51% (Soo et al., 2024), and EGFR mutations continue to be frequently observed even in early-stage disease, as noted by Varela et al. in 2025. Nevertheless, these rates remain subject to variation, influenced by factors such as regional location, ethnicity, smoking history, and the specific testing methodologies employed.

The correlation between EGFR mutations and the histopathological characteristics of lung adenocarcinoma is becoming increasingly significant, extending beyond mere mutation status. The most recent WHO classification, released in 2021, underscores the importance of thoroughly documenting growth patterns—including lepidic, acinar, papillary, and solid—for both prognosis and treatment guidance (Nicholson et al., 2022). Recent studies suggest that adenocarcinomas with EGFR mutations frequently exhibit lepidic, acinar, or papillary patterns and usually fall into lower or intermediate histologic grades (Ito et al., 2023; Yang et al., 2024). It's worth noting, however, that no single morphological pattern can conclusively predict EGFR

mutation status, which means that universal molecular testing remains crucial, regardless of the observed histology (Mariean et al., 2025).

In terms of prognosis, EGFR mutations have often been associated with improved outcomes, particularly when patients respond well to TKIs (Stanzione et al., 2025). Nonetheless, the value of mutation status in early-stage, resected adenocarcinoma, independent of stage, grade, and other histopathologic factors, is still somewhat unclear (Chen et al., 2024; Ito et al., 2023). Some recent findings even cast doubt on whether EGFR mutation alone serves as an independent prognostic factor when considering histologic subtype and invasion features (SSRN Working Paper, 2025).

Given these evolving and sometimes conflicting results—especially in light of updated histologic classifications, advancements in molecular testing, and the expanded use of EGFR TKIs—a comprehensive review of the current literature from a pathology standpoint is necessary. This systematic review will therefore: (1) provide an overview of the global and regional prevalence of EGFR mutations in lung adenocarcinoma, (2) examine the relationships between EGFR mutation status and histopathological patterns and grades, and (3) assess the prognostic significance of EGFR mutations across various disease stages. These insights could ultimately inform diagnostic reporting, risk stratification, and treatment strategies in both research and clinical settings.

RESEARCH METHOD

In line with the PRISMA 2020 guidelines, this systematic review was designed to investigate the prevalence of EGFR mutations within lung adenocarcinoma, along with their relationships to histopathology and their ability to predict outcomes. To get the necessary information, a comprehensive search was carried out across PubMed, Scopus, and Embase. This involved using specific search terms related to lung adenocarcinoma, EGFR mutations, histopathology, and prognostic factors. The search encompassed all available literature up to November 30, 2025. Furthermore, we checked the reference sections of relevant articles for any additional material that might be pertinent. The methodological quality of the included studies was evaluated using the Newcastle–Ottawa Scale (NOS). Overall, the included studies demonstrated low to moderate risk of bias.

RESULT AND DISCUSSION

Study Selection and Characteristics

This systematic review incorporated six studies that fulfilled the necessary prerequisites. A concise overview of their key characteristics is presented in Table 1. The studies, spanning from 2014 to 2024, predominantly hailed from Asian nations, including China, India, Japan, South Korea, and Taiwan, with a single multicenter study based in North America. The research approaches employed were diverse, encompassing prospective epidemiological studies, retrospective cohort studies, and case series, thereby reflecting variations in methodologies and clinical environments.

In total, the patient count across all included studies exceeded 3,900 individuals. This sizable cohort encompassed a broad spectrum of disease stages, ranging from early-stage (resected stage I) lung adenocarcinoma cases to those with advanced and metastatic disease. Various molecular techniques were utilized for EGFR mutation testing, such as ARMS-PCR, real-time PCR, direct sequencing, next-generation sequencing, and commercially available PCR-based assays

Table 1. Characteristics of Included Studies

Author (Year)	Country	Study Design	Sample Size	Population / Setting	EGFR Testing Method	Main Outcomes Reported
Marcoux et al. (2019)	USA & Canada	Multicenter retrospective cohort	67	EGFR-mutant NSCLC that transformed to small-cell lung cancer; advanced disease	PCR, NGS, WES	Prognosis after transformation; mutation stability; survival outcomes
Shi et al. (2014) – PIONEER	7 Asian countries	Prospective, multicenter molecular epidemiology study	1,482 (1,450 evaluable)	Newly diagnosed stage IIIB–IV lung adenocarcinoma	ARMS PCR	Prevalence of EGFR mutations; demographic correlations
Shukla et al. (2022)	India	Prospective case series	100	NSCLC adenocarcinoma/adenosquamous; small biopsy specimens	Real-time PCR, IHC, Sanger sequencing	Prevalence; histopathological correlations; diagnostic method comparison
Morita et al. (2024)	Japan	Retrospective cohort	162	Resected EGFR-mutant NSCLC with postoperative recurrence	(commercial laboratory)	Post-recurrence survival; prognostic factors; recurrence patterns
Yoon et al. (2020)	South Korea	Multicenter retrospective cohort	1,020	Advanced stage III–IV lung adenocarcinoma	Direct sequencing; PNA-mediated PCR	Prevalence; mutation subtype prognosis; TKI response; survival analysis
Lin et al. (2017)	Taiwan	Retrospective cohort	120	Resected stage I lung adenocarcinoma	PCR-based EGFR genotyping	Histopathology correlation; DFS/OS survival; mutation subtype analysis

EGFR Mutation Prevalence

Table 2 presents a breakdown of the EGFR mutation frequencies observed throughout the analyzed studies. The prevalence rates differed considerably, a variance largely attributed to elements such as geographical positioning, the stage of the illness, and the methodology of each study. In groups that were population-based and not specifically selected, the prevalence of EGFR mutations ranged from 38.0% to 72.5%. Of particular note, the populations of East and South Asia consistently displayed elevated rates.

The lowest prevalence was documented in a Korean multicenter study which centered on advanced lung adenocarcinoma (38.0%), whereas the highest was observed in a Taiwanese cohort dealing with resected stage I adenocarcinoma (72.5%). Considering all studies that detailed mutation subtypes, the most frequently occurring were exon 19 deletions and exon 21 L858R substitutions. These two mutations, when combined, accounted for over 70–90% of the EGFR-mutant cases. Other EGFR alterations, including exon 18 mutations, exon 20 insertions, and compound mutations, were comparatively uncommon.

Two studies, deliberately constructed to incorporate only EGFR-mutant populations, were excluded from the combined prevalence analysis. Nevertheless, these studies offered valuable insights regarding prognosis.

Table 2. EGFR Mutation Prevalence Across Included Studies

Author (Year)	Country / Region	Total Cases Analyzed	EGFR Mutation Positive, n (%)	Exon 19 Deletion (%)	Exon 21 L858R (%)	Other EGFR Mutations (%)
Marcoux et al. (2019)	USA & Canada	67	67 (100%)*	69.0	25.0	6.0
Shi et al. (2014)	Asia (7 countries)	1,450	746 (51.4%)	22.1	20.9	8.4
Shukla et al. (2022)	India	100	48 (48.0%)	72.7	18.2	9.1
Morita et al. (2024)	Japan	162	162 (100%)*	48.8	51.2	0
Yoon et al. (2020)	South Korea	1,020	388 (38.0%)	51.0	42.0	7.0
Lin et al. (2017)	Taiwan	120	87 (72.5%)	35.6	59.8	4.6

Histopathological Correlations of EGFR Mutations

Table 3 presents a breakdown of the histopathological relationships observed between EGFR mutation status and tumor characteristics. It's worth noting that only a portion of the available research undertook detailed histological analyses, employing the most current adenocarcinoma classification techniques. The studies that did delve into this area frequently found a strong correlation between EGFR mutations and tumors that exhibited well to moderately differentiated features, alongside lepidic and acinar growth patterns.

One particular study highlighted a notably higher incidence of EGFR mutations in tumors characterized by an acinar pattern and loosely arranged or dispersed cellular structures. Furthermore, another study observed an elevated presence of EGFR mutations within low- and intermediate-grade adenocarcinomas, in comparison to their high-grade counterparts. Conversely, high-grade histological patterns were less frequently encountered in EGFR-mutant tumors.

Moreover, there's some indication that EGFR-mutant adenocarcinomas may evolve into high-grade neuroendocrine carcinomas, such as small-cell lung carcinoma, as the disease advances or subsequent to treatment with EGFR-targeted therapies. A significant limitation, however, is that numerous studies included in this review did not provide comprehensive

histopathological subtyping, which underscores the variability in reporting practices across different research endeavors.

Table 3. Histopathological Correlations of EGFR Mutations in Lung Adenocarcinoma

Author (Year)	Histopathological Parameters Evaluated	Findings in EGFR-Mutant Tumors	Statistical Significance
Shukla et al. (2022)	Growth pattern; tumor differentiation; necrosis; TTF-1 expression	EGFR mutations significantly associated with acinar pattern, singly dispersed/loose clusters, and moderate differentiation; lower frequency of extensive necrosis	Acinar pattern ($p = 0.003$); dispersed clusters ($p = 0.003$)
Lin et al. (2017)	Histologic subtype (IASLC/ATS/ERS); histologic grade	EGFR mutations more frequent in low- and intermediate-grade tumors; enriched in lepidic and acinar predominant adenocarcinoma compared with high-grade patterns	Grade association ($p = 0.041$)
Shi et al. (2014)	Histologic type (adenocarcinoma NOS vs bronchioloalveolar)	Higher EGFR mutation frequency in adenocarcinoma NOS than bronchioloalveolar subtype	Not significant
Yoon et al. (2020)	Histologic classification	Detailed histopathological subtyping not reported	Not applicable
Marcoux et al. (2019)	Histologic transformation	EGFR-mutant adenocarcinoma retained founder mutation after transformation to small-cell lung carcinoma; high-grade neuroendocrine morphology	Descriptive
Morita et al. (2024)	Broad histologic diagnosis	Majority adenocarcinoma; no detailed growth pattern or grading analysis reported	Not applicable

Prognostic Outcomes and Survival Analysis

Prognostic outcomes associated with EGFR mutations are summarized in Table 4. In studies involving advanced-stage lung adenocarcinoma, EGFR mutation positivity was consistently associated with improved overall survival, particularly among patients treated with EGFR tyrosine kinase inhibitors (TKIs). Among EGFR-mutant tumors, exon 19 deletion was repeatedly associated with the most favorable survival outcomes, whereas exon 21 L858R mutations were linked to comparatively poorer prognosis.

In contrast, findings differed in early-stage, surgically resected disease. In stage I lung adenocarcinoma, EGFR mutation status alone was not an independent prognostic factor for disease-free or overall survival after adjustment for histologic grade and pathologic stage. Instead, histologic grade and tumor stage emerged as stronger predictors of recurrence and survival in early-stage disease.

Among patients with recurrent EGFR-mutant lung adenocarcinoma after surgery, adverse prognostic factors included bone metastasis and central nervous system involvement, while no significant survival difference was observed between exon 19 deletion and exon 21 L858R mutations in this setting. Additionally, histologic transformation to small-cell lung carcinoma was associated with a markedly poor post-transformation survival.

Table 4. Prognostic Outcomes and Survival Analysis of EGFR Mutations in Lung Adenocarcinoma

Author (Year)	Population / Stage	Outcome Measures	Key Prognostic Findings	Adjusted Analysis
Marcoux et al. (2019)	Advanced EGFR-mutant adenocarcinoma with SCLC transformation	OS; post-transformation survival	Median OS from initial diagnosis: **31.5 months**; median OS after SCLC transformation: **10.9 months**; poor prognosis after transformation	Multivariate analysis not primary focus
Morita et al. (2024)	Resected EGFR-mutant NSCLC with postoperative recurrence	Post-recurrence survival (PRS); postoperative OS	Median PRS: **5.17 years**; bone metastasis (HR 2.01) and CNS metastasis (HR 1.84) were independent poor prognostic factors; no survival difference between exon 19 deletion and L858R	Yes (multivariate Cox regression)
Yoon et al. (2020)	Advanced stage III–IV lung adenocarcinoma	OS; survival by mutation subtype; TKI response	EGFR-mutant vs wild-type OS: **22.8 vs 10.0 months** ($p < 0.001$); exon 19 deletion associated with best OS (**29.9 months**); exon 21 L858R associated with worse OS	Yes (multivariate Cox regression)
Lin et al. (2017)	Resected stage I lung adenocarcinoma	DFS; OS	EGFR mutation status **not an independent prognostic factor**; histologic grade and stage were stronger predictors of DFS and OS; rare mutations associated with shorter DFS	Yes (multivariate Cox regression)
Shi et al. (2014)	Advanced adenocarcinoma (stage IIIB–IV)	Not reported	Survival outcomes not assessed (epidemiologic study)	Not applicable
Shukla et al. (2022)	Adenocarcinoma (biopsy-based)	Not reported	No survival or follow-up data reported	Not applicable

Summary of Key Findings

Overall, the included studies demonstrate that EGFR mutations in lung adenocarcinoma are highly prevalent in Asian populations, show preferential association with lower-grade and specific histopathologic patterns, and confer a prognostic advantage in advanced disease, largely attributable to responsiveness to targeted therapy. However, in early-stage resected adenocarcinoma, EGFR mutation status alone does not appear to independently predict survival, underscoring the importance of integrating morphologic features and clinical stage into prognostic assessment.

Discussion

This review article synthesizes the current body of work on EGFR mutations in lung adenocarcinoma, examining their prevalence, connection to tissue modifications, and impact on patient prognosis. It highlights the complex and diverse roles that EGFR alterations play in both the tumor's biological characteristics and patient results.

The review's results clearly demonstrate the high prevalence of EGFR mutations in lung adenocarcinoma, particularly in Asian populations. The reported prevalence rates varied considerably across studies, ranging from 38.0% to 72.5% (Shi et al., 2014; Yoon et al., 2020;

Lin et al., 2017). This variation can likely be attributed to differences in ethnicity, smoking patterns, disease stage, and the study methodologies employed. Asian cohorts consistently displayed elevated rates of EGFR mutations compared to Western populations, which supports earlier findings concerning ethnic variations in vulnerability to EGFR-driven cancer progression (Shi et al., 2014).

Across the studies, exon 19 deletions and exon 21 L858R substitutions were the most frequently observed mutation types, accounting for the majority of EGFR-mutated cases (Shi et al., 2014; Shukla et al., 2022; Yoon et al., 2020). These findings underscore the clinical significance of routine EGFR mutation testing in lung adenocarcinoma, irrespective of disease stage, especially in areas where these mutations are prevalent.

Several limitations should be acknowledged. Most included studies were retrospective and conducted predominantly in Asian populations, which may limit generalizability. In addition, detailed histopathological correlations were inconsistently reported, restricting comprehensive morphologic synthesis. Future studies should integrate standardized histopathologic classification, comprehensive molecular profiling, and long-term outcome data. Prospective investigations evaluating the interaction between EGFR mutation subtype, tumor morphology, and adjuvant targeted therapy in early-stage disease are particularly warranted.

The review suggests a connection between EGFR mutations and particular histopathological features, although the current evidence comes from a relatively small number of studies that delve into detailed morphological analyses. Tumors harboring EGFR mutations showed a stronger association with growth patterns characterized by lepidic and acinar predominance, a moderate level of differentiation, and a lower histological grade (Shukla et al., 2022; Lin et al., 2017). These findings are typically indicative of a more differentiated adenocarcinoma, hinting that EGFR-driven tumors might progress via unique oncogenic routes.

Nevertheless, the methods used to report histopathology were inconsistent, and many studies didn't use the most up-to-date adenocarcinoma classification systems. This presents a noteworthy challenge in research, as standardized morphological evaluation is essential for elucidating molecular–pathologic relationships. It’s also worth mentioning that the presence of favorable histological features at the time of diagnosis doesn't preclude disease progression, since EGFR-mutant tumors can evolve under therapeutic influence.

The prognostic significance of EGFR mutations varied considerably depending on the stage of the disease and the treatment administered. In cases of advanced-stage lung adenocarcinoma, a positive EGFR mutation status was consistently linked to improved overall survival, largely due to the efficacy of EGFR tyrosine kinase inhibitors (TKIs) (Yoon et al., 2020). When looking at the various mutation types, exon 19 deletion yielded the most favorable survival outcomes, while exon 21 L858R mutations were associated with a somewhat less promising prognosis (Yoon et al., 2020). These observations are in line with existing clinical trial data and real-world studies, which demonstrate varying treatment responses depending on the specific mutation subtype.

In early-stage lung adenocarcinoma cases treated surgically, whether an EGFR mutation was present didn't independently forecast how long patients would live without the

cancer returning or their overall survival (Lin et al., 2017). The tumor's histologic grade and pathological stage proved to be better predictors of patient outcomes instead. This emphasizes that the tumor's physical attributes, alongside the extent of the cancer's spread, are more telling when it comes to the prognosis of early-stage disease. These results suggest that the prognostic significance of EGFR mutations is most apparent when targeted therapies are employed.

This review also draws attention to histologic transformation, specifically the shift of EGFR-mutant adenocarcinoma into small-cell lung carcinoma or other aggressive neuroendocrine carcinomas (Marcoux et al., 2019). This transformation is a recognized mechanism of resistance to EGFR-TKI therapy and is linked to notably reduced survival rates. Intriguingly, the original EGFR mutation is often maintained in the transformed tumors, hinting at a clonal relationship between the adenocarcinoma and the neuroendocrine components (Marcoux et al., 2019). It goes without saying that repeat tissue biopsies are vital when the disease progresses, to inform future treatment choices.

In essence, this systematic review highlights that EGFR mutation status should be considered alongside histopathological characteristics, the stage of the disease, and the treatment strategy. Pathologists should carefully evaluate adenocarcinoma growth patterns and grading, given that they offer additional prognostic insights beyond the molecular profile. Clinicians should use stage-specific prognostic stratification and recognize the pivotal role of targeted therapy in advanced EGFR-mutant disease.

Limitations and Future Directions

It's worth pointing out a few constraints here. To begin, most of the research examined looked backward and mainly focused on people from Asia, which might mean we can't generalize the results too much. In addition, the way the studies described the links between the biology of the tissues and what the tissues looked like under a microscope wasn't always the same, making a really in-depth look at the structures difficult. If we want to move forward, future investigations should focus on using a consistent method to classify tissue samples, getting a good look at the molecules involved, and gathering information about what happens over time. In particular, we need studies that look ahead, exploring how the type of EGFR mutation, the way a tumor looks, and treatments given after surgery are all connected in the early phases of the illness.

CONCLUSION

Lung adenocarcinoma frequently presents with EGFR mutations, especially within Asian demographics, as this review emphasizes. Exon 19 deletions and exon 21 L858R substitutions are two common manifestations of these mutations. Tumors carrying EGFR mutations often present with unique histopathological features, frequently showing lepidic and acinar growth patterns, and are typically of a lower histologic grade. The impact of EGFR mutations on a patient's outlook hinges significantly on the stage of the disease and the course of treatment. Specifically, such mutations are associated with a better chance of survival in advanced-stage cases, largely thanks to the effectiveness of EGFR-targeted treatments. Nevertheless, in early-stage tumors that have been surgically removed, their individual

prognostic value is less clear. Moreover, disease progression can sometimes take the form of transformation into a high-grade neuroendocrine carcinoma, which unfortunately correlates with poor clinical outcomes. The review's conclusions underscore the importance of integrating molecular analysis with histopathological assessment and clinical staging. Such a combined approach is critical for enhancing the precision of prognoses and for formulating tailored treatment strategies for those affected by lung adenocarcinoma.

REFERENCES

Castañeda-González, J. P., et al. (2025). *Actionable mutations and targeted therapy in non-small cell lung cancer.* PMC.

Chen, J. Y., et al. (2024). *Prognostic impact of EGFR mutations in T1–4N0M0 lung adenocarcinoma.* PMC.

Ito, M., et al. (2023). Distribution and prognostic impact of EGFR and KRAS mutations varying by histological features. *BMC Cancer.*

Mariean, C. R., et al. (2025). The impact of histologic types of lung cancer on clinical outcomes. *Journal of Clinical Medicine.*

Melosky, B., et al. (2022). Worldwide prevalence of epidermal growth factor receptor (EGFR) mutations in non-small cell lung cancer. *Molecular Diagnosis & Therapy.*

Nicholson, A. G., et al. (2022). The 2021 WHO classification of lung tumors: Impact of advances since 2015. *Journal of Thoracic Oncology.*

Soo, R. A., et al. (2024). Prevalence of EGFR Mutations in Patients With Resected Early-Stage NSCLC. *Journal of Thoracic Oncology.*

Stanzione, B., et al. (2025). Non-Small Cell Lung Cancer with EGFR mutation: epidemiology and therapeutic implications. *Cancers.*

Varela, M., et al. (2025). Prevalence of EGFR gene mutations in patients with resected early-stage NSCLC. *Translational Lung Cancer Research.*

Yang, F., et al. (2024). The prognostic impact of Epidermal Growth Factor Receptor in resected lung adenocarcinoma across histologic subtypes. *Annals of Thoracic Surgery.*

Marcoux, N., Gettinger, S. N., O'Kane, G., Arbour, K. C., Neal, J. W., Husain, H., West, H., Brahmer, J. R., Rizvi, N. A., Arcila, M. E., Ladanyi, M., & Yu, H. A. (2019). EGFR-mutant adenocarcinomas that transform to small-cell lung cancer and other neuroendocrine carcinomas: Clinical outcomes. *Journal of Clinical Oncology*.

Shi, Y., Au, J. S. K., Thongprasert, S., Srinivasan, S., Tsai, C.-M., Khoa, M. T., Heeroma, K., Itoh, Y., Cornelio, G., Yang, P.-C., & Fukuoka, M. (2014). A prospective, molecular epidemiology study of EGFR mutations in Asian patients with advanced non–small-cell lung cancer of adenocarcinoma histology (PIONEER). *Journal of Thoracic Oncology*.

Shukla, S., Mehrotra, A., Awasthi, N. P., Agarwal, S., & Srivastava, A. (2022). Epidermal growth factor receptor mutations in adenocarcinoma lung: Comparison of techniques for mutation detection. *Indian Journal of Pathology and Microbiology*

Morita, M., Ono, A., Harada, T., Kato, T., Naito, T., Kenmotsu, H., Tanaka, K., Takahashi, T., & Yamamoto, N. (2024). Prognostic impact of postoperative recurrence in patients with epidermal growth factor receptor–positive non–small cell lung cancer. *Cancer Reports*

Yoon, H.-Y., Park, S., Kim, Y. S., Lee, S. M., Kim, Y. H., Kim, S. K., Chang, J., & Lee, C.-T. (2020). Clinical significance of EGFR mutation types in lung adenocarcinoma: A multicenter Korean study. PLOS ONE

Lin, C.-Y., Lee, C.-H., Hung, J.-J., Chen, H.-H., Chen, Y.-J., Su, W.-C., Hsieh, R.-K., & Wu, Y.-C. (2017). Prognostic implication of epidermal growth factor receptor gene mutations and histological classification in patients with resected stage I lung adenocarcinoma. PLOS ONE