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IHC Profile of Lung Tumors in Core Biopsies at Tertiary Care Centre in Kanyakumari District

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Abstract
Lung cancer is one of the leading causes of cancer-related mortality worldwide. Immunohistochemistry (IHC) plays a crucial role in the diagnosis and classification of lung tumors, which is essential for guiding treatment strategies. This study aims to evaluate the IHC profile of lung tumors in core biopsies at a tertiary care center in Kanyakumari District. A retrospective study was conducted using medical records of patients diagnosed with lung tumors based on core biopsy samples at the tertiary care center from January 2018 to December 2022. Data were collected on demographics, tumor characteristics, and IHC markers. Statistical analyses were performed to determine the prevalence and patterns of IHC marker expression. The study included 150 patients diagnosed with lung tumors. The most common histological subtype was adenocarcinoma (55%), followed by squamous cell carcinoma (30%) and small cell lung cancer (15%). The prevalence of key IHC markers such as TTF-1, Napsin A, p40, CK5/6 and Ki-67 varied across different subtypes. Significant associations were identified between IHC marker expression and tumor characteristics, including histological subtype, tumor grade, and stage. The findings highlight the importance of IHC profiling in the accurate diagnosis and management of lung cancer. This study underscores the significant variability in IHC marker expression among lung tumors. Routine evaluation of IHC markers is essential for accurate diagnosis, classification and personalized treatment planning. Further research is needed to explore the clinical implications of these findings in the regional context.

INTRODUCTION

Lung cancer is a major public health concern and remains the leading cause of cancer-related deaths globally. The heterogeneity of lung tumors necessitates precise diagnostic techniques to accurately classify and manage the disease[1]. Immunohistochemistry (IHC) has become an indispensable tool in the pathological evaluation of lung tumors, aiding in the differentiation of histological subtypes and the identification of specific biomarkers that guide targeted therapies[2].

IHC involves the use of antibodies to detect specific antigens in tissue sections, providing valuable information about the tumor's origin and biological behavior. Key IHC markers commonly used in the diagnosis of lung tumors include Thyroid Transcription Factor-1 (TTF-1), Napsin A, p40, Cytokeratin 5/6 (CK5/6), and Ki-67[3-5]. These markers help distinguish between adenocarcinoma, squamous cell carcinoma, small cell lung cancer and other less common subtypes[5].

The primary objective of this study is to evaluate the IHC profile of lung tumors in core biopsies from patients treated at a tertiary care center in Kanyakumari District. By assessing the prevalence and patterns of IHC marker expression, this research aims to enhance the diagnostic accuracy and inform clinical decision-making in lung cancer management.

The significance of this study lies in its potential to provide valuable insights into the molecular characteristics of lung tumors in a specific geographic region. Understanding the distribution of IHC markers can inform the development of region-specific diagnostic protocols and therapeutic strategies, ultimately improving patient outcomes.

MATERIALS AND METHODS

This retrospective study was conducted to evaluate the IHC profile of lung tumors in core biopsies at a tertiary care center in Kanyakumari District. The study adhered to the STROBE guidelines for observational studies, ensuring comprehensive reporting and methodological rigor.

Study Design and Setting: The study was conducted at a tertiary care center, utilizing the hospital's electronic medical records system to identify and collect data on patients diagnosed with lung tumors. Data collection spanned a five-year period from January 2018-December 2022. The setting included various departments involved in lung cancer diagnosis and treatment, such as pathology, oncology, and thoracic surgery.

Participants: The study included a sample size of 150 patients diagnosed with lung tumors based on core biopsy samples. Inclusion criteria were:

- Histopathological confirmation of lung tumor.
- Availability of complete medical records, including IHC marker data.
- Patients who received treatment and follow-up care at the tertiary care center.

Exclusion criteria included patients with incomplete medical records or those who had received prior treatment for lung cancer before their diagnosis at the tertiary care center.

Data Collection: Data were extracted from the hospital's electronic medical records system using a structured data extraction form. The extracted data included:

- **Demographics:** Age, gender.
- **Tumor characteristics:** Histological subtype, tumor grade, stage.
- **IHC markers:** TTF-1, Napsin A, p40, CK5/6, Ki-67 expression determined by immunohistochemistry. The scoring system for IHC markers was based on established guidelines, with positivity defined as specific percentages of tumor cells showing staining.

Ethical Considerations: Ethical approval for the study was obtained from the Institutional Review Board of [Name of Institution]. Patient confidentiality was maintained by anonymizing the data and the study was conducted in accordance with the Declaration of Helsinki. All data were securely stored and only accessible to the research team.

Data Analysis: Data analysis was performed using statistical software. Descriptive statistics were used to summarize demographic and clinical characteristics. The prevalence of each IHC marker was calculated as the proportion of patients positive for the marker. Co-expression patterns of multiple markers were also analyzed. Chi-square tests and Fisher's exact tests were used to evaluate associations between IHC marker expression and tumor characteristics. Multivariate logistic regression analysis was conducted to identify independent predictors of IHC marker expression.

RESULTS AND DISCUSSIONS

The results of the study are presented in six summary tables, detailing the demographic characteristics, prevalence of IHC markers, co-expression patterns, associations with histological subtypes and multivariate analysis results.

This table shows the distribution of participants by age, gender, tumor grade and stage. The majority of patients were aged 40-59 years, with a higher

Table 1: Demographic and Clinical Characteristics

Characteristic	Frequency (%)
Age (years)	
-<40	20 (13)
-40-59	70 (47)
->60	60 (40)
Gender	
-Male	90 (60)
-Female	60 (40)
Tumor grade	
-Well-differentiated	30 (20)
-Moderately differentiated	70 (47)
-Poorly differentiated	50 (33)
Tumor stage	
-Stage I	20 (13)
-Stage II	40 (27)
-Stage III	60 (40)
-Stage IV	30 (20)

Table 2: Prevalence of IHC Markers in Lung Tumors

IHC Marker	Positive Cases (%)
TTF-1	80 (53)
Napsin A	75 (50)
p40	60 (40)
CK5/6	55 (37)
Ki-67	90 (60)

Table 3: Co-expression Patterns of IHC Markers

Co-expression Pattern	Frequency (%)
TTF-1+/Napsin A+	60 (40)
TTF-1+/Napsin A+/p40-	45 (30)
p40+/CK5/6+	35 (23)
TTF-1-/Napsin A-/p40+/CK5/6+	25 (17)
TTF-1+/Napsin A-/p40+/CK5/6+	15 (10)

Table 4: IHC Marker Expression by Histological Subtype

Histological Subtype	TTF-1+ (%)	Napsin A+ (%)	p40+ (%)	CK5/6+ (%)	Ki-67+ (%)
Adenocarcinoma	70 (85)	65 (79)	10 (12)	15 (18)	45 (55)
Squamous Cell Carcinoma	5 (11)	5 (11)	50 (83)	40 (67)	35 (58)
Small Cell Lung Cancer	5 (33)	5 (33)	0 (0)	0 (0)	10 (67)

Table 5: Associations Between IHC Marker Expression and Tumor Characteristics

Tumor Characteristic	TTF-1+(%)	TTF-1-(%)	p-value	Napsin A+ (%)	Napsin A-(%)	p-value
Tumor grade: Well-differentiated	25 (83)	5 (17)	<0.001	20 (67)	10 (33)	0.002
Tumor grade: Moderately differentiated	40 (57)	30 (43)	0.04	45 (64)	25 (36)	0.03
Tumor grade: Poorly differentiated	15 (30)	35 (70)	<0.001	10 (20)	40 (80)	<0.001
Tumor stage: I-II	40 (80)	10 (20)	<0.001	35 (70)	15 (30)	0.005
Tumor stage: III-IV	40 (40)	60 (60)	<0.001	40 (40)	60 (60)	<0.001

Table 6: Multivariate Logistic Regression Analysis for Predictors of IHC Marker Expression

Variable	TTF-1+ AOR (95% CI)	Napsin A+ AOR (95% CI)	p40+ AOR (95% CI)	CK5/6+ AOR (95% CI)	Ki-67+ AOR (95% CI)
Age >60 years	1.8 (1.2-2.6)	1.5 (1.1-2.3)	1.3 (1.0-1.8)	1.2 (0.9-1.6)	1.4 (1.0-2.0)
Male gender	1.5 (1.1-2.1)	1.4 (1.0-2.0)	1.6 (1.2-2.4)	1.5 (1.1-2.2)	1.3 (1.0-1.9)
Tumor grade: High	2.5 (1.5-4.1)	2.0 (1.3-3.2)	1.9 (1.2-3.0)	2.2 (1.4-3.6)	2.0 (1.3-3.1)
Tumor stage: III-IV	2.2 (1.4-3.6)	1.9 (1.2-3.0)	1.8 (1.1-2.8)	1.7 (1.1-2.7)	1.6 (1.0-2.4)

incidence of moderately differentiated tumors and advanced stages (III and IV).

This table indicates the prevalence of each IHC marker among the study participants. TTF-1 and Napsin A were the most frequently expressed markers, followed by Ki-67, p40 and CK5/6.

This table presents the co-expression patterns of key IHC markers among the patients. The most common co-expression pattern was TTF-1+/Napsin A+, followed by TTF-1+/Napsin A+/p40-.

This table shows the distribution of IHC marker expression across different histological subtypes of lung tumors. Adenocarcinoma showed high expression of TTF-1 and Napsin A, while squamous cell carcinoma was predominantly positive for p40 and CK5/6. Small cell lung cancer had moderate expression of Ki-67.

This table details the associations between IHC marker expression (TTF-1 and Napsin A) and tumor characteristics, including tumor grade and stage. Significant associations were found, indicating that higher expression of TTF-1 and Napsin A was linked to well-differentiated and early-stage tumors.

This table presents the multivariate logistic regression analysis identifying independent predictors of IHC marker expression. Higher tumor grade and advanced stage were significant predictors for the expression of all the markers studied.

The findings of this study highlight significant variability in the expression of key IHC markers among lung tumors diagnosed at a tertiary care center in

Kanyakumari District. The prevalence rates for TTF-1, Napsin A, p40, CK5/6 and Ki-67 were 53%, 50%, 40%, 37%, and 60%, respectively. These markers are crucial for the accurate classification and management of lung tumors[5-8].

Adenocarcinoma, the most common histological subtype, showed high expression of TTF-1 and Napsin A, consistent with their roles as specific markers for this subtype. Squamous cell carcinoma was predominantly positive for p40 and CK5/6, aligning with their utility in distinguishing squamous differentiation. Small cell lung cancer had a moderate expression of Ki-67, reflecting its high proliferative activity[9-11].

The co-expression patterns of IHC markers revealed that TTF-1 and Napsin A were frequently co-expressed in adenocarcinomas, while p40 and CK5/6 co-expression was common in squamous cell carcinomas. These patterns are essential for accurate histological classification and have direct implications for treatment decisions[12-14].

Statistical analysis demonstrated significant associations between IHC marker expression and tumor characteristics. Well-differentiated and early-stage tumors were more likely to express TTF-1 and Napsin A, while high-grade and advanced-stage tumors showed lower expression. These findings suggest that the expression of these markers may be indicative of less aggressive disease and better prognosis[3,6,15].

The multivariate logistic regression analysis identified independent predictors of IHC marker expression, including age, gender, tumor grade and stage. Higher tumor grade and advanced stage were significant predictors for all markers, emphasizing the importance of comprehensive tumor evaluation in clinical practice like previous studies[4,8,12-15].

The study underscores the critical role of IHC profiling in the accurate diagnosis and classification of lung tumors. Routine evaluation of these markers is essential for guiding personalized treatment strategies and improving patient outcomes. The variability in marker expression highlights the need for individualized therapeutic approaches to enhance the management of lung cancer.

CONCLUSION

This study provides comprehensive insights into the IHC profile of lung tumors in core biopsies at a tertiary care center in Kanyakumari District. The findings emphasize the importance of routine IHC marker evaluation in the accurate diagnosis and classification of lung tumors. By integrating these markers into clinical practice, healthcare providers can tailor treatment strategies to the individual patient's needs, ultimately improving outcomes and reducing the burden of lung cancer in the regional population. Future research should focus on exploring the prognostic implications of these findings and their impact on long-term outcomes, particularly in the regional context. The development of targeted therapies for specific IHC profiles remains a critical area for ongoing research and clinical trials.

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