Research identifies patterns of CD24, a novel biomarker for non-small cell lung carcinomas

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The May edition of the *Journal of Thoracic Oncology* features a study aimed to clarify expression patterns of a novel cancer biomarker, CD24, in non-small cell lung carcinomas (NSCLC) and to correlate the findings to clinicopathologic variables, such as performance status, age, gender and prognostic significance. Furthermore, the results associated CD24 expression with the new (seventh) edition of the TNM staging. In summary, the study concluded that high expression of CD24 was a negative independent prognostic factor for progression free and cancer-specific survival in NSCLC.

The metastasis-associated protein CD24 found within a tumor has been identified as a new prognostic factor and stem cell marker; however, the importance of the CD24 in NSCLCs has not been made clear through previously existing research. To clarify the understanding, the present study conducted a retrospective study of prognostic factor analysis by evaluating CD24 expression in 267 consecutive cases of NSCLC. Using a tissue microarray technique the team analyzed the immunohistochemistry that correlated with clinicopathologic parameters.

The specific study findings revealed that CD24-high expression was demonstrated in 33 percent of the NSCLC cases, specifically 87 of 267. Expression rate also associated more so with adenocarcinoma histology (39 percent) than in squamous cell carcinoma histology (23 percent). Patients with CD24-high tumors also tended to have a higher risk of disease progression and cancer-related death. Furthermore, CD24-high

expression aligned with new pathologic stages rather than old p-stages.

Prior to the revision of the TNM staging, the most important conventional prognostic factor for patient survival was tumor stage at the time of diagnosis, including tumor size, pleura invasion, involvement of regional lymph nodes and metastatic spread to distant organs. However, the revised guidelines found age, gender and performance status (PS), in addition to stage, all to be prognostic factors for survival. Within the current study, expression correlated with PS and new p-stage; furthermore, age correlated with progression free survival and cancer-specific survival, regardless of tumor histology.

"Biomarkers that are over-expressed during cancer progression are of special interest because they may not only be used to predict patient outcome but also serve as potential targets in cancer therapy like epidermal growth factor receptor (EGFR) gene," lead investigator Dr. Hyun Ju Lee relays the implications of the research findings.

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