



Correlation of increased *MALAT1* expression with pathological features and prognosis in cancer patients: a meta-analysis

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ABSTRACT. Metastasis-associated lung adenocarcinoma transcript 1 (*MALAT1*) has been identified as a potential cancer biomarker, yet the mechanism by which it influences the development of cancer remains unknown. In this study, we aimed to correlate *MALAT1* expression with pathological features and prognosis in cancer patients. Several databases were searched using combinations of keywords relating to *MALAT1* and cancer. After selection of relevant cohort studies according to strict criteria, a meta-analysis was conducted. Twelve studies were analyzed, involving 958 cancer patients. Elevated *MALAT1* expression was associated with poor prognosis and larger tumors [prognosis: hazard ratio = 3.11, 95% confidence interval (CI) = 1.98-4.23, P = 0.000; tumor size: odds ratio (OR) = 0.40, 95%CI = 0.21-0.74, P = 0.003]. However, no connection with histological grade, T-stage, lymph node (LN) metastasis, or distant metastasis was established (all P > 0.05). A correlation between increased

expression and poor prognosis was observed in the large and small sample-size subgroups (all $P < 0.05$), as was a relationship with large tumor size (OR = 0.30, 95%CI = 0.13-0.71, $P = 0.006$). Expression was correlated with T-stage and distant metastasis in the small sample-size subgroup (all $P < 0.05$), but no association was detected regarding histological grade, LN metastasis in either subgroup (all $P > 0.05$). Our findings demonstrate that elevated *MALAT1* expression correlates with large tumor size, advanced tumor stage, and poor prognosis, and might therefore be utilized to evaluate clinical pathological features and prognostic out come for cancer patients.

Key words: *MALAT1*; Protein expression; Cancer; Pathological features; Prognosis; Meta-analysis