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Identifying the effects of unprocessed *let-7a-1* and *let-7a-3* in non-small cell lung cancer

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ABSTRACT

MicroRNAs (miRNAs) are small, noncoding RNAs that regulate protein levels typically by interacting with the 3′ untranslated region (3′-UTR) of target messenger RNA (mRNAs) and are often aberrantly expressed in cancer. The *let-7* miRNA family members are commonly regarded as cancer suppressors, by down-regulating the expression of oncoproteins such as RAS, HMGA2, and MYC. However, prior work indicates that unprocessed *let-7* RNAs may be positively correlated with cancer phenotypes in lung cancer cell lines. Our study aims to identify the effects of unprocessed *let-7a-1* and *let-7a-3* in non-small cell lung cancer, by transfecting plasmids that express unprocessed *let-7a-1* and *let-7a-3* into 3 different lung cancer cell lines. We then proceeded to conduct functional assays to measure the differences in anchorage independent growth, cell proliferation, and cell migration in all cell lines transfected with unprocessed *let-7*, in contrast to cells transfected with a control vector and thus far determined that unprocessed *let-7a-1* can enhance anchorage independent growth. Thus, we created truncations of the *let-7a-1* miRNA to identify the *cis* regions of this miRNA that is responsible for the change in phenotype. Our results suggest that cells transfected with truncated, yet unprocessed *let-7a-1* have increased anchorage independent growth, a major hallmark of cancer cell. There is still a need to replicate the functional assays that were conducted while continuing to create constructs of both *let-7a-1* and *let-7a-3* in order to further identify the sequence of the miRNAs responsible for the enhanced cancer phenotypes.

KEYWORDS

microRNA, *let-7*, lung cancer, non-coding RNA