1-2020

Angiogenin mRNA Expression Levels in Prostate Cancer Tissue

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Recommended Citation

Yao, Bowen; Shigematsu, PhD, Megumi; Pawar, PhD, Kamlesh Ganesh; Pliatsika, MS, Venetia; and Kirino, PhD, Yohei, "Angiogenin mRNA Expression Levels in Prostate Cancer Tissue" (2020). *Phase 1.* Paper 2.
https://jdc.jefferson.edu/si_dh_2022_phase1/2

SKMC Class of 2022: SI/DH Abstract

Word count: 221

Angiogenin mRNA Expression Levels in Prostate Cancer Tissue

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Introduction: Prostate cancer is the most commonly diagnosed cancer in men and second leading cause of cancer deaths. Studies have shown that tRNA fragments are upregulated in prostate cancers and play important roles in carcinogenesis. This project looks at how tRNA cleaving enzyme angiogenin expression is regulated in prostate cancer tissues.

Methods: Clinical data and mRNA expression levels of selected tRNA cleaving enzymes were extracted from the TCGA website. mRNAs were sequenced using IlluminaGA_RNASeqV2 at University of North Carolina.

Results: 546 samples from 494 patients, with normal tissue from 53 patients were collected. ANG mRNA levels were lower in patients with higher Gleason scores(Intercept=1321.787362, regression coefficient= -87.05499452, R^2=0.038). ANG mRNA levels were inconclusive in different clinical T grade(p=0.15), but were lower in higher pathologic T grade(intercept=1100.484695, x variable=-166.9047227, R^2=0.038);

ANG expression was lower in patients with nodal involvement versus without(539.56 vs 673.58, p=0.005).

Discussion: Overall trend we found from the results were ANG mRNA expression levels are down regulated in patients that have more advanced disease versus early disease. This supports the hypothesis that ANG expression plays an interesting role in prostate cancer biology. This trend might be due to the negative feedback due to high levels of tRNA fragments however there is no single theory available to answer this question.

No references/tables/figures/appendices allowed.