New biomarkers for prognosis of aggressive prostate cancer

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A large number of men are diagnosed with prostate cancer each year, but many will not experience morbidity or mortality as a result of their cancers. Therefore, biomarkers for prostate cancer are necessary to carefully select patients for initial diagnostic biopsy or to facilitate care decisions for men who have already been diagnosed with prostate cancer. RNA-based approaches to biomarker discovery allow the investigation of non-coding RNAs, gene fusion transcripts, splice variants and multi-gene expression panels in tissue, urine or blood as opportunities to improve care decisions. In an effort to identify biomarkers of recurrence, we performed global RNA sequencing on 106 formalin-fixed, paraffin-embedded (FFPE) prostatectomy samples from 100 patients at three independent sites, defining a 24-gene signature panel (Sig24). The 24 genes in this panel have functions in cell cycle progression, angiogenesis, hypoxia, apoptosis, PI3K signaling, steroid metabolism, translation, chromatin modification and transcription. In our validation study, patients with high Sig24 scores had an increased risk of developing metastasis (HR: 3.78, 95% CI: 1.96-7.29, p<0.001) or experiencing prostate cancer specific mortality (PCSM) (HR: 6.54, 95% CI: 2.16-19.83, p<0.001) in an independent validation case cohort set of 235 patients from the Mayo Clinic. The findings of this study demonstrate the applicability of Sig24 for the prognosis of metastasis or PCSM following radical prostatectomy. Future studies investigating the combination of Sig24 with available prognostic tests may provide new approaches to improve risk stratification for patients with prostate cancer.

Speaker Biography

Carlos S Moreno is Associate Professor of Pathology and Laboratory Medicine and Biomedical Informatics at Emory University, where he is a Member of the Winship Cancer Institute in the Cancer Genetics and Epigenetics Program. He has obtained his BS and MS in Aeronautics and Astronautics from MIT and worked for NASA before he earned his PhD in Genetics and Molecular Biology from Emory University in 1998. He specializes in Cancer Bioinformatics and Cancer Genomics and his laboratory has used whole genome expression analysis and next-generation sequencing to identify biomarkers of aggressive disease in prostate cancer.

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