Transcriptomics analysis reveals unique immunoinflammatory signatures of nigerian prostate cancer

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Abstract

Background: Prostate cancer (PCa) is the leading cause of cancer death among Nigerian men, with most men presenting late and with high grade disease. Furthermore, improved PCa diagnosis and treatment could rely on genomics-driven precision approaches. Mounting evidence supports potential population enriched molecular features of cancer, however the extent of which is hampered due to a dearth of genomic data in diverse cohorts. This study, therefore, aims at utilizing transcriptomics analysis to deduce transcriptional states in PCa from Nigerian men.

Methodology: RNA was extracted from macro-dissected prostate tumor and adjacent normal tissue from 35 archival formalin fixed paraffin-embedded (FFPE) blocks from Gleason 8-9 cancers, of which 25 had cribriform morphologic architecture. High resolution hybrid-capture mRNA-seq libraries were sequenced using Illumina NovaSeq 6000 system and generated an average of 124 million read pairs per sample. Raw reads were processed using a custom pipeline based upon industry standard algorithms along with the deduction of genetic ancestry. Molecular annotation was also performed to investigate tumor and immune cell heterogeneity.

Result: The Nigerian data were compared with high grade PCa data of Caucasian obtained from TCGA. The Nigerian PCa tumors where characterized with uniquely enriched immune-inflammatory microenvironment which include crosstalk between dendritic cells and natural killer cells, and natural killer cell signaling. While the Nigerian tumors share more features of distal metastatic tumor, their enrichment in NKT Cells is a unique feature.

Conclusion: This represents the first report of RNA-seq analysis of PCa in Sub-Saharan Africa and the unique transcriptomics features of Nigerian PCa presents opportunities for precision intervention in addressing its burden in Nigeria