Men of African ancestry in particular have a high incidence, mortality, and worst prognosis for prostate cancer (PCa) among other racial and ethnic populations. Environmental and genetic factors have been accounted for at least partially as the underlying reasons for such disproportionate ethnic differences. Identification of hereditary genetic factors that predict PCa risk and aggressiveness in African men can assist epidemiologists, geneticists, and clinicians to target them for prevention, screening, and efficient treatment.

Inherited susceptibility for PCa aggressiveness in general and in African populations remains unknown. The development of the recent high throughput genotyping platforms has facilitated Genome Wide Association Studies allowing the detection and comparison of single nucleotide polymorphisms (SNPs) and novel risk-alleles in case-control studies in men with or without PCa. So far these studies have shown very limited ability for the identified PCa risk-associated SNPs or susceptibility loci to discriminate between high and less aggressive tumors.

Genetic linkage studies to identify familial-PCa predisposition loci, SNP, or chromosomes have initially provided some hope, but proved to have limited success. The largest linkage studies to identify susceptibility loci for aggressive PCa were conducted by International Consortium for Prostate Cancer Genetics (ICPCG) in 166 families who had at least three affected males with clinically aggressive disease. These studies identified few suggested linkage signals on chromosomes 6p22.3 (logarithm of odds [LOD] 3.0), 11q14.1-14.3 (LOD 2.4), and 20p11.21-q11.21 (LOD 2.5). An expanded follow-up study in familial PCa (presenting with aggressive disease) by the ICPCG identified LOD score higher than 3.0 at chromosome 8q24. However, no genetic variant was identified for this linkage signal. Alternatively, the candidate gene approach has been used to search selectively for gene- or pathway-specific SNPs or allelic variants underlying biological processes such as DNA repair, inflammation, metabolism, or hormone production.

In the study published in Asian Journal of Andrology by Cancel-Tassin et al., the rs16901979 SNP, located in region 2 of chromosome 8q24 was genotyped in 498 cases of histopathologically confirmed PCa and 541 control subjects from a distinct demographic and geographic location, the French Caribbean islands of Guadeloupe. The study population for PCa was selected from African men who had at least one parent born on the Caribbean island and with no history of hormonal therapy. Inclusion criteria for the control population were normal finding on digital rectal examination and total plasma prostate-specific antigen (PSA) levels < 75th percentile of the comparable age group for African-American men without PCa. Most research subjects (>91%) were from French West Indies. This study revealed an association between the identified AA genotype and the A-allele of the rs16901979 and increased risk of PCa. Stratification of the patients by disease aggressiveness based on Gleason score revealed that the combined AC + AA genotype were associated with a Gleason score ≥ 7 (odd ratio = 1.79, 95% confidence interval = 1.17–2.73, P = 0.007). Based on these data, authors concluded that the A-allele at rs16901979 in region 2 of 8q24 is associated with increased risk of PCa and disease aggressiveness. This study has confirmed the association between the A-allele and elevated risk of PCa observed in other populations of Africans, Caucasians, and Asians. However, the authors’ conclusion that there is an association between the SNP rs16901979 and the risk of more aggressive PCa in the study population is based on less stringent criteria for disease aggressiveness and limited sample size for lethal tumors. Availability of clinical stage (i.e., tumor node metastasis), PSA levels and Gleason score (< 6, 3 + 4, 4 + 3, and ≥ 8) for the study population should allow more acceptable criteria for disease aggressiveness. It appears that limited sample size (n = 45, 9.5% of total number of patients) for clinically lethal or aggressive tumors (Gleason ≥ 8) has forced dichotomization of Gleason score into < 7 and ≥ 7. This has diminished the strength of the study in differentiating aggressive from nonaggressive tumors and to link the SNP rs16901979 into PCa aggressiveness. On the other hand, this is an interesting study with a meaningful result showing that the SNP rs16901979 can discriminate intra-ethnic difference for PCa risk in a distinct African population.

Overall, it appears that identifying genetic variants to predict PCa susceptibility is more achievable than finding those responsible for or influencing disease aggressiveness. This is even more challenging if one considers only one SNP and not a signature of SNPs. The ultimate goal of identifying men of high risk for developing lethal PCa remains a challenge and an open question.

**COMPETING INTERESTS**

All authors declare no competing interests.

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