A novel genomic alteration of LSAMP associates with aggressive prostate cancer in African American men

Petrovics, Gyorgy; Li, Hua; Stümpel, Tanja; Tan, Shyh-Han; Young, Denise; Katta, Shilpa; Li, Qiyuan; Ying, Kai; Klocke, Bernward; Ravindranath, Lakshmi; Kohaar, Indu; Chen, Yongmei; Ribli, Dezs; Grote, Korbinian; Zou, Hua; Cheng, Joseph; Dalgard, Clifton L.; Zhang, Shimin; Csabai, Istvan; Kagan, Jacob; Takeda, David; Loda, Massimo; Scherf, Matthias; Seifert, Martin; Gaiser, Timo; McLeod, David G.; Szallasi, Zoltan Imre; Ebner, Reinhard; Werner, Thomas; Sesterhenn, Isabell A; Freedman, Matthew; Dobi, Albert; Srivastava, Shiv

Published in:
EBioMedicine

Link to article, DOI:
10.1016/j.ebiom.2015.10.028

Publication date:
2015

Document Version
Publisher's PDF, also known as Version of record

Link back to DTU Orbit

Citation (APA):
A novel genomic alteration of LSAMP associates with aggressive prostate cancer in African American men

Gyorgy Petrovics a,1, Hua Li a,1, Tanja Stümpe b,1, Shyh-Han Tan a,1, Denise Young a, Shilpa Katta a, Qiuyan Li c,2, Kai Ying b,2, Bernward Klocke b,2, Lakshmi Ravindranath a,2, Indu Kohara a, Yongmei Chen a, Dezso Ribli c,2, Korbinian Grote b,2, Hua Zou b,2, Joseph Cheng b,2, Clifton L. Dalgard a,2, Shimin Zhang a,2, István Csabai e,2, Jacob Kagan j, David Takeda d,3, Massimo Lod a,4, Sudhir Srivastava a,5, Iman Dezfouli a,5, Martin Seifert b,5, Timo Gaissl d,5, David G. McLeod a,6, Zoltan Szallas f,5, Reinhard Ebner g, Thomas Werner b,5, Isabell A. Sesterhenn h, Matthew Freedman a,7, Albert Dobi a,*, Shiv Srivastava a,**

a Center for Prostate Disease Research, Department of Surgery, Uniformed Services University of the Health Sciences and Walter Reed National Military Medical Center, Bethesda, MD 20814, USA
b Medical College, Xiamen University, Xiamen 36102, China
c Dana–Farber Cancer Institute, Harvard Medical School, Boston, MA 02215, USA
d Department of Physics of Complex Systems, Eötvös Loránd University, Budapest H-1117, Hungary
e Center for Biological Sequence Analysis, Department of Systems Biology, Technical University of Denmark, Lyngby, DK-2800, Denmark
f CytoTest Inc., Rockville, MD 20850, USA
g Institute of Anatomy, Physiology and Genetics, Collaborative Health Initiative Research Program, Uniformed Services University of the Health Sciences, Bethesda, MD 20814, USA
h Renal Pathology, Joint Pathology Center, Silver Spring, MD 20910, USA
i Cancer Biomarkers Research Group, Division of Cancer Prevention, National Cancer Institute, Bethesda, MD 20892, USA
j The Eli and Edythe L. Broad Institute, Cambridge, MA, USA
k Pathologisches Institut, Universität Mannheim, Medizinische Fakultät Mannheim der Universität Heidelberg, Mannheim D-68167, Germany
l Department of Urology, Walter Reed National Military Medical Center, Bethesda, MD 20814, USA
m Children’s Hospital Informatics Program at the Harvard-Massachusetts Institute of Technology Division of Health Sciences and Technology, Harvard Medical School, Boston, MA 20115, USA

Evaluation of cancer genomes in global context is of great interest in light of changing ethnic distribution of the world population. We focused our study on men of African ancestry because of their disproportionately higher rate of prostate cancer (CaP) incidence and mortality. We present a systematic whole genome analyses, revealing alterations that differentiate African American (AA) and Caucasian American (CA) CaP genomes. We discovered a recurrent deletion on chromosome 3q13.31 centering on the LSAMP locus that was prevalent in tumors from AA men (cumulative analyses of 435 patients: whole genome sequence, 14; FISH evaluations, 101; and SNP array, 320 patients). Notably, carriers of this deletion experienced more rapid disease progression. In contrast, PTEN and ERG common driver alterations in CaP were significantly lower in AA prostate tumors compared to prostate tumors from CA. Moreover, the frequency of inter-chromosomal rearrangements was significantly higher in AA than CA tumors. These findings reveal differentially distributed somatic mutations in CaP across ancestral groups, which have implications for precision medicine strategies.

© 2015 The Authors. Published by Elsevier B.V. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

1. Introduction

Men of African ancestry have a significantly higher rate of prostate cancer (CaP) incidence and mortality in the United States and globally (Siegel et al., 2015). Accumulating evidence from our group and others support the contention that biological and genetic alterations differ in prevalence between AA and CA CaP (Chornokur et al., 2011; Farrell et al., 2013; Martin et al., 2013; Pomerantz and Freedman, 2011; Powell et al., 2010). Recently, many tumor sequencing studies have
highlighted frequent alterations of ERG, PTEN and SPOP genes in early stages of CaP (Baca et al., 2013; Barbieri et al., 2012; Berger et al., 2011; Boutros et al., 2015; Grasso et al., 2012; Kumar et al., 2011; Taylor et al., 2010; Weischenfeldt et al., 2013) and of the androgen receptor (AR), p53 and PIK3CB and other genes in metastatic CaP or castration resistant prostate cancer (Robinson et al., 2015). However, the majority of these studies were performed in men of European ancestry. Motivated by the observation that the well-described TMPRSS2-ERG gene fusion significantly differs across ancestral populations (Blattner et al., 2014; Farrell et al., 2014; Khani et al., 2014; Magi-Galluzzi et al., 2011; Rosen et al., 2012) we sought to perform comprehensive whole genome analyses of prostate cancers from AA and CA men.

2. Materials and methods

2.1. Prostate cancer specimens, sample preparation and quality control

Prostate cancer samples selected for this study were archived specimens under IRB approved protocol from patients undergoing radical prostatectomy treatment at the Walter Reed National Military Medical Center (WRNMMC). Clinically localized primary prostate tumors were selected for whole genome sequencing from seven African American (AA) and seven Caucasian American (CA) patients. Histologically defined tumors with primary Gleason pattern 3 were manually dissected under microscope from frozen OCT-embedded 6 μm prostate tissue sections with ~80–95% tumor cell content (Table 1a). Hematoxylin and Eosin (H&E)-stained tissue sections were reviewed by I.A.S. to determine Gleason score and percentage composition of tumor at the site selected for DNA extraction. DNA was purified from the isolated tissues, as well as from peripheral blood lymphocytes (normal DNA control) of the corresponding patients using DNeasy Blood and Tissue DNA isolation kit (Qiagen). DNA samples were subjected to extensive quality control to verify structural integrity by agarose gel-electrophoresis. ERG fusion and expression status were determined by RT-PCR (Supplementary Fig. 1) and by immunohistochemistry (Furusato et al., 2010; Hu et al., 2008).

2.2. Validation of TMPRSS2-ERG fusion status by RT-PCR

TMPRSS2-ERG fusion positive cases were validated by RT-PCR. Approximately 40 ng of patient mRNA were reverse transcribed using Sensiscript (Qiagen, Germantown, MD) in the presence of random hexamer primers at 37 °C for 1 h. An additional reaction without reverse transcriptase was held in situ, and clusters were prepared for Read2 sequencing using the Illumina Paired-End Module. Paired-end sequence reads of 101 bases were generated using the Genome Analyzer IIX with v5 SBS reagent kits, as described in the Illumina Genome Analyzer operating manual. Data were processed using Real Time Analysis (RTA).

2.3. Whole genome sequencing

DNA samples were processed using the Illumina TruSeq DNA PCR-Free Sample Preparation kit, starting with 500 ng input and resulting in an average insert size of 310 bp. Cluster amplification, linearization, blocking and hybridization to the Read 1 sequencing primer were carried out on a cBOT. Following the first sequencing read, flow cells were held in situ, and clusters were prepared for Read2 sequencing using the Illumina Paired-End Module. Paired-end sequence reads of 101 bases were generated using the Genome Analyzer IIX with v5 SBS reagent kits, as described in the Illumina Genome Analyzer operating manual. Data were processed using Real Time Analysis (RTA).

2.4. Processing pipeline for analyses of whole genome sequence data

Germline samples were sequenced to at least 30 × depth followed by alignment and variant calling using the ELANDv2e algorithm in Consensus Assessment of Sequence And VAriation (CASA v 1.8) pipeline. DNA derived from tumors was sequenced to at least 30-fold haploid coverage. After alignment to reference genome Genome Reference Consortium Human Build 37 (GRCh37/hg19) and subtraction of the germline genome from tumor sequences, somatic variants were called using Strelka (for single nucleotide variants [SNVs] and Indels), Genomatix Mapper (www.genomatix.de) and BreakDancer (for structural variations [SVs]) (Chen et al., 2009), cn.MOPs (Klambauer et al., 2012) and Control-FREEC (Boeva et al., 2012) (for copy number variations [CNVs]). Somatic SNVs (one base-pair point mutations detected by single reads) initially called using Strelka (Saunders et al., 2012) (Supplementary Table 2) were validated using four other variant calling tools: Varscan2 (Koboldt et al., 2012), MuTect (Cibulskis et al., 2013; Roth et al., 2012) and Somatic Sniper (Larson et al., 2012) (Supplementary Table 3). SNVs that were detected by at least three variant calling tools were designated as high confidence SNVs (Wang et al., 2013) (Supplementary Table 4). SNVs that resulted in missense mutations, nonsense mutations (stop gain) and mutations affecting splice sites were presented in Supplementary Table 5. Indels, defined as small insertion and deletions of up to 300 bps, were called by single reads that were called by Strelka are listed in Supplementary Table 1. Somatic SVs, defined as large deletions, inversions, insertions, translocations detected by anomalous paired-end reads, were called by

<table>
<thead>
<tr>
<th>Sample ID</th>
<th>Race</th>
<th>Age</th>
<th>Pathologic Gleason score</th>
<th>Pathologic stage</th>
<th>Serum PSA (ng/ml)</th>
<th>TMPRSS2-ERG Status</th>
<th>Tumor Gleason score</th>
<th>Gleason 3 pattern of tumor (%)</th>
<th>Estimated tumor purity (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>GP02</td>
<td>AA</td>
<td>68</td>
<td>7 (4 + 3)</td>
<td>T3C</td>
<td>7</td>
<td>6 (3 + 3)</td>
<td>100</td>
<td>80</td>
<td>GP02</td>
</tr>
<tr>
<td>GP04</td>
<td>AA</td>
<td>51</td>
<td>7 (3 + 4)</td>
<td>T3A</td>
<td>8.3</td>
<td>7 (3 + 4)</td>
<td>95</td>
<td>80</td>
<td>GP04</td>
</tr>
<tr>
<td>GP10</td>
<td>AA</td>
<td>53</td>
<td>7 (3 + 4)</td>
<td>T3C</td>
<td>6.5</td>
<td>7 (3 + 4)</td>
<td>95</td>
<td>90</td>
<td>GP10</td>
</tr>
<tr>
<td>GP18</td>
<td>AA</td>
<td>48</td>
<td>7 (3 + 4)</td>
<td>T3A</td>
<td>3.7</td>
<td>6 (3 + 3)</td>
<td>100</td>
<td>80</td>
<td>GP18</td>
</tr>
<tr>
<td>GP12</td>
<td>AA</td>
<td>52</td>
<td>6 (3 + 3)</td>
<td>TX</td>
<td>3.8</td>
<td>6 (3 + 3)</td>
<td>100</td>
<td>90</td>
<td>GP12</td>
</tr>
<tr>
<td>GP13</td>
<td>AA</td>
<td>59</td>
<td>6 (3 + 3)</td>
<td>T2C</td>
<td>7.7</td>
<td>7 (3 + 4)</td>
<td>100</td>
<td>85</td>
<td>GP13</td>
</tr>
<tr>
<td>GP15</td>
<td>AA</td>
<td>44</td>
<td>6 (3 + 3)</td>
<td>TX</td>
<td>9.1</td>
<td>6 (3 + 3)</td>
<td>92</td>
<td>80</td>
<td>GP15</td>
</tr>
<tr>
<td>GP06</td>
<td>CA</td>
<td>58</td>
<td>7 (4 + 3)</td>
<td>T3C</td>
<td>7.4</td>
<td>7 (3 + 4)</td>
<td>100</td>
<td>95</td>
<td>GP06</td>
</tr>
<tr>
<td>GP11</td>
<td>CA</td>
<td>64</td>
<td>7 (3 + 4)</td>
<td>T2C</td>
<td>11.6</td>
<td>6 (3 + 3)</td>
<td>95</td>
<td>90</td>
<td>GP11</td>
</tr>
<tr>
<td>GP16</td>
<td>CA</td>
<td>49</td>
<td>7 (4 + 3)</td>
<td>T3A</td>
<td>22.7</td>
<td>7 (3 + 4)</td>
<td>85</td>
<td>90</td>
<td>GP16</td>
</tr>
<tr>
<td>GP01</td>
<td>CA</td>
<td>64</td>
<td>7 (3 + 4)</td>
<td>T3B</td>
<td>11.4</td>
<td>7 (3 + 4)</td>
<td>95</td>
<td>80</td>
<td>GP01</td>
</tr>
<tr>
<td>GP07</td>
<td>CA</td>
<td>69</td>
<td>6 (3 + 3)</td>
<td>TX</td>
<td>4</td>
<td>6 (3 + 3)</td>
<td>100</td>
<td>90</td>
<td>GP07</td>
</tr>
<tr>
<td>GP05</td>
<td>CA</td>
<td>60</td>
<td>6 (3 + 3)</td>
<td>TX</td>
<td>2.8</td>
<td>7 (3 + 4)</td>
<td>97</td>
<td>80</td>
<td>GP05</td>
</tr>
<tr>
<td>GP17</td>
<td>CA</td>
<td>67</td>
<td>7 (4 + 3)</td>
<td>T3A</td>
<td>7.4</td>
<td>7 (3 + 4)</td>
<td>95</td>
<td>80</td>
<td>GP17</td>
</tr>
</tbody>
</table>

Table 1a: Patient-specific features included in the study (patient number: GP02-18; Race: African American: AA, Caucasian American: CA, prostate specific antigen: PSA).
Genomatix Mapper and BreakDancer (www.genomatix.de). Genes with intergenic breakpoints, inversion and deletions that were called are presented in Supplementary Table 7. Structural variation breakpoints for ERG, LSAMP and PTEN that were detected by whole genome sequencing are tabulated in Supplementary Table 8. A subset of base-pair mutations and rearrangements were validated using Sanger sequencing (Supplementary Fig. 2) in order to assess the specificity of the detection algorithms (primers used are listed in Supplementary Table 1).

2.5. Detection of transcripts from ZBTB20 and LSAMP promoters by 5′ RACE

mRNA transcripts initiating from ZBTB20 and LSAMP promoters were detected by 5′-rapid amplification of cDNA ends (RACE) (Harvey and Darlison, 1991; Shi and Kaminskyj, 2000) using the SMARTer® RACE 5′/3′ kit (Clontech). In a coupled reaction, 10 ng of total RNA from patients reverse transcribed in the presence SMARTer IIA oligo into first-strand cDNA incorporated with the SMARTer sequence at the 5′ end. The first-strand cDNA is amplified in the presence of the universal primer and gene specific 5′ primers using two cycles of 94 °C for 30 s, 68 °C for 3 min followed by 28 cycles of 94 °C for 30 s, 68 °C for 30 s and 72 °C for 3 min. The absence of distinct bands prompted another round of amplification using nested primers (primers are listed in Supplementary Table 1). Amplified DNA products were analyzed by using a 2100 Bioanalyzer (Agilent) DNA prior to separation on agarose gel. Distinct bands were excised (10 for GP02 and 18 for GP10), gel purified, subcloned into pC-Blunt II-TOPO plasmids and transformed into One...
Shot TOP10 E. coli (Life Technologies). Six colonies from each transformation were picked for the isolation of plasmid DNA and analyzed by Sanger sequencing. The types of splice variants and how frequently each was detected are described in Supplementary Fig. 3.

2.6. Principal component analysis (PCA)

The ancestry of patients for the CPDR cohort of seven AA and seven CA patients together with the patients from The Cancer Genome Atlas (TCGA) (The Cancer Genome Atlas Research Network et al., 2013) were confirmed by principal component analysis using the EIGENSTRAT method from the EIGENSOFT package (Price et al., 2006). For the PCA of the 14 patients assessed by whole genome sequencing, 39,867 SNP markers were extracted from whole genome sequencing data, SNPs with less than 20× coverage were filtered out and the genotypes are inferred from alternate allele frequency (0 ~ 0.2: ref./ref.; 0.2 ~ 0.8: ref./alt; 0.8 ~ 1: alt/alt). By applying the sampling criteria to filter out SNPs with batch difference, total of 1353 SNPs were selected. The principal components were computed from a combined matrix of these 1353 SNPs genotype derived from the WGS data of the 7AA and 7CA samples and from the SNP array data from 415 HapMap Phase II reference samples representing three distinct reference populations: Northern and Western European ancestry (CEU), Africans of Yoruba ancestry in Ibadan, Nigeria (YRI), and Americans of African ancestry in Southwest of the United States (ASW). The computed ancestry of the seven AA and seven CA patients are shown to localize with ASW/YRI and with CEU populations, respectively, confirming identical classification to self-reported ethnicity (Supplementary Fig. 4).

The ancestry the TCGA cohort were established by using a CNV (SNP) array dataset (broad.mit.edu_PRAD.Genome_Wide_SNP_6. Level_3.184.2019.0) that contains genotype data determined by using the Affymetrix Genome-Wide Human SNP Array 6.0. The principal components used to determine the ancestry of this cohort were computed from a combined matrix consisting of 13,541 SNPs or genotypes of 320 TCGA “cases” and 552 HapMap Phase II “controls” representing four reference populations (Han Chinese in Beijing, China [CHB] in addition to CEU, YRI and ASW). The 13541 SNPs were filtered from a total of 39,867 SNPs based on having an observed minor allele frequency greater than 0.05, a significant diversity among reference populations (Krusal Wallis test p < 0.05 after Bonferroni correction), and no significant batch difference for the allele frequency between TCGA samples and HapMap Phase II samples. EIGENSTRAT was used to calculate the first two principal components corresponding to the two largest eigenvalues. TCGA cases that show similar principal scores to the control HapMap samples were assigned to the same population as that of the HapMap samples from the same cluster. This stratified the TCGA cases into 41 African Americans and 279 Caucasian Americans (Supplementary Fig. 5 and Supplementary Table 9).

Fig. 2. Significantly higher number of inter-chromosomal rearrangements and exclusive association of chromosome LSAMP deletion/rearrangement in prostate cancer of AA men. (a) Circos plots of AA and CA whole genomes indicate chromoplexy characteristic of prostate cancer genomes. Inter-chromosomal translocations are marked with purple. Inter-chromosomal rearrangements are marked by green. (b) Inter-chromosomal translocations are significantly more frequent events in AA prostate cancer genomes. (c) Wild type (WT), LSAMP locus rearrangements by large deletion (patient GP04), small deletion (GP2) or by duplication generating a ZBTB20-LSAMP gene fusion (GP10). (d) Confirmation of ZBTB20-LSAMP gene fusion by Sanger sequencing of the genomic fusion junction.
2.7. Frequency of LSAMP and PTEN deletions and TMPRSS2-ERG fusion in the TCGA SNP array data

The TCGA cohort with established ancestry provides an independent patient cohort to assess the frequency of LSAMP and PTEN deletions and TMPRSS2-ERG alterations in prostate adenocarcinoma (PRAD). To determine the deletions or copy number changes within LSAMP (3q13.31), PTEN and TMPRSS2-ERG loci, raw SNP data were first normalized using the CRMA v2 method from the AROMA package (Bengtsson et al., 2009). Integer copy number inference was performed with the ASCAT software suite (Van Loo et al., 2012). Copy numbers were normalized by chromosome-wide medians before the identification of deleted loci. Data from SNP arrays that failed to converge to an acceptable solution were omitted from analysis.

Principal component analysis was applied from the EIGENSTRAT package (Price et al., 2006) to establish the ancestry of patients (Supplementary Fig. 5).

2.8. Validation of LSAMP and PTEN deletion frequencies by interphase FISH assay

FISH analysis (Hopman et al., 1991) for the detection of deletions at the PTEN (Yoshimoto et al., 2006) and ZBTB20-LSAMP locus was performed on whole mounted sections and on prostate tissue microarrays (TMAs) constructed from a cohort of radical prostatectomy specimens as described in Merseburger et al. (2003). A PTEN locus-specific probe was generated by selecting a combination of clones within the peak region of common PTEN deletions near 10q23.3. These clones were tested in an iterative trial-and-error process to optimize signal intensity and specificity, resulting in a probe matching ca. 450 kbp covering PTEN and adjacent genomic sequences (Supplementary Fig. 6a). A control probe derived from chromosome 10-specific alpha satellite centromeric DNA, labeled with CytoGreen fluorescent dye was used for chromosome 10 counting. A ZBTB20-LSAMP locus-specific probe was constructed from bacterial artificial chromosome clones obtained from...
...nuclei. Tumor cells with at least two centromeres were counted. Prostate cancers in the United States (Siegel et al., 2015). We evaluated glands showed loss of allele. Benign prostatic glands and stroma served of evaluable tumor cells showed loss of allele or when more than 50% showed loss of allele. Focal deletions were called when more than 25% of evaluable tumor cells were more prevalent in CA vs. AA cases (26% vs. 7%, p = 0.007). Moreover, LSAMP deletion in AA men correlated with biochemical recurrence (BCR) and with pT3 tumors (p = 0.05) (Fig. 3c, Supplementary Table 10).

3.4. The mutation landscape of prostate cancers of African American and Caucasian men

We detected 261 somatically acquired SNVs in the coding sequence of 247 genes from 7 CA and 7 AA patients (Supplementary Table 5). A comparison of these SNVs against COSMIC and TCGA databases as shown in Fig. 1a, identified 43 SNVs that were previously described in prostate and/or other cancers (Baca et al., 2013; Barbieri et al., 2012; Forbes et al., 2015; Khani et al., 2014). The virtual absence of PTEN deletions in early stage prostate cancers of African American men

Recent studies noted frequency differences in PTEN deletion between AA and CA CaP (Blattner et al., 2014; Khani et al., 2014). The virtual absence of PTEN deletion observed in AA CaP whole genome sequence data shown here was striking (Fig. 1b). To validate these observations in an independent set of samples, we probed the PTEN locus by FISH in a tissue microarray, as described above. PTEN deletions were notably less frequent in AA (15%) compared to CA cases (63%) (p = 0.004) (Table 2a and 2b).
4. Discussion

Emerging data from our and other groups support biological and genetic differences between African American (AA) and Caucasian American (CA) CaP. While reports on comprehensive evaluations of primary CaP genomes or exomes have highlighted recurrent alterations (TMPRSS2-ERG, PTEN, SPOP and CHD1), these studies were focused on patients with Caucasian ancestry. ERG oncogenic activation via gene fusions and deletion of the PTEN tumor suppressor are major early tumor-igenic driver alterations in CaP genomes (Bigner et al., 1984; Li et al., 1997; Tomlins et al., 2005). Within the continuum of assessment of these alterations high frequencies in CA patients and lower frequencies in AA men were noted (Blattner et al., 2014; Farrell et al., 2014; Hu et al., 2008; Khani et al., 2014; Magi-Galluzzi et al., 2011; Petrovics et al., 2005; Rosen et al., 2012). In Asian subjects, CaP frequencies of ERG and PTEN alterations are the lowest (Blattner et al., 2014; Mao et al., 2010; Qi et al., 2014). The goal of this study was to delineate genomic features of AA and CA CaP focusing on early stages of the disease representing majority of cases at initial presentation in Western countries.

In summary, three recurrent genomic alterations (PTEN, LSAMP region and ERG) showed distinct prevalence between AA and CA CaP. This study discovered a novel deletion of LSAMP locus as a prevalent genomic alteration in AA CaP. Notably, this alteration is associated with rapid disease progression. Evaluation of the minimum site of deletion in SNP datasets of AA tumors suggests that the primary target of deletion is the LSAMP gene. LSAMP locus inactivation by recurrent deletions has been reported in osteosarcoma (Barøy et al., 2014; Kresse et al., 2009) and acute myeloid leukemia (Kühn et al., 2012) and by translocation in clear cell renal carcinoma (Chen et al., 2003) and ovarian carcinoma (Ntougkos et al., 2005). Single nucleotide polymorphism within the first intron of LSAMP has recently been shown to be a predictor of prostate-cancer-specific mortality (Huang et al., 2013). Further, alterations of ZBTB20, C4BP3 and GSK3B adjacent to LSAMP are less well understood but are suspected to have pro-tumorigenic functions in cancer (Chen et al., 2014; Kroon et al., 2014; Shi et al., 2011). Thus, the observed allelic loss of LSAMP in CaP is consistent with its tumor suppressor function reported in cancer.

Currently, chromoplexy through AR-mediated DNA breaks and faulty repair is a proposed mechanism of prostate cancer genomic rearrangements (Baca et al., 2013; Taylor et al., 2010). In our study we found significantly higher frequency of inter-chromosomal rearrangements in AA than in CA CaPs. Whether the chromoplexy initiating mechanism or the subsequent selection of tumor cells is different between AA and CA men needs to be further elucidated.

Taken together, this report highlights distinct features of AA CaP genome with emphasis on new findings on recurrent deletions of the LSAMP locus in AA CaP which associates with disease recurrence and identifies an aggressive subset of prostate cancers. These findings have broader implication towards the understanding of cancer genomes of currently underrepresented populations towards the development of ethnically informed diagnostic, prognostic marker and tailored therapeutical approaches.

Acknowledgements

This research was supported by funds from the Center for Prostate Disease Research, Uniformed Services University Program, Hu0001-10-2-0002 to DGM, the NCI/EDRN ACN12011-001-0 to SS, the NCI R01 CA162383-05 grant to SS, the H.L. Snyder Medical Foundation to MLF, the KMR-12-1-2012-0216 and OTKA-114560 grants to DR and IC, the Otto Monsted Foundation to IC and ZZ, and the Maizzone Foundation, the Breast Cancer Research Foundation, the Novo Nordisk Foundation, grants by MT-TR643/2012, KTIJA_NAP_13-2014-0021 to ZZ. The funders did not have any role in the in study design, data collection, data analysis, interpretation or writing of the report. The authors thank Dr. Madhvi Upender, Dr. Ahmed A. Mohamed, Dr. Allissa Dillman, Dr. Nicholas Griner, Dr. Shashwat Sharad, Dr. Zhaozhang Li, and Ms. London Toney for the experimental support and Mr. Stephen Doyle for his assistance with the art and graphics. The views expressed in this manuscript are those of the authors and do not reflect the official policy of the Department of the Army, Department of Defense or the US Government.

Appendix A. Supplementary data

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.ebiom.2015.10.028.

References


