Intratumoural evolutionary landscape of high-risk prostate cancer: the PROGENY study of genomic and immune parameters

M. Linch1,2,†, G. Goh1,3,†, C. Hiley4,5, Y. Shanmugabavan6, N. McGranahan1,5, A. Rowan5, Y. N. S. Wong1,7,8, H. King1, A. Furness7,8, A. Freeman9, J. Linares9, A. Akarca9, J. Herrero9, R. Rosenthal1,3, N. Harder10, G. Schmidt10, G. A. Wilson1,5, N. J. Birkbak1,5, R. Mitter11, S. Dentro12,13, P. Cathcart14, M. Arya6,15, E. Johnston16, R. Scott6, M. Hung6, M. Emberton6,15, G. Attardi17,18, Z. Szallasi19,20,21, S. Punwani16, S. A. Quezada7,8, T. Marafioli9, M. Gerlinger17,18, H. U. Ahmed6,22,23, * & C. Swanton1,2,5, ^

1Translational Cancer Therapeutics Laboratory, UCL Cancer Institute, London, UK; 2Department of Medical Oncology, University College London Hospitals NHS Foundation Trust, London, UK; 3Bill Lyons Informatics Centre, UCL Cancer Institute, London, UK; 4Division of Cancer Studies, King’s College London, London, UK; 5Translational Cancer Therapeutics Laboratory, The Francis Crick Institute, London, UK; 6Division of Surgery and Interventional Science, University College London, London, UK; 7Cancer Immunology Unit, UCL Cancer Institute, London, UK; 8Research Department of Haematology, UCL Cancer Institute, London, UK; 9Department of Histopathology, University College London Hospitals NHS Foundation Trust, London, UK; 10Definiens AG, Munich, Germany; 11Department of Bioinformatics and Biostatistics, The Francis Crick Institute, London, UK; 12Cancer Genomics Laboratory, The Francis Crick Institute, London, UK; 13Experimental Cancer Genetics, Welcome Trust Sanger Institute, Cambridge, UK; 14The Urology Centre, Imperial College London, London, UK; 15Centre for Medical Imaging, University College London, London, UK; 16Centre for Evolution and Cancer, The Institute of Cancer Research, London, UK; 17Department of Medical Oncology, Royal Marsden Hospital, London, UK; 18Centre for Biological Sequence Analysis, Technical University of Denmark, Lyngby, Denmark; 19Computational Health Informatics Program (CHIP), Harvard Medical School, Boston, USA; 20MTA-SE-NAP Brain Metastasis Research Group, Semmelweis University, Budapest, Hungary; 21Division of Surgery, Department of Surgery and Cancer, Imperial College London, UK; 22Department of Urology, Imperial College Healthcare NHS Trust, London, UK

*Correspondence to: Prof. Hashim Ahmed, Division of Surgery and Cancer, Imperial College London, Fulham Palace Road, London W6 8RF, UK. Tel: +44-203-311-6611; E-mail: hashim.ahmed@imperial.ac.uk
Prof. Charles Swanton, Translational Cancer Therapeutics Laboratory, The Francis Crick Institute, 1 Midland Road, London NW1 1AT, UK. Tel: +44-203-796-2047; E-mail: charles.swanton@crick.ac.uk
†Both authors contributed equally to this work.
^Joint corresponding authors.

Background: Intratumoural heterogeneity (ITH) is well recognised in prostate cancer (PC), but its role in high-risk disease is uncertain. A prospective, single-arm, translational study using targeted multiregion prostate biopsies was carried out to study genomic and T-cell ITH in clinically high-risk PC aiming to identify drivers and potential therapeutic strategies.

Patients and methods: Forty-nine men with elevated prostate-specific antigen and multiparametric-magnetic resonance imaging detected PC underwent image-guided multiregion transperineal biopsy. Seventy-nine tumour regions from 25 patients with PC underwent sequencing, analysis of mutations, copy number and neoepitopes combined with tumour infiltrating T-cell subset quantification.

Results: We demonstrated extensive somatic nucleotide variation and somatic copy number alteration heterogeneity in high-risk PC. Overall, the mutational burden was low (0.93/Megabase), but two patients had hypermutation, with loss of mismatch repair (MMR) proteins, MSH2 and MSH6. Somatic copy number alteration burden was higher in patients with metastatic hormone-naive PC than in those with high-risk localised PC, independent of Gleason grade. Mutations were rarely ubiquitous and mutational frequencies were similar for mHNPC and hrlPC patients. Enrichment of focal 3q26.2 and 3q21.3, regions containing putative metastasis drivers, was seen in MMRD patients. We found evidence of parallel evolution with three separate clones containing activating mutations of β-catenin in a single patient. We demonstrated extensive intratumoural and intertumoural T-cell heterogeneity and high inflammatory infiltrate in the MMR-deficient (MMRD) patients.
and the patient with parallel evolution of β-catenin. Analysis of all patients with activating Wnt/β-catenin mutations demonstrated a low CD8+/FOXP3+ ratio, a potential surrogate marker of immune evasion.

**Conclusions:** The PROGENY (PROstate cancer GENomic heterogeneitY) study provides a diagnostic platform suitable for studying tumour ITH. Genetic aberrations in clinically high-risk PC are associated with altered patterns of immune infiltrate in tumours. Activating mutations of Wnt/β-catenin signalling pathway or MMRD could be considered as potential biomarkers for immunomodulation therapies.

**Clinical Trials.gov Identifier:** NCT02022371

**Key words:** prostate cancer, intratumoural heterogeneity, neoepitopes, tumour infiltrating lymphocytes, wnt signalling, mismatch repair

---

**Introduction**

Prostate cancer (PC) is the second most common malignancy in men with an incidence of 1.1 million men per year leading to an estimated 307,000 deaths worldwide [1]. While the prognosis of clinically low-risk PC is excellent [2], there is significant mortality associated with clinically high-risk disease, with approximately 20%–25% 10-year cancer-specific mortality despite radical treatments [3].

A key challenge in PC is to identify patients with potentially lethal disease while avoiding the morbidity of overtreatment in patients with indolent disease. Accurate risk stratification has been confounded by underestimation of disease burden using standard transrectal ultrasound-guided biopsies and extensive tumour heterogeneity of primary PC [4–6]. A recent improvement on transrectal ultrasound-guided biopsies is targeted magnetic resonance imaging (MRI)-guided biopsies that increase the likelihood of sampling clinically significant disease [7].

Multi-regional sampling of tumours allows measurement of intratumoural heterogeneity, a prognostic entity in PC [8]. To date, in-depth exploration of genomic ITH with multiregion sequencing (M-Seq) in the primary PC has relied on prostatectomy patient series [9, 10] to provide good-quality tissue; however, this has enriched for clinically low- and intermediate-risk disease [5, 6].

Tumour infiltrating lymphocyte density has been shown, albeit inconsistently, to be prognostic in PC [11–13]. The impact of tumour genetics on prostate immunobiology is unclear and deciphering this could improve risk stratification, prognostication and immunotherapeutic approaches.

We conducted the PROGENY study (PROstate cancer GENomic heterogeneitY) to attain high-quality multi-regional prostate biopsies to determine the driver and evolutionary events of clinically high-risk PC at the time of diagnosis and to correlate genomic and immune parameters.

**Methods and materials**

**Patient selection**

Between September 2013 and December 2015, 49 men with a prostate-specific antigen ≥15, a multi-parametric MRI detectable lesion in the prostate and no prior prostate-directed biopsies or treatments were enrolled into the PROGENY study, with local ethics committee approval. Of these, 23 patients and a further 2 contemporaneous patients from the institutional biobank met the criteria for the planned genetic and T-cell analysis (supplementary Table S1 and Figure S1, available at *Annals of Oncology* online).

**Tissue procurement**

Multi-regional PC biopsies were obtained using multi-parametric MRI, image-fusion transperineal template targeting as described previously [7] (supplementary Figure S2, available at *Annals of Oncology* online). Blood samples were obtained before the biopsy for isolation of germline DNA.

**Sequencing studies**

Tumour DNA was extracted using the Allprep Micro Kit (Qiagen, CA) and germline DNA extracted with the DNase Blood & Tissue Kit (Qiagen, MD) following the manufacturer’s instructions. Further details are contained in the supplementary data, available at *Annals of Oncology* online.

**Immunohistochemistry**

Single and multiplexed IHC was carried out as described previously [14]. Antibody details are in supplementary Table S2, available at *Annals of Oncology* online. TM and ML jointly carried out quantification of inflammatory infiltrate (INIF), blinded to patient characteristics. Samples with ≥8% (median of all samples) INIF (15/25 patients) in any one region were subjected to digital image analysis. These correlated well with the manual estimation (R² = 0.71) (supplementary Figures S3 and S4, available at *Annals of Oncology* online).

**Results**

**The extent of intratumoural heterogeneity in high-risk PC**

Across 25 prospectively recruited patients, M-Seq from 79 tumour regions identified a total of 4484 exonic somatic nucleotide variations (SNV) (3382 non-silent), of which 1962 were ubiquitous, 95 were shared and 2027 were private (Figure 1A). The overall estimation of exonic SNV burden was 0.93 mutations per megabase (median, range, 0.18–33 per megabase), consistent with prior studies in PC [15].

The overall fraction of the genome subject to somatic copy number alterations (SCNAs) was 23.1% (median, range 1.9%–41.6%). Of this fraction, a median of 52.3% (range 2.1%–95.3%) was heterogeneous (Figure 1A). The degree of SNV and SCNA heterogeneity among the tumours was positively correlated (Figure 1B) (r = 0.49, P = 0.013, Pearson’s).

Two patients, BP0001 and PR0103, had markedly elevated SNV rates. BP0001 had a previous diagnosis of Lynch Syndrome and was found to harbour a germline mutation in *MSH6* (p.G39E, rs1042821) and a somatic heterozygous deletion encompassing the region encoding for *MSH2* and *MSH6*, resulting...
in a hemizygous variant in *MSH6*. PR0103 had a somatic 10 Mb deletion overlapping *MSH2* and *MSH6* and a 5 kb somatic deletion across *MSH2*, leading to biallelic loss of *MSH2*. IHC of *MSH2* and *MSH6* in both of these patients showed complete loss of protein expression in the tumours (supplementary Figures S5 and S6, available at *Annals of Oncology* online).

**Genomic events enriched in patients presenting with metastatic disease**

After the diagnostic biopsy, 12/25 patients were found to have metastatic disease on imaging (mHNPC) and 13 patients had localised PC with high risk for metastatic disease (hrlPC).
mHNPC primary tumours had significantly higher burden of SCNAs compared with hrlPC tumours (29.6% ± 10.6% versus 12.5% ± 8.9%, P = 7.57 × 10⁻⁴, Mann–Whitney U test) (Figure 1C) and this was independent of Gleason grade. Comparing mHNPC and hrlPC patients, there was no significant difference in the proportion of heterogeneous SCNAs (P = 0.89, Mann–Whitney U test), overall mutational burden (P = 0.74, Mann–Whitney U test) (Figure 1D), or proportion of heterogeneous mutations (P = 0.11, Mann–Whitney U test).

To explore the relative frequency of SNVs and SCNAs in mHNPC and hrlPC, we focused on driver genes identified in previous PC series (Figure 2) [16, 17]. We found no significant differences between mHNPC and hrlPC tumours. However, there was a significant enrichment of 3q26.2 and 3q21.3 gains in mHNPC compared to hrlPC tumours (5/12 versus 1/13 and 3/12 versus 1/13, respectively) (Figure 3), which remained significantly enriched after controlling for the differing levels of SCNAs.

**Parallel evolution of wnt/β-catenin pathway**

We observed one tumour (PR0139) with three distinct CTNNB1 mutations, all previously described gain-of-function mutations

---

**Figure 2.** Clonal and subclonal driver events in prostate cancer. List of driver genes previously reported as significantly mutated in primary prostate cancer (blue), metastatic castrate-resistant prostate cancer (mCRPC) (grey), or both (black). Ubiquitous ETS fusion (purple), homozygous loss (dark blue), heterozygous deletion (blue), amplification (red) in each tumour is depicted by a coloured square, and heterozygous events are indicated with a triangle. Nonsynonymous mutations are depicted as smaller squares, whether missense (green), frameshift (yellow) or nonsense (dark blue). Clonal and subclonal mutations are indicated by a purple and orange outline, respectively. Known recurrent mutations in TP53, PIK3CA, CTNNB1 and BRAF are indicated with a red star. The barplots on the right are an aggregate of clonal/ubiquitous or subclonal/heterogenous events in each gene across all samples. Metastatic hormone naive prostate cancer (mHNPC); high-risk localised prostate cancer (hrlPC).
in exon 3 of \textit{CTNNB1} leading to stabilisation of $\beta$-catenin and activation of Wnt/$\beta$-catenin signalling (Figure 4A). Phylogenetic analysis of the clonal structure in this tumour revealed that all 3 \textit{CTNNB1} mutations were in three separate subclones (Figure 4B), providing strong evidence for parallel evolution leading to activation of the Wnt/$\beta$-catenin pathway in this tumour.

Temporal order of driver events in clinically high-risk PC

To explore the relative timing of driver events in PC, we utilised a modified version of Pyclone to cluster the mutations (supplementary Methods, available at \textit{Annals of Oncology} online). Consistent with previous reports about PC tumourigenesis [18, 19], we observed ETS fusions and mutations or loss of \textit{TP53} to be early (clonal) events (Figure 2 and supplementary Table S3, available at \textit{Annals of Oncology} online), \textit{PTEN} a later event (60% clonal), and mutations or deletions of chromatin modifiers (\textit{KMT2C}, \textit{KMT2D} and \textit{CHD1}) as a later (subclonal) event (Figure 2).

The landscape of SCNs was also highly consistent with previous studies [15, 17], (Figure 3). In general, we observed that the majority of recurrent SCNA peaks were early events across most tumours in the cohort, aside from 8q and 7p gains, which occurred heterogeneously in 7/13 and 4/6 tumours.

Next, we investigated the mutational processes in the two patients with defective MMR (supplementary Figure S7, available at \textit{Annals of Oncology} online). BP0001, who had germline \textit{MSH2} and \textit{MSH6} aberrations, had a high proportion of ubiquitous mutations. The landscape of SCNAs was also highly consistent with previous studies [15, 17], (Figure 3). In general, we observed that the majority of recurrent SCNA peaks were early events across most tumours in the cohort, aside from 8q and 7p gains, which occurred heterogeneously in 7/13 and 4/6 tumours.
associated with Signature 6 (DNA repair) compared with PR0103 (41.3% versus 8.6%) in keeping with loss of MMR as an early tumourigenic process. Conversely, ubiquitous mutations in PR0103 were mainly associated with Signature 1 (age), suggesting that MMRD was not an initial driver of this tumour, but rather the acquired biallelic loss of \textit{MSH2} was a later event that provided a selective advantage, possibly through an accelerated mutation rate.

**T-cell infiltrate heterogeneity and neoantigen burden**

There was considerable variation in the total inflammatory infiltrate (INIF) (CD8$^+$ or CD4$^+$ and/or FoxP3$^+$ cells in tumour region) between patients (Figure 5A), as well as between different regions within each patient. This intratumoural heterogeneity of INIF is well illustrated by PR0123, where 4 separate core biopsies have different levels of INIF (mean 15%, range 5%–25%) (Figure 5B).

We noted that both PR0103 and BP0001 had extensive INIF (maximal infiltrate >20% of all nucleated cells per biopsy) (2/2) compared with patients without MMR deficiency, where only 6/23 had extensive INIF. Patients PR0112 and PR0129 had ubiquitous and heterozygous loss of \textit{MLH1} and \textit{MSH2} respectively, but this was not associated with high mutational burden or high INIF. As mutational load has been reported to correlate with neoantigen load and neoantigens can elicit a clonal expansion of neoantigen reactive T- (NART) cells [20–22], we hypothesised that the abundant INIF in these MMRD deficient tumours might be related to a high neoantigenic burden. Consistent with this, PR0103 and BP0001 displayed a high neoantigen burden. However, extending this analysis to all 25 patients in this cohort, there was no association between neoantigen burden nor clonal neoantigen burden and INIF (supplementary Figure S8, available at Annals of Oncology online).

**Wnt signalling and modulation of immune response**

Activation of tumour intrinsic Wnt/\(\beta\)-catenin signalling in melanoma has recently been reported to lead to T-cell exclusion from the tumour preventing anti-tumour immunity [23]. However, PR0139 who had parallel evolution of activated \(\beta\)-catenin, had high levels of CD8$^+$ infiltrate (Figure 5A), but was noted to also have high FOXP3$^+$ levels giving a low CD8$^+$/FOXP3$^+$ ratio. A low ratio of tumour-infiltrating CD8$^+$ and FOXP3$^+$ lymphocytes is increasingly being recognised as a measure of immune suppression and as a potential prognostic indicator [24–26].
In our cohort, the 15 patients with levels of INIF at or above the median underwent digital pathology analysis. Of these patients, 7/15 had activating mutations in the Wnt pathway (gain-of-function CTNNB1 mutations, RSPO2 amplification, and deletion of APC, RNF43 and ZNRF3 [17, 27]). We observed a significantly lower CD8⁺/FOXP3⁺ ratio in patients with tumours containing activating mutations of the Wnt pathway compared with wild-type tumours (2.65 ± 1.2 versus 6.08 ± 5.0, \(P = 0.043\), Mann–Whitney U test) (Figure 5C).

**Discussion**

We have conducted the largest prospective clinical cohort study of M-Seq in high-risk PC patients and carried out an integrated genomic and tumour immune infiltrate analysis. Uniquely, we have compared M-Seq of diagnostic prostate biopsies from mHNPC and hrPC and demonstrated increased SCNA in mHNPC patients, consistent with previous reports correlating biochemical recurrence following prostatectomy with high SCNA in localised disease [28]. We observed no differences in SNV frequency between mHNPC and hrPC patients, which is surprising given the large differences seen in other studies between localised PC and pre-treated metastatic castrate-resistant prostate cancer [17, 29]. This may be a consequence of the small sample size or may suggest that unlike SCNA changes, SNV accumulation is a later evolutionary event, possibly as a result of the selective pressure of treatment. In this study, there was enrichment for gains of 3q26.2 and 3q21.3 in mHNPC patients. Both amplicons contain genes previously implicated in PC, e.g. 3q26.2...
Annals of Oncology

contains PRKCI, expression of which is associated with biochemical relapse following prostatectomy [30]. Interestingly, these gains in copy number are early evolutionary events, and the fact that these focal gains are enriched in patients presenting with metastatic disease suggests that some PCs are hard-wired to be aggressive.

We describe the first report of parallel evolution of Wnt signalling in PC, where 3 separate gain-of-function mutations of β-catenin (CTNNB1) were identified in a single tumour. This is similar to the distinct TMRPRS-ERG fusions identified in several regions of the primary prostate tumour [5] and alterations of SETD2, PTEN and KDM5C in renal cancer [31]. Parallel evolution of the Wnt pathway, a pathway already implicated in PC cell growth, proliferation and epidermal to mesenchymal transition [32], points to its biological importance in PC. Unlike mouse melanoma models, where tumour intrinsic Wnt/β-catenin signalling led to T-cell exclusion from the tumour [23], we observed that patients with activated Wnt/β-catenin signalling can have normal or high levels of INIF, but that this is predominantly CD8+ /FOXP3+ low, consistent with a dysfunctional T-cell response. Future studies will be needed to further elucidate the role and mechanism of Wnt/β-catenin signalling in immune modulation in human PC, which is of particular interest given the number of potential novel drugs targeting this pathway.

We identified two patients with hypermutation associated with MMR deficiency and high INIF, the latter being similar to a report of 12/16 (75%) men at risk of Lynch syndrome and diagnosed with PC having significant INIF [33]. Similar to reports in advanced PC [34], our hIPC patients with MMRD had complex structural rearrangements of DNA repair genes MSH2 and MSH6 leading to inactivation. Overall however, we did not demonstrate an association with INIF and neoepitope burden, but given the small number of patients with DNA repair aberrations in this series, this analysis is underpowered. MMRD deficiency has been associated with response to immune checkpoint inhibition in a large biomarker validation study. Lancet 2017; 389: 815–822. We have demonstrated extensive intratumoural heterogeneity of INIF in primary PC. The impact of this on prognosis and predicting treatment response is unknown, but future studies testing INIF as a potential biomarker will need to consider testing multiple tumour regions or developing a liquid biopsy strategy.

In conclusion, our findings reveal how mutational and SCNA changes may drive aggressive metastatic PC. We show that activated Wnt signalling is correlated with immune suppression in primary PC, and suggest that activated Wnt/β-catenin, MMR, high INIF and the CD8+/FOXP3− ratio should be explored as predictive biomarkers for immunotherapeutics in prostate cancer.

Disclosure

The authors have declared no conflicts of interest.

References


Funding

This work was supported by Prostate Cancer Foundation. CS, ML, ME, SAQ and TS are supported by the National Institute for Health Research, the University College London Hospitals Biomedical Research Centre (no grant numbers apply). ML has received support from a BMS II-ON grant (no grant numbers apply). ME is a UK National Institute of Health Research (NIHR) Senior Investigator. CS, HUA and ML are supported by the Cancer Research UK University College London Experimental Cancer Medicine Centre (no grant numbers apply). CS is Royal Society Napier Research Professor. This work was supported by the Francis Crick Institute (no grant numbers apply) which receives its core funding from Cancer Research UK (FC001169), the UK Medical Research Council (FC001169), and the Wellcome Trust (FC001169); by the UK Medical Research Council (grant reference MR/FC001169/1); CS is funded by Cancer Research UK (TRACERx), the CRUK Lung Cancer Centre of Excellence, Stand Up 2 Cancer (SU2C), the Rosetrees Trust, NovoNordisk Foundation (ID 16584), the Prostate Cancer Foundation, the Breast Cancer Research Foundation (BCRF), the European Research Council (THESEUS) (no grant numbers apply). HUA acknowledges funding from the Medical Research Council (UK), the Pelican Cancer Foundation Charity, Prostate Cancer UK, St Peters Trust Charity, Prostate Cancer Research Centre the Wellcome Trust, National Institute of Health Research-Health Technology Assessment Programme and the US National Institute of Health-National Cancer Institute (no grant numbers apply). SAQ is funded by a CRUK Career Development Fellowship, CRUK Biotherapeutic Programme Grant, World Wide Cancer Research, and a Cancer Research Institute Investigator Award (no grant numbers apply). ZS is supported by the Breast Cancer Research Foundation, Basser Foundation, Mazzone Foundation, EU FP7 project PREDICT, the Széchenyi Program, Hungary (KTIA_NAP_13-2014-0021) and the NovoNordisk Foundation (ID 16854). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the article.