Elucidating Drivers of Neuroendocrine Plasticity in Mouse Models of Prostate Cancer

Rodrigo Romero^{1*}, Cassandra Burdziak^{2*}, Patrick McGillivray^{2*}, Harmanpreet Kaur¹, Perianne Smith¹, Meril Takizawa^{2,3}, Brigita Meškauskaitė^{2,3}, Ignas Masilionis^{2,3}, Marisa Mariani^{2,3}, Karolis Kumpaitis^{2,3}, Nikhita Pasnuri^{2,3}, Catherine Snopkowski^{2,3}, Huiyong Zhao⁴, Elisa DeStanchina⁴, Ronan Chaligné^{2,3}, Dana Pe'er^{2,5,6} (peerd@mskcc.org) and Charles L. Sawyers^{1,5,6} (sawyersc@mskcc.org)

¹Human Oncology and Pathogenesis Program, MSKCC, New York, NY, USA

⁶Co-corresponding

Abstract: Lineage plasticity is a hallmark of cancer that enables tumor cells to evade therapies and develop resistance. Understanding the molecular drivers of plasticity is crucial for managing treatment resistance in the clinic. We previously established a novel mouse model of the neuroendocrine lineage plasticity in prostate cancer, identifying Rb1 loss, tumor microenvironment input, and Ascl1 expression as key factors for the neuroendocrine transition. Using advanced single-cell sequencing and spatial transcriptomics alongside integrative computational methods, we confirm the dynamic nature of this adenocarcinoma-to-neuroendocrine transition, revealing significant transcriptional and epigenetic heterogeneity within tumor populations. This process is characterized by sharp phenotypic shifts at key transition points, with the identification of a rare transitory tumor population bridging these two extremes. Our findings nominate several transcription factors co-expressed with Ascl1 as potential drivers of the neuroendocrine transition. Lineage tracing with single cell molecular barcoding uncovers a striking polyclonal origin of the neuroendocrine transition, where multiple transition-competent luminal adenocarcinoma clones independently converge upon a plastic cell state. This dynamic state is defined by progressive activation of neuroendocrine programs, sharp induction of AP-1 activity, and engagement of cell-intrinsic inflammatory pathways. These findings shed additional light into coregulated genetic and transcriptional programs governing therapy resistance and tumor evolution. By pinpointing these critical molecular players, our work opens new avenues for disrupting lineage plasticity, offering promising therapeutic strategies to overcome treatment resistance in prostate cancer.

Funding Acknowledgements: R.R. was supported by the by National Institutes of Health (NIH) Translational Research Oncology Training Program (T32CA160001), Charles H. Revson Senior Fellowship in Biomedical Science (22–23), the Malcolm S. Forbes Postdoctoral Fellowship, and the Prostate Cancer Foundation Young Investigator Award. We acknowledge the use of the Integrated Genomics Operation Core, funded by the NCI Cancer Center Support Grant (CCSG, P30 CA08748), Cycle for Survival, Marie-Josée and Henry R. Kravis Center for Molecular Oncology and the Alan and Sandra Gerry Metastasis and Tumor Ecosystems Center. This work was supported by the Howard Hughes Medical Institute; NIH grants CA193837, CA092629, CA224079, CA155169, CA008748 and CA274492 and U54CA209975. The content is solely the responsibility of the authors and does not necessarily represent the official views of the NIH, Howard Hughes Medical Institute, Damon Runyon Cancer Research Foundation or the Charles H. Revson Foundation. D.P. and C.L.S. are Howard Hughes Medical Institute investigators.

Conflicts of Interest Disclosure Statement: C.L.S. served on the Board of Directors of Novartis (2013-2025), is a cofounder of ORIC Pharmaceuticals and is a co-inventor of the prostate cancer drugs enzalutamide and apalutamide, covered by US patents 7,709,517; 8,183,274; 9,126,941; 8,445,507; 8,802,689; and 9,388,159 filed by the University of California. C.L.S. is on the scientific advisory boards for the following biotechnology companies: Beigene, Blueprint Medicines, CellCarta, Column Group, Foghorn, Housey Pharma, Nextech, PMV Pharma and ORIC. D.P. is on the scientific advisory board of Insitro. The other authors declare no competing interests.

²Program for Computational and Systems Biology, SKI, MSKCC, New York, NY, USA

³Single Cell Analytics Innovation Lab, MSKCC, New York, NY, USA

⁴Antitumor Assessment Core Facility, MSKCC, New York, NY, USA

⁵Howard Hughes Medical Institute, Chevy Chase, MD, USA

^{*}These authors contributed equally