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EDITORIAL

Bringing Access to the Full Spectrum of Cancer Research: A Call for Papers

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Abbreviations: AACR, American Association for Cancer Research; FDA, Food and Drug Administration; HPV, human papilloma virus; ICGC, International Cancer Genome Consortium; LMICs, low- and middle-income countries; TCGA, The Cancer Genome Atlas.

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Cancer is a keyword in innumerable stories of both loss and hope. In 2012, 14.1 million people were diagnosed with cancer worldwide, with an estimated 8.2 million deaths annually [1]. The disease burden is daunting, yet long-term investment of resources in research is now yielding cause for optimism. For example, the United States Food and Drug Administration (FDA) has approved over 30 cancer drugs within the past three years [2], many of which were designed in response to insights gained from genomic investigations and developed to specifically target a gene or protein that is required for tumor growth, spread, or survival.

Understanding the clonal evolution of a cancer and the mutations that accrue over time could result in even more precise therapies. Recent findings from the cancer genomics field have also revealed the extent to which cancers are not just heterogeneous among people but also within an individual [3,4]. Propelled by improved technologies such as single-cell sequencing, longitudinal studies on an individual can trace a cancer's development over time and through metastases, providing guidance for potentially individualized therapies.

As an open-access journal committed to publishing outstanding research and commentaries on the major challenges to human health worldwide, *PLOS Medicine* endeavors to provide a prominent venue for publishing global cancer research. With growing and aging populations, low- and middle-income countries (LMICs) are disproportionately affected by the increasing numbers of cancers worldwide, with more than 60% of the world's total cancer cases and 70% of the deaths occurring in Africa, Asia, and Central and South America [1]. In lower-resource settings, the situation is made worse by the lack of early detection and access to treatment. Recent Policy Forum articles in *PLOS Medicine* have outlined key components to the establishment of national childhood cancer strategies in LMICs [5] and strategies to improve cancer care for cervical cancer in LMICs, including scale-up of human papilloma virus (HPV) vaccination and integration of care and prevention services with HIV and maternal services [6]. Given that disparities also exist in access to cancer care within high-income countries (e.g., for lung cancer treatment [7]), *PLOS Medicine* welcomes submissions of research that provides solutions to access to care within both low- and high-resource settings.

Reducing the burden of cancer means addressing the full spectrum of contributing conditions. Accordingly, in recent months, *PLOS Medicine* has published research on topics ranging from identifying and improving environmental and lifestyle-related exposures [8,9,10] to optimizing the benefits and reducing the harms of screening [11,12,13,14], as well as translating basic science towards state-of-the art treatments [3,4,15,16] and ensuring that such interventions are available to all who need them [7,17].

Within this spectrum, the editorial team believes that translational genomics represents a "state of the art" wavelength, able to illuminate both basic pathophysiology and therapeutic

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decisions and options. The editorial team is actively engaging with the cancer genomics community, both through our academic editors, such as Andrew Beck (Dana-Farber/ Harvard Cancer Center) who discussed the importance of open access to cancer genomics data in a recent editorial [18], and also via our attendance at key conferences in 2015. Two consortia that provide broad public access to cancer sequence data are The Cancer Genome Atlas (TCGA, http://cancergenome.nih.gov/) and International Cancer Genome Consortium (ICGC, https://icgc.org/). We are very pleased to feature an accompanying interview blog [19] with Francis Ouellette, Associate Director of Informatics and Biocomputing at the Ontario Institute for Cancer Research, who discusses the remit of the ICGC and TCGA projects, how these projects have generated a tidal wave of data that has reshaped how people consider analyzing such datasets, and his hopes for how these findings will translate into clinical applications.

To coincide with the meeting of the American Association for Cancer Research (AACR), to be held in Philadelphia from April 18 to 22, 2015, *PLOS Medicine* is launching a Cancer Research Collection [20], an open-access collection of recently published articles representing the full spectrum of clinically relevant cancer research and commentary, from translational to clinical to epidemiological. To expand the collection, and to support the mission we share with the AACR to conquer cancer through research and education, we are issuing a call to the clinical genomics and cancer research community for papers that provide novel insights into cancer heterogeneity, progression, and translational and clinical medicine, with strong potential to advance patient care, public policy, or clinical research agendas. Papers submitted in response to the call for papers will be included in the collection if accepted for publication. Please submit a presubmission inquiry to the editorial team at http://www.editorialmanager.com/pmedicine/default.aspx.

Author Contributions

Wrote the first draft of the manuscript: CG. Wrote the paper: CG LN TM AR LP PS. Agree with manuscript results and conclusions: CG LN TM AR LP PS. All authors have read, and confirm that they meet, ICMJE criteria for authorship.

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