

## Overcoming Intratumor Heterogeneity of Polygenic Cancer Drug Resistance with Improved Biomarker Integration<sup>1</sup>

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### Abstract

Improvements in technology and resources are helping to advance our understanding of cancer-initiating events as well as factors involved with tumor progression, adaptation, and evasion of therapy. Tumors are well known to contain diverse cell populations and intratumor heterogeneity affords neoplasms with a diverse set of biologic characteristics that can be used to evolve and adapt. Intratumor heterogeneity has emerged as a major hindrance to improving cancer patient care. Polygenic cancer drug resistance necessitates reconsidering drug designs to include polypharmacology in pursuit of novel combinatorial agents having multitarget activity to overcome the diverse and compensatory signaling pathways in which cancer cells use to survive and evade therapy. Advances will require integration of different biomarkers such as genomics and imaging to provide for more adequate elucidation of the spatially varying location, type, and extent of diverse intratumor signaling molecules to provide for a rationale-based personalized cancer medicine strategy.

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### Introduction

In Sun Tzu's book *The Art of War*, method and discipline are part of the five constant factors governing one's deliberations, which are considered necessary to achieve success. In other words, proper assessment of the strengths and weaknesses of your capabilities and those of your opponent are crucial before engagement. For many centuries, surgery was the only treatment option available for cancer patients. Advancements in anesthesia, antiseptic practices, blood transfusions, and antibiotics were landmark achievements providing for the field of "surgical oncology" to develop. However, during this time the observation of cancer cell spread or metastasis necessitated additional developments including radiation therapy and chemotherapy. Initially, the use of drugs involved cytotoxic chemotherapy for killing rapidly proliferating cancer cells, which evolved to combination therapy using drugs with different molecular mechanisms and toxicity profiles. It has long been rationalized that the ability to eliminate a tumor required identification of a druggable target presented by the tumor, which could be exploited as a differentiable vulnerability (either by presence or amount) apart from the host organism.

### Attack by a Stratagem

The exquisite scientific progress achieved over the past few decades have had a major impact in improving our understanding of tumor treat-

ment sensitivity and response to therapeutic interventions. In the current post-genomic era, a clearer picture is emerging revealing an ever increasing complex array of interconnected adaptable signaling pathways on which defined pathogenic driver mutations emerge and on which tumor cells become addicted to for survival. This understanding led to the establishment of a new generation of cancer drugs termed molecularly targeted cancer therapies developed to block the growth and spread of cancer through interfering with specific signaling molecules involved in tumor growth and progression. Molecularly targeted agents offered the ability to potentially treat genetically defined subgroups of patients by focusing on cellular and molecular alterations specific to their individual cancer. Major clinical advances were anticipated to be achieved through the development and use of targeted agents based on the belief that targeted cancer therapies would be more effective than traditional chemotherapy and radiotherapy. It was also hoped that targeted cancer agents would provide additional

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benefits because while being less harmful to normal cells, systemic side effects would be if not ameliorated altogether, at least minimized, thus improving a patient's overall quality of life. Furthermore, individualization of cancer patient care was now seen as possible, as confirmation of the presence of a particular target within a tumor could be achieved in a relatively straightforward manner through molecular genomic analysis of an individual patient's tumor using a biopsy sample obtained from a patient's tumor. By matching the drug to the tumor target, major clinical successes seemed to be well within reach.

### Variation in Tactics

Experience has now showed that targeted therapies have limitations that include potential for tumor cells to develop resistance. For example, some patients have developed resistance to imatinib (Gleevec) through a mutation in the *BCR-ABL* gene that alters the shape of the protein so that its affinity for drug binding is reduced, decreasing treatment efficacy. In fact, a wide variety of tumor cell adaptations in signaling molecules may occur following exposure to targeted agents, providing the cells with an opportunity to gain the upper hand through acquired resistance, thus escaping elimination. Typically, alternative targeted therapies that could possibly overcome the acquired resistance are not available nor are the specific cellular adaptations that occurred easily determined in real time. Owing to these issues in part, targeted therapies are being used in combination with other targeted therapies or with traditional chemotherapy and radiation therapy to provide for a more aggressive treatment approach.

What was described thus far was an overall approach to cancer treatment from the perspective of an individual tumor mass having a single or major oncogenic driver that can be targeted following identification of the target through analysis of a biopsy sample. However, we now know that the composition of tumors can be comprised of many different cell subpopulations, each which can harbor different genotypic and phenotypic characteristics leading to a diversity of biologies. This knowledge can be very disconcerting, leaving one with the feeling of "two steps forward and one step backwards" in the war on cancer. The impact associated with the relatively recent understanding of the presence of significant intratumor heterogeneity on tumor therapy cannot be underestimated. Multiple cellular subpopulations with different genetic and phenotypic characteristics along with their associated tremendous three-dimensional spatial variation within a single lesion portends the fact that a specific lesion does not have a single target but rather multiple oncogenic targets that must be overcome to achieve optimized therapeutic benefit [Yap TA (2012). *Sci Transl Med* 4, 127].

### Terrain

There are potentially a myriad of factors that can contribute to intratumor heterogeneity. For example, heterogeneous cellular microenvironments within a tumor mass can act to drive regional phenotypic evolution and diversity with associated genetic mutations. For example, spatially distinct regions within a tumor with limited blood flow would have low oxygenation levels that could lead to tumor cells adapted to a microenvironment of acidosis and hypoxia resulting in augmented survival pathways and enhanced resistance to chemoradiation. Moreover, genetic instability within a tumor cell population provides opportunities for the emergence of spatially varying cells expressing alternate oncogenes and tumor suppressor genes further complicating the development of an adequate treatment strategy for an individual tumor.

Recent findings have in fact revealed significant intratumor heterogeneity, and branched evolution was present in primary renal carcinomas and associated metastatic sites using multiregion sequencing [Gerlinger M (2012). *N Engl J Med* 366, 892]. In this study, multiregion genetic analysis of four different tumors revealed that intratumor heterogeneity was present in every tumor analyzed. Tumors were found to have spatially separated heterogeneous somatic mutations, patterns of allelic imbalance, and chromosomal imbalances that led to phenotypic intratumor diversity and uniformity. It was also shown that a single tumor-biopsy specimen only revealed a minority of genetic aberrations (including mutations, allelic imbalance, and ploidy) that were actually present in the tumor mass. Thus, characterization of intratumor heterogeneity using next-generation sequencing necessitates our rethinking of how best to approach the development of effective personalized medicine, which, until now, has relied on single biopsy samples to delineate the mutational landscape of a patient's cancer. It is clear that genomic analyses using single tumor-biopsy specimens underestimate the overall mutational burden of tumors because the presence of significant intratumor heterogeneity requires the issue of sampling bias to be addressed to achieve improved outcome.

Intratumor heterogeneity of protein function may nurture tumor adaptation through a Darwinian selection process leading to improper selection of drugs resulting in an ineffective and thus disastrous treatment outcome. Due to limitations in information obtainable from single tumor-biopsy samples, the presence of intratumor heterogeneity is anticipated to provide abridged information related to the true tumor genomic landscape resulting in unending challenges to development of personalized medicine for cancer patients. Due to the presence of intratumor heterogeneity, intrinsic and acquired resistance to cytotoxic chemotherapy, ionizing radiation, and molecularly targeted drugs is an unavoidable consequence including the need to target multiple oncogenic drivers of the tumor. One proposed solution is to use the information related to polygenic drug resistance to develop a rationally designed approach using combinatorial targeted therapy to address the heterogeneity of targets disseminated throughout the tumor mass. One of the key issues related to combination therapies is the potential for severe and undesirable side effects. In an effort to minimize these toxicities, new approaches to drug development are incorporating simultaneous targeting moieties within a single structurally designed molecule [Guerrant W (2012). *J Med Chem* 55, 1477]. Development of novel multivalent ligands to modulate several cancer targets simultaneously may provide a useful approach for combating the inherent intratumor heterogeneous diversity of protein function encountered in clinical experience.

### The Use of Spies

The concept of significant spatially varying somatic mutations along with the need to delineate the major contributors of such within an individual's tumor necessitates the need for obtaining additional multiregional information to optimize therapy and to predict treatment outcome. Obtaining multiple biopsies may be problematic especially in patients with multifocal metastatic disease and following treatment wherein a tumor may adapt and thus gain resistance to the intervention in real time. An alternate proposed strategy is to use state-of-the-art clinical imaging modalities to complement the information obtained from genetic analysis to further characterize tumor spatial heterogeneity [Basu S (2011). *Eur J Nucl Med Mol Imaging* 38, 991]. Imaging can be used to reveal intratumor phenotypic heterogeneity that likely reflects the underlying and spatially corresponding genetic

**Table 1.** Summary of Published Articles.

Subject	2010	2011	2012
Cancer genetics	[14,37,45,51,64,67,69–71,90,92,93,100,104]	[123,137,139,143,146,160,164,180,205,206,209]	[231,232,235,238,239,250,258,261,263,268,269,273,278,283,289,294,299,303,320,323]
Cell and tumor biology	[1,2,5,8,10,15–17,19,21,22,30–33,35,36,40,41,44,48,52,53,55,56,58,59,61–63,65,66,73,74,79–81,83,85,86,89,91,94–96,98,99,101,103,105]	[107–109,115–117,124,130,132–136,141,145,151,152,154,156,161,163,168,171,173,174,176,181,182,188,191–197,199,201,208,210–214]	[216–220,222,224,227,228,233,234,236,237,244,248,249,256,257,260,262,267,271,275,279,282,284,286,290–292,301,302,304–306,313–317,319]
Experimental therapeutics	[4,6,7,11,20,27,28,38,46,50,54,60,87,88,106]	[112,114,119–122,127,129,138,140,142,147–149,167,172,175,184–186,189,190,202–204,207,215]	[221,225,226,240,242,246,253,254,259,266,270,274,276,280,281,287,288,293,296,297,300,308–310,312,321,322,324]
Tumor immunology	[13,29,43,57,68,78,97]	[110,113,159,166,170,178,179,187,198,200]	[229,230,245,251,277,285,307,318]
Epidemiology and prevention	[39]		
Cancer imaging	[25,75,84]	[118,128,131,150,153,165,183]	[247,252,255,264,265]
Clinical investigations	[3,9,12,23,24,26,34,42,47,49,77,82,102]	[125,169]	[223,243]
Animal models	[18,76]	[111,126,144,177]	[241,311]

diversity. For example, positron emission tomography, magnetic resonance imaging (MRI), and computed tomography (CT) all provide multislice high-resolution anatomic as well as functional images that can be repeated over time before, during, and following treatment intervention. These imaging modalities are well suited for interrogating the three-dimensional landscape of tumors noninvasively and over time. While traditional clinical assessment of tumor images is conducted by a trained radiologist, the complexities and subtleties of spatially varying signal intensities may be difficult to extract and interpret by the naked eye. Traditionally, whole-tumor statistical averages (histograms) of quantified imaging metrics have been used to characterize tumors before and following treatment. However, this type of analysis relegates the spatial information to a whole-tumor average measurement. More recently, emergence of a voxel-by-voxel-based approach for quantifying changes over time spatially has been found to provide more sensitivity for detecting changes over time during therapy as well as retaining the spatial information within the anatomic context of the tumor [Galban CJ (2011). *Clin Cancer Res* 17, 4760]. The voxel-based method has been applied across imaging modalities and provides new opportunities to assess intratumor heterogeneity [Laymon CM (2012). *Magn Reson Imaging* 30, 1278]. Additional approaches for assessment of tumor heterogeneity using digital image post-processing algorithms include texture analysis methods [Davnull F (2012). *Insights Imaging*].

Imaging can provide significant and timely clinical patient management support, as it can provide rapid and objective assessment of tumor therapeutic response. However, response to therapeutic intervention may be initially successful, but rapid emergence of spatially varying resistance is likely and development of a noninvasive imaging approach with the ability to detect this eventuality in a timely manner would allow for rapid deployment of alternate interventions that would be anticipated to optimize therapeutic outcome. Diffusion-weighted MRI has been shown to provide a sensitive measure of tumor response throughout the course of treatment. In addition, diffusion-weighted MRI was reported to be sensitive enough to detect real-time emergence of resistance in an animal tumor model [Lee KC (2006). *Cancer Res* 66, 4692]. The overall ability of imaging metrics to delineate spatially varying and treatment-associated changes in tumor structure and function provides complementary information to biopsy-derived molecular genetic information related to tumor target presentation and will ultimately improve drug selection and patient care.

## Summary

As described above, genotypic and phenotypic diversity has a tremendous impact on cancer growth and intervention. The journal *Neoplasia* provides peer-reviewed diverse information related to basic cancer biology, as it relates to clinical relevance and serves as a rapid conduit to disseminate relevant and timely information to the international community. Exemplifying the significant diversity of articles published in *Neoplasia* over the past 3 years, articles that cover areas of cancer research including cell and tumor biology, imaging, genetics, experimental therapeutics, and clinical investigations are published (Table 1). The readership of *Neoplasia* is provided with broad-based state-of-the-art information comprising many key pieces of the overall oncology puzzle. Furthermore, the immediate availability of *Neoplasia* articles to the world-wide clinical cancer research community is a key feature of *Neoplasia*, allowing authors' research findings to be made available to the largest possible readership ensuring that published articles will have a significant impact. Finally, as the Editor in Chief and, along with the Editorial Board, we have been pleased with the overall success that this effort has in serving the cancer research community. We thank the scientific groups who have entrusted the dissemination of their research findings to our publication and we look forward to continued progress in knowledge, which will be used to improve cancer patient care and outcome.

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