Pharmacologic Biomarkers in the Development of Stratified Cancer Medicine

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Abstract
Clinical pharmacologic research plays a vital role in cancer drug development. In recent years, biomarker studies have become integral to this process, specifically the use of pharmacologic biomarkers in the development of targeted therapies and their translation to clinical practice. In this overview, we discuss the validation of pharmacodynamics (PD) biomarkers and highlight the circulating tumor DNA as a promising cancer biomarker to illustrate how PD biomarkers can be powerful tools for guiding treatment strategies. We provide insights into PD biomarker approaches for future development of novel therapies and their role in cancer medicine.

See all articles in this CCR Focus section, "Progress in Pharmacodynamic Endpoints."
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Introduction
Clinical pharmacology is the science of drugs in the prevention, treatment, and control of disease in humans. A comprehensive understanding of the principles of clinical pharmacology is essential for any clinician to deliver optimal therapeutics to individual patients. Clinical pharmacology is divided into three important disciplines that are interrelated: pharmacokinetics (PK; absorption, distribution, metabolism, and elimination), pharmacogenetics (PG; genes that regulate PKs, including drug metabolizing enzyme and drug transporter genes, and genes for pharmacologic targets), and pharmacodynamics (PD, pharmacologic effects manifested as a clinical response or adverse effect; Fig. 1; ref. 1). It is the dependence of PD (drug action) on PK and PG that is a central theme in the six articles presented in this CCR Focus section (2–7). Our understanding of PD has greatly improved over the past two decades and most drug effects are the result of interactions with specific macromolecules or targets that induce a biochemical, physiologic, or molecular change. Hertz and McLeod (2) eloquently point out that although, in oncology, PD can influence both PK and PD and these are determined of-mechanism PD) and phenotypic effects (proof-of-concept PD) in the tumor. Furthermore, genetic factors can influence both PK and PD and these are determined by PG biomarkers.

• Predisposition biomarkers to predict the risk of developing cancer, for example, germ line mutations in tumor-suppressor genes such as BRCA1 and BRCA2.
• Screening biomarkers for early cancer detection, and hence, more effective management, in the general or at risk population, for example, prostate-specific antigen.
• Diagnostic biomarkers to define the exact type of tumor to be treated, for example, cellular and molecular pathology.
• Prognostic biomarkers for estimating the likely disease course and, hence, the most appropriate management strategy, for example, radiologic and pathologic assessments.
• Predictive biomarkers for selecting the most appropriate therapy, for example, molecular target assessment to identify the appropriate targeted therapy (predictive biomarkers are also referred to as "theranostics" and "companion diagnostics").

Pharmacologic biomarkers, as discussed extensively in this CCR Focus section, to demonstrate that active drug levels are achieved (PK biomarkers) and that these are associated with adequate drug-target interaction (proof-of-mechanism PD) and phenotypic effects (proof-of-concept PD) in the tumor. Furthermore, genetic factors can influence both PK and PD and these are determined by PG biomarkers.
Surrogate response biomarkers to detect clinical activity before volumetric changes in the tumor have occurred, for example, changes in circulating tumor markers or functional imaging such as PET and MR.

**Validation of PD Biomarkers**

Validation of a PD biomarker addresses whether the biomarker achieves its purpose in a carefully defined clinical setting and the population of interest. A critical distinction should be made between when a biomarker undergoes method validation versus clinical qualification. Analytic method validation is the process of assessing the assay, its performance characteristics, and the optimal conditions that will ensure the reproducibility and accuracy of the assay. Clinical qualification is the evidentiary process of linking a biomarker with biologic processes and clinical endpoints (8), and is equivalent to clinical validation recently defined by Parkinson and colleagues (9). Although “validation” and “qualification” have been used interchangeably in the literature, the distinction should be made to properly describe the particular phase the PD biomarker is transitioning through in the drug development process. The term “validation” is usually reserved for analytic methods, and “qualification” for biomarker evaluation in relation to a clinical endpoint (8, 10). Both validation and qualification processes are intertwined and their integration guides biomarker development with the overriding principle of linking the biomarker with its intended use (11).

It is also important to point out that biomarker method validation is distinct from PK validation and routine laboratory validation. A “fit-for-purpose” approach for biomarker method development and validation is derived from the concept that assay validation should be tailored to meet the intended purpose of the biomarker study. Method validation should demonstrate the reliability of the assay for the intended application, with the rigor of the validation process increasing from the initial validation required for exploratory purposes to the more advanced validation that is needed to demonstrate the evidentiary status of the biomarker (11). Fit-for-purpose method validation is an umbrella terminology that is used to describe distinct stages of the validation process, including prevlabation, exploratory and advanced method validation, and in-study method validation. Method validation is, thus, a continuous and iterative process of assay refinement with criteria that are driven by the application of the biomarkers with increasing rigor at each successive validation step, focusing on method robustness, cross-validation, and documentation control.

In 2001, the U.S. Food and Drug Administration (FDA) issued a guidance for industry on “bioanalytical method validation” for assays to support PK studies that are specific for small-molecule drugs and which are not directly related to the validation of biomarker assays. As an update, in September 2013, the FDA issued a revised draft guidance that includes biomarkers and diagnostics (12), and to ensure the development of validated analytic tests, the revised draft guidance established six fundamental parameters for the validation of a biomarker assay: accuracy, precision, selectivity, sensitivity, reproducibility, and stability. Although the recommendations in this guidance pertain to the validation of assays to measure in vivo biomarker concentrations in biologic matrices, such as blood or urine, the above parameters can be extended to any sample type or assay platform used in analytic method validation.
The concept of biomarker qualification has become integrated within the drug development process. The qualification of biomarkers as tools for efficient drug development originated from the FDA Critical Path Initiative and the FDA Guidance for Industry on Pharmacogenomic Data Submissions (13). The guidance defined a valid biomarker as one that is measured in an analytic test system with well-established performance characteristics, and for which there is an established scientific framework or body of evidence that elucidates the physiologic, toxicologic, pharmacologic, or clinical significance of the test results. The classification of biomarkers is context-specific (14), and this context-specific concept resulted in the qualification process of biomarkers being defined as "a conclusion that within the stated context of use, the results of assessment with a biomarker can be relied upon to adequately reflect a biological process, response, or event, and support use of the biomarker during drug development." The term "context of use" describes the setting(s) in which the biomarker is qualified, and boundaries within which the available data justify its use. In January 2014, the FDA issued the latest guidance document on the qualification process for drug development tools (15). Biomarkers are measured using specific devices, and biomarker qualification cannot be achieved without analytic and clinical validation of at least one device to measure the biomarker. It is essential that the assays used to measure the biomarker are analytically validated in a sequence of trials to generate the evidence to support the use of the biomarker in the given context of use. The qualification data incorporate consensus methods and evidence that associates biomarker measurements with sufficient clinical outcomes. Examples of the qualification of biomarkers for use in the development of oncology drugs can be best illustrated with the qualification of circulating tumor cells (CTC; ref. 16) and the qualification of imaging-based biomarkers (17), as measures of clinical benefit. Biomarker qualification is also observed in the codevelopment of biomarkers (in the form of "diagnostic" tests) and drugs with the use of these biomarkers being limited to the application of the drug (18). Codevelopment imposes the necessity to generate specific guidelines describing analytic test validation (sensitivity and specificity of the assays), clinical test validation (ability of the assays to detect and predict diseases), and clinical utility.

In this CCR Focus section, Kinders and colleagues (3) provide excellent examples of the challenges that can be encountered in the implementation of PD biomarkers in the evaluation of targeted therapies, using proof-of-mechanism and proof-of-concept PD biomarkers that are relevant to the development of poly(ADP-ribosе)polymerase inhibitors as case examples. Importantly, the authors highlight the potential of using surrogate normal tissues, for example, peripheral blood mononuclear cells and skin biopsies. However, the data derived from such studies, although of value in confirming that potentially effective drug levels are being achieved, are not a substitute for studies on tumor material, although the latter may not of course always be clinically accessible. As a consequence a number of laboratories have investigated the utility of circulating tumor DNA (ctDNA) and CTCs in biomarker studies.

Circulating Tumor DNA as a Biomarker

Cell-free fragments of DNA are shed into the bloodstream by cells undergoing apoptosis or necrosis and in patients a proportion of the fragmented DNA in circulation is derived directly from the tumor. Although the circulating cell-free DNA, also known as ctDNA, may arise from tumor necrosis, apoptosis or active secretion, the exact mechanism remains unknown (19). Recent advances in sequencing technologies have enhanced the sensitivity and accuracy of DNA analysis, allowing for the genotyping of somatic genomic alterations in ctDNA. ctDNA contains genetic defects identical to those of the tumors themselves, enabling the detection of cancer-associated genetic alterations that include point mutations, rearrangements, amplifications, and aneuploidy.

In recent years, ctDNA has shown promise as a noninvasive cancer biomarker. The concept that ctDNA represents a sensitive biomarker of tumor burden, and, hence, has potential as both a prognostic and surrogate response biomarker, has come to fruition with the demonstration that ctDNA can relate to tumor staging and prognosis. Studies in solid tumors such as melanoma, ovarian, breast, and colon cancers have evaluated the potential utility of this approach to define tumor dynamics during therapy for patients with advanced disease (20–24). Specifically, detection of KRAS mutations in ctDNA can help with drug monitoring and, thus, early identification of patients who develop resistance to EGF receptor blockade (19, 20). This potential role was further confirmed in two recent studies (25, 26) with Bettegowda and colleagues demonstrating the sensitivity of ctDNA for detection of clinically relevant KRAS gene mutations at 87.2% and its specificity was 99.2% (27). They also detected ctDNA across 14 tumor types that had not yet metastasized or released detectable CTCs, and found ctDNA at relatively high concentrations in the patients with metastatic cancer and at lower but detectable concentrations in those with localized cancers. Together, these findings suggest that ctDNA could be a reliable biomarker for early detection as well as for determining optimal treatment, and monitoring resistance.

The ability to detect and enumerate ctDNA offers broad clinical applications that have not been feasible with routine sequencing of tumor tissue or other circulating or imaging biomarker measurements. The relatively short half-life (approximately 2 hours) of ctDNA allows measurement of changes that take place over a short timeframe (hours), rather than months as seen with conventional volumetric measures of radiographic response or progression, making the measurement of ctDNA an ideal candidate marker of tumor dynamics (28). The high degree of specificity of ctDNA allows for interrogation of tumor-specific molecular alterations in the circulation as mutations found in ctDNA would be absent in matched normal DNA. Furthermore, in terms of sensitivity, ctDNA is abundant and readily detectable in most patients with advanced cancer; in cases with lower levels of ctDNA such as in early-stage
disease or minimal residual disease, detection may still be possible using advanced genomic methodologies. The analysis of ctDNA has considerable potential in the assessment of molecular heterogeneity, for monitoring tumor dynamics, identifying genetic determinants of therapy, and evaluating treatment response, as well as detecting acquired resistance and developing potential strategies to circumvent this. Thus, ctDNA is a broadly applicable, sensitive, and specific biomarker that can be a powerful tool for guiding treatment strategies in cancer. However, it will be necessary to develop standardized methodologies for ctDNA analyses and validation in large prospective clinical trials, before implementing this “liquid biopsy” approach widely in the clinic.

PD Biomarker Approaches and Issues Addressed in This Edition

Complementing and extending the potential of ctDNA as a biomarker in PD studies are investigations using CTCs. The article by Yap and colleagues (4) in this CCR Focus section demonstrates the exciting progress that has been made in using CTCs in PD studies, in addition to the extensively investigated role of CTCs as prognostic and surrogate response biomarkers. Correctly, the authors emphasize the two key issues of CTC heterogeneity and the potential for differences in PD readouts in CTCs versus those in the original solid tumor lesion. A particular issue in using CTCs for PD studies in that cells in the blood will be exposed to plasma drug concentrations, which may or may not be the same as drug levels achieved in solid tumors, emphasizing the more general point that PK and PD should not be considered in isolation, but as the two sides of the same pharmacologic “coin.”

Although the direct measurement of tumor drug levels is extremely challenging, the article by van der Veldt and Lammertsma (5) demonstrates the potential of PET tracers in this context, as exemplified by the radiolabeled taxanes [18F]paclitaxel and [11C]docetaxel. These tracers provided significant insights into PK and biodistribution models, enhancing predictive ability by addressing the question of whether or not the drug achieves active tumor levels. In addition, the authors report that the induction of the ABCB1 transporter apparently reduced tumor uptake. These data, if confirmed, have tremendous clinical implications as accumulation was variable and associated with tumor perfusion, but not tumor size. Of concern was the observation that less than 1% of total uptake associated with tumor perfusion, but not tumor size. However, the drug administered accumulated the tumors, highlighting the importance of approaches designed to enhance drug delivery. Notwithstanding the low overall level of tumor drug uptake, higher tumor uptake was related to tumor response in patients with lung cancer. Furthermore, the enticing data presented on the interaction between bevacizumab and docetaxel were particularly impressive. In patients with non–small cell lung cancer, bevacizumab seemed to reduce both perfusion and the net influx rate of [11C]docetaxel, an effect that persisted for at least 4 days, suggesting that careful thought should be given to the sequence of antiangiogenic agent/chemotherapy drug combination regimens. Although this article demonstrates the potential of PET imaging in providing hard data on the distribution of drugs, the real value will come in showing target expression, and data are now emerging on both PK and PD.

The most successful class of targeted therapies to date in cancer medicine are the oncogenic kinase inhibitors or antagonists, either small molecule or antibody based. These drugs are the “poster children” for personalized/refined/precision medicine and provide unequivocal evidence that molecular insights into the disease can lead to significant improvements in outcomes. As the development of kinase inhibitors has evolved the critical role of predictive and PD biomarkers has become ever more clearly apparent, and Gainor and colleagues (6) provide an excellent overview of lessons learned and challenges still faced in lung cancer. Again, these authors emphasize the issue of accessing a hard-to-biopsy tumor for biomarker studies, and the potential of surrogate tissues, CTCs, ctDNA, and imaging for PD studies in lung cancer.

Finally, the interplay between genome-wide association study (GWAS) and candidate single-nucleotide polymorphism (SNP) studies is well laid out in the reviews of Low and colleagues (7) and Hertz and McLeod (2), respectively. GWAS and candidate SNP studies are both necessary to fully understand the PG of a drug, and most PG candidate SNP approaches assume that the key drug metabolizing enzymes and transporters involved have been defined. There are now at least three commercially available platforms for studying drug metabolism and transporter genes. On the other hand, GWAS offers a hypothesis-free approach for generating insights into genetic determinants of PK and PD, as well as understanding of the mechanisms and pathways of underlying gene–phenotype interactions. Nonetheless, both approaches (GWAS and candidate SNP) have their limitations, in particular, the failure to provide functional information. However, both approaches have strengths and the sequential use of GWAS to identify candidate SNPs that can then be translated into focused SNP panels, as illustrated in the article by Hertz and McLeod (2) is a viable route to clinical application. Coordination in the development of clinical PG biomarkers for routine use is critical and a number of national and international consortia have been established to do so.

Conclusions

As cancer becomes the primary cause of death from disease in an increasing number of developed countries, and the overall incidence of cancer increases with aging populations, the need for more effective therapies becomes ever-more pressing. After many decades of investment in basic cancer research, insights into cancer biology are now being translated into new treatments that offer real hope for both current and future generations of patients with cancer. Importantly, in developing and optimizing these new therapies, the quality
and intensity of science that led to their discovery must be sustained during their clinical evaluation, and biomarker studies are a vehicle for so doing. Specifically, predictive, PK, proof-of-mechanism PD, proof-of-concept PD, and surrogate response biomarker studies are the tools that facilitate highly quality clinical pharmacologic research, without which the early clinical development of targeted therapies as well as their routine use in cancer medicine will not be viable. The articles in this CCR Focus section highlight both the considerable potential as well as many of the pitfalls of biomarker research. However, the significant progress made already gives confidence that, through integrated targeted drug and biomarker studies, progress seen in the chemotherapy of cancer will be maintained.

Disclosure of Potential Conflicts of Interest

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References


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