New Strategies in Renal Cell Carcinoma: Targeting the Genetic and Metabolic Basis of Disease

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Abstract

The development of new forms of treatment of advanced renal cell carcinoma over the past two decades has been primarily focused on targeting the VHL/HIF pathway. The recent identification of mutations of chromatin-remodeling genes in clear-cell renal carcinoma (ccRCC), of genomic heterogeneity, and of a Warburg-like metabolic phenotype in advanced disease has had a profound effect on our understanding of the evolution of ccRCC and on potential approaches to personalized therapy. Early approaches to therapy for patients with advanced type I papillary RCC that have centered around the MET/HGF pathway will expand as more genomic information becomes available. Sporadic and familial type II papillary renal cell carcinoma are characterized by enhanced aerobic glycolysis and share an antioxidant response phenotype. In fumarate hydratase–deficient RCC, fumarate-induced succination of KEAP1 activates Nrf2 signaling. CUL3 and Nrf2 mutations as well as an Nrf2 activation phenotype are found in sporadic type II papillary RCC. Therapeutic approaches designed to target the Nrf2 pathway as well as to impair blood flow and glucose delivery in these cancers that are highly dependent on a robust tumor vasculature and on ready availability of glucose for energy production and glycolysis are in development.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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Learning Objectives

Upon completion of this activity, the participant should have a better understanding of the strategies currently in use and under investigation for therapy for renal cell carcinoma and of the biologic rationale underlying novel therapeutic strategies.

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Background

Renal cell carcinoma (RCC) affects more than 270,000 individuals annually worldwide, and there are nearly 120,000 deaths each year due to this disease (1). Patients with relatively small, localized (T1) disease treated surgically have excellent 5- and 10-year survival rates (95%). However, in patients with advanced disease (T4 or M1), the 2-year survival was less than 20% before the advent of targeted agents directed against the VHL/HIF pathway. Our ability to better manage patients with advanced disease has been largely driven by a better understanding of the genetic and biochemical alterations underlying these tumors. Over the past two decades, it has become clear that RCC is not a single disease but is made up of a number of different types of cancer that occur in this organ, each with a different histology, a different clinical course, responding differently to therapy, and caused by different genes. The morphologic classification of RCC is on its way to becoming obsolete as we discover the genomic and molecular drivers of these diseases. Much of what has been learned about the genetic basis of RCC has come from study of the inherited forms of RCC, including von Hippel–Lindau (clear-cell RCC), hereditary papillary renal carcinoma (type I papillary RCC), and hereditary leiomyomatosis RCC (type II papillary RCC; refs. 2, 3). Over the past decade, significant progress has been made in the development of targeted therapeutic approaches for patients with advanced RCC (4). However, despite the advent of these new
agents, most patients with advanced RCC progress on therapy and many will eventually die of this disease.

Clear-cell RCC (ccRCC) is the most common type of RCC and accounts for 75% of cases. The VHL tumor suppressor gene, located on the short arm of chromosome 3, is the gene for the inherited form of ccRCC associated with von Hippel–Lindau (5) and has been found to be mutated or methylated in a high percentage of tumors (~90%) from patients with ccRCC (6, 7). The VHL protein forms a complex with elongin C, elongin B, and CUL2 to target the hypoxia-inducible factors, HIF1α and HIF2α, for ubiquitin-mediated degradation (8–10). This is an oxygen-sensing process; in normoxia, HIF prolyl hydroxylase (PHD) transfers hydroxyl groups to two prolines in HIF, which enables the VHL complex to target and degrade HIF. In hypoxia, PHD does not hydroxylate HIF, the VHL complex cannot target and degrade HIF, and HIF accumulates. HIF1α and HIF2α are transcription factors that regulate the transcription of a number of hypoxia-responsive genes, such as VEGF, platelet-derived growth factor, and glucose transporters GLUT1 and GLUT4. Understanding the VHL/HIF pathway has provided the foundation for the development of a number of targeted therapeutic approaches for the treatment of patients with advanced ccRCC, leading to the development and FDA approval of several agents that target this pathway. Tensirolimus and everolimus, which target the mTOR pathway, have also been approved for advanced RCC. While these agents have had remarkable clinical effect, up to a 45% response rate and increased progression-free survival rates, virtually all eventually develop progressive disease (11).

Papillary RCC, which accounts for 15% of RCC, is made up of a heterogeneous group of cancers that encompasses multiple histologic subtypes, including type I papillary RCC and type II papillary RCC. Although inhibition of the VEGF or mTOR signaling pathways has led to some clinical benefits, the effect is marginal and the prognosis remains poor for patients with advanced disease (12).

**On the Horizon**

**Clear cell renal cell carcinoma**

**Targeting the VHL/HIF pathway**

Why is targeting the VHL/HIF pathway in ccRCC only partially successful clinically? Is it because we need to develop more effective ways to target this pathway or because we need to identify and target other genes associated with the development of this disease. The use of more target-specific, potent VEGFR inhibitors has not been shown to improve efficacy but may be associated with a better toxicity profile. Concurrent inhibition of VEGFR and MET, Tie2, FGFR, and mTOR pathways are being evaluated; however, complete remissions and long-term responses are rare with these strategies (11). Functional studies have long suggested that HIF2α (versus HIF1α) is the critical downstream target of VHL (13, 14) and that inhibition of HIF2α can suppress the ability of a VHL−/− tumor to form tumors in xenograft models (15, 16) and HIF2α SNPs have been linked to an increased risk of developing RCC (17, 18). Genetic and functional studies have implicated HIF1α as a chromosome 1q4 kidney cancer suppressor gene (19) and chromosome 1q4 loss has been found to be associated with poor prognosis (20). A number of strategies have been developed to target HIF2α. The Molecular Targets Laboratory at the National Cancer Institute (Bethesda, MD) has isolated a number of agents that have been shown to inhibit HIF2α transcriptional activity that will need to be further studied in *in vitro* and *in vivo* models to develop specificity and effectiveness (21–24). Zimmer and colleagues have reported small-molecule inhibitors of HIF2α translation based on enhancing the binding activity of IRP1 to the iron responsive element (IRE) in the 5′-untranslated region of the HIF2α message (25, 26). Utilizing a similar approach, tempol, a stable nitroxide that activates IRP1 toward IRE binding, has been shown to decrease HIF2α and its downstream targets in VHL−/− RCC cell line models (27). The role of this agent alone or in combination with other antitumor agents will need to be evaluated in *in vitro* and *in vivo* models. Additional approaches involving autophagic degradation of HIF2α (28), targeting proteosomal degradation of VHL missense mutations (29), and targeting the hypoxia-associated factor-mediated regulation of HIF2α-dependent transcription during hypoxia are being evaluated (30, 31).

**Chromatin-remodeling gene mutations**

Dalgleish and colleagues opened a new chapter in our understanding of the genetic basis of ccRCC and the role of systematic screens to determine genomic architecture when they reported the identification of inactivating mutations of genes involved in histone modification, such as the histone H3 lysine 36 methyltransferase SETD2 and the histone H3 lysine 4 dimethylase KDM5C (32). This work was followed shortly by the identification of truncating mutations of the SWI/SNF chromatin-remodeling complex gene, PBRM1, and BAP1, a deubiquitase that is the catalytic subunit of the Polycomb repressive deubiquitinase complex, in ccRCC, highlighting the fundamental role of aberrant chromatin biology in this disease (33, 34). The Cancer Genome Atlas (TCGA) performed a comprehensive molecular characterization of more than 400 ccRCCs and identified 19 significantly mutated genes, including VHL and other chromosome 3 genes such as PBRM1, SETD2, and BAP1, as well as KDM5C, PTEN, MTO1, TP53, and PIK3CA. Mutations in the chromatin regulators, SETD2, BAP1, and PBRM1 were each differentially associated with altered expression patterns with a distinct set of downstream effects, reflecting different roles for chromatin remodeling in the transcriptome (35). A number of findings have highlighted the importance of driver mutations of chromatin-remodeling genes in ccRCC. In large studies, somatic mutations of BAP1 have been correlated with decreased overall survival, and a straightforward immunohistochemical assay has been developed to assess BAP1 levels (7, 35–38). In addition, germline BAP1 mutations have been found to be the driver mutations in families characterized by an increased incidence of early onset, bilateral, multifocal ccRCC (39, 40). Intensive efforts are currently under way to determine the functional consequences of inactivation of chromatin remodeling genes in ccRCC to provide the foundation for the development of effective forms of therapy targeting these gene pathways. Simon and colleagues have recently identified alterations in chromatin organization and transcript profiles in ccRCC associated with SETD2 mutations in a large cohort of primary human kidney tumors (41) as a first step in developing actionable targets in SETD2-deficient ccRCC. The findings that SETD2 has been shown to be required for DNA double-strand break repair and activation of the p53-mediated checkpoint (42), that SETD2-dependent histone H3K36 trimethylation is required for homologous recombination repair and genome stability (43), and that cells lacking SETD2 activity display microsatellite instability and an elevated spontaneous...
mutation frequency characteristic of DNA mismatch repair-deficient cells (44) opens the door to therapeutic approaches targeting genomic instability in SETD2-deficient RCCs.

Genomic heterogeneity in ccRCC

In studies that have profound implications for both understanding ccRCC tumor evolution as well as for the development of effective strategies for therapy of this disease, Gerlinger and colleagues performed multiregion exome sequencing (M-seq) in large tumors from 10 patients (all except two of whom presented with metastatic disease) and identified pronounced intratumoral heterogeneity (45, 46). VHL gene mutation, which was found in each sample, was considered to be a "truncal" mutation as it was uniformly present in all segments. PBRM1 was found to be mutated in a portion of the tumors and was also considered to be truncal in those subsets. Other driver mutations, found in the chromatin-remodeling genes BAP1, KDM5C, and SETD2, genes in the phosphoinositide 3-kinase (PI3K)–mTOR pathway (mTOR, PIK3CA, TSC2, PTEN) and TP53, were found only in "branch" segments of the tumors and each portion of the tumors was found to have a unique spectrum of branch mutations. As more portions of the tumors were samples, more tumor heterogeneity was identified, suggesting that even these studies underestimate the true extent of heterogeneity of driver mutations in ccRCC (45–47).

These studies raise a number of very fundamental questions. First, what is the best way to detect driver mutations in ccRCC? One approach could involve performing M-seq on the primary kidney tumor to identify druggable driver mutations for therapy. Another approach could involve performing M-seq on tumor material from metastatic tumors, considering that the tumor that has already metastasized might be most likely to contain the critical driver mutations. The second and more critical question is how should we develop a therapy for a tumor with such genomic heterogeneity. One approach would be to continue to focus on developing more effective approaches to targeting the primary truncal mutation (the VHL pathway). When more information about the effect of mutations in chromatin-remodeling genes such as SETD2 and BAP1 becomes available, approaches targeting these pathways will be evaluated.

Targeting the metabolic basis of ccRCC

Integrative analysis in the TCGA study revealed that high-grade, high-stage ccRCC from patients with poor survival showed evidence of a metabolic shift, involving downregulation of genes involved in the TCA cycle, decreased PTEN and AMPK protein levels, upregulation of the glutamine transporter and pentose phosphate pathway genes, and increased acetyl-CoA carboxylase protein (35). The finding of a metabolic shift involving dependence on the pentose phosphate shunt, decreased AMPK, increased glutamine transport, and fatty acid production is consistent with the findings of VHL-deficient ccRCC lines that preferentially use glutamine-dependent reductive carboxylation for lipid biosynthesis (48), which is regulated by citrate levels and sensitizes VHL-deficient carboxylation for lipid biosynthesis (48), which is regulated by citrate levels and sensitizes VHL-deficient RCC to glutamine deprivation (49). The balance between reductive carboxylation and glucose catabolism in VHL-deficient cells is coordinated by nicotinamide transhydrogenase (50). The finding of a Warburg shift in ccRCC, consistent with that seen in fumarate hydratase (FH)-deficient RCC (51), provides a number of opportunities for targeted therapies (Fig. 1). A number of potential targets are available, including glutaminase, AMPK, FAS, and LDHA. Agents targeting AMPK, such as metformin and AICAR, have shown antitumor activity in vitro RCC cell line models (52). Glutaminase inhibitors have shown efficacy in VHL-deficient RCC cell line models (49) and are currently being evaluated in clinical trials. Intense efforts are under way to identify an effective LDHA inhibitor appropriate for clinical use.

Papillary RCC

Type I papillary RCC

Type I papillary RCC occurs in a sporadic, noninherited as well as a hereditary form. Hereditary papillary kidney (HPRC) cancer is an autosomal dominant hereditary cancer syndrome in which affected individuals are at risk for the development bilateral, multifocal type I papillary RCC (53). The gene for HPRC, localized to the long arm of chromosome 7, was found to be the proto-oncogene MET (54). Activating mutations in the tyrosine kinase domain of MET are found in the germline of patients affected with HPRC (54, 55). Kidney tumors from patients affected with both HPRC and sporadic papillary RCC are characterized by polysomy of chromosome 7, and nonrandom duplication of the mutant MET allele has been found in tumors from patients affected with HPRC (56). Hereditary and sporadic type I papillary RCC share a distinct morphologic phenotype (57), and MET mutations have been found in 13% of sporadic type I papillary tumors.

The identification of oncogenic MET mutations in patients affected with HPRC and in a subset of patients with sporadic papillary RCC led to a multicenter phase II study of foretinib, an inhibitor of Met, VEGFR2, RON, and AXL tyrosine kinases, in patients with sporadic as well as HPRC-associated papillary RCC. The overall response rate was 13.5%, with a median progression-free survival of 9.3 months, which was considerably higher than that seen in historical controls treated with agents targeting mTOR or VEGFR pathways (58). In a subgroup analysis, 5 of 10 (50%) patients with HPRC with germline MET mutations were found to have a partial response to therapy, versus 5 of 57 (9%) non-HPRC patients. Sufficient pathway review was not available to determine whether type I papillary RCC responded better than type II papillary RCC (58). A clinical trial evaluating the effect of INC280, an agent that selectively targets Met, in patients with papillary RCC is under way. Trials are currently being planned to evaluate the effect of a number of agents that target Met in patients with both papillary and nonpapillary RCC. The TCGA papillary RCC project is currently under way to provide more insights into the genetic characteristics of both type I and type II papillary RCC and will hopefully identify driver mutations that will guide future trials in this disease.

Type II papillary RCC

Type II papillary kidney cancer is an aggressive and often lethal form of RCC (2, 3). As is the case with type I papillary RCC, there are both sporadic as well as familial forms of type II papillary RCC. The hereditary form of type II papillary RCC occurs in hereditary leiomyomatosis and RCC (HLRCC). HLRCC is an autosomal dominant hereditary cancer syndrome in which patients are at risk for the development of cutaneous and uterine leiomyomas and a very aggressive, lethal form of type II papillary RCC that has a propensity to spread when the primary tumor is very small.
HLRCC is characterized by germline mutation of the gene for the Krebs cycle enzyme, FH (62).

**Warburg model of cancer**

In FH-deficient RCC, oxidative phosphorylation is impaired and the cells undergo a shift to aerobic glycolysis, consistent with the Warburg effect (63, 64). FH-deficient RCC cells are unusually dependent on glucose for proliferation and glycolysis to generate the increased ATP needed for rapid proliferation (65). In FH-deficient RCC, fumarate accumulates and inhibits HIF PHD, resulting in accumulation of HIF1 and increased transcription of its targets, such as VEGF and GLIIT1, which leads to the increased vascularity and glucose transport needed to provide increased nutrients for rapid growth and proliferation and for ATP production needed in cells characterized by a decrease in oxidative phosphorylation (Fig. 2; ref. 66). Diminished AMPK levels have been found in FH-deficient RCC cells, resulting in reduced phosphorylation of...
acetyl CoA carboxylase, which would be expected to increase fatty acid synthesis. In addition, phospho-S6 ribosomal protein, a downstream mTOR effector, was also found to be activated in FH-deficient RCC cells (51, 67). Finally, FH-deficient RCC is characterized by a glutamine-dependent reductive carboxylation in which glutamine is the primary carbon source for lipid biosynthesis (Fig. 2; ref. 68).

KEAP1/Nrf2 antioxidant response pathway

As FH-deficient RCC is characterized by increased oxidative stress and elevated levels of reactive oxygen, effective antioxidant response is critical for continued growth (69). In FH-deficient RCC, increased levels of fumarate induce succination of multiple proteins including the KEAP1 protein, which, as part of an E3 ubiquitin ligase complex with CUL3, targets the NRF2 transcription factor for degradation. Succination of KEAP1 inactivates KEAP1 and inhibits NRF2 degradation, resulting in activation of the NRF2 antioxidant response element (ARE) transcription pathway. While mutation of FH is rarely seen in sporadic type II papillary RCC, recent studies have reported activation of the NRF2 pathway in sporadic type II PRCC due to inactivating mutations of CUL3 or activating mutations of NRF2. An intense effort is under way to develop therapeutic agents that target the NRF2 ARE pathway.
Summary

Although enormous progress has been made over the past 20 years in our understanding of the genetic basis and development of targeted therapeutics for ccRCC, we still have a long way to go. For ccRCC, we need better approaches for targeting both the VHL/HIF2α as well as chromatin-remodeling gene pathways. Given the profound genomic heterogeneity in ccRCC, it is most likely that successful strategies will need to target both truncal as well as branch driver mutations. Ongoing genomic studies in papillary RCC will hopefully identify novel driver mutations and pathways for this disease. For type I papillary RCC, the MET pathway seems particularly promising. For type II papillary RCC, targeting the tumor vascularity and glucose transport/glycolysis and targeting the KEAP1/NRF2 pathway also appear to be promising approaches. It is hoped that ongoing metabolomic and functional studies will identify novel metabolic pathways to target in both clear-cell and papillary RCC.

Authors’ Contributions

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