Metastatic solid tumors are almost invariably fatal. Patients with disseminated small-cell cancers have a particularly unfavorable prognosis, with most succumbing to their disease within two years. Here, we report on the genetic and functional analysis of an outlier curative response of a patient with metastatic small-cell cancer to combined checkpoint kinase 1 (CHK1) inhibition and DNA-damaging chemotherapy. Whole-genome sequencing revealed a clonal hemizygous mutation in the Mre11 complex gene RAD50 that attenuated ATM signaling which in the context of CHK1 inhibition contributed, via synthetic lethality, to extreme sensitivity to irinotecan. As Mre11 mutations occur in a diversity of human tumors, the results suggest a tumor-specific combination therapy strategy in which checkpoint inhibition in combination with DNA-damaging chemotherapy is synthetically lethal in tumor cells but not normal cells with somatic mutations that impair Mre11 complex function.

SIGNIFICANCE: Strategies to effect deep and lasting responses to cancer therapy in patients with metastatic disease have remained difficult to attain, especially in early-phase clinical trials. Here, we present an in-depth genomic and functional genetic analysis identifying RAD50 hypomorphism as a contributing factor to a curative response to systemic combination therapy in a patient with recurrent, metastatic small-cell cancer. Cancer Discov; 4(9); 1014–21. © 2014 AACR.

See related commentary by Peng et al., p. 988.
INTRODUCTION

Curative therapy for patients with metastatic solid tumors remains elusive. Even with the much-heralded advent of targeted inhibitors of oncogenic signaling pathways, drug resistance and disease progression occur in essentially all patients. We sought to define the mechanistic basis of a dramatic and durable response to systemic therapy in a 51-year-old woman originally diagnosed with an invasive small-cell cancer of the ureter (Supplementary Fig. S1A and S1B). Small-cell variants, a rare histologic subtype that can arise throughout the urothelial tract, is associated with a particularly poor prognosis. Following initial surgical resection and a short course of adjuvant chemotherapy (etoposide and cisplatin), her disease rapidly recurred. After a second surgery to remove recurrent and metastatic tumors in her kidney and retroperitoneal lymph nodes, the patient again recurred with progressive metastatic disease, prompting enrollment in an open-label phase I clinical trial of AZD7762, an ATP-competitive checkpoint kinase inhibitor (CHK1/2), and weekly irinotecan, a topoisomerase I inhibitor (1). Within 5 months, the patient achieved a complete response that has proved durable despite discontinuation of drug therapy nearly 3 years ago (Fig. 1A and B). We performed whole-genome sequencing (WGS) of the tumor and matched normal tissue from this patient to investigate the genetic basis of this outlier example of curative systemic cancer therapy.

RESULTS

WGS of tumor DNA from the second surgery and matched normal blood revealed a complex somatic tumor genome (Fig. 1C). We identified 19,011 somatic point mutations and small insertions and deletions (indels), of which 147 were located in protein-coding or noncoding RNA regions of the genome (Supplementary Table S1). Overall, the somatic mutation rate was 7.06 mutations per million bases, similar to the only other reported WGS of a metastatic urothelial cancer reported to date (2). This genome also had a substantial number of DNA copy-number alterations (CNA), as is typical of p53-mutant bladder cancers (the tumor harbored a TP53 point mutation; ref. 3). CNAs were the source of approximately 60% of all structural rearrangements identified in this tumor genome, the burden of which was high (Supplementary Table S2).

As WGS was performed on the recurrent tumor specimen obtained after etoposide-cisplatin therapy but before trial enrollment, we sought to determine whether the candidate driver mutations identified arose early in molecular time by analyzing the diagnostic tumor sample collected pre-etoposide-cisplatin therapy. Using a capture-based approach partially customized using the WGS findings (see Methods; Supplementary Fig. S2A), we deeply sequenced 281 genes (Supplementary Tables S3 and S4). This confirmed that most of the mutations identified by WGS of the recurrent tumor affecting known cancer genes were present in the treatment-naive diagnostic tumor (Fig. 1D). Others preexisted therapy but were not selected for, and still others arose later in molecular time, as they were present but subclonal only in the post-etoposide-cisplatin tumor.

We then performed an integrated analysis using the mutation, DNA copy number, and tumor clonality data generated by the WGS analysis together with the sum of information on pathways proximal to the mechanism of drug action to prioritize genomic aberrations that may have contributed to this patient’s exceptional response. In addition to the mutation in TP53 (A161T), mutations identified in ATR and RAD50 were particularly noteworthy from the perspective of this patient’s profound response to checkpoint inhibitor-based combination therapy (Supplementary Fig. S2B–S2D). Although both were missense mutations, in silico analyses suggested that whereas ATRR578S was unremarkable, the RAD50L1237F mutant was deemed the likely contributor to the profound response to systemic therapy observed in this patient. Several lines of evidence supported this prediction. The ATR mutation was heterozygous, affected the poorly conserved H585 residue (Supplementary Fig. S2C), did not reside in a protein domain or motif of known significance, was not recurrently mutated nor was among a pattern of clustered mutations at this site (data not shown), and was not affected by a focal CNA, arguing against selection for the ATR mutation during tumorigenesis (see Supplementary Data).

Conversely, the weight of the in silico evidence suggested that the novel missense mutation in RAD50 (L1237F) was a potential sensitizing lesion contributing to the profound response to systemic therapy observed in this patient. RAD50 is a component of the Mre11 complex, a multisubunit nuclease composed of RAD50, MRE11A, and NBN (4), mutations of which are associated with DNA repair deficiency. This RAD50L1237F allele was clonal in the index patient (present in 100% of tumor cells; Supplementary Fig. S3) and accompanied by focal deletion of the wild-type allele (Fig. 2A), with corresponding tumor-specific reduction of RAD50 protein expression confirmed by IHC (Supplementary Fig. S4A–S4D). Furthermore, this mutation is situated in the D-loop of RAD50 (Fig. 2B), a region that influences ATP hydrolysis (5, 6). Recent structural analyses indicate that ATP hydrolysis has a profound effect on the functionality of the Mre11 complex, which senses double-strand breaks (DSB) and governs the DNA-damage response (DDR; ref. 7). Analyzing the mutational landscape of RAD50 in 7,494 sequenced tumors across 28 tumor types (Supplementary Table S5 and Supplementary Data) revealed that not only do approximately 4% of all human tumors harbor Mre11 complex mutations but a subset of these cluster in regions adjacent to the L1237F-mutant D-loop motif of the RAD50 protein in diverse tumors (Fig. 2B). Notably, these mutations were most common in urothelial bladder and colorectal tumors (11% and 8%, respectively), the latter of which are often treated with irinotecan-based regimens (8). In addition, RAD50L1237F is a very highly conserved residue, along with several of the other RAD50-mutant alleles detected (Fig. 2C). Essentially all Rad50 orthologs have a leucine (L, Leu) at the position corresponding to human residue 1237. Bacteriophage T4 Rad50 is an exception, possessing a phenylalanine (F, Phe) at this position (Fig. 2C). This suggested that the L1237F mutation would be hypomorphic rather than inactivating, with the gene product retaining some residual function. Finally, structural analysis of the Rad50 dimer confirmed
the clustering of the L1237F mutation in the index tumor genome with other mutant alleles observed in diverse tumor types, which together affect the D-loop motif and Walker B elements adjacent to ATP binding (Fig. 2D). In summary, in silico analysis predicted that although ATR H585D was likely a passenger mutation, the L1237F mutation and others observed in RAD50 in additional tumors may exert a significant functional impact.

We exploited the high degree of evolutionary conservation of the RAD50 D-loop to assess the functional significance of RAD501237F by modeling this and other tumor-associated alleles in S. cerevisiae. Six rad50-mutant yeast strains were...
established: rad50L1240F (the yeast version of the mutation in the tumor genome), as well as mutations predicted to exert minor and major effects on D-loop structure (rad50L1240A and rad50L1240R, respectively; see Methods; Supplementary Table S6). In addition, we established rad50-mutant strains harboring D-loop (D1238N, rad50D1241N) and non–D-loop but highly conserved (Q1259K, rad50Q1262K) mutations identified in breast and endometrial carcinomas, respectively.

All three rad50L1240 mutations appeared to destabilize the Rad50 protein, as the steady-state levels of the rad50L1240F and rad50L1240A gene products were reduced compared with wild-type, whereas Rad50L1240R was nearly undetectable (Fig. 3A). Conversely, the rad50L1241N and rad50Q1262K mutants had levels of Rad50 similar to wild-type cells. Nevertheless, although these mutations had differing effects on Rad50 expression levels, the Mre11 complex itself remained intact, as indicated by coimmunoprecipitation with Mre11 (Fig. 3A). We further confirmed the apparent selection for RAD50 hemizygosity in the tumor (mutation and LOH), as only diploid strains expressing homozygous rad50L1240F/L1240F (or rad50L1240F haploid cells) exhibited impaired survival following camptothecin (an analog of irinotecan) treatment (Supplementary Figs. S5 and S6).

**Figure 2.** D-loop and adjacent mutations in RAD50. A, DNA copy number segmentation inferred from WGS of the index case indicates a focal heterozygous loss spanning the RAD50 locus on 5q31.1, deleting the wild-type allele (as indicated by the sequence logo representing the allelic frequency), retaining only RAD50L1237F, the RAD50L1237F mutation (red) is present in the D-loop of the ATPase domain near the Walker B motif (top and bottom, schematic of RAD50 protein at multiple scales). Directly adjacent appear a cluster of mutations in diverse malignancies (black). B, conservation of the RAD50 D-loop motif and adjacent sequence is indicated across 9 organisms in which the mutated leucine and adjacent aspartate residues are highlighted in green and yellow, respectively, along with the positions of other mutations. The mutation position for human and yeast (in brackets) is given and indicated by arrowheads (Hs, Homo sapiens; Mn, Mus musculus; Dm, Drosophila melanogaster; At, Arabidopsis thaliana; Sc, Saccharomyces cerevisiae; Sp, Schizosaccharomyces pombe; Ec, Escherichia coli; Pf, Pyrococcus furiosus; T4, Bacteriophage T4). D, the three-dimensional structure of the Rad50 dimer indicating the position of the affected subunit with mutations colored in red. Inset, position of mutant residues within close proximity to bound ATP.
These data indicate selection for RAD50 hypomorphism in the index patient through mutation and LOH (Fig. 2A), resulting in the retention of only a single-mutant allele with compromised function.

As the curative response in the index patient occurred in the setting of combined inhibition of topoisomerase I and the DNA-damage checkpoint pathway, we assessed whether checkpoint inhibition was synergistic with rad50<sup>L1240F</sup> in the presence of camptothecin by examining drug sensitivity in a checkpoint-competent background, the rad50<sup>Δ</sup> mec1<sup>Δ</sup> double mutants were at least 500-fold more sensitive to camptothecin than either of the single mutants (Fig. 3B). Other D-loop mutants exhibited variable camptothecin sensitivity, with rad50<sup>D1241N</sup> sharing a pattern similar to L1240F, whereas rad50<sup>Hs</sup>L1240N was as sensitive as rad50Δ cells. These results indicate that L1237F-mutant cells are strongly dependent on the remaining intact checkpoint pathway for survival upon DNA damage by topoisomerase I inhibition. This synthetic lethal interaction likely accounts for the apparent hypersensitivity of the index patient’s RAD50<sup>L1237F</sup>–mutant cells to cotreatment with irinotecan and AZD7762.

Figure 3. RAD50 hypomorphism attenuates ATM signaling, synergizing with checkpoint inhibition to confer chemotherapy sensitivity. A, although the Rad50<sup>L1237F</sup>–mutant cells exhibited only mild camptothecin sensitivity in a checkpoint-competent background, the rad50<sup>L1240F</sup> mec1<sup>Δ</sup> double mutants were at least 500-fold more sensitive to camptothecin than either of the single mutants (Fig. 3B). Other D-loop mutants exhibited variable camptothecin sensitivity, with rad50<sup>D1241N</sup> sharing a pattern similar to L1240F, whereas rad50<sup>Hs</sup>L1240N was as sensitive as rad50Δ cells. These results indicate that L1237F-mutant cells are strongly dependent on the remaining intact checkpoint pathway for survival upon DNA damage by topoisomerase I inhibition. This synthetic lethal interaction likely accounts for the apparent hypersensitivity of the index patient’s RAD50<sup>L1237F</sup>–mutant cells to cotreatment with irinotecan and AZD7762.
As the Mre11 complex also regulates the DDR kinase ATM, we next assessed the functional status of Tel1 (the yeast ATM ortholog and Mec1 paralogue) in rad50 mutants. In mec1Δ sae2Δ mutants, cells that are only able to respond to DNA damage through Tel1 via a functional Mre11 complex (see Supplementary Data; refs. 10, 11), rad50Δ L1237F triple-mutant cells had a sensitivity to both camptothecin and the DNA-damaging agent methyl methanesulfonate equal to that of rad50-mutant mec1Δ alone, indicating defective activation of Tel1 in Rad50 D-loop–mutant cells (Fig. 3B and Supplementary Fig. S7). Next, we examined DNA damage–dependent activation of Rad53, which, as a downstream substrate of Tel1 analogous to human Chk2, can only be activated by Tel1 in the absence of Mec1. Although methyl methanesulfonate treatment induced Rad53 phosphorylation levels in wild-type cells, and some additional Rad53 stimulation is apparent upon Sae2 loss, sae2Δ cannot rescue Rad53 phosphorylation levels in any of the rad50 mutants tested (Fig. 3C and Supplementary Fig. S8). This attenuation of Rad53 phosphorylation levels in the triple mutants confirms that Tel1 (ATM) signaling is defective in the Rad50-mutant cells.

As Tel1 kinase activity is important for telomere maintenance, we assessed the impact of this molecular phenotype on telomere length in the rad50 mutants. As in previous studies that showed significantly shorter telomeres resulting from tel1Δ and Tel1 kinase-dead strains (12), we also witnessed shorter telomeres in the rad50-mutant cells (Supplementary Fig. S9). This observation, along with the defect in Rad53 phosphorylation in Mec1-deficient cells, suggests that ATM activation was compromised in the rad50L1237F index responder. In sum, the results suggest that the marked sensitivity of the rad50L1237F–mutant tumor to irinotecan was due, at least in part, to simultaneous inhibition of both the ATR (by AZD7762) and ATM (by rad50L1237F) axes of the DDR.

We further recapitulated these findings in mammalian cells. We engineered mouse embryonic fibroblasts (MEF) in which the sole source of Rad50 was rad50L1237F. Upon treatment with the Chk1 inhibitor and camptothecin, these cells had reduced phosphorylation of the substrate Kap1 at Ser824, an ATM-dependent site (Supplementary Fig. S10A). Consequently, these cells had reduced γH2AX formation following irradiation (Supplementary Fig. S10B), confirming the ATM signaling defect. Moreover, although colony formation was reduced significantly upon irinotecan treatment irrespective of genotype, this was greatest upon cotreatment with the Chk1 inhibitor in rad50L1237F cells (Supplementary Fig. S10C).

DISCUSSION

In summary, we find that a hypomorphic mutation in RAD50 accompanied by LOH identified by WGS of an extreme outlier responder likely contributed to a complete and durable response to irinotecan in combination with a selective inhibitor of CHK1. The rad50L1237F mutant was both clonal and arose early, suggesting that RAD50 dysfunction may have contributed to tumor initiation, perhaps in combination with mutant p53, by potentiating the profound structural remodeling of this patient’s tumor genome. Although our functional results indicate that rad50L1237F confers dramatically enhanced sensitivity to the combination of irinotecan and CHK1 inhibition, additional factors may have contributed to the profound and durable response observed. For example, the clonal nature of this responder’s tumor, with 95.1% of all somatic mutations identified present in the dominant tumor clone (Supplementary Fig. S3), may have contributed to the depth and durability of the response. It has been suggested that extensive subclonal mutations in treatment-naïve patients are associated with a shorter time to relapse and a worse outcome (13). The limited subclonal structure of this patient’s tumor may, therefore, have resulted in a less-tolerant environment for the selection and outgrowth of a preexisting resistant clone. This may have been especially true given the dose-dense weekly cytotoxic treatment regimen used, which may not have allowed the tumor sufficient time to adapt a fitter and more resistant clone.

In addition to demonstrating the indispensability of the D-loop of RAD50 for proper ATM activation and downstream checkpoint signaling (Fig. 3D), the hypomorphic nature of the rad50L1237F allele is noteworthy. Whereas the somatic mutation was defective, innocuous D-loop alanine substitutions (rad50Δ L1240A and rad50Δ L1241A) had only a very mild impact, despite these residues being so highly conserved. Thus, there is considerable plasticity in the D-loop sequence that produces a narrow solution space in which RAD50 hypomorphism can be achieved through somatic mutation. This illustrates the potential importance of functional rather than fully inactivating mutations of highly conserved components of essential cellular systems like the DDR to various malignant phenotypes, including treatment sensitivity.

Although D-loop mutations in RAD50 have been studied previously (5, 14), our phenotypic characterization of the somatic rad50L1237F allele revealed new insights into RAD50 function that may be exploited therapeutically. Whereas RAD50 mutation produced a negligible DSBR repair defect, ATM activation was severely impaired. This resulted in marked synergy with inhibition of the ATR–CHK1 axis of the DDR in the setting of cotreatment with a DNA damage-inducing cytotoxic chemotherapy (Fig. 3E). These data suggest a tumor-specific combination therapy strategy in which checkpoint inhibition in combination with DNA-damaging chemotherapy is synthetically lethal in tumor cells but not in normal cells with somatic mutations impairing Mre11 complex function. Indeed, as we found Mre11 complex mutations along with those in ATM to be present in a significant minority of patients across diverse human cancer types (Supplementary Table S5), these data argue for the development of inhibitors of checkpoint control generally and also targeted inhibitors of the Mre11 complex specifically or its synthetic lethal partners (such as ATM). As suggested by prior studies, this combinatorial approach may prove particularly effective in p53-mutant patients, as was the case in the index patient described here (15). This synthetic lethality is thus analogous to the use of PARP inhibitors in patients with BRCA1/2 mutations and highlights the potential utility of targeting DNA repair pathways in combination with mutagenic chemotherapies in patients who have a tumor-restricted defect in DDR. Finally, this work highlights that the value of whole-genome analyses of extreme outlier phenotypes is not limited to targeted therapeutics or the
Sample Preparation and Sequencing

Clinical information and tumor and normal tissues were obtained from patients with informed consent and in accordance with Institutional Review Board approval at Memorial Sloan Kettering Cancer Center (New York, NY; MSKCC IRB #89-076). For the index case on which WGS was performed, DNA was extracted from frozen tumor tissue using the DNEasy Blood and Tissue Extraction Kit (Qiagen). Ten-micrometer thick frozen tumor from frozen tumor tissue using the DNEasy Blood and Tissue Extraction Kit (Qiagen). Ten-micrometer thick frozen tumor

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RAD50 IHC

IHC for RAD50 was performed on a 4-μm thick FFPE tissue section of the tumor from the salvage nephrectomy (same specimen undergoing WGS). A primary monoclonal anti-RAD50 antibody was used and diluted to 1:100, CC1 standard (ab89; Abcam). Staining was assessed with a Ventana Discovery XT Automated System with DAB Map kit detection system (Ventana Medical Systems).

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Authors’ Contributions


Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): H. Al-Ahmadie, G. Iyer, P. Kim, G.K. Schwartz, M.F. Berger, D.B. Solit, B.S. Taylor


Other (created yeast strains, performed yeast experiments, assisted with yeast data interpretations and writing of the yeast data experimental part): M. Hohl

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REFERENCES


Synthetic Lethality in ATM-Deficient RAD50-Mutant Tumors Underlies Outlier Response to Cancer Therapy

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