Microsatellite instability (MSI) is displayed by approximately 15% of colorectal cancers (CRC). Defective DNA mismatch repair generates mutations at repetitive DNA sequences such as those located in the double strand break (DSB) repair gene MRE11. We assessed the mutational status of MRE11 in a panel of 17 CRC cell lines and 46 primary tumors and found a strong correlation with MSI status in both cell lines and tumors. Therefore, we hypothesized that deficiency in MRE11 may sensitize CRC cells to poly(ADP-ribose) polymerase (PARP-1) inhibition based on the concept of synthetic lethality. We further assessed the activity of the PARP-1 inhibitor, ABT-888, in CRC cell lines and observed preferential cytotoxicity in those MSI cell lines harboring mutations in MRE11 compared with both wild-type cell lines and microsatellite stable (MSS) cell lines. A significant correlation between MRE11 expression levels and cytotoxicity to ABT-888 at 10 μM was observed ($R^2 = 0.915$, $P < 0.001$). Using two experimental approaches, including short hairpin RNA knocking down MRE11 in the wild-type and MSS cell line SW-480 and a second cell line model transfected with mutant MRE11, we experimentally tried to confirm the role of MRE11 in conferring sensitivity to PARP-1 inhibition. Both models led to changes in proliferation in response to ABT-888 at different concentrations, and a drug–response effect was not observed, suggesting a possible contribution of additional genes. We conclude that MSI colorectal tumors deficient in DSB repair secondary to mutation in MRE11 show a higher sensitivity to PARP-1 inhibition. Further clinical investigation of PARP-1 inhibitors is warranted in MSI CRCs. Cancer Res; 71(7); 2632–42. ©2011 AACR.
proteins involved in the nonhomologous end joining and homologous recombination pathways. Experimental evidence shows a direct interaction between PARP-1 and MRE11 reflected by the fact that PARP-1 is apparently required for rapid accumulation of MRE11 at DSB sites (12). Therefore, tumor cells harboring mutations of genes involved in homologous recombination such as BRCA1, BRCA2, and MRE11 are particularly vulnerable to DNA damage. Our aim in this study was to assess the activity of the PARP-1 inhibitor ABT-888 in CRC cell lines harboring a mutation in the homologous recombination gene MRE11 that frequently accompanies MMR deficiency.

Materials and Methods

Cell lines and primary tumor samples

A total of 17 CRC cell lines were selected for experiments based on microsatellite status obtained from the Wellcome Trust Sanger Institute Cancer Genome Project (13) as detailed in Supplementary Table S1. Cell lines were purchased from the American Type Culture Collection. MSI status was also confirmed independently in cell lines, as well as the presence of mutations in the principal oncogenes for CRC. Cells were grown in DMEM/F12 medium supplemented with 10% fetal bovine serum and 1% penicillin/streptomycin. SW480/SN3 and its derivative SM1.3 expressing a construct for bovine serum and 1% penicillin/streptomycin. SW480/SN3 and HT Sequence Detection System. Two sets of primers were designed to assess the independent expression levels of the MRE11 wild type and the mutant transcript, 1 set for PARP-1 and 1 for GAPDH that was used as an endogenous control. Primer sequences and PCR conditions are available upon request. The relative expression of the wild type and mutant transcript of MRE11 and PARP1 was calculated by ΔCt normalization to the expression of GAPDH.

Immunofluorescence

Cells were cultured on coverslips, fixed, and processed as previously described (14). For each cell line, Rad51 and γH2AX foci were quantified following fixation of cells 24 hours after being seeded (t = 0) and 18 hours after irradiation (7.5 Gy; t = 18). Samples were imaged with an Olympus FV500 confocal microscope (Olympus America) with a 60× objective. For quantification of Rad51 and γH2AX foci, at least 100 cells were visually scored for each condition by 2 independent observers. Cells with ≥5 foci were scored as positive and the percentage of positivity was compared at baseline and 18 hours following irradiation for 3 cell lines (SW620, HCT15, and SW48).

Irradiation

Cells were irradiated using a Philips RT250 (Kimtron Medical) at a dose rate of ~2 Gy/min in the University of Michigan Comprehensive Cancer Center Experimental Irradiation Core.

Statistical analysis of association between expression and mutational status of MRE11

Comparisons of expression levels between cell lines grouped by MRE11 mutational status across 3 categories were performed using the rank-based, Kruskal-Wallis ANOVA test followed by post hoc Dunn’s test for pairwise differences among groups (MRE11 homozygous vs. heterozygous mutants, MRE11 homozygous mutants vs. wild type, MRE11 heterozygous mutants vs. wild-type) using SAS version 9.1. Nonparametric methods were used to protect against violation of normality assumption given the limited sample size.

Analysis of gene expression data of tumor samples

RNA isolation and microarray procedures were used. Primary tumors were obtained at the time of surgical resection, after which they were snap frozen in liquid nitrogen at −80°C, embedded in optimum cutting temperature freezing media (Miles Scientific), cryotome sectioned, stained with hematoxilin and eosin, and evaluated by a surgical pathologist. Areas with >70% tumor cellularity were identified for RNA isolation. Selected sections of tumor samples were homogenized in Trizol (Invitrogen), and total cellular RNA was purified according to the instructions of the manufacturer, with additional purification using RNeasy spin columns (Qiagen). RNA quality was assessed by 1% agarose gel electrophoresis, and samples were included only if the 18S and 28S bands were discrete and approximately equal. Expression levels were measured in 2 batches using Affymetrix U133A

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and U133A Plus 2.0 arrays. Preparation of target cRNA, hybridization, and scanning were performed according to the protocols of the manufacturer.

**Statistical analysis of microarray data**

Expression analyses were carried out in the R-software using the package Bioconductor (16). Expression data in both batches were first subjected to quality assessment by creating the density plot of the log-intensity and RNA degradation plot corresponding to each sample. For all 331 samples, MAS 5.0-calculated signal intensities were normalized using the quantile normalization procedure implemented in robust multiarray analysis (17, 18) and the normalized data were log2 transformed. Sample-specific median centering and scaling by the standard deviation were additionally applied. Filtering was done to exclude probe sets that were not expressed or probe sets that exhibited low variability across samples. Expression values were required to be above the lower quartile of all expression measurements in at least 25% of samples, and the interquartile range across the samples on log2 scale was required to be at least 0.5. After preprocessing and quality assessment, the 2 batches were aligned. Probes of the U133A array present in the U133A Plus 2.0 were selected and quantile normalized to mimic the distribution of the U133A array. Five samples had been hybridized in both arrays and served to verify that the correlation of the expression was adequate for the majority of the probes. A total of 331 samples and 419,473 probe sets were subjected to further analysis. Two-class comparison of MSI versus MSS tumors was carried out by 2-sample t-test to yield a list of differentially expressed probe sets, discriminating between the 2 biologic states of interest under consideration. We had information on MSI status available from 300 patients whose characteristics are detailed in Supplementary Table S3. The issue of multiple testing was addressed by using adjusted P values after controlling for the overall false discovery rate by Benjamini and Hochberg method (BH-adjusted P values; ref. 19). We also evaluated the local false discovery rate associated with our probe selection procedure by using the locfdr package in R (20).

**Gene expression data sources, selection of probes from gene expression data sets submitted to the Connectivity Map Build 02 and generation of compound lists**

Bioinformatic approaches to identify the level of enrichment between gene expression profiles characterizing MSI tumors and gene changes induced in vitro by the PARP-1 inhibitor phenanthridinone and others were assessed using the Connectivity Map (21). We used 5 different data sets characterizing MSI-H tumors. Four of them were previously published and retrieved directly from their original publications (22–25). Criteria followed for selection of probe sets and detailed lists have been published previously (26). The fifth data set was generated from a total of 300 colorectal fresh frozen tumors collected from the MECC study and analyzed in 2 batches. The first batch was hybridized to the Affymetrix U133A chip and the second one to U133A Plus 2.0 (Supplementary Table S3). The final list of probe sets defining gene expression of MSI-H compared with MSS tumors was selected based on the strength of multiplicity adjusted P values (cutoff, P < 0.001) and ratio of mean expression values across the 2 groups (cutoff fold-change >1.3 and <0.7). It contained 442 upregulated and 480 downregulated probe sets as detailed in Supplementary Tables S4 and S5.

**Cytotoxicity experiments, dose–response data, and IC50 calculations of ABT-888 in cell line models**

ABT-888 (A-861695, Abbott Laboratories) was obtained from Axxora. Stock concentrations of 1 mM were maintained in DMSO and were dissolved in supplemented medium to obtain 6 serial dilutions (1 nM to 50 μM). Cytotoxicity experiments were performed in 4 homozygous MRE11 mutant, 1 heterozygous, and 3 wild-type cell lines. One thousand cells were seeded in triplicate per well and after 24 hours medium was replaced with medium containing 6 different concentrations of ABT-888. In control wells, cells were fed with standard medium. After 6 days of treatment cell viability was estimated using WST-1. Cell viability was estimated on the basis of their ability to metabolize the tretazolium salt WST-1 to formazan by mitochondrial dehydrogenases. Quantification of absorbances was analyzed using a Spectramax 190 (Molecular Devices Corporation). The percentage of surviving cells at each concentration relative to the nontreated group was calculated. The IC50 was then estimated by fitting a sigmoid shaped dose–response curve. Differences in drug sensitivity comparing the mean IC50 of 3 independent experiments for every cell line and cell proliferation data at a certain drug concentration (10 μM) between cell lines classified by MRE11 poly(T)11 mutational status were determined using Kruskal-Wallis ANOVA as described previously. In addition, correlation between the levels of expression of the mutant transcript of MRE11 poly(T)11 and the percentage of growth inhibition induced by ABT-888 at 10 μM was examined by Spearman’s coefficient of rank correlation test. P < 0.05 was considered to indicate statistical significance. These calculations were performed using SAS version 9.1.

**Cell cycle analysis**

For cell cycle analysis, cells were washed in cold PBS, fixed in 70% ethanol, washed, resuspended in 25 μg/mL Propidium iodine (PI) with 100 μg/mL RNase A (BD Pharmigen), and incubated for 30 minutes at 37°C. Fluorescence was measured on a BD Biosciences FACScalibur flow cytometer within 1 hour. Data were analyzed using the MODFIT 2.0 program (Verity Software House).

**Stable knockdown of MRE11 in SW-480 cells**

Several lentiviral-based plasmids containing a short hairpin RNA (shRNA) to human MRE11 were purchased from Open Biosystems. Nonsilencing (mock) shRNAs were used as negative controls. The sequence of the MRE11-specific 22-mer shRNA with highest efficacy and reported here was
AGGCCATGAACATGAGTGTAAA. Experimental procedures for shRNA transfection were done according to the Open Biosystems technical manual. Stable clones were generated by transfecting SW480 cells in 6-well dishes with 2 μg of each of the shRNA plasmids using FuGeneHD (Roche) according to the manufacturer's recommendations. Forty-eight hours after transfection, the cells were placed under selection with 2.0 μg/ml puromycin (Sigma-Aldrich), splitting them when the cells reached confluence. Multiple clones from the same transfection were pooled and grown under puromycin selection. Successful knockdown of specific gene products was confirmed by qRT-PCR as described earlier.

Results

Microsatellite unstable colorectal cancer cell lines are associated with mutations in \textit{MRE11 poly(T)11}

Mutations in coding microsatellite tracts of \textit{MRE11} and \textit{RAD50} were assessed in a panel of 17 CRC cell lines. None of the MSS cell lines was mutated in \textit{MRE11} or \textit{RAD50}. All MSI-high (MSI-H) cell lines harbored a mutation in the polyT(11) tract located in the intron 4 of \textit{MRE11}. Three had monoallelic and 5 had biallelic mutations. Only 3 cell lines harbored mutations in an exonic polyA(9) repeat of \textit{RAD50} (Table 1; Supplementary Table S1), and all of them were MSI. Therefore, we decided to focus our attention on \textit{MRE11}. To confirm the frequency of the \textit{MRE11}-intron 4 mutation, we genotyped 46 tumors from the MECC study (Supplementary Table S2). Eighteen out of 22 (82%) of MSI tumors harbored a mutation in \textit{MRE11} compared with 0% of MSS tumors (P < 0.001). Among the 22 MSI tumors with \textit{MRE11} mutations, 36% of tumors had biallelic mutations.

Mutations of \textit{MRE11} are not associated with an increase of \textit{PARP-1} expression

Because the Intron 4-\textit{MRE11} mutation generates a change in splicing that leads to skipping of exon 5, we decided to assess the expression of \textit{MRE11} in 10 CRC cell lines. Two sets of primers for the mutant and the wild-type transcripts of \textit{MRE11} were designed (Fig. 1A). Those cell lines harboring biallelic mutations in \textit{MRE11} showed a significant decrease in the levels of the wild-type transcript of \textit{MRE11} and an increase in the mutant transcript compared to wild-type cells (P < 0.05; Fig. 1B and C). In contrast, cell lines with monoallelic mutations showed intermediate expression levels of the mutant transcript compared with wild-type cells (P < 0.05; Fig. 1C). In addition, we assessed the basal levels of \textit{PARP-1} expression and no differences were observed between \textit{MRE11} mutant and wild-type cell lines (Fig. 1D).

MSI-II tumors present with changes in gene expression related to the homologous recombination pathway

Once we observed that deficiency in \textit{MRE11} exists among MSI tumors, our interest was focused on assessing if the homologous recombination pathway showed evidence of deregulation in MSI tumors. Therefore, we examined the expression levels of those genes integrated in the KEGG pathway hsa03440 using data from a total of 300 CRCs from the MECC study (Supplementary Table S3). As shown in Fig. 2A and Supplementary Table S6, a total of 14 of 30 genes were significantly differentially expressed in MSI-H compared with MSS tumors (BH-adjusted P < 0.005; ref. 19). \textit{MRE11} and \textit{RAD50} probe sets showed a lower expression in MSI-H tumors and simultaneously other probe sets such as \textit{PARP-1} were significantly upregulated, probably due to the deficiency in the MRN complex proteins (Fig. 2B). These data provide evidence of significant differential expression of the homologous recombination pathway in MSI tumors.

Mutations of \textit{MRE11} induce higher levels of unrepaired DNA damage and attenuate the formation of Rad51 foci after irradiation

To determine the effect of \textit{MRE11} mutation on homologous recombination repair, we measured Rad51 focus formation at baseline and in response to radiation-induced DNA damage. We found that Rad51 focus formation following irradiation in the wild-type and monoallelic \textit{MRE11} mutant cell lines was significantly increased from baseline. However, the cell line harboring a biallelic mutation did not exhibit Rad51 mobilization upon irradiation. This observation highlights the impairment of DSB repair by the homologous recombination pathway in cell lines deficient in \textit{MRE11} (Fig. 11). Furthermore, we investigated the degree of unrepaired DNA damage in cell lines with different \textit{MRE11} mutational statuses by quantifying γH2AX with immunofluorescence (data not shown). In all 3 cell lines, irradiation induced an increase in the levels of unrepaired DNA damage, as expected. Under baseline conditions, the cell line SW-48 harboring biallelic mutations in \textit{MRE11} presented with more cells positive for γH2AX foci as compared with the wild-type cell line SW-620 and the monoallelic mutant HCT-15, suggesting that \textit{MRE11} mutation results in accumulation of DNA damage in otherwise unperturbed cells.

A gene expression profile of MSI-II tumors is anticorrelated with changes induced by the \textit{PARP-1} inhibitor phenanthridinone

Based on this deficiency in DSB repair exhibited by MSI tumors, we hypothesized that \textit{PARP-1} inhibitors might have a

Table 1. Frequency of the \textit{MRE11 poly(T)11} mutation in cell lines and primary CRC

<table>
<thead>
<tr>
<th>Cell lines, n</th>
<th>MSI</th>
<th>MSS</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>\textit{MRE11 poly(T)11} mutation, n (%)</td>
<td>8</td>
<td>9</td>
<td>&lt; 0.001</td>
</tr>
<tr>
<td>Yes</td>
<td>8 (100)</td>
<td>0 (0)</td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>0 (0)</td>
<td>9 (100)</td>
<td></td>
</tr>
<tr>
<td>Primary tumors, n</td>
<td>22</td>
<td>24</td>
<td></td>
</tr>
<tr>
<td>\textit{MRE11 poly(T)11} mutation, n (%)</td>
<td>18 (82)</td>
<td>0 (0)</td>
<td>&lt; 0.001</td>
</tr>
<tr>
<td>Yes</td>
<td>18 (82)</td>
<td>0 (0)</td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>4 (18)</td>
<td>24 (100)</td>
<td></td>
</tr>
</tbody>
</table>
role in the treatment of this tumor subtype based on the concept of synthetic lethality. In addition, we searched for in silico data supporting this biologically driven hypothesis using a systems biology tool. We interrogated the Connectivity Map (21) database to determine if gene expression changes induced in cell line models after treatment with first generation PARP-1 inhibitors such as phenanthridinone, NU-1025, and 1,5-Isoquinolinediol were anticorrelated with different gene expression profiles characterizing MSI-H tumors using 2 different measures: the enrichment score and the connectivity score. Strong evidence of anticorrelation between both phenanthridinone and NU-1025 and MSI-H tumors was found in 3 of 5 gene expression data sets. In the case of phenanthridinone enrichment (\( \text{enrichment score} < 0.95 \)) and connectivity scores

Figure 1. A, a polyT(11) tract located at the intron 4 is the target for mutations in MSI tumors. Shortening in 1 or more nucleotides causes changes in the splicing that induce complete skipping of exon 5 and protein truncation. Two sets of primers were designed to measure the levels of the wild type (wt) and the mutant transcript (mut) of MRE11; B-D, levels of expression of the wt and mut transcript of MRE11 as well as PARP-1 assessed by qRT-PCR in 10 CRC cell lines.
Low levels of MRE11 wild-type transcripts increase the sensitivity to the PARP-1 inhibitor ABT-888 in MSI-H cell lines

We selected ABT-888 to assess the effects of a novel PARP-1 inhibitor in a CRC model deficient in MRE11. We used 3 wild-type, 1 monoallelic, and 4 biallelic mutants of MRE11 cell lines for these experiments. Because the monoallelic mutant cell line has intermediate expression levels of the MRE11 mutant transcript but closer to wild-type cells, we decided to group it along with them for IC50 and cytotoxicity at 10 μM comparisons. A significant difference in cytotoxicity was found at 10 μM concentration between biallelic mutants and wild-type plus monoallelic mutants (44.5% vs. 80.65%, P = 0.028; Fig. 4A) and a 2.5-fold difference in IC50 when compared between these 2 groups (8.9 vs. 22.23 μM, P = 0.028; Fig. 4B). Then we studied the correlation between levels of expression of the mutant transcript of MRE11 and cytotoxicity to ABT-888 at a concentration of 10 μM showing a significant association between both (R = −0.9048, P = 0.0046; Fig. 4C). Cell cycle changes revealed an arrest in G1 and a decrease in S-phase after treatment with ABT-888 in MRE11 biallelic mutants (Fig. 4D), consistent with expectation given the mechanism of PARP inhibitors.

Finally, we conducted experiments using 2 different approaches to diminish the expression of MRE11. First, shRNA was used to knock down the expression of MRE11 in a wild-type MRE11 and MSS cell line to further assess its role as a mediator of the effect of PARP-1 inhibition. As depicted in Fig. 5A, we were able to achieve a significant, but incomplete, knockdown of MRE11 gene expression in the SW-480 cell line. We observed differences in proliferation between mock shRNA and MRE11 shRNA stable transfectants when 50 μM of ABT-888 was used, pointing toward a potential role of MRE11 as responsible for the drug effects (Fig. 5B). Therefore,
a second validation experiment using the cell line SW-480/SN3 and its derivative SM1.3 was performed. SM1.3 was originally transfected with an expression construct for Δ3-7MRE11 lacking exons 5 to 7 that was originally cloned from the CRC cell line HCT-116. Experiments using this cell line were designed to confirm the role of MRE11 mutations in conferring sensitivity to PARP inhibitors. We assessed the expression of the wild-type transcript of MRE11 in the parental SW-480/SN3 and in SM1.3 observing that the derivative cell line SM1.3 expressed less than 20% of the parent line’s MRE11 transcript levels, supporting its utility as an appropriate model (Fig. 5A).

Cytotoxicity assays comparing ABT-888 in these 2 cell lines showed a higher response by SM1.3 to PARP inhibition at 10 μM, consistent with the trends of the results obtained with the shRNA approach. However, SM1.3 did not show a differential response at 50 μM, suggesting either a threshold effect or an imperfect dose–response relationship when compared with the previous shRNA knockdown approach (Fig. 5C).

**Discussion**

Genetic instability in MSI tumors is secondary to the presence of a deficiency in the MMR system that introduces a myriad of mutations in downstream genes (27). One of these gene targets is MRE11, a gene that is implicated in homologous recombination. MRE11 forms a multiprotein complex with RAD50 and NBS1 that signals double strand DNA breaks and then recruits other proteins that initiate DNA repairing.

**Table 2.** Enrichment results obtained from the application to the Connectivity Map to 5 different data sets defining MSI CRCs

<table>
<thead>
<tr>
<th>Data set</th>
<th>Compound name</th>
<th>Dose (μM)</th>
<th>Cell line</th>
<th>Connectivity score</th>
<th>Enrichment score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vilar</td>
<td>Phenanthridinone</td>
<td>51</td>
<td>MCF7</td>
<td>-0.68</td>
<td>-0.98</td>
</tr>
<tr>
<td>Banerjea</td>
<td>Phenanthridinone</td>
<td>51</td>
<td>MCF7</td>
<td>-0.61</td>
<td>-0.94</td>
</tr>
<tr>
<td>Watanabe</td>
<td>Phenanthridinone</td>
<td>51</td>
<td>MCF7</td>
<td>0</td>
<td>0.62</td>
</tr>
<tr>
<td>Koinuma</td>
<td>Phenanthridinone</td>
<td>51</td>
<td>MCF7</td>
<td>-0.60</td>
<td>-0.95</td>
</tr>
<tr>
<td>Kruhoffer</td>
<td>Phenanthridinone</td>
<td>51</td>
<td>MCF7</td>
<td>0</td>
<td>0.54</td>
</tr>
<tr>
<td>Vilar</td>
<td>NU-1025</td>
<td>100</td>
<td>MCF7</td>
<td>0</td>
<td>0.523</td>
</tr>
<tr>
<td>Banerjea</td>
<td>NU-1025</td>
<td>100</td>
<td>MCF7</td>
<td>-0.243</td>
<td>-0.4</td>
</tr>
<tr>
<td>Watanabe</td>
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<td>100</td>
<td>MCF7</td>
<td>-0.56</td>
<td>-0.93</td>
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<tr>
<td>Koinuma</td>
<td>NU-1025</td>
<td>100</td>
<td>MCF7</td>
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<td>0.408</td>
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<td>Kruhoffer</td>
<td>NU-1025</td>
<td>100</td>
<td>MCF7</td>
<td>0.46</td>
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<tr>
<td>Vilar</td>
<td>1,5-Isoquinolinediol</td>
<td>100</td>
<td>HL60</td>
<td>0</td>
<td>0.650</td>
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<tr>
<td>Banerjea</td>
<td>1,5-Isoquinolinediol</td>
<td>100</td>
<td>HL60</td>
<td>-0.51</td>
<td>-0.86</td>
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<td>Watanabe</td>
<td>1,5-Isoquinolinediol</td>
<td>100</td>
<td>HL60</td>
<td>0</td>
<td>-0.642</td>
</tr>
<tr>
<td>Koinuma</td>
<td>1,5-Isoquinolinediol</td>
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<td>HL60</td>
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<td>-0.53</td>
</tr>
<tr>
<td>Kruhoffer</td>
<td>1,5-Isoquinolinediol</td>
<td>100</td>
<td>HL60</td>
<td>0</td>
<td>0.656</td>
</tr>
</tbody>
</table>

**NOTE.** Enrichment and connectivity scores for every data set are presented. These scores are intended to reflect the correlation between gene expression changes induced in cell line models after treatment with first-generation PARP-1 inhibitor and those gene expression profiles characterizing MSI-H tumors coming from different data sets. The enrichment score indicates the strength of this correlation and the connectivity score is relative to the rest of drugs tested in the Connectivity Map. The absolute value of both ranges from +1 to −1 and refers to the level of correlation or anticorrelation with the original signature of interest. Phenanthridinone, NU-1025, and 1,5-Isoquinolinediol are first-generation PARP inhibitors, with phenanthridinone being the compound with the most consistent results.
We have observed frequent mutations in an specific poly(T)11 tract located in the intron 4 of MRE11 in MSI colorectal tumors that is consistent with previous reports (28, 29), thus confirming that MSI is strongly associated with this MRE11 mutation.

At the present time, deficiency in homologous recombination has been therapeutically exploited in those tumors exhibiting mutations in BRCA1 and BRCA2 (30). This novel therapeutic approach is based on the fact that simultaneous deficiency in 2 genes may introduce lethality in a biologic system that otherwise would be tolerant to the loss of one of them (31). Although the role of BRCA1 and BRCA2 is more predominant in homologous recombination than MRE11, our hypothesis is that other components of this pathway may also predict an increase in the sensitivity to PARP-1 inhibitors. In terms of the biology of DSB repair, we have shown that cell lines harboring biallelic mutations in MRE11 did not effectively promote homologous recombination expressed by the
mobilization of Rad51. Moreover, biallelic mutant cell lines presented with higher levels of unrepaired DNA damage in basal conditions. Consistent with our hypothesis, we then demonstrated that those CRC cell lines displaying MSI and harboring biallelic mutations in MRE11 have greater sensitivity to PARP-1 inhibition. However, the effect of PARP-1 inhibition is abrogated when 1 wild-type allele of MRE11 is retained. This point has been illustrated in our data by the fact that a heterozygous cell line had similar sensitivity to PARP-1 inhibition to those with both alleles intact. A similar effect has been reported in the preclinical testing of these compounds in BRCA-1 and -2 deficient models. Therefore, we suggest that those patients with MSI tumors harboring biallelic mutations in MRE11 may represent a target population for the use of PARP-1 inhibitors in patients with MSI CRCs. We have shown that tumors with biallelic mutations represent approximately 36% of the total of MRE11 mutants. Finally, we tested several shRNA constructs in 2 different MSS CRC cell lines, SW-480 and HT-29, to functionally validate the contribution of MRE11 to PARP-1 sensitivity. We initially observed that those

Figure 5. A, levels of MRE11 wild-type transcript in transfected cells with a shRNA plasmid against MRE11 and in the derivative cell line SM1.3 that has been transfected with an expression construct for Δexons MRE11 lacking exons 5 to 7. Levels of expression were normalized to mock cells and to the parental cell line SW480/SN3, respectively. B, proliferation after treatment with ABT-888. Note a difference in proliferation between SW-480 transfected with shRNA anti-MRE11 plasmid and SW-480 transfected with a mock plasmid at 50 µM and also between SM1.3 and its parental cell line at 10 µM. C, expression levels of the wild-type transcript of MRE11 compared to levels expressed in the original panel of cell lines.
transfections with highest efficacy knocking-down the expression of MRE11 induced lethality in the cells. The validation experiments were first performed in a SW-480 transfected with a shRNA that achieved a level of downregulation of only 25%. Despite this limited suppression, we observed a higher sensitivity to PARP-1 inhibitors at 50 μM of ABT-888 following this level of decreased MRE11 expression. In addition, we performed a second set of validation studies using a cell line model transfected with a transcript that contains a mutation in MRE11 lacking exons 5 to 7 and leads to dramatically lower levels of the wild-type MRE11 at 80% of the baseline compared with the parental cell line. Again we observed that PARP inhibition exerted a higher effect on the derivative cell line SM1.3 at a lower concentration of the drug of 10 μM but not at 50 μM. Therefore, these data are not entirely consistent with dose–response inhibition across all concentrations, and suggest that either inhibitory thresholds might not be perfectly modeled by our transfection system, or that other genetic variation may contribute to PARP sensitivity. In fact, we have been able to identify by using gene expression profiling other candidate genes that are involved in the homologous recombination pathway and significantly deregulated in MSI-H tumors.

To our knowledge, this is the first communication on the activity of PARP-1 inhibitor in a solid tumor harboring a deficiency in a DNA repair pathway other than BRCA1 and BRCA2, thus suggesting broader applications of this therapeutic strategy. Therefore, our study also provides preclinical rationale for an ongoing phase II clinical trial exploring the activity of a different PARP-1 inhibitor in colorectal tumors stratified by MSI status (NCT00912743). In addition, we suggest that combinations of other therapies inducing DSB such as radiation or irinotecan may enhance the effects of PARP-1 inhibitors in MSI CRCs and are warranted in the future.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Acknowledgments

We want to thank Mark Meuth and Amil Ganesh from the Institute of Cancer Studies (Sheffield, UK) for providing us with cell lines for validation experiments. The raw data as well as the data set with the statistical tests have been deposited in the National Center for Biotechnology Information’s GEO database and are accessible through GEO Series number GSE26468.

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6. Duval A, Hamelin R. Mutations at coding repeat sequences in misexpression of MRE11 at 80% of the baseline compared with the parental cell line. Again we observed that PARP inhibition exerted a higher effect on the derivative cell line SM1.3 at a lower concentration of the drug of 10 μM but not at 50 μM. Therefore, these data are not entirely consistent with dose–response inhibition across all concentrations, and suggest that either inhibitory thresholds might not be perfectly modeled by our transfection system, or that other genetic variation may contribute to PARP sensitivity. In fact, we have been able to identify by using gene expression profiling other candidate genes that are involved in the homologous recombination pathway and significantly deregulated in MSI-H tumors.

To our knowledge, this is the first communication on the activity of PARP-1 inhibitor in a solid tumor harboring a deficiency in a DNA repair pathway other than BRCA1 and BRCA2, thus suggesting broader applications of this therapeutic strategy. Therefore, our study also provides preclinical rationale for an ongoing phase II clinical trial exploring the activity of a different PARP-1 inhibitor in colorectal tumors stratified by MSI status (NCT00912743). In addition, we suggest that combinations of other therapies inducing DSB such as radiation or irinotecan may enhance the effects of PARP-1 inhibitors in MSI CRCs and are warranted in the future.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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