ERCCI and ERCC2 Polymorphisms Predict Clinical Outcomes of Oxaliplatin-based Chemotherapies in Gastric and Colorectal Cancer: A Systemic Review and Meta-analysis

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Key words: Chemotherapy, DNA repair, Meta-analysis, Pharmacogenetics, Platinum

Short title: NER gene polymorphisms and platinum therapy

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Translational Relevance

Combination treatment of oxaliplatin and fluoropyrimidines is the standard treatment for gastric and colorectal cancer, which improves patients’ response and overall survival. The nucleotide excision repair (NER) pathway is responsible for removal of DNA adducts caused by oxaliplatin and thus may influence chemotherapeutic efficacy. Our meta-analysis provided evidence of an association between NER ERCC1 rs11615C>T and ERCC2 rs13181T>G SNPs and clinical outcomes in gastric and colorectal cancer patients receiving oxaliplatin-based chemotherapy in both Asians and Caucasians. Our results suggest that it is feasible to use a pharmacogenomic approach to predict clinical outcomes of oxaliplatin-treated gastric and colorectal cancer patients.
Abstract

Purpose: Nucleotide excision repair (NER) modulates platinum-based chemotherapeutic efficacy by removing drug-produced DNA damage. To summarize published data on the association between polymorphisms of NER genes (ERCC1 and ERCC2) and responses to oxaliplatin-based chemotherapies, we performed a meta-analysis of gastric and colorectal cancer for commonly studied polymorphisms ERCC1 rs11615C>T and ERCC2 rs13181T>G.

Patients and methods: In 17 previous published studies, 1787 cancer patients were treated with the oxaliplatin-based regimen. Primary outcomes included therapeutic response (TR) (i.e., complete response + partial response vs. stable disease + progressive disease), progression-free survival (PFS) and overall survival (OS). We calculated odds ratio (OR) or hazard ratio (HR) with 95% confidence intervals (CI) to estimate the risk or hazard.

Results: We found consistent and clinically substantial risk or hazard for TR, PFS and OS in the oxaliplatin-treated gastric and colorectal cancer patients with an ethnic discrepancy. For ERCC1 rs11615C>T, the T allele was associated with reduced response, PFS and OS in Asians (TR: OR, 0.53 and 95% CI, 0.35-0.81; PFS: HR, 1.69 and 95% CI, 1.05-2.70; and OS: HR, 2.03 and 95% CI, 1.60-2.59). For ERCC2 rs13181T>G, the G allele was associated with reduced response, PFS and OS in Caucasians (TR: OR, 0.56 and 95% CI, 0.35-0.88; PFS: HR, 1.41 and 95% CI, 1.02-1.95; and OS: HR, 1.42 and 95% CI, 1.11-1.81).

Conclusions: NER ERCC1 rs11615C>T and ERCC2 rs13181T>G polymorphisms are useful prognostic factors in oxaliplatin treatment of gastric and colorectal cancer. Larger studies and further clinical trials are warranted to confirm these findings.
Introduction

Fluoropyrimidines are essential in the treatment of gastric and colorectal cancer in advanced stages and have shown survival benefit, compared with the best supportive care (1, 2). Oxaliplatin is the new generation of platinum drugs that improve response rate and survival after adding to the 5-Fu/leucovorin (LV) regimen. Combination treatment of 5-Fu/LV plus oxaliplatin (FOLFOX) is now considered the standard treatment for gastric and colorectal cancer, with a response rate of over 40% for the first-line treatment (3, 4). Despite the efficacy of combined chemotherapies, a large proportion of patients display varying levels of resistance, indicating that the therapeutic efficacy has a remarkable inter-individual variability. Since DNA kinking is the major feature of platinum-DNA adducts that block DNA replication and lead to cancer cell death (5, 6), which is recognized and repaired by the nucleotide excision repair (NER) pathway, it is conceivable that the inter-individual difference in the NER capacity may influence the efficacy of oxaliplatin-based chemotherapy and clinical outcomes of the treated cancer patients.

ERCC1 and ERCC2 proteins are major components of the NER complex, acting as the rate-limiting enzymes in the NER pathway. Several common and putatively functional single nucleotide polymorphisms (SNPs) of ERCC1 and ERCC2 have been identified, of which ERCC1 rs11615 and rs3212986 SNPs (C118T and C8092A) have some effects on ERCC1 mRNA expression (7), whereas ERCC2 rs1799793 and rs13181 SNPs (Asp312Asn [G>A] and Lys751Gln, [T>G], respectively) SNPs are associated with suboptimal DNA repair capacity (8, 9). Previous studies have suggested that ERCC1 is a promising predictive marker for response to the platinum-based chemotherapy, because of its low expression associated with increased chemotherapeutic sensitivity (10). Therefore, these ERCC1 and ERCC2 SNPs may be useful prognostic markers for treatment with platinum agents.
Because published reports of an association between NER SNPs and clinical outcome of platinum-based chemotherapy from individual studies are not consistent, we performed a systemic review and meta-analysis to assess the evidence of effects of \textit{ERCC1} rs11615C>T and \textit{ERCC2} rs13181T>G SNPs on the efficacy of oxaliplatin-based chemotherapy in gastric and colorectal cancer patients.

\textbf{Patients and Methods}

\textbf{Study selection}

We searched for relevant publications before June 1\textsuperscript{st}, 2010 in English literature by using electronic MEDLINE and EMBASE databases with the following terms “\textit{ERCC1}”, “\textit{ERCC2 or XPD}” or “\textit{ERCC}”, “gastric or stomach cancer”, “colon or colorectal cancer”, “polymorphism or variant”, and “treatment or chemotherapy”. References of the retrieved articles were further screened for earlier original studies. The inclusion criteria were as follows: advanced, recurrent, or metastatic gastric or colorectal cancer; treated purely by regimens of FOLFOX (oxaliplatin plus 5-Fu/leucovorin) or XELOX (oxaliplatin plus capecitabine, a drug which converts to 5-Fu in vivo) (excluding neoadjuvant chemotherapy); cancer histologically or pathologically confirmed; East Asian (China, Korea and Japan) or Caucasian (European descendents) ethnicities; and \textit{ERCC1} rs11615C>T and or \textit{ERCC2} rs13181T>G genotyped. The corresponding authors were contacted to obtain missing information, and some studies were excluded if critical missing information was not obtained by our repeated requests. Abstracts, unpublished reports and articles with sample size less than 45 or written in non-English language were also excluded.
**Statistical methods**

We estimated the odds ratio (OR) for objective response versus no response after platinum-based chemotherapy \([\text{CR+PR vs. PD+SD, using the WHO criteria (11) or the Response Evaluation Criteria in Solid Tumors criteria (RECIST) (12)}]\). Progression-free survival (PFS) and overall survival (OS) were evaluated by pooled Cox proportional hazard ratios (HRs) and 95% confidence intervals (CIs) using published methods (13) because a meta-analysis of summary results is statistically as efficient as a joint analysis of individual participant data (14). We assessed the between-study heterogeneity by using the Cochran’s Q test with a significance level of \(P < 0.05\). We performed initial analyses with a fixed-effect model and confirmatory analyses with a random-effect model, if there was significant heterogeneity. We used inverted funnel plots and the Egger’s test to examine the effect of publication bias. We compared the difference in the effect estimates between subgroups as described previously (15). All \(P\) values were two-sided, and all analyses were performed using the Stata software (Stata Corporation, Texas) and Review Manager (v5.0; Oxford, England).

**Results**

We identified 65 related publications by initial screening (as of June 1\(^{st}\), 2010), of which 21 publications seemed to meet the inclusion criteria. We excluded one study, in which data were inestimable and authors were unreachable (16), two studies that used other chemotherapeutic agents (i.e. irinotecan and cetuximab) in addition to FOLFOX or XELOX (17, 18), and one study with study sample size less than 45 (19) (Fig. 1). As a result, the final data pool consisted of 17 studies, including 1787 cancer patients (Table 1).
**ERCC1 rs11615C>T**

**Objective response**

Nine studies including 855 patients were eligible for the final analysis. In the dominant model, the minor variant T allele was not associated with objective response in all patients (T/T+C/T versus C/C: OR, 0.89; 95% CI, 0.50-1.57) (Fig. 2A), and no single study altered the result substantially by the sensitivity test. However, stratified analysis by ethnicity showed a significant difference in the estimates of effect between Asians and Caucasians (\(P = 0.002\)), and the T allele was associated with a significantly lower objective response rate in Asians (OR, 0.53; 95% CI, 0.35-0.81). When only colorectal cancer was included, the OR was similar to that of the overall patients (OR, 0.88; 95% CI, 0.42-1.87) (Table 2). No publication bias was detected by either the funnel plot or Egger’s test (data not shown).

**Progression-free survival**

Eleven studies including 1230 patients were eligible for the final analysis. The T allele was associated with a non-significant increase of hazard for PFS in all patients (T/T+C/T versus C/C: HR, 1.33; 95% CI, 0.94 to 1.87) (Fig. 2B), and the single study by Paré et al. (20) showed substantial influence over the pooled result, the exclusion of which elevated the HR significantly (HR, 1.46; 95% CI, 1.07 to 1.99). Although stratified analysis by ethnicity showed a clinically substantial and statistically significant increase in the hazard of progression in Asian patients (HR, 1.69; 95% CI, 1.05 to 2.70), further comparison did not show significant difference in the estimates of effect between Asians and Caucasians (\(P = 0.147\)). When only colorectal cancer was included, the HR was similar to that of overall patients (HR, 1.39; 95% CI, 0.89 to 2.17) (Table 2). No publication bias was detected by either the funnel plot or the Egger’s test (data not shown).
**Overall survival**

Nine studies including 968 patients were eligible for the final analysis. There appeared a significant effect of ERCC1 rs11615C>T polymorphism on OS in all patients (T/T+C/T versus C/C: HR, 1.51; 95% CI, 1.02 to 2.24) (Fig. 2C). Further analysis demonstrated substantial influence from the single study of Chang et al. (21), the exclusion of which led to loss of significance of the pooled result (HR, 1.36; 95% CI, 0.92 to 2.02). Stratified analysis indicated a more pronounced effect in Asian patients (HR, 2.03; 95% CI, 1.60 to 2.59), compared with the Caucasian patients (HR, 1.10; 95% CI, 0.60 to 2.03), and a marginally significant difference existed in the estimates of effect between these two ethnicities ($P = 0.064$). When only colorectal cancer was included, the T allele was associated with a non-significant increased hazard of death (HR, 1.55; 95% CI, 0.87 to 2.77) (Table 2). No publication bias was detected by either the funnel plot or the Egger’s test (data not shown).

**ERCC2 rs13181T>G**

**Objective response**

Six studies including 625 patients were eligible for the final analysis. The G allele was associated with a reduced objective response in all patients (G/G+G/T versus T/T: OR, 0.53; 95% CI, 0.37-0.78) (Fig. 3A), and no single study influenced the pooled result substantially. In stratified analyses, the association remained significant in subgroups of Caucasians (OR, 0.56; 95% CI, 0.35-0.88) and colorectal cancer (OR, 0.52; 95% CI, 0.35-0.77) (Table 2). No publication bias was detected by either the funnel plot or the Egger’s test (data not shown).
Progression-free survival

Eight eligible studies of 931 patients were included in the final analysis, only two of which included Asians. Overall, there was a substantial effect of the G allele on progression hazard in all patients (G/G+G/T versus T/T: HR, 1.41; 95% CI, 1.06-1.89) (Fig. 3B and Table 2), and no single study influenced the pooled result substantially. In stratified analyses, the significance remained in subgroups of Caucasians (HR, 1.41; 95% CI, 1.02 to 1.95) and colorectal cancer (HR, 1.50; 95% CI, 1.11-2.02) (Table 2). No publication bias was detected by either the funnel plot or the Egger’s test (data not shown).

Overall survival

Six studies including 669 patients were eligible for the final analysis, again only two of which included Asians. The G allele was associated with a non-significant increase in the hazard of death in all patients (G/G+G/T versus T/T: HR, 1.54; 95% CI, 0.96 to 2.50) (Fig. 3C and Table 2), and the single study by Keam et al. (22) had a substantial influence over the pooled result, the exclusion of which elevated the HR significantly (HR, 1.77; 95% CI, 1.11 to 2.84). In stratified analyses, the significance remained in subgroups of Caucasians (HR, 1.42; 95% CI, 1.11-1.81), and colorectal cancer (HR, 1.77; 95% CI, 1.11-2.84). No publication bias was detected by either the funnel plot or the Egger’s test (data not shown).

Discussion

In this meta-analysis, we provided evidence of an association between ERCC1 rs11615C>T and ERCC2 rs13181T>G SNPs and clinical outcomes of Asians and Caucasians patients, respectively, with gastric and colorectal cancers that were treated by oxaliplatin-based research.
chemotherapy.

Previous studies showed that clinical outcomes, measured as either tumor progression or survival, were better in patients susceptible to higher levels of platinum-induced DNA adduct (23, 24). Resistance to platinum may result from numerous mechanisms (25), among which NER is the predominant mechanism for moderate levels of platinum resistance seen clinically (26). There is evidence that cancer patients with congenital NER mutations are sensitive to platinum treatment and that hypersensitivity of testicular cancer to cisplatin is due to DNA repair deficiency (27, 28). ERCC1 and ERCC2 are two key rate-limiting enzymes in the multistep NER process. ERCC1, in collaboration with XPF protein, is involved in DNA lesion recognition, whereas ERCC2 is a subunit of human transcriptional initiation factor TFIIH with ATP-dependent helicase activity. Therefore, functional ERCC1 and ERCC2 SNPs may contribute directly to phenotypes of drug sensitivity by modifying related genes’ functions and reflect platinum sensitivity as an inborn trait.

Our meta-analysis used objective response, PFS and OS as primary parameters to assess the influence of NER SNPs on clinical outcomes of oxaliplatin-based chemotherapy, because these parameters are intrinsically correlated but not necessarily consistent with one another. Most often, a low objective response rate suggests tumor resistance to the chemotherapeutic regimen and a short PFS and OS is very likely the consequence. However, a high objective response rate may lead to an increased PFS and OS, or no survival benefit at all (29), demonstrating the necessity of including all three parameters to make a comprehensive assessment. In our meta-analysis, ERCC1 rs11615 T allele was a biomarker of low objective response, short PFS and OS in Asian patients, whereas ERCC2 rs13181 G allele showed significant or marginally significant association with low objective response, short PFS and OS in overall patients, Caucasians and colorectal cancer subgroups. Although some single studies may have influenced the significance of the pooled results,
the association tendency was obvious with or without these studies. The consistent changes of three parameters strongly suggested that *ERCC1* rs11615C>T and *ERCC2* rs13181T>G both had an effect on oxaliplatin-based chemotherapy and that objective response could be a useful surrogate of survival in oxaliplatin-treated gastric and colorectal cancer patients.

Our results could be reasonably explained by the biological significance of these two SNPs. The rs11615 T allele of *ERCC1* polymorphism was found to be associated with high mRNA expression of the corresponding gene (30), whereas the rs13181 G allele of *ERCC2* polymorphism was found to be associated with a low number of X-ray induced chromatid aberrations (8). Functional studies confirmed a substantial influence of the *ERCC1* rs11615C>T and *ERCC2* rs13181T>G SNPs on the phenotype of NER capacity (7, 31, 32), and possessing the TT genotype of *ERCC2* rs13181T>G SNP was associated with the risk of sub-optimal DNA repair up to seven fold, compared with the GG/GT genotype (8). Hence, patients carrying the *ERCC1* rs11615 T or *ERCC2* rs13181 G allele may have higher DNA repair capacity that could effectively reduce the anticancer effect of oxaliplatin, leading to poor prognosis of these patients.

Notably, there was an apparent ethnic discrepancy in the prognostic values between Asians and Caucasians, and statistical test also confirmed the existence of ethnical difference in the estimates of effect for the *ERCC1* allele. As shown in Table 1, there was a remarkably lower prevalence of *ERCC2* rs13181 G allele in Asians than in Caucasians, which might explain the lack of effect of *ERCC2* rs13181T>G SNP in Asian patients. However, it is interesting to find that there was no predictive value of *ERCC1* rs11615C>T SNP in Caucasians, even though the rs11615 T allele was much more common in Caucasians than in Asians. Although the underlying mechanisms are not clear, numerous factors may have played a role, such as gene-gene interaction from different
genetic background, and gene-environmental interaction from different lifestyles. Additional large studies are warranted to investigate these possibilities.

Despite our efforts to make an accurate and comprehensive analysis, limitations of our meta-analysis need to be addressed. First, some data were excluded from our analysis because of loss of contact (16) or missing in the original study (33), which could cause some bias in our estimates but was unlikely to change our major conclusions, because Spindler et al. showed no association between ERCC1 rs11615C>T polymorphism and PFS in Caucasians (33), and Liu et al. showed no association between ERCC2 rs13181T>G polymorphism and OS in Asians (16), which were consistent with our findings. Second, most of the included studies were retrospective and differed significantly in study designs. In addition, the frequencies of ERCC1 rs11615 T and ERCC2 rs13181 G alleles were also substantially different among patient populations with different ethnicity. All these may have caused wide and significant heterogeneity between studies. Third, our analysis largely used unadjusted estimates, because not all published studies presented adjusted estimates or when they did, the estimates were not adjusted by the same potential confounders. However, when only those studies with the available adjusted estimates were used, the conclusions were not significantly changed (data now shown). Fourth, we were unable to analyze the association between ERCC1 and ERCC2 SNPs and platinum toxicities, because few studies provided this information or used different toxicity profiles. Finally, oxaliplatin is not used as a single compound but in combination with 5-Fu in the regimen, and unfortunately, we were unable to investigate potential gene-gene interactions between NER variants and folate metabolizing gene variants because of the limited publications available on this topic.

Overall, our meta-analysis demonstrated that ERCC1 rs11615C>T and ERCC2 rs13181T>G SNPs might be useful prognostic factors for assessing clinical outcomes of oxaliplatin-based
chemotherapies (FOLFOX or XELOX) in gastric and colorectal cancers. However, future prospective studies with large sample sizes and better study designs are required to confirm our findings.

Disclosure of Potential Conflicts of Interest:

The authors have declared no conflicts of interest.

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Role of the authors:

Ming Yin, Jingrong Yan, Qingyi Wei conceived the ideas, conducted literatures search and data collections; Eva Martinez-Balibrea, Francesco Graziano, Heinz-Josef Lenz, Hyo-Jin Kim, Jacques Robert, Seock-Ah Im, Wei-Shu Wang, Marie-Christine Etienne-Grimaldi provided the raw data of their original studies, and all authors contributed to the writing, revising, and approval for final submission.
### Table 1. Studies on oxaliplatin-based chemotherapy and ERCC1 (rs11615C>T) and ERCC2 (rs13181T>G) polymorphisms included in the meta-analysis.

<table>
<thead>
<tr>
<th>Study</th>
<th>Country</th>
<th>Tumor</th>
<th>Drug</th>
<th>No.</th>
<th>Biomarkers</th>
<th>SNPs</th>
<th>Allele Freq</th>
</tr>
</thead>
<tbody>
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<tr>
<td>Chang 2009 (21)</td>
<td>Taiwan</td>
<td>Colorectal</td>
<td>FOLFOX</td>
<td>168</td>
<td>TR, OS, PFS</td>
<td>rs11615</td>
<td>T: 0.254</td>
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<td>Lai 2009 (34)</td>
<td>Taiwan</td>
<td>Colorectal</td>
<td>FOLFOX</td>
<td>188</td>
<td>TR, OS, PFS</td>
<td>rs13181</td>
<td>G: 0.080</td>
</tr>
<tr>
<td>Keam 2008 (22)</td>
<td>Korea</td>
<td>Gastric</td>
<td>FOLFOX</td>
<td>73</td>
<td>TR, OS, PFS</td>
<td>rs11615</td>
<td>T: 0.260</td>
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<td></td>
<td></td>
<td>rs13181</td>
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<tr>
<td>Liang 2008 (35)</td>
<td>China</td>
<td>Colorectal</td>
<td>FOLFOX or XELOX</td>
<td>99</td>
<td>TR, PFS</td>
<td>rs11615</td>
<td>T: 0.288</td>
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<td>Korea</td>
<td>Gastric</td>
<td>FOLFOX</td>
<td>75</td>
<td>TR, OS, PFS</td>
<td>rs11615</td>
<td>T: 0.240</td>
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<td>Huang 2008 (37)</td>
<td>China</td>
<td>Gastric</td>
<td>FOLFOX</td>
<td>89</td>
<td>OS, PFS</td>
<td>rs11615</td>
<td>T: 0.281</td>
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<td>China</td>
<td>Colorectal</td>
<td>FOLFOX or XELOX</td>
<td>113</td>
<td></td>
<td>rs11615</td>
<td>T: 0.323</td>
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<td>Caucasians</td>
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<tr>
<td>Le Morvan 2007 (39)</td>
<td>France</td>
<td>Colorectal</td>
<td>FOLFOX or XELOX</td>
<td>59</td>
<td>TR, OS, PFS</td>
<td>rs13181</td>
<td>G: 0.381</td>
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<tr>
<td>Paré 2008 (20)</td>
<td>Spain</td>
<td>Colorectal</td>
<td>FOLFOX</td>
<td>126</td>
<td>TR, OS, PFS</td>
<td>rs11615</td>
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<td></td>
<td>rs13181</td>
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<tr>
<td>Park 2001 (40)</td>
<td>USA</td>
<td>Colorectal</td>
<td>FOLFOX</td>
<td>70</td>
<td>TR</td>
<td>rs13181</td>
<td>G: 0.421</td>
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<td>Chua 2009 (41)</td>
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<td>Colorectal</td>
<td>FOLFOX</td>
<td>115</td>
<td>TR, OS, PFS</td>
<td>rs11615</td>
<td>T: 0.635</td>
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<td>Spindler 2010 (42)</td>
<td>Denmark</td>
<td>Colorectal</td>
<td>XELOX</td>
<td>66</td>
<td>TR, PFS</td>
<td>rs11615</td>
<td>T: 0.652</td>
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<td>Viguier 2005 (43)</td>
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<td>Colorectal</td>
<td>FOLFOX</td>
<td>61</td>
<td>TR</td>
<td>rs11615</td>
<td>T: 0.557</td>
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<td>Colorectal</td>
<td>FOLFOX</td>
<td>166</td>
<td>PFS</td>
<td>rs11615</td>
<td>T: 0.557</td>
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<td>rs13181</td>
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<td>Colorectal</td>
<td>FOLFOX</td>
<td>106</td>
<td>OS, PFS</td>
<td>rs11615</td>
<td>T: 0.505</td>
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<td>Colorectal</td>
<td>FOLFOX or XELOX</td>
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<td>PFS</td>
<td>rs11615</td>
<td>T: 0.615</td>
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<td>rs13181</td>
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<td>FOLFOX</td>
<td>117</td>
<td>TR, OS, PFS</td>
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<td>rs13181</td>
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<td>HapMap^</td>
<td>China</td>
<td>(normal)</td>
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<td>137</td>
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<td>rs11615</td>
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<td>136</td>
<td></td>
<td>rs13181</td>
<td>G: 0.095</td>
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<td></td>
<td>Europe</td>
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<td>rs11615</td>
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<td></td>
<td>rs13181</td>
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</table>

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^Allele freq are shown as T allele of ERCC1 rs11615 and G allele of ERCC2 rs13181.

^PFS data was not available.

^Data from http://hapmap.ncbi.nlm.nih.gov/cgi-perl/gbrowse/hapmap3r3_B36/
Table 2. Analysis of the association between *ERCC1* rs11615C>T and *ERCC2* rs13181T>G polymorphisms and objective response, PFS and OS

<table>
<thead>
<tr>
<th>Objective response</th>
<th>Study</th>
<th>Fixed effect (Cases)</th>
<th>Random effect (T/T+C vs. C/C)</th>
<th>Phetb</th>
<th>Study</th>
<th>Fixed effect (Cases)</th>
<th>Random effect (T/T+C vs. C/C)</th>
<th>Phetb</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>ERCC1 rs11615C&gt;T</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>All</td>
<td>9 (855)</td>
<td>0.81 (0.58-1.12)</td>
<td>0.89 (0.50-1.57)</td>
<td>0.005</td>
<td>11</td>
<td>1.33 (1.15-1.54)</td>
<td>1.33 (0.94-1.87)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Asian</td>
<td>4 (378)</td>
<td>0.53 (0.35-0.81)</td>
<td>0.55 (0.31-0.98)</td>
<td>0.158</td>
<td>5 (504)</td>
<td>1.79 (1.45-2.21)</td>
<td>1.69 (1.05-2.70)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Caucasian</td>
<td>5 (477)</td>
<td>1.47 (0.89-2.43)</td>
<td>1.44 (0.68-3.02)</td>
<td>0.103</td>
<td>6 (726)</td>
<td>1.00 (0.81-1.23)</td>
<td>1.07 (0.72-1.59)</td>
<td>0.004</td>
</tr>
<tr>
<td>Colorectal only</td>
<td>7 (707)</td>
<td>0.77 (0.54-1.12)</td>
<td>0.88 (0.42-1.87)</td>
<td>0.002</td>
<td>8 (993)</td>
<td>1.38 (1.17-1.64)</td>
<td>1.39 (0.89-2.17)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td><strong>ERCC2 rs13181T&gt;G</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>All</td>
<td>6 (625)</td>
<td>0.53 (0.37-0.78)</td>
<td>0.53 (0.36-0.78)</td>
<td>0.588</td>
<td>8 (931)</td>
<td>1.37 (1.15-1.63)</td>
<td>1.41 (1.06-1.89)</td>
<td>0.010</td>
</tr>
<tr>
<td>Asian</td>
<td>2 (261)</td>
<td></td>
<td></td>
<td></td>
<td>2 (261)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Caucasian</td>
<td>4 (364)</td>
<td>0.56 (0.35-0.88)</td>
<td>0.56 (0.35-0.89)</td>
<td>0.368</td>
<td>6 (670)</td>
<td>1.33 (1.09-1.62)</td>
<td>1.41 (1.02-1.95)</td>
<td>0.022</td>
</tr>
<tr>
<td>Colorectal only</td>
<td>5 (552)</td>
<td>0.52 (0.35-0.77)</td>
<td>0.52 (0.35-0.77)</td>
<td>0.472</td>
<td>7 (858)</td>
<td>1.42 (1.19-1.71)</td>
<td>1.50 (1.11-2.02)</td>
<td>0.008</td>
</tr>
</tbody>
</table>

aStudy: the number of studies included in the analysis.
bPhet: *P*-value of between-study heterogeneity.
References


10. Vilmar A, Sorensen JB. Excision repair cross-complementation group 1 (ERCC1) in platinum-


27. Furuta T, Ueda T, Aune G, Sarasin A, Kraemer KH, Pommier Y. Transcription-coupled
35. Liang J LH, Yao R, Liang H, Wu G. ERCC1 Asn118Asn polymorphism as predictor for cancer


43. Viguier J, Boige V, Miquel C, et al. ERCC1 codon 118 polymorphism is a predictive factor for


Figure legend

Fig. 1. Study flow chart for the process of selecting the eligible publications.

Fig. 2. Forest plot of (A) objective response; (B) progression-free survival; and (C) overall survival in gastric and colorectal cancer patients treated with oxaliplatin-based therapies by ERCC1 rs11615C>T polymorphism (T/T+C/T vs. C/C, reference group = C/C).

Fig. 3. Forest plot of (A) objective response; (B) progression-free survival; and (C) overall survival in gastric and colorectal cancer patients treated with oxaliplatin-based therapies by ERCC2 rs13181T>G polymorphism (G/G+G/T vs. T/T, reference group = T/T).
Figure 1

65 relevant studies identified and screened

- 44 studies excluded by title or abstract examination

21 reports retrieved for further evaluation

- 1 study with data inestimable and author unreachable
- 2 studies used other agents
- 1 study with sample size < 45

17 reports finally included

- 14 reports of ERCC1 C113T
- 9 reports of ERCC2/XPD Lys751Gln
Clinical Cancer Research

ERCC1 and ERCC2/XPD Polymorphisms Predict Clinical Outcomes of Oxaliplatin-based Chemotherapies in Gastric and Colorectal Cancer: A Systemic Review and Meta-analysis

Ming Yin, Jingrong Yan, Eva Martinez-Balibrea, et al.

Clin Cancer Res  Published OnlineFirst January 28, 2011.

Updated version  Access the most recent version of this article at: doi:10.1158/1078-0432.CCR-10-2169

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