RESEARCH ARTICLE

Single Nucleotide Polymorphisms in the NER Pathway and Clinical Outcome of Patients with Bone Malignant Tumor

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Abstract

The effects of polymorphisms in ERCC5, ERCC6, XPC, CCNH and MMS19L on osteosarcoma response to chemotherapy and the survival of the affected patients were assessed. Genotyping of ERCC5, ERCC6, XPC, CCNH and MMS19L was performed by PCR-RFLP assay. The median PFS was 12.8 months, and the median OS was 18.6 months. Individuals carrying homozygous genotypes of ERCC5 rs17655 and ERCC5 rs1047768 were more like to have good response to treatment, while those carrying homozygous genotypes of MMS19L rs29001322 showed poor response. Osteosarcoma patients carrying TT genotype of ERCC5 rs1047768 showed a significantly longer PFS (16.8 months) and OS (21.4 months) than CC genotype, with HRs(95% CI) of 0.31 (0.10-0.93) and 0.32 (0.06-0.97), respectively. Conversely, those with the TT genotype of MMS19L rs29001322 demonstrated shorter PFS and OS, the HRs (95% CI) being 2.23 (1.08-4.15) and 4.62 (1.45-16.08), respectively. Our findings showed polymorphisms in ERCC5 rs1047768 and MMS19L rs29001322 to be associated with clinical outcome of osteosarcoma patients undergoing chemotherapy.

Keywords: Single Nucleotide polymorphisms - osteosarcoma - chemotherapy - clinical outcome

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Introduction

Osteosarcoma derives from primitive bone-forming mesenchymal cells, and is the most common bone malignant tumor found in children and adolescents. Osteosarcoma often occurs during rapid skeletal growth with more than half of them developing in the long bones (Hattinger et al., 2010). Chemotherapy with methotrexate, cisplatin and adriamycin followed by surgery and post-operative chemotherapy were the standard treatment of osteosarcoma. Although these advanced treatment, almost 30% of these patients relapse or occur metastasis (Chou and Gorlick, 2006). The clinical response to chemotherapeutics is influenced by multiple factors, including genetic and environmental factors.

Previous pharmacogeneitc studies have shown that the gene polymorphisms are correlated with the drug metabolism and transport (Zhou et al., 2008). It is suggested that deficiencies in DNA repair capacity could have a role in cancer onset or progression, and could have a role in affecting the response to DNA damaging agents (Goode et al., 2002; Le et al., 2006; Martin and Hamilton, 2008). Four main different pathways of DNA repair processes participate into repairing various types of DNA damages. Particularly, the nucleotide excision repair (NER) pathway repairs bulky lesions, and has been associated with tumor progression and response to platinum-based chemotherapy (Reed, 1998; Stoehlmacher et al., 2004). Various studies have indicated the SNPs of NER genes are related with the response to chemotherapy in osteosarcoma (Caronia et al., 2009; Biason et al., 2012; Dogan et al., 2012). But the response to chemotherapy of osteosarcoma by SNPs in the NER pathway, including ERCC5, ERCC6, XPC, CCNH and MMS19L, has not been identified. Therefore, in our study, we aimed to assess the effect of polymorphisms in ERCC5, ERCC6, XPC, CCNH and MMS19L on the response to chemotherapy in osteosarcoma, and the survival of these patients.

Materials and Methods

Subjects, treatments and clinical variables

One hundred and eighty two consecutive patients diagnosed with osteosarcoma were enrolled between May 2006 and May 2009 in our hospitals. All the cases were histologically confirmed. All the patients were followed up every two months by telephone until death or the end of follow-up. All samples were obtained with written informed consent from patients or their relatives. The ethnical approval of the study was gained from the Ethics Committee of the Xinxiang Medical University.

Patients were treated preoperatively with 25 mg/m^2 adriamycin intravenous on days one for three days, or 14 g/m^2 methotrexate plus 35 mg/m^2 cisplatin on day one for three days. After surgery, the adjuvant chemotherapy included methotrexate 10 g/m^2 on day one, 25 mg/m^2

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Table 1. Clinical Characteristics of Subjects

		Patients	
		No	%
Age, yr (Mean±SD)	15.3±8.2		
Sex	Female	72	39.6
	Male	110	60.4
Subtype	Osteoblastic	104	57.1
	Chondroblastic	47	25.6
	Not specified	31	17.3
Location	Femur	94	51.4
	Tibia	61	33.7
	Arm	15	8.4
	Central	12	6.5
Response to treatment	Good	94	51.6
	Poor	88	48.4
Metastasis	No	97	53.2
	At diagnosis	48	26.1
	At follow-up	38	20.7
Status at the end of follow-up	Alive	109	59.9
	Dead	73	40.1

Table 2. Allele Frequencies of Gene Polymorphisms in 182 Patients Treated with Chemotherapy

Gene	SNP	Alleles	MAF	Wide-type	Hetero-zygous	Homo-zygous
ERCC5	rs1047768	C/T	0.4881	131	35	16
ERCC6	rs2228526	A/G	0.1566	80	76	27
XPC	rs2228001	A/C	0.3439	136	28	18
CCNH	rs2266690	C/T	0.1378	131	34	17
17MMS19L	rs29001322	C/T	0.3054	80	76	26

cisplatin or adriamycin, 0.45 mg/m^2 one day one for three days, 500 mg/m^2 cyclophosphamide on day one for three days, and 1.5 mg/m^2 vincristine on day one for one day. The response to chemotherapy was evaluated in accordance with the response evaluation criteria from European Organization for Research and Treatment of Cancer. The response was assessed after four weeks of treatment. The response to chemotherapy was divided into good responders and poor responders. The good responders were defined as complete response or partial response, and the poor responders were defined as stable disease or progressive disease. Overall survival (OS) was calculated from the date of entry to the date of death or last clinical follow-up.

DNA extraction and quantification

Genomic DNA was extracted from peripheral blood lymphocytes using the Qiagen Blood Kit (Qiagen, Germany) according to the manufacturer's instructions. The DNA extraction was determined by Agarose gel electrophoresis method. When a stripe was shown, the DNA was successfully extracted. Genotyping of ERCC5, ERCC6, XPC, CCNH and MMS19L was performed by PCR-RFLP assay. The forward and reverse primers for polymerase chain reaction (PCR) amplification and single base extension (SBE) assays was determined by Primer 5.0 software. Polymerase chain reaction (PCR) conditions were used as follows: an initial melting step of 5 min at 94°C; 35 cycles of denaturation for 30 s at 94°C; annealing for 30 s at 64°C; extension for 60s at 72°C, followed by a 5 min final extension at 72°C.

Table 3. Response to Platinum-based Chemotherapy According to Genotypes

Genotype	Cases				χ^2	*P* value
	Good responder N=94	%	Poor responder N=88	%		
ERCC5 rs1047768						
CC	60	63.5	72	81.3		
CT	21	22.1	14	16.3		
TT	14	14.4	2	2.4	11.24	<0.05
ERCC6 rs2228526						
AA	38	40.4	42	47.2		
AG	40	42.2	36	40.8		
GG	16	17.4	11	12	0.7	0.71
XPC rs2228001						
AA	68	72.5	67	76.6		
AC	15	16.2	13	14.5		
CC	11	11.3	8	8.8	0.42	0.81
CCNH rs2266690						
CC	70	74.5	61	69.7		
CT	16	17.2	18	20.1		
TT	8	8.3	9	10.2	0.6	0.74
MMS19L rs29001322						
CC	49	52.2	31	35.4		
CT	36	38.4	39	44.8		
TT	9	9.4	17	19.7	6.37	<0.05

Statistical analysis

Follow-up began on the first day of participating. The overall survival was the time from study entry until death regardless of cause. All statistical tests are two sided. All analyses were performed using the Statistical Package for the Social Sciences (SPSS) software 13.0 for windows. The main statistical method used is the Cox Hazard regression model. Survival distributions were estimated by using the Kaplan-Meier method and assessed using the log-rank test. The association between genotype and survival was estimated by hazard ratios (HR) their confidence intervals (CI) from multivariate Cox proportional hazards model. The adjusted hazard ratios (HR) with 95% CI was used to assess the association between ERCC5, ERCC6, XPC, CCNH and MMS19L polymorphisms and OS of osteosarcoma. P value less than 0.05 was considered to be significant. All tests were two-sided and analyzed by SPSS 11.0 software.

Results

The clinical characteristics of 182 osteosarcoma patients were shown in Table 1. The median age of the patients at the diagnosis was 15.3±8.2 years (range 8.5 to 31.6 years). At the time of recruitment, only 33% of the patients were older than 18 years, and 60.5% of them were males. More than 50% of them patients were osteosarcoma, whereas the remainders were osteoblastic and chondroblastic osteosarcoma. Most of the location of cancer was in Femur (51.4%), and followed by tibia (33.7%) and arm (8.4%). Among 182 patients, 51.6% of them showed good response to treatment, and 46.8% of the patients showed metastasis at diagnosis or follow-up. At the end of follow-up, 73 patients died and 109 patients were alive. At the time of final analysis on May 2012, the median follow-up was 41.5 months.

Table 4. Univariate Analysis of Gene Polymorphisms in Relation to PFS and OS

Gene		PFS				OS			
	Case	event	Median (month)	Log-rank	HR(95%CI)[1]	event	Median (month)	Log-rank	HR(95%CI)[1]
ERCC5 rs1047768									
CC	131	75	11.2		1. 0	58	14.7		1
CT	35	14	15		0.70(0.33-1.44)	11	19.4		0.51(0.20-1.22)
TT	16	4	16.8	<0.05	0.31(0.10-0.93)	4	21.4	<0.05	0.32(0.06-0.97)
ERCC6 rs2228526									
AA	80	43	13.1		1	34	18.3		1
AG	76	36	13.6		0.89(0.49-1.57)	28	18.7		0.76(0.37-1.51)
GG	27	14	13.4	0.51	0.95(0.42-2.32)	11	19.1	0.13	0.92(0.33-2.57)
XPC rs2228001									
AA	136	71	12.2		1	56	18.2		1
AC	28	14	13.4		0.96(0.44-2.02)	11	19		0.91(0.34-2.36)
CC	18	9	13.6	0.29	0.95(0.36-2.38)	6	19.2	0.29	0.77(0.21-2.61)
CCNH rs2266690									
CC	131	64	14.1		1	51	20.3		1
CT	34	19	12.8		1.14(0.57-2.25)	15	18.4		1.31(0.54-3.17)
TT	17	10	12.6	0.73	1.20(0.46-2.97)	7	19	0.31	1.32(0.37-4.69)
MMS19L rs29001322									
CC	80	32	16.5		1	26	22.5		1
CT	76	41	11.4		1.34(0.74-2.45)	32	16.8		1.69(0.81-3.51)
TT	26	20	10.9	<0.05	2.23(1.08-4.15)	15	17.1	<0.05	4.62(1.45-16.08)

[1]Adjusted for potential risk factors, including sex, age, location of tumor and metastasis

The genotypic frequencies of the five SNPs were showed in Table 2. All the SNPs were common SNPs with minor allele frequencies between 0.13 and 0.48. 94 patients were classified as good responders. The results of tumor response to treatment by genotype were showed in Table 3. We found significant difference in the response to treatment in the polymorphisms in ERCC5 rs1047768 and MMS19L rs29001322 (P<0.05). Individuals carrying with homozygous genotypes of ERCC5 rs1047768 were more like to have good response to treatment, while those carrying homozygous genotypes of MMS19L rs29001322 had significantly poor response to treatment (Table 3). No evidence of association was found for the other polymorphisms in the

In our study, the median PFS was 12.8 months, and the median OS was 18.6 months. Patients carrying TT genotype of ERCC5 rs1047768 showed a significantly longer median PFS (16.8 months) and OS (21.4 months) than CC genotype, and the PFS and OS showed significant different among the genotypes of ERCC5 rs1047768 by log-rank test (Table 4). By Cox proportional hazards model after adjusting for potential confounding factors, we found the hazard ratio(HR) and its 95% confidence interval (95% CI) for PFS in patients with TT genotype of ERCC5 rs1047768 were 0.31(0.10-0.93) when compared with CC genotype. We found a significantly decreased risk of death from osteosarcoma among patients carrying TT genotype of ERCC5 rs1047768, and HR (95% CI) was 0.32(0.06-0.97).

Reversely, we found patients carrying TT genotype of MMS19L rs29001322 were associated with a moderate risk of progressive disease, and a heavy risk of death from osteosarcoma. The log-rank test showed the polymorphism in MMS19L rs29001322 was associated with poor PFS and OS in osteosarcoma patients, and the HRs(95% CI) were 2.23(1.08-4.15) and 4.62(1.45-16.08) by Cox proportional hazards model, respectively.

Discussion

Osteosarcoma is a rare disease, and accounts for eighth most common cancer in children. Customized chemotherapy according to reliable molecular prognostic and predictive markers could play an important role in the treatment of patients with cancer. Many preclinical and clinical studies have extensively investigated the association between expression levels of DNA repaired gene and chemotherapy response in osteosarcoma patients. In our study, we found SNPs of ERCC5 and MMS19L could predict the response to chemotherapy and clinical outcome of osteosarcoma patients receiving chemotherapy by multivariate analysis.

Our findings have important prognostic and therapeutic implications. Tumors with dysfunctional ERCC5 expression would be predicted to demonstrate sensitivity to cisplatin. ERCC5 (ERCC5) is a structure-specific endonuclease, which participates in two incision steps that are critical to the DNA repair process. ERCC5 cleaves the damaged DNA 3' to the damaged site, nonenzymatically participates in the 5' incision mediated by the ERCC1 and ERCC4 heterodimer, and stabilizes the DNA repair complex to the damaged DNA. ERCC5 levels are associated with cytotoxicity to cisplatin and iofulven, and potentially to be an important therapeutic target (Koeppel et al., 2004).

Recently studies have indicated that ERCC5 is involved in the efficacy of cisplatin neoadjuvant chemotherapy in various cancers (Ott et al., 2011; Liu et al., 2012; Massuti et al., 2012). The low efficiency genotypes involved in DNA repair and replication may contribute to the difference in susceptibility of cancer. Only one previous study has indicated high expression of ERCC5 identifies a highly sensitive population of sarcomas with significantly improved treatment outcome (Schöffski et al., 2011). Our study also has showed variation of ERCC5 is correlated

with good response to cisplatin in osteosarcoma.

MMS19 splice variants have specific distinct functional domains, and this gene exerts its function in repairing and transcripting. Specific MMS19 domains a specific role in NER pathway and transcription and contributes to regulating the switch between transcription and NER (Hatfield et al., 2006). Previous two studies reported that the association between MMS19L and risk of cancer or its prognosis (McWilliams et al., 2009; Zhang et al., 2012). Our study has showed polymorphism in MMS19 is associated with good response of cisplatin chemotherapy in osteosarcoma, and our study provides evidence for further study to clarify their association.

There were some limitations in our study. Firstly, the sample size is relatively small in our study, which would decrease the statistical power of our study and thus lower the power to find the differences between groups. Secondly, lots of factors involved in cellular response to chemotherapy. However, we only analyzed nine SNPs of DNA repair genes, and some other factors might have interaction with these nine SNPs. Thus some bias may be existed. Therefore, in order to confirm our findings, we are currently analyzing a panel of 30 genes of metabolizing and DNA repair enzymes in a perspective study involving more than 200 patients.

In conclusion, some SNPs in the NER pathways are correlated with response to chemotherapy and prognosis of osteosarcoma, especially for SNPs of ERCC5 and MMS19. Our findings would provide important evidence for prognostic and therapeutic implications in osteosarcoma.

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