The following Gynecologic Oncology Group (GOG) member institutions participated in this translational research study: University of Alabama at Birmingham, Duke University Medical Center, Abington Memorial Hospital, University of Rochester Medical Center, Walter Reed Army Medical Center, Wayne State University, University of Minnesota Medical School, Emory University Clinic, University of Mississippi Medical Center, Colorado Gynecologic Oncology Group PC, University of California at Los Angeles, University of Washington, University of Pennsylvania Cancer Center, Milton S. Hershey Medical Center, Georgetown University Hospital, University of Cincinnati, University of North Carolina School of Medicine, University of Iowa Hospitals and Clinics, University of Texas Southwestern Medical Center at Dallas, Indiana University Medical Center, Wake Forest University School of Medicine, Albany Medical College, University of California Medical Center at Irvine, Tufts-New England Medical Center, Rush-Presbyterian-St Luke's Medical Center, State University of New York (SUNY) Downstate Medical Center, University of Kentucky, Community Clinical Oncology Program, The Cleveland Clinic Foundation, Johns Hopkins Oncology Center, SUNY at Stony Brook, Eastern Pennsylvania GYN/ONC Center PC, Washington University School of Medicine, Cooper Hospital/University Medical Center, Columbus Cancer Council, University of Massachusetts Medical Center, Fox Chase Cancer Center, Medical University of South Carolina, Women's Cancer Center, University of Oklahoma, University of Virginia, University of Chicago, Tacoma General Hospital, Thomas Jefferson University Hospital, Case Western Reserve University, Tampa Bay Cancer Consortium, North Shore University Hospital, Brookview Research Inc.

Supplemental Patients and Methods

The *ERCC1* codon 118 and *C8092A* polymorphisms were detected by polymerase chain reactions (PCR), followed by pyrosequencing. For codon 118, a 413-base pair region was amplified in a standard PCR mixture consisting of 100 ng of template DNA, 400 mmol/L of a biotin-labeled forward primer 5′/5Bio/GTG-CGA-GGA-GGC-AGG-AGG-TGT-GGG-3′, 400 mmol/L of the reverse primer 5′-TGT-TGC-ACT-GGG-CAC-CTC-CAG-GCC-3′ (IDT DNA, Coralville, IA), 200 μmol/L of each dNTP (Promega, Madison, WI), 10× buffer containing $MgCl_2$, and 0.3 units of HotMaster TAQ (Eppendorf, Hamburg, Germany). The reaction began with a 94°C incubation for 2 minutes and was followed by 35 cycles of denaturation at 94°C for 1 minute, annealing at 65°C for 1 minute, and elongation at 72°C for 2 minutes. There was a final elongation at 72°C for 10 minutes. A 255-base pair region for *C8092A* was amplified in a PCR mixture consisting of template DNA plus 200 mmol/L of the forward primer 5′/TGA-GCC-AAT-TCA-GCC-ACT-3 and 200 mmol/L of the biotin-labeled reverse primer 5′-/5Bio/TAG-TTC-CTC-AGT-TTC-CCG-3 (IDT DNA), as above.

For both reactions, 10 μL of the amplimer was visualized on an ethidium bromide–stained agarose gel under ultraviolet light. Twenty microliters of the PCR product were then prepared for genotyping by combining the PCR product with 20 μL of water, 40 μL of binding buffer (10 nmol/L Tris-HCL, 2 M NaCl, 1 mmol/L EDTA, 0.1% Tween-20, pH 7.6), and 3.0 μL of streptavidin-coated sepharose beads (Amersham, Piscataway, NJ). The DNA was washed in 70% ethanol and then released from the beads into 38.8 μL of annealing buffer (20 mmol/L Tris-Acetat, 2 mmol/L $MgAc_2$, pH 7.6) and 1.2 μL of the 10 μmol/L sequencing primer. The sequencing primer for codon 118 was 5′-ACG-TCG-CCA-AAT-TCC-CAG-GG-3′ and the primer for *C8092A* was 5′/AGG-CCG-GGA-CAA-GAA-GCG-GA-3. The samples were heated to 95°C for 2 minutes and then allowed to cool to room temperature. Pyrosequencing was completed using the PSQ96 MA and the SQA reagent kit (Biotage, Uppsala, Sweden).

Relationship Between *ERCC1* Polymorphisms, Disease Progression, and Survival in the Gynecologic Oncology Group Phase III Trial of Intraperitoneal Versus Intravenous Cisplatin and Paclitaxel for Stage III Epithelial Ovarian Cancer

Table A1.

Full Multivariate Cox Regression Model for *ERCC1* Polymorphisms and Clinical Outcome

			PFS			OS		
ERCC1 Genotype		No. of Patients	HR	95% CI	*P*	HR	95% CI	*P*
All participants[*†]								
Codon 118					.415			.393
	C/C	40	1.00			1.00		
	C/T	101	1.17	0.73 to 1.89		0.72	0.43 to 1.22	
	T/T	92	0.94	0.57 to 1.54		0.87	0.51 to 1.47	
C8092A					.031			.038
	C/C	131	1.00			1.00		
	C/A or A/A	112	1.40	1.03 to 1.90		1.43	1.02 to 2.01	
IP arm subset[†‡]								
Codon 118					.965			.771
	C/C	17	1.00			1.00		
	C/T	51	1.04	0.46 to 2.38		0.73	0.30 to 1.77	
	T/T	38	0.97	0.42 to 2.24		0.82	0.34 to 2.00	
C8092A					.021			.026
	C/C	61	1.00			1.00		
	C/A or A/A	45	1.73	1.09 to 2.76		1.81	1.08 to 3.06	
IV arm subset[†‡]								
Codon 118					.393			.873
	C/C	23	1.00			1.00		
	C/T	50	1.37	0.73 to 2.56		0.91	0.45 to 1.82	
	T/T	54	1.05	0.55 to 1.98		1.03	0.53 to 2.03	
C8092A					.585			.510
	C/C	70	1.00			1.00		
	C/A or A/A	57	1.12	0.74 to 1.69		1.16	0.74 to 1.83	

Abbreviations: PFS, progression-free survival; OS, overall survival; HR, hazard ratio; IP, intraperitoneal cisplatin and paclitaxel; IV, intravenous cisplatin and paclitaxel.

↲* Adjustments were made for patient, age, race, Gynecologic Oncology Group performance status, histologic cell type, tumor grade, residual disease status, and treatment arm.

↲† Similar results and conclusions were observed for the reduced multivariate Cox models for PFS and OS with adjustments for the prognostic factors including histology cell type (clear cell/mucinous *v* other histologic subtypes), residual disease status (macroscopic *v* none or microscopic), and treatment arm (IP *v* IV).

↲‡ Adjustments were made for patient, age, race, Gynecologic Oncology Group performance status, histologic cell type, tumor grade, and residual disease status in women randomly assigned to the IP or the IV treatment arm. Testing was performed to determine whether there was statistical evidence of an interaction between the codon 118 or the *C8092A* polymorphism in *ERCC1* and treatment in this cohort ($P > .05$).