Waf-1 (p21) and p53 Polymorphisms in Breast Cancer

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Abstract

p53 is a transcription factor for Waf-1/p21, a cyclin-dependent kinase inhibitor. Certain polymorphic variants of Waf-1 and p53 have been evaluated for their association with cancer risk. Previous studies indicated that certain p53 polymorphisms confer an increased risk of breast cancer [odds ratios (ORs) and 95% confidence intervals (CIs) = 2.9, 1.4 – 6.3 Carcinogenesis (Lond.), 17: 1313, 1996; 2.5, 1.3 – 4.8 Cancer Epidemiol. Biomark. Prev., 6: 105, 1997; and 1.5, 1.1 – 2.0, Anticancer Res., 18: 2095, 1998]. The primary objectives of this study were to test the hypotheses that the serine variant (codon 31 transversion) in the third base of codon 31 of Waf-1 is also involved in this process and that there is an interaction between Waf-1 and p53 polymorphisms. To do this, Waf-1 and p53 genotypes were determined for women enrolled in a breast cancer case-control study (Caucasians, African-Americans and Latinos; 487 Waf-1 and 504 p53 genotypes were obtained). Multivariate logistic regression was used to evaluate possible associations between Waf-1 and p53 polymorphisms, race, and menopause. The primary aim was to determine whether an interaction between Waf-1 and p53 existed. Whereas multivariate analysis suggested associations between breast cancer and inheritance of Waf-1ser31 in African-Americans (OR, 2.32; 95% CI = 0.66 – 5.60; n = 37 cases and 65 controls) and Latinos (OR, 2.22; 95% CI = 0.71 – 6.89; n = 30 cases and 75 controls), and inheritance of p533 – 2 – 1 in Caucasians (OR, 3.15; 95% CI = 1.14 – 8.89; n = 93 cases and 187 controls), we did not see an interaction between Waf-1ser31 and p533 – 2 – 1. Consistent with the finding that p533 – 2 – 1 is a risk factor for Caucasian women was the observation of a strong interaction between race and p53 (P < 0.01).

Introduction

Cell cycle control is critical for normal growth and differentiation, and its disruption can lead to tumor growth and progression. Cell cycling is regulated by cyclins, catalytic partners of the cyclins. A variety of cyclin-cdk complexes is formed during distinct phases of the cell cycle and is necessary for progression. Waf-1 (p21), is a nonspecific cdk inhibitor (1). Cell cycle arrest at the G1-S phase restriction point is mediated through up-regulation of Waf-1 by p53, and the associated inhibition of G1 cyclins-cdk2 complexes. p53 is a tumor suppressor gene that maintains homeostasis through Waf-1-mediated induction of G1 arrest or Bax-mediated apoptosis (2). In the presence of DNA damage after exposure to a carcinogen, up-regulation of p53 and subsequently Waf-1 could delay progression past the G1 restriction point. Mutations in either p53 or Waf-1 may lead to loss of this homeostatic control during human carcinogenesis. The fact that 50% of all human cancers contain p53 mutations highlights its vital role in cell cycle regulation (3).

Polymorphisms in these cell cycle regulation genes have been reported, and their frequencies are dependent on race (4 – 6). At least four polymorphisms have been described for Waf-1 (4, 5). A nucleotide substitution polymorphism (C/A transversion) in the third base of codon 31 of Waf-1 results in a serine/arginine amino acid substitution. This polymorphism has been implicated in breast cancer, cervical adenocarcinoma, and endometrial cancer (7 – 9). At least 14 polymorphisms have been confirmed for human p53. Five are in exons (codons 21, 36, 47, 72, and 213), and 9 are in introns (intron numbers 1 – 3, 6, 7, and 9; Ref. 6). There are >120 previous studies that have sought an association between p53 polymorphisms and cancer, and though no clear consensus has been reached, 3 studies suggest that a haplotype of 3 of these polymorphisms represent a breast cancer risk factor (6, 10 – 13).

This study represents a first step to evaluate polymorphisms present in a series of genes that constitute a biological pathway. In this case the pathway is that of cell cycle control that is closely associated with cellular homeostasis that works to prevent tissue overgrowth and tumorigenesis. This is analogous to genes that constitute metabolic pathways where inheritance of a defective member results in an inborn error in metabolism leading to common elements of pathology, e.g., glycogen storage diseases (14).

It is possible that different allelic variants of more than one gene are more or less effective suppressors of the G1 → S progression. The objective of this study was to test the hypothesis that inheritance of minor allelic variants of either Waf-1 or p53 is associated with increased susceptibility for breast cancer either independently or together. Earlier studies indicated p53 – 1 – 2 – 1 is a risk factor for breast cancer in Caucasian women (11, 12). This study is in continuation of the previous study providing expansion of the p53 database; it additionally examines the Waf-1 polymorphism and seeks a potential interaction between p53 and Waf-1.

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2 The abbreviations used are: cdk, cyclin-dependent kinase; OR, odds ratio; CI, confidence interval; PCR, polymerase chain reaction; RFLP, restriction fragment length polymorphism.
Materials and Methods

**Human Samples.** A detailed description of the population has been reported previously (11, 15). Breast cancer cases and controls were enrolled from patients presenting at the Mount Sinai Medical Center, New York, NY, between September 1994 and February 1996. Of 1690 eligible women identified, 1101 (65%) agreed to participate; participation rates were comparable regardless of race or diagnosis (15). From these, 175 incident breast cancer cases were matched on age and race with 175 women who had no diagnosis of breast disease and 181 controls. There were 303 Caucasians (102 cases and 201 controls), 117 African-Americans (41 cases and 76 controls), and 111 Latinas (32 cases and 79 controls). Informed consent was administered according to the Institutional Review Board Guidelines, and additional approval was obtained from the National Institute for Occupational Safety and Health, Human Studies Review Board. Ethnicity was self-described, and menopausal status was defined previously. Blood samples (30 ml) were obtained at the time of interview and were used as the source of DNA for genetic analyses.

**Determination of Waf-1 and p53 Genotypes.** The Waf-1 codon 31 polymorphism was determined by PCR-RFLP according to a method published previously (5). A 100-bp genomic amplicon was generated with Waf-1-specific primers (forward 5' AGA ACC CAT GCG GCA GCA AGG 3', reverse 5' TGG ATG CAG CCC GCC ATT AGC 3'; 100 pmol; Life Technologies, Inc., Rockville, MD), in a reaction mixture (50 µl) containing AmpliTag Gold (1 unit; Perkin-Elmer, Foster City, CA), deoxynucleotide triphosphates (100 µM; Promega, Madison, WI), and Tris-HCI/KCl/MgCl2 (100/500/2.5 mm, respectively; Perkin-Elmer). Thermal cycling (35 rounds of denaturation, annealing, and extension) proceeded at 94°C for 30 s, 53°C for 1 min, and 72°C for 1 min with a final extension of 5 min. The PCR products were digested with BstPI for 1 h at 37°C according to the manufacturer’s instructions, and fragments were separated on a Nusieve agarose gel (4%). DNA fragments were stained with ethidium bromide (0.5 µg/ml) and analyzed using an Eagle Eye II image system (Stratagene, La Jolla, CA). Haplotypes for three p53 polymorphisms were determined according to a PCR-RFLP method published previously (11).

**Statistical Analysis.** Exact methods and the χ² test were used to compare the gene frequencies of p53 and Waf-1 in the control populations of three racial groups, African-American, Latina, and Caucasian. The χ² test was also used to determine whether the genotype frequencies reported in our population conformed to Hardy-Weinberg population laws. SAS statistical software was used to conduct all of the statistical analyses (16).

Within racial groups, exact methods and χ² tests were used to compare Waf-1 and p53 allelic frequencies in breast cancer cases and controls. For the Waf-1 minor variant, statistical comparisons were made initially by collapsing the homozygous minor variants into one group (presence of at least one high risk allele) versus the presence of the major variant Waf-1 A1 as the referent group. ORs and 95% CIs were also calculated comparing the homozygous only minor variant (presence of two Waf-1 A2 alleles) to the presence of only one minor variant and the major variant (presence of only one Waf-1 A2 or Waf-1 A1). Similar analysis was conducted for the p53Y27R2 allele.

Logistic regression was used to evaluate the significance of associations between breast cancer and the potential risk factors Waf-1, p53, race, and menopause. Each main effect term was first tested individually using the likelihood ratio test followed by two-way interactions for each pair of significant main effects. Resulting ORs were then calculated using the multivariable model with all of the significant main effects and interactions.

**Results**

The frequency of the minor (serine) allele of Waf-1 in Caucasians was found to be 0.1, consistent with published reports (5, 17), but the allelic frequencies of Waf-1 by race were found to vary (Table 1). The minor allele frequencies for African-Americans and Latinas were 0.27 and 0.24, respectively. These are significantly different when compared with Caucasians (χ² = 20.23, P = 0.001 and χ² = 14.78, P = 0.001, respectively). It should be noted that an excess of serine homozygotes was found in both Caucasian controls and in Caucasian cases (P = 0.01 and 2 × 10⁻⁶; Table 1, HW column).
Haplotypes, comprising three biallelic polymorphisms of p53 were reported previously for 365 women enrolled in this study (11). We expanded this database and added results for an additional 139 women to reevaluate the association between p53 and breast cancer and to test the hypothesis of a gene-gene interaction between the minor Waf-1 variant and polymorphisms in its transcription factor p53. Haplotypes were designated according to the original nomenclature (10). Thus, p53 haplotypes were generated for 504 of the 531 women included in the age- and race-matched case-control study. When an association between the p53 haplotype and breast cancer was reexamined in the expanded database no change in overall conclusions was observed. Inheritance of p53 haplotype conveyed a breast cancer risk of almost 2 (OR, 1.96; 95% CI = 1.14–3.40).

Logistic regression was then used to examine the question of interactions and significance associations between the potential breast cancer risk factors Waf-1, p53, race, and menopause. Interestingly, the results indicated that, without simultaneously considering other variables, Waf-1, p53, race, and menopause status were not significantly associated with risk of breast cancer. The two-way interactions between p53 and race was statistically significant (P < 0.01), whereas that between Waf-1 and race was not (P = 0.15). p53 was strongly associated with increased odds of breast cancer among Caucasians (OR, 3.15; 95% CI = 1.14–8.89). No association was found between breast cancer and inheritance of p53 haplotype in either African-Americans (OR, 1.29; 95% CI = 0.54–3.10) or Latinas (OR, 0.52; 95% CI = 0.12–2.16). Waf-1 was found to be potentially associated with breast cancer in African-Americans (OR, 2.32; 95% CI = 0.66–5.60) and Latinas (OR, 2.22; 95% CI = 0.71–6.89). Interestingly, Waf-1 was not associated with breast cancer risk in Caucasians (OR, 1.10; 95% CI = 0.35–3.50). The two-way interaction between Waf-1 and p53 showed almost no association with disease, either before or after adjusting for race (P > 0.9 and P = 0.15, respectively). ORs for different combinations of race, p53, and Waf-1 are given in Table 2. We recognize that a relatively small number of study subjects used to approach this type of analysis could have contributed to the failure to find an association.

**Discussion**

Waf-1 plays a direct role in mediating p53-induced G1 arrest and p53 is its transcription factor. Whereas p53 is mutated in 20–40% of human breast cancers, Waf-1 is mutated in relatively few (3, 7, 18). Moreover, relative phenotypic expression of Waf-1 and p53 appears to be important in breast cancer where tumors expressing both genes were less aggressive than those expressing only one (19). No formal case-control study has yet investigated a potential role for the Waf-1 codon 31 polymorphism in human breast carcinogenesis, although it has been studied in oral, esophageal, lung, ovarian, endometrial, and prostate cancers (4, 8, 20, 21).

This study tested the new hypothesis that the minor codon 31 Waf-1 variant (serine, F = 0.10 Caucasians, 0.27 Latinas, and 0.34 African-Americans) is involved in human breast carcinogenesis. We have also attempted to investigate a potential gene-gene interaction between polymorphisms in the cdk inhibitor Waf-1 and its transcription factor p53. To do this, Waf-1 and the p53 genotypes were determined for breast cancer cases (160 and 165, respectively) and controls (327 and 339, respectively) among three ethnic groups (Caucasians, African-Americans, and Latinas).

Earlier studies concluded that the p53 haplotype represents a breast cancer risk factor (10–13). This association was particularly strong for post-menopausal Caucasian women (OR, 2.5; 95% CI = 1.3–4.8; n = 365; Ref. 11). In addition, the haplotype frequencies were found to vary among different racial groups. This study has been extended here by increasing the database from 365 to 504, and the data remain consistent with the original findings.

When the age- and race-matched breast cancer case-control population was considered as a whole, Waf-1 was not found to be associated with breast cancer. Interestingly, however, when each racial group was considered separately, the odds of breast cancer for the inheritance of the minor, codon 31, Waf-1 allele (serine) was increased in both Latinas and African-Americans but not Caucasians. Although differences seen for Waf-1 were not significant and are likely attributable to small numbers, when the study group is broken down by race, they are provocative.

For p53, the data are consistent with the original findings and those from independent studies (10, 11, 13). Inheritance of the p53 haplotype appears to be a breast cancer risk factor for Caucasian women and stronger in postmenopausal breast cancer (OR, 2.67; 95% CI = 1.35–5.28) than premenopausal breast cancer (OR, 1.09; 95% CI = 0.42–2.84). However, these data must be treated with caution, because the sample size is small and the CI for postmenopausal women are inclusive of that for premenopausal women.

Logistic regression was additionally used to seek interactions between the p53 and Waf-1 polymorphisms. No gene-gene interaction was found. Taking the implication of the p53 haplotype in Caucasian breast cancer and the trend toward inheritance of the Waf-1p53 haplotype in Latina and African-American breast cancers together, these data still suggest that this point in the pathway to the G1-restriction point is critical in breast cancer irrespective of race.

Furthermore, significant variation in Waf-1 allele frequency between racial groups was observed, where the minor allele frequencies for Caucasians, African-Americans, and Latinas were 0.10, 0.27, and 0.24, respectively. This finding is

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**Table 2** Regression analysis for Waf-1–p53 interaction for risk of breast cancer

Results of logistic regression model to evaluate potential associations between Waf-1 and p53 polymorphisms, race, menopause, and breast cancer risk. The likelihood ratio test was used to test each main effect term individually. Two-interactions for each pair of significant main effects were tested. All significant main effects and interactions were considered in a multivariable model to generate the ORs.

<table>
<thead>
<tr>
<th>Population (n)</th>
<th>Inherited putative “at risk” alleles</th>
<th>Waf-1</th>
<th>p53</th>
<th>Waf-1 + p53</th>
</tr>
</thead>
<tbody>
<tr>
<td>None</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Caucasians (280)</td>
<td>1.52 (0.48–3.90)</td>
<td>1.10</td>
<td>(0.35–3.50)</td>
<td>3.15 (1.14–8.89)</td>
</tr>
<tr>
<td>African-Americans (102)</td>
<td>1.0</td>
<td>2.32</td>
<td>(0.66–5.60)</td>
<td>1.29 (0.54–3.10)</td>
</tr>
<tr>
<td>Latinas (105)</td>
<td>1.86 (0.63–5.47)</td>
<td>2.22</td>
<td>(0.71–6.89)</td>
<td>0.52 (0.12–2.16)</td>
</tr>
</tbody>
</table>
consistent with literature reports for the frequency of this Waf-1 polymorphism (5, 17). Thus, any attempt to base power calculations on the data presented in this report needs to consider each racial group separately.

A previous study has linked the Waf-1, codon 31 polymorphism with phenotypic expression of the gene (7). In that study, frozen tissues were obtained from a Caucasian tumor bank, and the minor allele was associated with increased expression in endometrial cancer but not breast or ovarian cancer. However, the Waf-1 genotypic distribution was similar to that observed here (7).

Studies of some other cancers have noted associations between the Waf-1, codon 31 polymorphism and cancer risk. These include prostate and cervical adenocarcinomas, cancers of the head and neck, and some lung cancers (5, 8, 22, 23). Although, Waf-1 expression may be linked with prognosis in breast cancer and possibly progression in endometrial cancer, the codon 31 polymorphism has not been associated previously with risk of breast or ovarian cancers (7, 8, 19, 22, 23).

For p53, there are eight studies of the codon 72 polymorphism in breast cancer; however, none of them make strong suggestions, and we also thank Dr. Douglas P. Landsittel for assistance with statistical analysis.

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We thank Drs. Dan S. Sharp and Val Vallathyan for insightful comments and suggestions, and we also thank Dr. Douglas P. Landsittel for assistance with statistical analysis.

References

Correction

Polymorphisms in Breast Cancer

In the article on polymorphisms in breast cancer in the January 2002 issue of *Cancer Epidemiology, Biomarkers & Prevention* (1), the authors mistakenly, but consistently, referred to the serine allele (S) of *Waf-1* as the minor allele when in fact the minor allele is arginine (R) and the major allele is serine. This error appears in the Abstract (line 11), Introduction (last paragraph), Results (lines 1 and 8), and Discussion (paragraph 4, line 6). In addition, the headings to Table 1 are similarly incorrectly labeled. Because the authors stated hypotheses and analyzed data based on the “minor” allele frequencies, this error does not affect the Conclusions.

Reference

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