Polymorphisms in the DNA Repair Gene XPD: Correlations with Risk and Age at Onset of Basal Cell Carcinoma

Marianne Dybdahl, Ulla Vogel, Gerda Frentz
Håkan Wallin, and Bjorn A. Nexo
National Institute of Occupational Health, DK-2100 Copenhagen, Denmark [M. D., U. V., H. W., B. A. N.], and Institute of Preventive Medicine, Kommunehospitalet, DK-1399 Copenhagen, Denmark [G. F.]

Abstract

The XPD protein has a dual function, both in nucleotide excision repair and in basal transcription. We have studied the role of two nucleotide substitutions in the XPD gene, one in exon 23 leading to an amino acid substitution (Lys751Gln) and one silent in exon 6 in relation to basal cell carcinoma (BCC). Both are two-allele polymorphisms, with the nucleobases A and C at the given positions. We genotyped psoriasis patients with and without BCC and nonpsoriatic persons with and without BCC (4 × 20 persons). The choice to study psoriasis patients was motivated by their high genotoxic exposure via treatment and their high relative rate of early BCC. Subjects carrying two A alleles (AA genotype) in exon 23 were at 4.3-fold higher risk of BCC than subjects with two C alleles (95% CI, 0.79–23.57). In addition, the mean age at first skin tumor for BCC cases with the AA genotype was significantly lower than the mean age for BCC cases with the AC or CC genotype (P = 0.012). Thus, the variant C-allele of exon 23 may be protective. The exon 6 genotype was associated with the risk of BCC among the psoriasis patients; psoriasis patients carrying two A alleles in exon 6 were at 5.3-fold higher risk of BCC than psoriasis patients with two C alleles (95% CI, 0.78–36.31). For the psoriatics, the mean age at onset of BCC for cases with the AA genotype was marginally lower than the mean age for cases with genotype AC or CC (P = 0.060). Our results raise the possibility that the polymorphisms in the XPD gene may be contributing factors in the risk of BCC development. They are, therefore, important candidates for future studies in susceptibility to cancer.

Introduction

A complex system of DNA repair enzymes has a vital role in protecting the genome of the cell from carcinogenic exposure. A considerable interindividual variation in DNA repair capacity has been observed in the general population, and it has been reported that individuals with a nucleotide excision repair capacity below the population mean are at increased risk of developing skin and lung cancer (1, 2). Like many other phenotypical traits, the variation in DNA repair capacity is probably genetically determined. Given the known association between DNA repair capacity and cancer (most clearly demonstrated by xeroderma pigmentosum patients that are defective in genes in the nucleotide excision pathway and have a 1000-fold increased risk of getting BCC4; Ref. 3), sequence variation of DNA repair genes has the potential to be cancer risk factors in the population.

The XPD gene encodes a helicase involved in the nucleotide excision repair pathway (4). In addition to repair, the XPD gene also has a function in basal transcription. Because XPD has been found to be a subunit of the transcription factor IIH required for all transcription by the RNA polymerase II, it is an essential gene (5). Consistent with this, it has recently been reported that inactivation of the XPD gene in mice leads to embryonic lethality in the preimplantation stage (6).

In a previous report, five different two-allele polymorphisms were found in the coding sequence of the XPD gene (7); and in a more recent study, several two-allele polymorphisms in five different DNA repair genes were reported (8). The variant alleles existed at frequencies ranging from 0.04 to 0.45 in a group of 12 healthy individuals. These DNA repair gene variations remain to be studied in cohorts of cancer cases and their controls in which the finding of a higher incidence of a certain allele in cancer patients than in healthy individuals could suggest that this allele is a contributing factor in an individual’s risk of cancer.

Psoriasis patients are via their treatment exposed to a variety of genotoxic agents, including coal tar, psoralen, and methotrexate. Presumably as a consequence of the treatment psoriasis patients are at increased risk of getting BCC (9). The risk is particularly increased among young psoriasis patients (relative risk 12; age group, 30–39 years). Young psoriasis patients, therefore, offer an attractive study group for an attempt to elucidate the role of protective mechanisms, i.e., DNA repair, in relation to cancer.

In the present study, we analyzed two known XPD polymorphisms: one silent nucleotide substitution and one amino

4 The abbreviations used are: BCC, basal cell carcinoma; OR, odds ratio; CI, confidence interval.
acid substitution (7, 8) in relation to BCC in psoriasis patients and apparently normal individuals (3). Because both polymorphisms alter a restriction site, we developed two PCR/RFLP based assays. We performed genotyping of psoriasis patients with and without BCC and nonpsoriatic persons with and without BCC (4 × 20 persons). For both polymorphisms, we found that the distribution of the genotypes differed between cases and controls, and that the genotype was associated with the age at which the skin cancer patients had their first tumor and possibly the risk of BCC.

Materials and Methods

Study Subjects. Four groups, each consisting of 20 persons, participated in the study (Table 1). Group 1 included persons with a diagnosis of both psoriasis and BCC, group 2 included persons with diagnosed psoriasis, group 3 included persons with a diagnosis of BCC, and group 4 included healthy persons.

All BCC subjects were identified from a population-based cohort of persons treated by Danish dermatologists in the year 1995. The index group consisted of those with both BCC and psoriasis who fulfilled these criteria: (a) age in 1995 < 50 years; and (b) clinically verified diagnosis of psoriasis. The diagnosis of BCC was clinically and histologically confirmed. The other study groups were matched to the index group by age and sex. The group of psoriasis patients without BCC was selected from among patients treated in the years 1992–1995 for psoriasis by dermatologists who participated in the national cohort study 1995. The group of control subjects was recruited from the participating institutes from among personnel and relatives. All of the control subjects were genetically independent. Persons who had received psoriatic treatments (i.e., UV-radiation, psoralen and UV-A light, bucky rays, coal tar, and oral methotrexate) during the last 3 months before blood collection were excluded. The 40 patients with BCC differed from the average patient in the national cohort with BCC in that the ratio of male:female was 1:3 against 6:5 in the cohort, and the average age at first BCC was 38.3 years (± 5.7) against 56.5 years (± 14.0) in the cohort. Subjects completed an extensive questionnaire on risk factors for skin cancer and provided a blood sample. All of the study persons were Caucasians; the majority was blue- or gray-eyed. Fair skin was more frequent in group 3 (14 persons) than in the other groups (4–8 persons). There was a tendency that persons in group 1 had been treated for psoriasis for a longer time than those of group 2, and also that the treatments were more intense.

All of the subjects gave written informed consent. The study was conducted in accordance with the Helsinki declaration and was approved by the local medical ethical committee.

DNA Extraction and PCR Analysis. Genomic DNA was extracted from 3–5 × 10⁶ granulocytes obtained from a blood specimen. The DNA was extracted with the Puregene DNA Isolation Kit (Gentra Systems, Minneapolis, MN).

The PCR primers were synthesized by TAG-Copenhagen Aps (Copenhagen, Denmark). The polymorphic site in exon 6 was amplified using forward primer 5’-TGG AGT GCT ATG GCA GGA TCT CTG-3’ and reverse primer 5’-CCA TGG GCA TCA AAT TCC TGG GA-3’. The polymorphic site in exon 23 was amplified using forward primer 5’-ATC CTG TCC CTG TCC GTG GCC ATT C-3’ and reverse primer 5’-TGT GGA CGT GAC AGT GAG AAA T-3’. The PCR reactions were initially optimized using the PCR Optimization Kit (Boehringer-Mannheim, Mannheim, Germany).

The PCR reactions were performed in a 25-μl reaction volume containing: 20 mM Tris-HCl, 50 mM KCl (pH 8.4), 1.0 mM MgCl₂, 0.2 mM each deoxynucleotide triphosphate, 1.0 μM each primer, 0.5 units of Taq DNA polymerase (Life Technologies, Denmark), and 50–200 ng of genomic DNA. The cycling conditions were: initial denaturation at 96°C for 1 min, 30 cycles of denaturation at 94°C for 30 s, primer annealing at 60°C for 30 s, primer extension at 72°C for 1 min, and finally an extension at 72°C for 2 min.

Restriction Enzyme Analysis. For both polymorphisms, only two alternative nucleotides (A and C) have been identified by DNA sequencing (7, 8); therefore, in the following, we will only consider A and C as possible allele types.

Exon 6. PCR product (10 μl) was digested with 3 units of TfiI enzyme (New England Biolabs, Beverly, MA) in a 20-μl reaction mixture, as suggested by the manufacturer, for 1.5 h and separated on a 2.0% agarose gel. The A but not the C allele in exon 6 has a TfiI restriction site within the 652-bp amplified PCR product. In addition, there is a second TfiI restriction site within the amplified fragment that serves as an internal control for digestion. The three possible genotypes are defined by three distinct banding patterns: CC (56-, 596-, and 596-bp fragments), CA (56-, 114-, 482-, and 596-bp fragments), and AA (56-, 114-, and 482-bp fragments).

Exon 23. PCR product (5 μl) was digested with 15 units of Psrl enzyme (Life Technologies) in a 20-μl reaction mixture as suggested by the manufacturer for 1 h and separated on a 2.0% agarose gel. The A but not the C allele in exon 23 has a Psrl restriction site within the 324-bp amplification product. In addition, there is a second Psrl restriction site within the amplified fragment that serves as an internal control for digestion. The three possible genotypes are defined by three distinct banding patterns: AA (100- and 224-bp fragments), AC (66-, 100-, 158-, and 224-bp fragments), and CC (66-, 100-, and 158-bp fragments).

Host Cell Reactivation Assay. The assay was performed basically as described by Athas et al. (10). Briefly, the assay measures the ability of host lymphocytes to repair a UV-damaged reporter gene inserted into a plasmid DNA that is transfected into the lymphocytes.

Statistical Methods. The ORs and 95% CIs were calculated to assess the relationship between each polymorphism and BCC. The χ² test was used to compare the distribution of the genotypes between BCC cases and controls. A one-sided heteroscedastic t test was used to compare the ages of first BCC between the genotypes. For both polymorphisms, the mean age of having two A alleles (AA) was compared with the mean age of having one C allele (AC), and to the mean age of having one or two C alleles (AC and CC).

Results

We have performed a study of BCC in relation to XPD gene polymorphisms using PCR/RFLP based assays in psoriasis patients with and without BCC and nonpsoriatic persons with and without BCC (4 × 20 persons). Table 1 summarizes the

---

**Table 1** Distribution of age and sex in the study groups

<table>
<thead>
<tr>
<th>Group</th>
<th>n</th>
<th>Age (years)</th>
<th>Males</th>
<th>Females</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 (BCC + psoriasis)</td>
<td>20</td>
<td>47.1 ± 4.0</td>
<td>5</td>
<td>15</td>
</tr>
<tr>
<td>2 (psoriasis)</td>
<td>20</td>
<td>46.9 ± 3.8</td>
<td>5</td>
<td>15</td>
</tr>
<tr>
<td>3 (BCC)</td>
<td>20</td>
<td>46.8 ± 3.5</td>
<td>5</td>
<td>15</td>
</tr>
<tr>
<td>4 (control)</td>
<td>20</td>
<td>46.1 ± 3.6</td>
<td>5</td>
<td>15</td>
</tr>
</tbody>
</table>

* Mean ± SD.
distribution of age and sex for the study persons. We analyzed two polymorphisms: one amino acid substitution and one silent nucleotide substitution; the distribution of the genotypes in the study groups is shown in Table 2.

**Exon 23.** The $A\rightarrow C$ polymorphism in exon 23 at nucleotide position 35931 gives rise to the amino acid substitution Lys$\rightarrow$Gln. In our study population, the variant allele C had an average frequency of 0.32, which agrees with a previous study (7). The distribution of genotype by case-control status was comparable between psoriasis and nonpsoriasis patients (Table 2). Among all of the BCC cases, 95% carried at least one A allele, and 53% were homozygotes (genotype AA). Among all of the controls, 83% carried at least one A allele, and 43% were AA. The association between exon 23 genotype and risk of BCC is shown in Table 3, and all ORs are calculated relative to subjects with the AA genotype. Subjects with the AA or AC genotypes were at higher risk of skin cancer; the ORs were 5.3 (95% CI, 0.78–36.31) and 3.3 (95% CI, 0.66–16.03), respectively.

We also found an association between the exon 23 genotype and the age at which the BCC cases had their first skin tumor (Fig. 1). The mean ages at first cancer for the genotypes AA, AC, and CC were 39, 43, and 42 years, respectively, indicating that subjects with two A alleles may have a higher risk of early BCC than subjects with one or two C alleles. The mean age at first tumor for cases with the AA genotype was significantly lower than the mean age for the AC and CC genotypes combined ($P = 0.012$). Comparing the mean ages for the AA and AC genotypes gave a similar result. The small number of cases with the CC genotype ($n = 3$) limits the ability to compare the AA or AC genotype with the CC genotype.

**Exon 6.** The $A\rightarrow C$ polymorphism in exon 6 at nucleotide position 22541 does not result in an amino acid change. The average frequency of the variant allele A in exon 6 was 0.48 in this study population, which is in agreement with a previous report (7). Among only the psoriasis patients did we observe a difference in the distribution of genotypes between the cases and controls (Table 2). Among psoriasis patients with BCC, 85% carried at least one A allele and 30% were homozygotes (AA). Among psoriasis patients without BCC, 60% carried at least one A allele and only 15% were AA. The association between exon 6 genotype and risk of BCC is shown in Table 3, and the ORs are calculated relative to subjects with the CC genotype. Subjects with the AA or AC genotype were at higher risk of skin cancer; the ORs were 5.3 (95% CI, 0.78–36.31) and 3.3 (95% CI, 0.66–16.03), respectively.

The association between the genotype of exon 6 and the age at onset of skin cancer was seen only in psoriasis patients and is presented in Fig. 2. For the psoriasis patients, the mean ages at first tumor for the genotypes AA, AC, and CC were 39, 43, and 42 years, respectively, indicating that subjects with two A alleles may have a higher risk of early BCC than subjects with one or two C alleles. The mean age at first cancer for cases with the AA genotype was marginally lower than the mean age for cases with the AC and CC genotypes combined ($P = 0.060$). Comparing the mean ages for the AA and AC genotypes gave a similar result. The small number of cases with the CC genotype ($n = 3$) precludes statistical significance when comparing the
AA or AC genotype with the CC genotype. For the nonpsoriasi- 
atics, the mean ages at first tumor for the genotypes AA, AC, 
and CC were 42, 39, and 41 years, respectively.

The PCR/RFLP assay did not allow us to identify the 
haplotype, but the combinations of the genotypes in exon 6 and 
exon 23 are summarized in Table 4. Interestingly, a person 
being homozygous CC in exon 23 (11%) was always homozy-
gous CC in exon 6, and a person being homozygous AA in exon 
6 (24%) was always homozygous AA in exon 23. There was a 
large proportion of individuals being heterozygous for the nu-
cleotide variations in both exon 6 and exon 23 (28%). These 
data indicate strong linkage disequilibrium in the material and 
would be consistent with an absence of the exon6' exon23' 
haplotype.

Previously we have measured the DNA repair capacity in 
this study population by use of a host cell reactivation assay in 
lymphocytes, but we found no relationship of the DNA repair 
capacity with any of the two polymorphisms studied. In another 
study of the same population, we have reported the level of 
DNA damage by single cell gel electrophoresis (comet-assay) 
and the DNA repair capacity by unscheduled DNA synthesis in 
lymphocytes (11). Neither of these two parameters correlated 
with any of the polymorphisms.

Discussion

Here we report from a study of two polymorphisms in the DNA 
repair gene XPD (7, 8) in relation to a cancer disorder. For both 
polymorphisms, we found that the distribution of genotypes 
differed between the study groups, and that the genotype was 
associated with the age at which the skin cancer patients had 
their first tumor and possibly the risk of BCC.

The frequencies of the A and C alleles in exon 23 were 
0.68 and 0.32, respectively, in our study population. We found 
that the A allele was associated with an increased risk of BCC. 
Forty-eight percent of our population was homozygous AA, and 
they had a more than 4-fold higher risk of BCC than individuals 
being homozygous CC (11%). Also the heterozygotes (geno-
type AC) had a higher risk of BCC that was almost 4-fold 
increased. In addition, we found that BCC cases with the AA 
genotype developed their first tumors at an earlier age than 
cases with the AC or CC genotype. The data suggest that the C 
allele has a protective influence against the cancer.

The A→C variation in exon 23 gives rise to the amino acid 
substitution Lys→Gln, which is a change from a basic to a 
polar amino acid. The nucleotide variation is located about 50 
bases upstream from the poly(A) signal, and could possibly 
 improve the function of the XPD protein.

The nucleotide substitution in exon 6 appears to be very 
common in the population, inasmuch as the frequency of the 
least common allele A in our study was 0.48. Only among the 
psoriasis patients did we find an association of the genotype 
with the risk of BCC. Twenty-three percent of the psoriasis 
patients had the genotype AA in exon 6, and they had a more 
than 5-fold higher risk of BCC than the psoriasis patients with 
the CC genotype (28%). The heterozygotes (genotype AC) had 
a more than 3-fold higher BCC risk. We also observed that the 
psoriasis patients with BCC who carried at least one A allele 
developed their first skin tumor earlier in life than the psoriasis 
patients with BCC carrying two C alleles.

The nucleotide substitution in exon 6 does not change an 
amino acid. It could conceivably affect the stability of the 
mRNA or disturb protein synthesis by converting a high-usage 
codon to a low-usage codon in the 5′ proximal region of the 
gene (12–14). It is, however, important to emphasize that the 
XPD polymorphisms studied need not be directly responsible 
for the differences in cancer risk. Another possible explanation 
is that the polymorphisms may cosegregate with another 
difference in XPD, whose function (or lack of function) contrib-
utes to the development of malignancy. Finally, ERCCI is 
located close to XPD on chromosome region 19q13.2–13.3, 
along with DNA ligase and XRCCI (15, 16), and these genes 
may also cosegregate with the polymorphisms. All of the four 
genes are important elements in repairing DNA damage.

We do not understand why the exon 6 polymorphism 
had an effect only in the psoriasis groups. It is possible, that 
the nucleotide variation in exon 6 has no detectable conse-
quences under ordinary circumstances but only becomes important under excessive genotoxic stress. Psoriasis pa-
sients are via their treatment exposed to a variety of geno-
toxic agents including coal tar, psoralen, and methotrexate, 
and eventually the DNA damage induced by these treatments 
may exceed the capacity of individuals who are homozygous 
for the variant A allele in exon 6.

Interpretation of our data is limited by the lack of knowl-
edge about the functional significance of the polymorphisms on 
the XPD gene. None of the nucleotide variations in XPD are 
located in any known or hypothesized helicase/ATPase do-
 mains (17), which might be expected given that inactivation 
of these domains causes loss of function as well as disease or

---

preimplantation lethality (6, 18). The XPD protein is a subunit of transcription factor TFIIH, which contains at least nine subunits. It is possible, that variations in the XPD subunit may cause minor structural changes that could modulate its interactions with other subunits, thereby modifying the overall transcriptional activity of the complex.

This preliminary study raise the possibility of an association of BCC development with two polymorphisms in the XPD gene, which makes this gene an important candidate for studies in susceptibility to commonly occurring forms of cancer. However, additional studies with larger sample sizes are required to detect the small effects observed. Future case-control studies of these two and other sequence variants identified in the XPD gene (8) and characterization of the functional significance of these variants will help to an understanding of the role of the XPD gene in cancer etiology.

Acknowledgments

We thank Jette Petersen and Dr. Lisbeth E. Knudsen for helping to organize the recruitment of the subjects in the study; Drs. Margrethe Gade, Birgit Albrechtsen, and E.A. Knudsen for help with the examination of the subjects; and Birgitte Korsholm for excellent assistance with the laboratory work.

References

Polymorphisms in the DNA Repair Gene XPD: Correlations with Risk and Age at Onset of Basal Cell Carcinoma

Marianne Dybdahl, Ulla Vogel, Gerda Frentz, et al.

Cancer Epidemiol Biomarkers Prev 1999;8:77-81.

Updated version  Access the most recent version of this article at:
http://cebp.aacrjournals.org/content/8/1/77

Cited articles  This article cites 17 articles, 8 of which you can access for free at:
http://cebp.aacrjournals.org/content/8/1/77.full.html#ref-list-1

Citing articles  This article has been cited by 50 HighWire-hosted articles. Access the articles at:
/content/8/1/77.full.html#related-urls

E-mail alerts  Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions  To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions  To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.