

## RESEARCH COMMUNICATION

## NAD(P)H:quinone oxidoreductase 1 (NQO1) Pro187Ser Polymorphism and Colorectal Cancer Predisposition in the Ethnic Kashmiri Population

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### Abstract

The C609T single nucleotide polymorphism of the NAD(P)H:quinone oxidoreductase 1 (NQO1) gene has been identified as an important risk parameter for the susceptibility to colorectal cancer. We here carried out a case-control study and examined the genotype distribution of NQO1 C609T (Pro189Ser) using the polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) approach, to investigate the possible role of this SNP as a risk factor in colorectal cancer development in Kashmir, India. We investigated the genotype distribution in 86 CRC cases in comparison with 160 healthy subjects and also focused on clinicopathological variables in the CRC cases. The observed genotype frequencies in cases and controls were significantly different [OR=1.64; 95%CI=0.94-2.86]. We also found a significant association between the Ser/Ser variant form with age group, smoking status, tumor location, nodal status/ higher tumor grade and with exposure to pesticides. Therefore, we suggest that the NQO1 C609T SNP is involved either in susceptibility or development of CRC in the ethnic Kashmiri population.

**Key Words:** Colorectal cancer - NQO1 - polymorphism - RFLP, restriction digestion - Kashmir

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### Introduction

Colorectal cancer (CRC) is a major cause of mortality and morbidity worldwide being the third most common malignancy in the world (Center et al., 2009). The incidence of this malignancy shows considerable variation among racially or ethnically defined populations in multiracial/ethnic countries. Kashmir has been reported as a high-incidence area for gastrointestinal cancers (Mir et al., 2005; Murtaza et al., 2006). In Kashmir valley colorectal cancer is the third most common, after esophageal and gastric cancers (Sameer et al., 2009).

In 1955, Lars Ernster and Franco Navazio identified an unusual nicotinamide nucleotide-dependent oxidoreductase in rat liver which they named as diphtheria toxin (DT) diaphorase now known as NAD(P)H:quinone oxidoreductase 1 (NQO1) (Chen et al., 2000). NQO1 is located on chromosome 16q22, is 20 kb in length and has 6 exons and 5 introns. NQO1 is a flavoprotein which functions as a homodimer. The physiological dimer has one catalytic site per monomer. Each monomer consists of 273 amino acids. NQO1 is expressed in human epithelial and endothelial tissues and at high levels throughout many human solid tumors. NQO1 is a mainly cytosolic enzyme although it has also been localized in smaller amounts to mitochondria, endoplasmic reticulum and nucleus (Ross et al., 2004; Chao et al., 2006). The

enzyme is generally considered as a detoxification enzyme because of its ability to reduce reactive quinones and quinone-imines to less reactive and less toxic hydroquinones by its unique ability to use either NADH or NADPH as reducing cofactors (Siegel et al., 2004). Because of its reducing capability NQO1 prevents the generation of semiquinone free radicals and reactive oxygen species with its unique property of transferring two electrons at a time to quinone, thus protecting cells from oxidative damage (Chen et al., 2000; Winski et al., 2002).

As most genes are subject to genetic variation so is NQO1 gene, so far two important single nucleotide polymorphisms have been discovered in this gene. One C>T base transition at position 465 of the NQO1cDNA and other C>T base transition mutation at position 609 (Chen et al., 1999). An inactivating SNP involving a base change from cytosine to thymine at base 609 of the NQO1 gene which replaces proline with serine residue at codon 187 in the encoded protein is the most actively studied one. This SNP occurs at a frequency of 50% in the human population, with 10% being homozygous for T alleles (Begleiter et al., 2006). However, these percentages vary in different ethnic groups, with a frequency rate of 2% to 5% in Caucasians and Blacks, and 20% in Asians (Kelsey et al., 1997). The NQO1 TT (Ser/Ser) form of the NQO1 protein has little or no activity as has been demonstrated

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by various studies on both human cell lines and primary human tissues (Siegel D et al., 1999), while as the cells which have heterozygous alleles i.e., CT (Pro/Ser) has approximately half of the NQO1 enzyme activity (Mitrou et al., 2007; Chao et al., 2006).

A number different clinical studies have been carried out on NQO1 genotype, most of which have shown an increased frequency of the NQO1 TT allele in patients with renal (Schulz et al., 1997), urothelial (Schulz et al., 1997), esophageal (Zhang et al., 2003; Sarbia et al., 2003), bladder (Park et al., 2003), breast (Menze et al., 2004), and gastric (Zhang et al., 2003; Sarbia et al., 2003) cancers and both pediatric (Wiemels et al., 1999; Krajcinovic et al., 2002) and adult leukemias (Smith et al., 2001; Naoe et al., 2000) compared with healthy controls. These findings suggest that the active form of NQO1 may provide protection from some carcinogen-induced cancers. However, a limited studies have been carried out on colorectal cancer, but whatever literature available till date suggest that NQO1 CT heterozygous condition might be a risk factor for the predisposition of malignancy (Chao et al., 2006; Begleiter et al., 2006; Mitrou et al., 2007). A recent meta-analysis suggested a statistically significant association of the NQO1 heterozygous genotype (CT) with a moderately elevated risk of developing colorectal cancer (Chao, 2006); while as the homozygous variant genotype (TT) was not associated with colorectal cancer risk. The risk of sporadic colorectal cancer has been linked to exposure to carcinogenic compounds in food, such as heterocyclic amines in fried meat (Felton et al., 1991). As has been hypothesized previously (Mitron et al., 2007) NQO1 activity might influence the risk of colorectal cancer in individuals exposed to NQO1 metabolising compounds as NQO1 expressed in the intestinal tract plays an important role in detoxifying dietary carcinogenic compounds, and the loss of enzyme activity may increase susceptibility to colorectal cancer (Chao et al., 2006).

Therefore, we carried out a case-control study in our population to determine if this NQO1 polymorphism is associated with an altered risk of developing colorectal cancer as many dietary habits (Sameer et al , 2010, Mir, 2005; Murtaza et al, 2006; Siddiqi, 1992 ) of our population have already been established as risk factors for the development of GIT cancers. We also investigated whether there was a link between these risk factors and the NQO1 genotype and colorectal cancer predisposition.

## Materials and Methods

### Study population

This study included 86 consecutive primary colorectal cancer patients. All CRC patients were recruited from Department of Surgery, Sher-I-Kashmir Institute of Medical Science from March 2008 to August 2009. Tumor types and stages were determined by two experienced pathologists. Blood samples of 160 age and sex matched cases with no signs of any malignancy were collected for controls. The mean age of both patient and control groups was 52 years old, and 56 of patients and 104 of controls were >50 years old or older. See Table 1 for details. Data on all CRC patients were obtained from personal

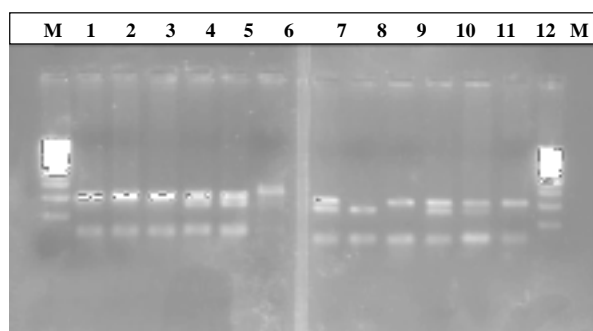
interviews with patients and or guardians, medical records and pathology reports. The data collected included sex, age, dwelling, tumor location, Dukes Stage, lymph node status, pesticide exposure, Bleeding PR. All patients and or guardians were informed about the study and their will to participate in this study was taken on predesigned questionnaire (Available on request). The collection and use of tumor and blood samples for this study were previously approved by the appropriate Institutional Ethics Committee.

### DNA extraction & Polymerase chain reaction-restriction fragment length polymorphism

DNA extraction was performed using any one of the previously described techniques. Previously reported primers: Forward primer 5'-TCC TCA GAG TGG CAT TCT GC-3' and Reverse primer 5'- TCT CCT CAT CCT GTA CCT CT-3' (Park et al., 2003) were used for the amplification of the 230bp target region within the NQO1 gene.

PCR was carried out in a final volume of 25 µL containing 50 ng genomic DNA template, 1X PCR buffer (Biotools) with 2 mM MgCl<sub>2</sub>, 0.4 µM of each primer (Genescript), 50 µM dNTPs (Biotools), and 0.5 U DNA polymerase (Biotools). For PCR amplification, the standard program was used as follows: one initial denaturation step at 94°C for 7 min, followed by 35 denaturation cycles of 30 s at 94°C, 30 s of annealing at 58°C, and 30 s of extension at 72°C, followed by a final elongation cycle at 72°C for 5 min. For RFLP, the PCR product of NQO1 Pro187Ser was digested with HinfI (2 U at 37°C for 16 h) (Fermentas). In case of NQO1 Pro187Ser polymorphism Pro/Pro wild was identified by 191 bp band while Ser/Ser variant was identified by 151 bp band and heterozygous Pro/Ser variant displayed two bands (191 bp and 151bp) (Figure 1).

DNA fragments were electrophoresed through a 2-3% agarose gel for resolution. The genotypes of >20% of the samples were double blindly reassessed to confirm the results by two independent researchers. A positive control for each polymorphism was used for 50% of samples.



**Figure 1. Restriction Fragment Length Polymorphism Analysis of NQO1 Pro187Ser using HinfI Enzyme.**

HinfI enzyme cleaves the Variant (Ser/Ser) resulting in the 151bp band while as Wild (Pro/Pro) is represented by 191bp band. Lane M: 100bp ladder; Lanes 1-3,9 & 12 show Wild (Pro/Pro) form; Lanes 4,5,7,10 & 11 show Heterozygous (Pro/Ser) form; and Lane 8 shows Variant (Ser/Ser) form; Lane 6 shows uncleaved amplicon

**Table 1. Frequency Distribution Analysis of Selected Demographic and Risk Factors in Colorectal Cancer Cases and Controls**

Variable	Cases (n=86)	Controls (n=160)	P Value
Age group	≤50	30 (34.9%)	1
	>50	56 (65.1%)	
Gender	Female	37 (43.0%)	0.764
	Male	49 (67.0%)	
Dwelling	Rural	59 (68.6%)	0.565
	Urban	27 (31.4%)	
Smoking status	Never	31 (36.0%)	0.102
	Ever	55 (64.0%)	
Pesticide exposure	Never	33 (38.4%)	0.200
	Ever	53 (61.6%)	

**Table 2. NQO1 Genotype Frequencies in Cases & Controls and Associations with CRC Risk**

TP53 Codon 72 Genotype	Cases (n= 86)	Controls (n=160)	OR (95% CI)
Pro/Pro	53 (61.6%)	116 (72.5%)	1.00 (Ref)
Pro/Ser	29 (33.7%)	39 (24.4%)	1.62 (0.91-2.91)
Ser/Ser	4 (4.6%)	5 (3.1%)	1.75 (0.45-6.78)
Pro/Ser+Ser/Ser	33 (38.4%)	44 (27.5%)	1.64 (0.94-2.86)

#### Statistical analysis

Observed frequencies of genotypes in CRC were compared to con-trols using chi-square or Fisher exact tests when expected frequencies were small. The chi-square test was used to verify whether genotype distributions were in Hardy-Weinberg equilibrium. Statistical significance was set at  $P < 0.05$ . Statistical analyses were performed with PASW version 18 Software.

## Results

A total of 86 colorectal cancer patients and 160 control subjects were included in this study. The patients comprised 49 males and 37 females (M/F ratio = 1.32) and the control subjects consisted of 88 males and 72 females (M/F ratio = 1.2). Mean age in patient and control groups was 52 years. No significant gender- or age-related differences were observed between the groups ( $P > 0.05$ ). Further more, out of 86 confirmed cases of CRC, 81 cases were sporadic, 4 were FAP and one case was HNPCC. All but one case were adenocarcinoma and only one was squamous cell carcinoma (SCC) of basal cell type, 59 rural and 27 urban, 36 cases had carcinoma in colon and 50 in rectum and 55 were smokers and 31 non smokers. See Table 1 & Table 2 for further details.

The genotype distribution of C609T SNP of the NQO1 in the healthy control population was similar to a previous report (Beglieter et al., 2006). However, we observed an decreased incidence of NQO1 Pro/Pro but increased incidence of the NQO1 Ser/Ser genotype in patients with colorectal cancer compared with healthy controls [Table 2]. The overall hazard ration of the NQO1 Ser allele in patients with colorectal patients was 1.62 (95% CI = 0.94-2.86) and it was found statistically significant ( $p < 0.05$ ). Overall, both heterozygous CT genotype (Pro/Ser) and the homozygous variant TT genotype (Ser/Ser) was associated with a modestly elevated risk for colorectal

**Table 3. Association between the NQO1 Gene Polymorphism and Clinico-pathologic Characteristics in Cases (n=86)**

Variables	Group I	Group II	OR (95% CI)
Age group	≤50=30 (34.9%)	>50=56 (65.1%)	
Pro/Pro	13	40	1 (Ref)
Pro/Ser	14	15	2.87 (1.09- 7.50)
Ser/Ser	3	1	9.23 (0.88- 96.6)
Pro/Ser+Ser/Ser	17	16	3.27 (1.29- 8.25)
Gender	Male=49 (67.0%)	Female=37 (43.0%)	
Pro/Pro	28	25	1 (Ref)
Pro/Ser	11	18	0.54 (0.22-1.37)
Ser/Ser	1	3	0.29 (0.02-3.04)
Pro/Ser+Ser/Ser	12	21	0.51 (0.21-1.24)
Dwelling	Rural = 59 (68.6%)	Urban = 27 (31.4%)	
Pro/Pro	40	13	1 (Ref)
Pro/Ser	17	12	0.46 (0.17-1.21)
Ser/Ser	2	2	0.32 (0.04-2.54)
Pro/Ser+Ser/Ser	19	14	0.44 (0.17-1.11)
Smoking status	Never = 31 (36.0%)	Ever = 55 (64.0%)	
Pro/Pro	29	24	1 (Ref)
Pro/Ser	1	28	0.03 (0.00- 0.23)
Ser/Ser	1	3	0.28 (0.03- 2.82)
Pro/Ser+Ser/Ser	2	31	0.05 (0.01- 0.25)
Tumor location	Colon = 36 (41.9%)	Rectum = 50 (58.1%)	
Pro/Pro	28	25	1 (Ref)
Pro/Ser	5	24	0.18 (0.06- 0.56)
Ser/Ser	3	1	2.67 (0.26- 27.4)
Pro/Ser+Ser/Ser	8	25	0.28 (0.10- 0.74)
Nodal status	Involved = 48 (55.8%)	Not = 38 (44.2%)	
Pro/Pro	36	17	1 (Ref)
Pro/Ser	9	20	0.21 (0.08- 0.56)
Ser/Ser	3	1	1.42 (0.14- 14.6)
Pro/Ser+Ser/Ser	12	21	0.27 (0.11-0.67)
Tumor grade	A+B = 38 (44.2%)	C+D = 48 (55.8%)	
Pro/Pro	17	36	1 (Ref)
Pro/Ser	20	9	4.70 (1.77-12.5)
Ser/Ser	1	3	0.70 (0.07- 7.29)
Pro/Ser+Ser/Ser	21	12	3.70 (1.48- 9.24)
Pesticide Exposure	Never = 33 (38.4%)	Ever = 53 (61.6%)	
Pro/Pro	14	39	1 (Ref)
Pro/Ser	17	12	3.95 (3.94-10.3)
Ser/Ser	2	2	2.78 (0.36- 21.7)
Pro/Ser +Ser/Ser	19	14	3.78 (1.50- 9.50)
Bleeding PR/Constipation	Yes = 60 (69.8%)	No = 26 (30.2%)	
Pro/Pro	35	18	1 (Ref)
Pro/Ser	22	7	1.62 (0.58-4.49)
Ser/Ser	3	1	1.54 (0.15-15.9)
Pro/Ser+Ser/Ser	25	8	1.61 (0.60-4.27)
Tumor type*	Mucinous=33 (38.5%)	Non= 52 (60.5%)	
Pro/Pro	20	33	1 (Ref)
Pro/Ser	12	16	1.24 (0.49-3.14)
Ser/Ser	1	3	0.55 (0.05-5.65)
Pro/Ser+ Ser/Ser	13	19	1.13 (0.46-2.77)
p53 status	Wild-type = 42 (48.8%)	Mutated = 44 (51.2%)	
Pro/Pro	29	24	1 (Ref)
Pro/Ser	11	18	0.51 (0.20-1.27)
Ser/Ser	2	2	0.83 (0.11-6.32)
Pro/Ser + Ser/Ser	13	20	0.54 (0.22-1.30)

\*One was SCC

cancer {OR = 1.62; 95% CI = 0.91-2.91) and OR = 1.75; 95% CI = 0.45-6.78 respectively}.

The correlation of NQO1 C609T polymorphic status and the clinicopathologic characteristics was carefully analyzed. It was found that the Ser/Ser variant status was

significantly related to the age group, smoking status, tumor location, nodal status/ higher tumor grade and with exposure to pesticides, but not with other variables (Table 3).

## Discussion

Although most polymorphisms are functionally neutral, some affect regulation of gene expression or the function of the coded protein (Costa et al., 2008). But Considering the potential role of NQO1 in modulating various diet and tobacco smoke-related compounds, we assessed the one most common SNP of NQO1 C609T (Pro187Ser) in an ethnic Kashmiri population for the first time since the role of NQO1 polymorphism in relation to colorectal cancer risk has not been reported from this part of the world.

As reported previously in various studies on Kashmiri population (Mir et al., 2005; Sameer et al., 2009 & 2010), it has been proven beyond doubt that our population is exposed to a special set of environmental and dietary risks which include consumption of sun-dried and smoked fish and meat, dried and pickled vegetables, red chilly, Hakh (a leafy vegetable of Brassica family), hot noon chai (salted tea) and Hukka (water pipe) smoke. As previously reported, the etiology and incidence of various GIT cancers in this population has been attributed to a probable exposure to nitroso compounds, amines and nitrates reported to be present in these local food stuffs most of which have been shown to contain important irritant and carcinogens (Siddiqi et al., 1992; Murtaza et al., 2006).

As has been reported previously by two studies on a rat model of colon carcinogenesis, the presence of an NQO1 inactivating polymorphism may represent a genetic factor that predisposes individuals to colorectal cancer (Begleiter et al., 2003; Sivananthan et al., 2005). In this study we analysed 86 colorectal cancer patients in relation to 160 healthy controls in order to examine the role of the C609T SNP in the NQO1 gene in the development of colorectal cancer in Kashmiri population. Cancer patients and healthy control subjects were well-matched for age, gender, ethnic distribution, and tobacco. We found a 1.62-fold greater incidence of the NQO1 CT genotype and 1.75-fold greater incidence of the NQO1 TT genotype in patients with colorectal cancer and compared with the healthy control population (Table 2). This finding is in agreement with several previous studies of the role of the NQO1 base 609 polymorphism in colon cancer risk (Lafuente et al., 2000; Hou et al., 2005; Begleiter et al., 2006; Chao et al., 2006; van der Logt et al., 2006).

We also found a relation between the increased incidence of NQO1 TT genotype and smoking status of the colorectal patients. This relation was in tune with the previous studies (Hou et al., 2005; Begleiter et al., 2006) where smoking status have been found to be an important risk factor for modulating the role of NQO1 enzymatic activity for predisposition of colorectal cancer. NQO1 protects cells from carcinogens in cigarette smoke by direct scavenging of quinone substrates and inhibiting the formation of CYP1A1-generated metabolites and subsequent binding to DNA (Joseph et al., 1994). NQO1

Ser187 allele has been linked to decreased NQO1 enzyme activity (Parkinson et al., 2003; Siegel et al., 2004). Thus, the presence of variant NQO1 leads to decreased detoxification ability which in turn may result in greater doses in smokers of B[a]P reactive metabolites at the cellular level, yielding increased risks for associated diseases which serve as the platform for the development of malignancy (Hou et al., 2005).

In addition to the already reported clinic-pathological risk factors, we also found a significant association of the NQO1 Ser allele with age group, smoking status, tumor location, nodal status/ higher tumor grade and with exposure to pesticides, identifying all of them as the potential risk factors for colorectal cancer.

Hence, in this study which has been carried for the first time in the Kashmir valley, we observed a significant correlation between the Ser/Ser variant NQO1 status with various clinicopathological variables in this ethnic Kashmiri population. Although these correlation need to be authenticated in large sample study in future, so as to help in better discernment of racial differences and in determining aggressiveness of colorectal cancer.

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