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Original Research

Analysis of rs25487 (Arg399Gln) in *XRCC1* in Sudanese Diagnosed with Nasopharyngeal Carcinoma and Its Possible Risk Factors

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Abstract

Nasopharyngeal carcinoma (NPC) is a multifactorial malignancy influenced by genetic susceptibility and environmental exposures. The *XRCC1* Arg399Gln (rs25487) polymorphism has been associated with NPC risk in several populations; however, evidence from African populations remains scarce. This study investigated the association between the *XRCC1* Arg399Gln polymorphism and NPC susceptibility in a Sudanese population. A case-control study was conducted including 71 patients with histopathologically confirmed NPC and 71 cancer-free controls recruited through the Upper Aerodigestive Tract Biobank. Genomic DNA was extracted from peripheral blood samples, and the *XRCC1* Arg399Gln polymorphism was genotyped using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP). Associations between genotype distributions, genetic models, and NPC risk were evaluated using crude odds ratios (ORs) with 95% confidence intervals (CIs). Environmental exposures, including cigarette smoking, alcohol consumption, and intake of salted fish "*Kajeek*" , were also compared between cases and controls. Genotype frequencies did not differ significantly between cases and controls. Compared with the Arg/Arg genotype, neither the Arg/Gln genotype (OR = 0.73, 95% CI: 0.34-1.54; *P* = 0.400) nor the Gln/Gln genotype (OR = 0.63, 95% CI: 0.21-1.91; *P* = 0.410) was associated with NPC susceptibility.

No significant associations were observed under dominant, recessive, or allelic genetic models. Cigarette smoking and alcohol consumption were not associated with NPC risk, while salted fish intake showed a borderline association (OR = 2.28, 95% CI: 0.99-5.23; *P* = 0.055). The study had approximately 80% power to detect an odds ratio of 2.6 or greater. No significant association was observed between the *XRCC1* Arg399Gln polymorphism and NPC susceptibility in this Sudanese population. Although limited by sample size, this study provides the first data on the distribution of the *XRCC1* Arg399Gln polymorphism among Sudanese patients with NPC. It contributes valuable baseline evidence from an understudied African population.

Keywords
Nasopharyngeal carcinoma; *XRCC1*; Arg399Gln polymorphism; DNA base excision repair; genetic susceptibility; case-control study; salted fish "*Kajeek*" consumption; African population

1. Introduction

Nasopharyngeal carcinoma (NPC) is a relatively uncommon malignancy worldwide; however, its incidence varies markedly across geographic regions and ethnic groups, with the highest burden observed in Southern China, Southeast Asia, and parts of North Africa [1]. NPC is a multifactorial disease resulting from complex interactions among genetic susceptibility, environmental exposures, and viral infection, particularly Epstein-Barr virus (EBV). Environmental risk factors, including cigarette smoking, alcohol consumption, preserved foods rich in nitrosamines, , and salted fish intake, have been implicated in NPC development, although their relative contributions vary among populations [2-12].

The X-ray repair cross-complementing group 1 (*XRCC1*) gene encodes a scaffold protein that plays a central role in the base excision repair (BER) pathway, which repairs DNA damage induced by oxidative stress, ionizing radiation, and chemical carcinogens. Functional polymorphisms within *XRCC1* may alter DNA repair efficiency and thereby influence individual susceptibility to cancer. Among these polymorphisms, Arg399Gln (rs25487), caused by a guanine-to-adenine substitution in exon 10, has been the most extensively investigated in molecular epidemiological studies.

Numerous case-control studies and several meta-analyses have examined the association between the *XRCC1* Arg399Gln polymorphism and NPC susceptibility. Although many studies, particularly those conducted in East and Southeast Asian populations, have reported an increased NPC risk associated with the Gln allele, findings remain inconsistent across different ethnic groups [13-17]. These discrepancies may reflect differences in genetic background, allele frequencies, environmental exposures, study design, and sample size. Consequently, replication studies in previously uninvestigated populations are important for assessing the consistency and generalizability of reported genetic associations across diverse ethnic groups.

Despite the relatively higher incidence of NPC in parts of North Africa, data on genetic susceptibility to NPC in African populations remain scarce. To the best of our knowledge, no previous study has investigated the association between the *XRCC1* Arg399Gln (rs25487)

polymorphism and NPC susceptibility in the Sudanese population. Establishing baseline genetic epidemiological data in understudied populations is important for improving our understanding of population-specific genetic variation. It may contribute valuable evidence for future pooled analyses involving African populations.

Therefore, the present study investigated the association between the *XRCC1* Arg399Gln (rs25487) polymorphism and susceptibility to nasopharyngeal carcinoma in a Sudanese population and described the distribution of selected environmental exposures, including cigarette smoking, alcohol consumption, and intake of salted fish, known in Sudan as "*Kajeek*", among cases and controls.

2. Materials and Methods

2.1 Study Population and Sample Collection

This case-control study included 71 patients with histopathologically confirmed nasopharyngeal carcinoma (NPC) and 71 cancer-free controls recruited through the Upper Aerodigestive Tract Biobank. Peripheral blood samples and epidemiological data were obtained from the biobank following informed consent and approval by the appropriate institutional ethics committee.

Demographic characteristics and information on environmental exposures were collected at recruitment using a standardized interviewer-administered questionnaire maintained by the biobank. Information collected included age, sex, cigarette smoking, alcohol consumption, and the intake of salted fish "*Kajeek*".

Participants were classified as smokers if they reported current or previous regular cigarette smoking. Alcohol consumers were defined as participants reporting current or previous alcohol consumption. Salted fish consumption was recorded as a binary variable (yes/no) based on participants' habitual consumption.

2.2 DNA Extraction

Genomic DNA was extracted from peripheral blood samples using the innuPREP Blood DNA Mini Kit (Analytik Jena AG, Germany) according to the manufacturer's instructions. DNA concentration and purity were assessed before PCR amplification.

2.3 Genotyping of the XRCC1 Arg399Gln Polymorphism

The *XRCC1* Arg399Gln (rs25487) polymorphism was genotyped using the polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) technique. Primer sequences were designed using Primer3 software and verified using the NCBI BLAST database. The primer sequences were: Forward: 5′-GGACTGTCACCGCATGCGTCGG-3′, Reverse: 5′-GGCTGGGACCACCTGTGTT-3′. These primers amplified a 149 bp fragment containing the rs25487 polymorphic site.

PCR amplification was carried out in a final reaction volume of 20 µL containing 5 µL genomic DNA, 1 µL of each primer, and 13 µL nuclease-free water using the Maxime PCR PreMix Kit (iNtRON Biotechnology, Republic of Korea), which contains i-Taq™ DNA polymerase, dNTPs, reaction buffer, and gel loading dye. Amplification was performed using a FlexCycler thermal cycler (Analytik Jena, Germany) with the following cycling conditions: initial denaturation at 94°C

for 4 minutes, followed by 35 cycles of denaturation at 94°C for 40 seconds, annealing at 55°C for 30 seconds, extension at 72°C for 30 seconds, and a final extension at 72°C for 10 minutes. PCR products were digested overnight at 37°C with MspI (5 U/µL; Vivantis, Malaysia). Digested fragments were separated by electrophoresis on a 3% agarose gel prepared in 1× TBE buffer. Fifteen microliters of each digestion product together with 5 µL of a 100 bp DNA ladder were loaded into each well and electrophoresed at 100 V for approximately 1 hour. DNA fragments were visualized under ultraviolet illumination using a gel documentation system and recorded using Essential UVPro1 software.

The Arg allele contains an MspI restriction site and generates fragments of 115 bp and 34 bp, whereas the Gln allele lacks the restriction site and remains as an undigested 149 bp fragment. Consequently, the Arg/Arg, Arg/Gln, and Gln/Gln genotypes were identified by fragment patterns of 115/34 bp, 149/115/34 bp, and 149 bp, respectively. Because the 34 bp fragment is very small, it was not consistently resolved on the 3% agarose gel, which is a recognized limitation of agarose-based PCR-RFLP assays. Therefore, genotype assignment was based primarily on the presence of the clearly resolved 149 bp and 115 bp fragments, which provide the characteristic digestion patterns required to distinguish the three genotypes (Figure 1).

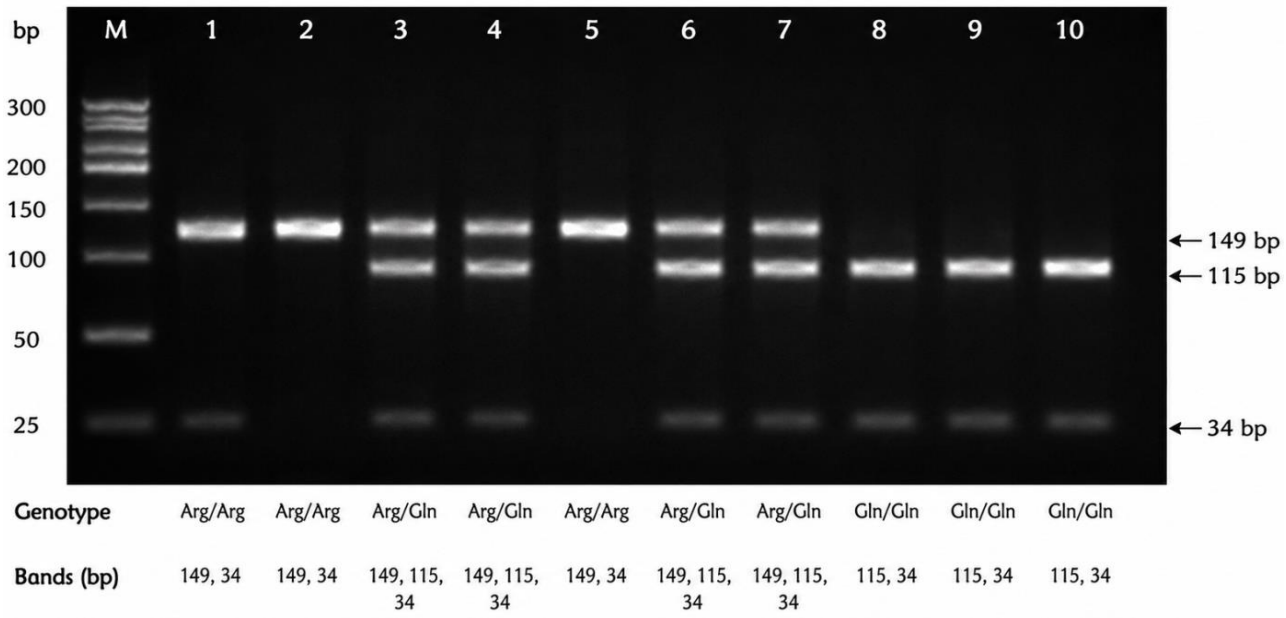

Figure 1 PCR-RFLP genotyping of the XRCC1 rs25487 (Arg399Gln) polymorphism. Representative agarose gel electrophoresis showing the three genotypes identified by polymerase chain reaction–restriction fragment length polymorphism (PCR-RFLP). Lane M: 100 bp DNA ladder. Lanes 1, 2, and 5: homozygous wild-type (Arg/Arg) genotype, showing fragments of 149 bp and 34 bp. Lanes 3, 4, 6, and 7: heterozygous (Arg/Gln) genotype, showing fragments of 149 bp, 115 bp, and 34 bp. Lanes 8, 9, and 10: homozygous variant (Gln/Gln) genotype, showing fragments of 115 bp and 34 bp. The 34 bp fragment appears faint due to its small size.

2.4 Genotyping Quality Control

DNA extraction, PCR amplification, restriction digestion, and electrophoresis were performed according to standardized laboratory protocols. Samples with weak or ambiguous digestion patterns were re-amplified and re-digested before genotype assignment. Genotypes were independently evaluated by two blinded investigators. Genotypes were successfully determined for all 142 study participants, resulting in a 100% genotyping call rate. In addition, the genotype distribution among controls was evaluated for Hardy-Weinberg equilibrium to serve as an internal quality control measure.

2.5 Statistical Analysis

Statistical analyses were performed using R software (version 4.5.1). Continuous variables are presented as means and ranges, whereas categorical variables are expressed as frequencies and percentages. Differences in demographic characteristics and environmental exposures between cases and controls were evaluated using the Pearson chi-square test or Fisher's exact test, where appropriate. Crude odds ratios (ORs) and 95% confidence intervals (CIs) were calculated to estimate the association between the *XRCC1* Arg399Gln polymorphism and NPC susceptibility.

Genotype frequencies were analyzed under codominant, dominant, recessive, and allelic genetic models, with the Arg/Arg genotype serving as the reference category. The genotype distribution in the control group was assessed for Hardy-Weinberg equilibrium using the Pearson chi-square goodness-of-fit test. Statistical significance was defined as a two-sided P value < 0.05.

A power analysis was conducted to evaluate the detectable effect size for the available sample size. Based on 71 cases and 71 controls, a two-sided significance level of 0.05 and 80% statistical power, the study was adequately powered to detect an odds ratio of approximately 2.6 or greater, indicating that it had sufficient power to detect relatively large genetic effects but limited power to detect the modest associations previously reported for the *XRCC1* Arg399Gln polymorphism.

2.6 Ethical Approval Statement

This study was conducted as part of the Upper Aerodigestive Tract research project and was reviewed and approved by the National Research Ethics Review Committee on 16 June 2014 (NO:UADT/6.2014). All procedures were performed in accordance with the ethical standards of the responsible committee and the Declaration of Helsinki. Written informed consent was obtained from all participants before enrollment.

3. Results

A total of 142 participants were included in the study, comprising 71 patients with histopathologically confirmed nasopharyngeal carcinoma (NPC) and 71 cancer-free controls. The demographic characteristics of the study population are summarized in Table 1. The patient group included 51 males and 20 females, whereas the control group comprised 47 males and 24 females. The mean age was 38.6 years (range, 12-75 years) among patients and 37.0 years (range, 11-75 years) among controls. No significant differences in age or sex distribution were observed between the two groups ($P > 0.05$).

Table 1 Demographic characteristics and environmental exposures among study participants.

Variable	Cases (n = 71)	Controls (n = 71)	OR (95% CI)	*P* value
Male sex	51 (71.8%)	47 (66.2%)	-	-
Mean age (years)	38.6 ± SD*	37.0 ± SD*	-	-
Smoking	24 (33.8%)	20 (28.2%)	1.30 (0.64-2.63)	0.586
Alcohol consumption	8 (11.3%)	8 (11.3%)	1.00 (0.35-2.83)	1.000
Salted fish "*Kajeek*" intake	24 (33.8%)	13 (18.3%)	2.28 (0.99-5.23)	0.055

The distribution of selected environmental exposures is presented in Table 1. No statistically significant associations were observed between NPC and cigarette smoking (OR = 1.30, 95% CI: 0.64-2.63; *P* = 0.586) or alcohol consumption (OR = 1.00, 95% CI: 0.35-2.83; *P* = 1.000). Consumption of salted fish was more common among patients than controls and showed a borderline association with NPC risk (OR = 2.28, 95% CI: 0.99-5.23; *P* = 0.055).

The genotype distribution of the *XRCC1* Arg399Gln (rs25487) polymorphism is presented in Table 2. Among patients, 23 (32%) carried the Arg/Arg genotype, 40 (56%) carried the Arg/Gln genotype, and 8 (11%) carried the Gln/Gln genotype. Among controls, the corresponding frequencies were 18 (25%), 43 (61%), and 10 (14%), respectively. The genotype distribution among controls was consistent with Hardy-Weinberg equilibrium (χ^2 = 3.65, *P* = 0.056).

Table 2 Association between the *XRCC1* Arg399Gln polymorphism and risk of nasopharyngeal carcinoma.

Genetic model	Cases n (%)	Controls n (%)	OR (95% CI)	*P* value
Genotype model				**0.625†**
Arg/Arg	23 (32.4)	18 (25.4)	Reference	-
Arg/Gln	40 (56.3)	43 (60.6)	0.73 (0.34-1.54)	0.400
Gln/Gln	8 (11.3)	10 (14.1)	0.63 (0.21-1.91)	0.410
Dominant model (Arg/Gln + Gln/Gln vs. Arg/Arg)	48 (67.6)	53 (74.6)	0.71 (0.34-1.47)	0.350
Recessive model (Gln/Gln vs. Arg/Arg + Arg/Gln)	8 (11.3)	10 (14.1)	0.77 (0.29-2.09)	0.620
Allelic model (Gln vs. Arg allele)	56/142 (39.4)	63/142 (44.4)	0.82 (0.52-1.31)	0.410

† Overall comparison of genotype frequencies using Pearson's chi-square test.

Using the Arg/Arg genotype as the reference category, no statistically significant association was observed between *XRCC1* Arg399Gln and NPC susceptibility. Compared with the Arg/Arg genotype, the Arg/Gln genotype yielded an OR of 0.73 (95% CI: 0.34-1.54; *P* = 0.400), whereas the Gln/Gln genotype yielded an OR of 0.63 (95% CI: 0.21-1.91; *P* = 0.410). Likewise, no statistically significant associations were identified under the dominant, recessive, or allelic genetic models (Table 2).

Allele frequencies are summarized in Table 3. The Arg allele frequency was 60.6% among patients and 55.6% among controls, whereas the Gln allele frequencies were 39.4% and 44.4%,

respectively. No statistically significant difference in allele distribution was observed between the two groups.

Table 3 Allele frequencies of the *XRCC1* Arg399Gln polymorphism among NPC patients and controls.

Allele	Cases n (%)	Controls n (%)	OR (95% CI)	*P* value
Arg	86 (60.6)	79 (55.6)	Reference	-
Gln	56 (39.4)	63 (44.4)	0.82 (0.52-1.31)	0.410

A post hoc power analysis demonstrated that, with 71 cases and 71 controls, the study had approximately 80% power to detect an odds ratio of 2.6 or greater at a two-sided significance level of 0.05. Consequently, the study was underpowered to detect the modest genetic effects reported in previous studies.

4. Discussion

The present case-control study investigated the association between the *XRCC1* Arg399Gln (rs25487) polymorphism and susceptibility to nasopharyngeal carcinoma (NPC) in a Sudanese population. To the best of our knowledge, this is the first study to evaluate this polymorphism in Sudanese patients with NPC and one of the few conducted in an African population. The genotype distributions of the *XRCC1* Arg399Gln polymorphism were comparable between cases and controls, and no statistically significant association was observed under the codominant, dominant, recessive, or allelic genetic models. Similarly, cigarette smoking, alcohol consumption, and salted fish intake were not significantly associated with NPC risk in the present cohort.

The *XRCC1* gene plays a central role in the base excision repair (BER) pathway by coordinating the repair of DNA damage induced by reactive oxygen species and environmental carcinogens. Functional variation in this gene may alter DNA repair capacity and consequently influence individual susceptibility to malignancy. Among the reported polymorphisms, Arg399Gln (rs25487) has been the most extensively investigated because it is located within the BRCT1 domain, which mediates interactions with other DNA repair proteins.

Our findings are consistent with several studies reporting no significant association between *XRCC1* Arg399Gln and NPC susceptibility. However, they differ from studies reporting a positive association, particularly among East Asian populations, where the 399Gln allele has been associated with an increased risk of NPC. Meta-analyses have likewise reported a modest increase in NPC susceptibility among carriers of the variant allele, particularly in Asian populations [5, 8, 18-20]. However, not all studies have demonstrated this association. Investigations from North African populations and several individual studies from China have reported no significant relationship between *XRCC1* Arg399Gln and NPC risk [6, 9, 21]. These inconsistencies likely reflect differences in ethnic background, allele frequencies, environmental exposures, study design, and sample size. Consequently, replication studies in previously uninvestigated populations remain important for evaluating the generalizability of genetic associations across diverse populations.

The absence of a significant association in the present study does not necessarily contradict previous reports. Rather, it suggests that the contribution of *XRCC1* Arg399Gln to NPC susceptibility may be modest and population-dependent. The post hoc power analysis indicated

that the present study had adequate statistical power to detect relatively large genetic effects (odds ratio ≥ 2.6) but was underpowered to identify the modest effect sizes (approximately 1.3-1.8) reported in previous meta-analyses. Therefore, the possibility of a weak association cannot be excluded and should be investigated in larger studies involving Sudanese and other African populations.

In addition to the genetic analysis, selected environmental exposures routinely collected through the Upper Aerodigestive Tract Biobank were evaluated to provide epidemiological context for the study population. No statistically significant associations were observed between NPC risk and cigarette smoking or alcohol consumption, while salted fish intake demonstrated only a borderline association. These findings differ from studies conducted in endemic regions, particularly Southern China, where preserved foods and tobacco exposure have consistently been implicated in NPC development [3, 4, 22-26]. Such discrepancies may reflect differences in dietary habits, environmental exposures, lifestyle factors, and sample size between populations. Furthermore, exposure information in the present study was recorded as categorical variables without detailed assessment of duration or cumulative exposure, which may have limited the ability to detect exposure-response relationships. Gene-environment interaction analyses were not performed due to limited sample size and statistical power.

The present study contributes baseline genetic epidemiological data from an understudied African population. Although previous meta-analyses have included several hundred participants from predominantly Asian populations, data from Sudan and most of sub-Saharan Africa remain scarce. Because allele frequencies and environmental exposures vary substantially among different ethnic groups, population-specific studies are important for expanding the global evidence base. They may contribute valuable data to future pooled analyses and meta-analyses.

The present study has several limitations. First, the relatively modest sample size limited statistical power to detect the small genetic effects previously reported for *XRCC1* Arg399Gln and precluded stable multivariable analyses that could adjust for potential confounding variables. Second, although environmental exposure data were available, formal gene-environment interaction analyses were not conducted due to limited sample size and insufficient statistical power. Future studies involving larger cohorts should evaluate interaction effects using multivariable regression models or other approaches, such as multifactor dimensionality reduction (MDR). Third, environmental exposures were based on self-reported questionnaire data and were recorded as binary variables; consequently, information regarding exposure duration, frequency, and cumulative lifetime exposure was unavailable. Fourth, Epstein-Barr virus (EBV) status, a major determinant of NPC pathogenesis, was not available for the study participants and therefore could not be incorporated into the analysis. Finally, although PCR-RFLP remains a reliable and widely used genotyping technique, the 34 bp digestion fragment generated by the MspI enzyme was not consistently resolved on the 3% agarose gel because of its small size. Genotype assignment was therefore based primarily on the clearly resolved 149 bp and 115 bp fragments. Future studies may benefit from using higher-resolution electrophoretic techniques, such as native polyacrylamide gel electrophoresis (PAGE), or sequence-based genotyping methods to further improve genotype discrimination.

5. Conclusion

In conclusion, no statistically significant association was observed between the *XRCC1* Arg399Gln (rs25487) polymorphism and susceptibility to nasopharyngeal carcinoma in this Sudanese population under codominant, dominant, recessive, or allelic genetic models. Likewise, cigarette smoking, alcohol consumption, and salted fish "*Kajeek*" intake were not significantly associated with NPC risk in this cohort. Although these findings do not support a major role for *XRCC1* Arg399Gln in NPC susceptibility among Sudanese individuals, they provide the first population-specific data for Sudan and contribute to the limited body of evidence from African populations. Larger multicenter studies incorporating comprehensive environmental exposure assessment, EBV status, and additional DNA repair gene variants are warranted to better define the contribution of DNA repair pathways to NPC susceptibility across diverse populations.

Author Contributions

Sarah Ahmed: laboratory analysis, results interpretation and manuscript drafting. Marwa M. Mohammed: Data analysis, data retrieval and manuscript writing. Heba Mohammed: Biobank data retrieval, quality assurance and manuscript writing. Sana Magzoub: Samples quality assurance, data analysis, and manuscript writing. Mona Ellaithi: Project PI, Methodology, and writing of the manuscript.

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Competing Interests

The authors declare no conflicts of interest related to this study.

Data Availability Statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

AI-Assisted Technologies Statement

Artificial intelligence (AI) tools were used solely for basic grammar correction and language refinement in the preparation of this manuscript. Specifically, OpenAI's ChatGPT was employed to improve the readability and linguistic clarity of the English text. All scientific content, data interpretation, and conclusions were developed independently by the author. The authors have thoroughly reviewed and edited the AI-assisted text to ensure its accuracy and accept full responsibility for the content of the manuscript.

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