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ASSOCIATION OF BASE EXCISION REPAIR PATHWAY GENES *OGG1*, *XRCC1* AND *MUTYH* POLYMORPHISMS AND THE LEVEL OF 8-OXO-GUANINE WITH INCREASED RISK OF COLORECTAL CANCER OCCURRENCE

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Abstract

Objectives: Reduced efficiency of DNA repair systems has long been a suspected factor in increasing the risk of cancer. In this work authors investigate influence of selected polymorphisms of DNA repair genes (*XRCC1*, *OGG1* and *MUTYH*) and level of oxidative damage (measured as level of 8-oxo-guanine, 8-oG) on modulation of the risk of colorectal cancer. **Material and Methods:** In group of 324 patients with colorectal cancer the occurrence of polymorphic variants in Ser326Cys of *OGG1*, Arg399Gln of *XRCC1* and Gln324His of *MUTYH* were studied with TaqMan technique. In addition level of 8-oG in isolated DNA was determined. **Results:** Studied polymorphisms of *OGG1*, *XRCC1* and *MUTYH* genes influence the risk of CRC: *OGG1* Ser326Cys (OR = 1.259, 95% CI: 1.058–1.499, p = 0.007), *XRCC1* Arg399Gln (OR = 2.481, 95% CI: 1.745–3.529, p < 0.0001) and *MUTYH* Gln324His (OR = 1.421, 95% CI: 1.017–1.984, p = 0.039) increase the risk. At the same time, studies examined level of 8-oG for each of the genotypes in both the patient and control group, and have shown that *OGG1* Ser326Cys and *XRCC1* Arg399Gln are associated with elevated 8-oG level, while *MUTYH* Gln324His is not, suggesting, that in case of *OGG1* Ser326Cys and *XRCC1* Arg399Gln CRC risk modulation is connected to mechanisms associated with 8-oG levels. **Conclusions:** This work shows that patients with CRC not only have an increased level of 8-oG and that the studied polymorphisms modulate risk of cancer, but also indicate a relationship between these 2 phenomena, which may contribute to a better understanding of the mechanism of neoplastic process in case of reduced effectiveness of DNA repair mechanisms. Int J Occup Med Environ Health. 2022;35(5):625–33

Key words:
***XRCC1*, DNA repair, *OGG1*, *MUTYH*, oxidative stress, cancer**

INTRODUCTION

Despite ongoing research and progress in both diagnosis and treatment, an rising number of colorectal cancer (CRC) cases can be observed. In 2012 according to Global Cancer Observatory (GLOBOCAN) there were 1 360 000 new CRC cases, which accounted for 9.7% of all newly diagnosed cancers, and CRC was the third most common cancer after breast and lung cancer [1]. Due to the complexity and variety of variants, the exact etiology of the disease remains unknown, however, several factors have been identified

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which may contribute to escalated risk of developing the disease. Genetic factors come to the fore, however, environmental factors should not be underestimated, and in most cases it is expected that the final underlying factor will be the coexistence of the above-mentioned factors. Within the group of genetic predisposition factors, DNA repair systems play a special role. It has been shown that the decrease in the efficacy of DNA repair systems is a key element modulating the occurrence of CRC. The relationship between mutations in the DNA Mismatch Repair (MMR) genes and the increased risk of hereditary nonpolyposis colorectal cancer (HNPCC) in which genetic changes within the *MSH2* gene are observed in approx. 60% of patients [2,3], gave rise to search for a similar effect on CRC incidence in other types of DNA repair systems. Particular attention was paid to Base Excision Repair (BER) and Nucleotide Excision Repair (NER) and a number of studies have proved that alterations in those repair systems can increase the risk of CRC [4]. It should be emphasized, however, that often results are ambiguous and sometimes contradictory [5]. This may be due to the differentiation of factors affecting the oncogenesis process. As mentioned above, colorectal cancer is most likely a result of co-interactions of endogenous and exogenous factors. The latter include most of all reactive oxygen species (ROS) [6]. Increased levels of oxidative stress caused by ROS may damage DNA in a way that can lead to oncogenesis [7]. DNA is damaged by ROS in many different ways, but the most common effect is the formation of 8-oxo-guanine (8-oG), modified guanine that can result in a mismatched pairing with adenine resulting in G to T and C to A substitutions. For this reason, the quick and effective removal of 8-oG is extremely important. The effect of 8-oG on the increased risk of cancer has been shown not only for CRC [8], but also for head and neck cancer [9] and lung cancer [10]. In a properly functioning cell, the 8-oG removal from the DNA is provided by BER, mainly by 8-oG glycosylase, also known as OGG1 [11]. The 8-oxo-guanine glycosylase interacts with other BER proteins, therefore, it is responsible for maintaining the genomic stability and defending against potential cancerous transformation.

The aim of this study was to investigate the effect of BER gene polymorphisms *OGG1* Ser326Cys, *XRCC1* Arg399Gln and *MUTYH* Gln324His on the modulation of CRC risk. Moreover, these data are supplemented with the levels of 8-oG broken down into each of the tested variants, in order to assess the possible impact of the effectiveness of antioxidant mechanisms on the risk level.

MATERIAL AND METHODS

Population of study

The source of DNA were lymphocytes from peripheral blood. In this study 324 patients of The Military Medical Academy Memorial Teaching Hospital – Central Veterans' Hospital in Łódź, Poland, were included. Before sample collection CRC was confirmed histopathologically in case of every patient and any other neoplastic disease was the exclusion criterion. One hundred eighty-nine men and 135 women (with the age of M±SD 67±7 years) were enrolled in the study; 320 cancer free patients admitted to the hospital for other reasons served as control group (age corresponding to the age of the studied group, $p < 0.05$). History of any neoplastic disease was the exclusion criterion for the control group. Research was approved by the bioethics committee of the Medical University of Lodz.

DNA isolation and genotyping

QIAamp DNA Blood Mini Kit from Qiagen was used to isolate DNA in accordance with the manufacturer's instructions; 200 µl of blood was used for each isolation.

Polymorphisms Ser326Cys of *OGG1* gene (reference SNP cluster ID 1052133 – rs1052133), Arg399Gln of *XRCC1* gene (rs25487) and Gln324His of *MUTYH* gene (rs3219489) were studied with TaqMan technique. The authors used 25 µl of reaction mixture: 1 µl of isolated DNA, 1 µl TaqMan

Table 1. The refSNP's and thermal conditions used in the PCR reaction in 324 patients with colorectal cancer, The Military Medical Academy Memorial Teaching Hospital in Łódź, Poland, 2019

Variable	Gene		
	OGG1	*XRCC1*	*MUTYH*
Polymorphism	Ser326Cys	Arg399Gln	Gln324His
RefSNP	rs1052133	rs25487	rs3219489
Position	chr3:9757089	chr19:43551574	chr1:45331833
Alleles	C>G/C>T	T>C/T>G	C>A/C>G

Thermal conditions: 1. 95°C – 10 min, 2. 92°C – 15 s, 3. 60°C – 1 min, 4. Step 2 and 3 – 45×.
Dyes: ROX, HEX, FAM, ref. dye: ROX.

probes, 13 µl of premix with polymerase and 10 µl of water. Thermocycler Startogene Mx3005P was used to perform the reaction. Reference SNP cluster IDs and thermal conditions are shown in Table 1. Randomly selected 10% samples were subject to repeat genotyping process to confirm copiability. All of the samples were genotyped randomly and case/control status of sample was hidden during genotyping.

8-oxo-guanine levels

To assess 8-oG levels in DNA samples HT 8-oxo-dG ELISA II Kit (R&D Systems) was used. Final DNA concentration of 500 µg/ml, measured with Microliter UV/Vis Spectrophotometer – Picodrop, was used. Reaction is immunobased and allows detection and quantitation of 8-oG in biological samples, including DNA. Reaction was performed according to manufacturer's instruction. Sensitivity of the kit is at 2 nmol (0.57 ng/ml) 8-OHdG which allows the detection of minimal amounts of the modified base. However, it should be noted that apart from the generally known limitations resulting from the ELISA method, in this particular case the measurement takes place on isolated DNA, which means that the obtained value indicates the level of 8-oG incorporated in the DNA molecule, but there is no information about the amount of 8-oG that was previously removed by repair systems.

Statistical analysis

The genotypes frequency was assessed with Hardy-Weinberg law using the χ^2 test. Risk modulation of CRC was calculated using means of multivariate regression analysis (odds ratio – OR) with confidence interval (CI) of 95%. The 8-oxo-guanine levels were compared among studied groups by analysis of variance using single factor one-way ANOVA test. In case of unequal means of the 3 populations, a t-test to test each pair of means was performed. In order to determine the equality of 2 population's variances we performed F-test and depending on the result two-sample assuming unequal variances t-test or two-sample assuming equal variances t-test was used.

RESULTS

Genotyping

The results state that Ser/Cys genotype of Ser326Cys polymorphism of *OGG1* gene (as presented in Table 2) increases the risk of colorectal cancer (OR = 1.259, 95% CI: 1.058–1.499, p = 0.007). Similar effect was observed for Arg/Gln genotype of Arg399Gln polymorphism of *XRCC1* gene (OR = 2.481, 95% CI: 1.745–3.529, p < 0.0001) and Gln allele (OR = 1.351, 95% CI: 1.076–1.696, p = 0.009) as well as Gln/His genotype of Gln324His polymorphism of *MUTYH* gene (OR = 1.421, 95% CI: 1.017–1.984, p = 0.039) (Table 2).

Table 2. The distribution of genotypes, allele frequencies and the analysis of the odds ratio (OR) for polymorphism of genes in 324 patients with colorectal cancer and the control group, The Military Medical Academy Memorial Teaching Hospital in Łódź, Poland, 2019

Variable	Group [n]		OR (95% CI)	p
	studied	control		
Ser326Cys polymorphism of *OGG1* gene				
Ser/Ser	96	119[a]	1 (ref.)	–
Ser/Cys	203	158[a]	1.259 (1.058–1.499)	**0.007**
Cys/Cys	21	37[a]	0.704 (0.386–1.281)	0.249
Ser	395	396	1 (ref.)	–
Cys	245	232	1.059 (0.844–1.329)	0.624
Arg399Gln polymorphism of *XRCC1* gene				
Arg/Arg	79	131[b]	1 (ref.)	–
Arg/Gln	208	139[b]	2.481 (1.745–3.529)	**<0.0001**
Gln/Gln	31	40[b]	1.285 (0.745–2.218)	0.368
Arg	366	401	1 (ref.)	–
Gln	270	219	1.351 (1.076–1.696)	**0.009**
Gln324His polymorphism of *MUTYH* gene				
Gln/Gln	108	125[c]	1 (ref.)	–
Gln/His	189	154[c]	1.421 (1.017–1.984)	**0.039**
His/His	18	33[c]	0.631 (0.336–1.185)	0.150
Gln	405	404	1 (ref.)	–
His	225	220	1.020 (0.809–1.286)	0.862

[a] Genotype distribution in Hardy-Weinberg equilibrium, $\chi^2 = 0.156$.
[b] Genotype distribution in Hardy-Weinberg equilibrium, $\chi^2 = 0.742$.
[c] Genotype distribution in Hardy-Weinberg equilibrium, $\chi^2 = 0.151$.
Ser326Cys polymorphism of *OGG1* gene: 320 participants in the studied group and 314 in the control group.
Arg399Gln polymorphism of *XRCC1* gene: 318 participants in the studied group and 310 in the control group.
Gln324His polymorphism of *MUTYH* gene: 315 participants in the studied group and 312 in the control group.
Bolded are variables that statistically significantly modulate the risk of CRC.

8-oxo-guanine levels

As initial study 8-oG levels comparison for both the healthy subjects and the patient group was performed, revealing that the mean level for patients was increased (28 615 nmol compared to 58 744 nmol/DNA (μg/μl), p = 0.05). Secondly, measurement of 8-oG levels in relation to specific genotypes showed that group with Ser/Cys genotype of the *OGG1* gene had statistically significantly higher level than remaining 2 genotypes. As shown in Figure 1a:

- in case of control group: 42.23 8-oG nmol/DNA (μg/μl) for Ser/Cys vs. 22.92 8-oG nmol/DNA (μg/μl) for Ser/Ser and 20.69 8-oG nmol/DNA (μg/μl) for Cys/Cys,
- in case of patients: 106.00 8-oG nmol/DNA (μg/μl) for Ser/Cys vs. 36.54 8-oG nmol/DNA (μg/μl) for Ser/Ser and 33.69 8-oG nmol/DNA (μg/μl) for Cys/Cys).

This situation is observed both within the patient group and the control group. The same result was observed for the genotype Arg/Gln of *XRCC1* gene, and once again

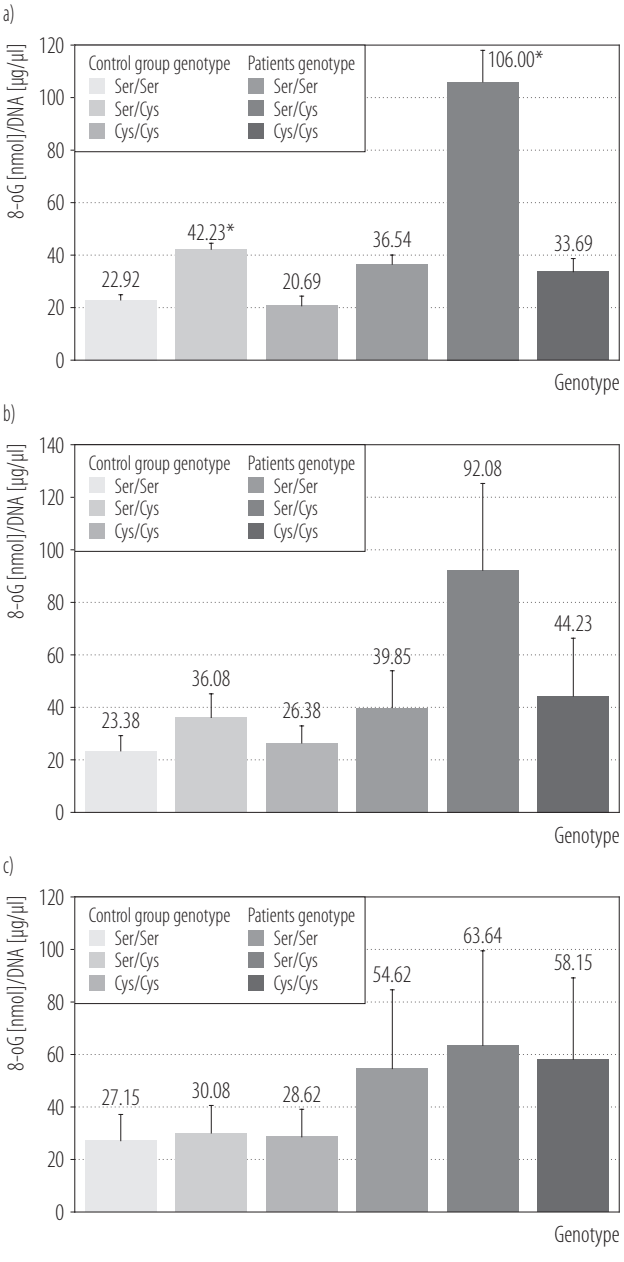
8-oG level was higher for both patients and control groups when compared to other 2 genotypes. As shown in Figure 1b:

– in case of control group: 36,08 8-oG nmol/DNA (μg/μl) for Arg/Gln vs. 23,38 8-oG nmol/DNA (μg/μl) for Arg/Arg and 26,38 8-oG nmol/DNA (μg/μl) for Gln/Gln,
– in case of patients: 92,08 8-oG nmol/DNA (μg/μl) for Arg/Gln vs. 39,85 8-oG nmol/DNA (μg/μl) for Arg/Arg and 44,23 8-oG nmol/DNA (μg/μl) for Gln/Gln.

However, this was not the case with the *MUTYH* gene, where no statistically significant differences in 8-oG levels between genotypes were observed (Figure 1c).

DISCUSSION

The ability of human cells to repair DNA damage is one of the key mechanisms that protect our body against cancer. The firmness of the genome should be a priority since its violation can lead to the accretion of mutations and, consequently, to cancerogenesis. Such a situation can be observed in the case of a decrease in the effectiveness of DNA repair mechanisms. Such a situation can be observed in the case of a decrease in the effectiveness of DNA repair mechanisms, and one of the most common damages resulting from such dysfunction will be those generated by reactive oxygen species. Among DNA lesions resulting from ROS action 8-oG is the most frequent and can lead to discrepancy in base paring [11]. Oxidation of guanine to 8-oG is repaired primarily by DNA glycosylase OGG1, a part of Base Excision Repair mechanism [12]. OGG1 has been shown to interact with XRCC1 [13] and MUTYH [14]. The polymorphisms of all these genes, due to their key function, have been studied in terms of risk modulation in wide spectrum of cancer types, including lung cancer [15], head and neck cancer [16], pancreatic and breast cancer [17] or gallbladder cancer [18]. In case of colorectal cancer *OGG1* Ser326Cys has been shown to increase risk [19], not modulate risk at all [20] or decrease risk [21]. *XRCC1* Arg399Gln increases the risk of CRC [22] or is considered not to have an influence [23]. Finally *MUTYH* Gln324His is considered to be risk factor for CRC occurrence [24].



* p<0.05.

Figure 1. The 8-oxo-guanine levels in CRC patients and control group for genotypes of a) Ser326Cys polymorphism of *OGG1* gene, b) Arg399Gln polymorphism of *XRCC1* gene, and c) Gln324His polymorphism of *MUTYH* gene in 324 patients with colorectal cancer, The Military Medical Academy Memorial Teaching Hospital in Łódź, Poland, 2019

In this study authors have shown that all 3 of those polymorphisms are connected to increased risk of CRC incidence – *OGG1* Ser326Cys (OR = 1.259, 95% CI: 1.058–1.499, p = 0.007), *XRCC1* Arg399Gln (OR = 2.481, 95% CI: 1.745–3.529, p < 0.0001) as well as *MUTYH* Gln324His (OR = 1.421, 95% CI: 1.017–1.984, p = 0.039). The causes of inaccuracies, and sometimes even contradictions in the literature data, and thus the comparison of our results to the available results, are to be found in the differences in the studied populations, such as race, abundance, exposure to additional risk factors (smoking, alcohol consumption). The main reason behind the inconsistent reports in this regard is the multifactorial nature of carcinogenesis. For a better understanding of the processes that may underlie at the increased risk of CRC in polymorphisms of studied genes, 8-oG levels were measured. Colorectal cancer patients showed a significantly higher level of oxidative damage measured as the level of 8-oG. This is a result to be expected due to the decreased level of antioxidant mechanisms in cancer patients as well as due to the increased level of oxidative stress during treatment. Previous studies indicate the potential role of BER proteins in regulating the level of 8-oG and the impact of this regulation on the risk of CRC, especially in the case of MUTYH [25]. However, there are no reports on the detailed impact of individual BER protein polymorphisms on the level of 8-oG, so authors compared this levels for patients and control groups broken down into all 3 genotypes of the studied genes. Results indicate that *OGG1* Ser326Cys not only, as mentioned above, increases the risk of CRC, but also is connected to increased level of 8-oG in case of patients as well as in healthy individuals. This supports theory, that Ser326Cys polymorphism increases CRC risk due to OGG1 decreased activity – accumulating 8-oG resulting from reduced efficacy of OGG1 leads to increased risk of malignant transformation. Although Janssen et al postulated that there is no connection betweenSer326Cys polymorphism inDNA glycosylase 1 and 8-oG damage repair efficiency in case of lymphocytes [26] authors believe that this may not be the case when it comes to colorectal cancer cells. In the case of a reduction in OGG1 expression, the likely effect will be an increase in the level of mutation and the resulting increase in the intensity of neoplastic transformation, what has been proved by studies that described cancers identified as having reduction in the *OGG1* expression, such as head and neck cancer [27] stomach cancer [28] or brain cancer [29]. Moreover activity of DNA repair proteins can be different in lymphocytes and in tissue, as proven by Janik et al [30] in case of lymphocytes compared to lung cells. The same mechanism can be postulated for XRCC1 which has been shown to closely interact with OGG1 [13] and according to obtained results in case of Arg399Gln may escalate CRC risk and is associated with elevated level of 8-oG. Available data seem to support that theory since Arg399Gln *XRCC1* patients revealed lower 8-oG incision activity in their lung tissues in non-small-cell lung carcinoma [30]. However, the same phenomenon was not observed with *MUTYH* Gln324His, which elevates CRC risk but is not associated with increased level of 8-oG. Although all 3 of these proteins (OGG1, XRCC1 and MUTYH) work together for the removal of oxidative damage from DNA, including 8-oG, MUTYH must modulate the risk of CRC occurrence due to other mechanisms than ineffectiveness in repairing oxidized guanine. It is possible that the function of MUTYH in the removal of 8-oG may be taken over by another protein, since different strategies exist to avert the danger of damage caused by ROS [31], therefore, despite the dysfunction of MUTYH, no increase in 8-oG levels will be observed, and the carcinogenic effect will be induced by some other process in which MUTYH is also involved. What may be this process remains unknown, therefore authors postulate that further research in this area is needed.

The results obtained in this study by no means are complete and comprehensive explanation of the mechanism of carcinogenesis resulting from the presence of the polymorphisms studied, however, the potential con-

nection between genotypes and changes in the amount of 8-oG may contribute to broadening the knowledge of how this process occurs. Several processes are involved in neutralizing oxidative stress, each of which plays an important role in maintaining oxidative homeostasis in the cell. Bioactive antioxidant compounds (vitamin C, glutathione, vitamin E) and enzyme systems (superoxide dismutase, catalase, peroxiredoxins) guard the level of reactive oxygen species and ensure that key cell components, including DNA, are not damaged. However, when this happens, DNA repair systems are one of the last lines of defense against introducing potentially carcinogenic changes to DNA. Oxidative stress may include an increase in the level of reactive oxygen species resulting from 2 sources – internal and external factors. In the light of the obtained results, the special role of effective ROS removal should be emphasized, especially in terms of environmental factors, which everyone can directly influence. Limiting exposure to elements that increase oxidative stress (tobacco smoking, excessive exposure to UVB radiation, inadequate nutrition) and promotion of attitudes supporting the reduction of oxidative stress (proper diet) can significantly reduce the risk of cancer and, if it occurs, increase the effectiveness of therapy. In this study, role of weakened DNA repair mechanisms and their clear effect on increasing the risk of colorectal cancer, *inter alia*, by affecting the 8-oG level was shown. It should be clearly emphasized, however, that 8-oG is only 1 of the effects of oxidative stress, and the method of measuring oxidative damage by evaluating the 8-oG level gives a picture of only a fragment of the full situation. At the same time, a situation in which an increased level of 8-oG can be observed in patients with CRC, in authors' opinion this fact can be used as a diagnostic tool in the detection of early forms of cancer. If it is confirmed that the enhanced CRC mechanism with reduced BER protein activity is based on increased 8-oG levels, it would seem reasonable to include antioxidant defense agents in cancer treatment.

CONCLUSIONS

Ser/Cys genotype of Ser326Cys polymorphism of *OGG1* gene, Arg/Gln genotype of Arg399Gln polymorphism of *XRCC1* and Gln/His genotype of Gln324His polymorphism of *MUTYH* gene increase CRC risk. The 8-oG level in CRC patients is higher than in the control group. At the same time Ser326Cys of *OGG1* gene and Arg399Gln of *XRCC1* polymorphisms are connected to highly increased 8-oG level. It may suggest that CRC risk modulation is associated with a decrease in activity in the removal of 8-oG, for which responsible may be impaired DNA repair, while underlying cause of elevated CRC risk in case of Gln/His genotype of Gln324His polymorphism of *MUTYH* gene must be due to some other mechanism, since it is not connected with increased 8-oG level.

REFERENCES

1. Ferlay J, Soerjomataram I, Dikshit R, Eser S, Mathers C, Rebelo M, et al. Cancer incidence and mortality worldwide: sources, methods and major patterns in GLOBOCAN 2012. Int J Cancer 2015;136:E359-386. https://doi.org/10.1002/ijc.29210.
2. Vasen HF, Stormorken A, Menko FH, Nagengast FM, Kleibeuker JH, Griffioen G, et al. MSH2 mutation carriers are at higher risk of cancer than MLH1 mutation carriers: a study of hereditary nonpolyposis colorectal cancer families. J Clin Oncol Off J Am Soc Clin Oncol 2001;19:4074–80. https://doi.org/10.1200/JCO.2001.19.20.4074.
3. Vasen HF, Watson P, Mecklin JP, Lynch HT. New clinical criteria for hereditary nonpolyposis colorectal cancer (HNPCC, Lynch syndrome) proposed by the International Collaborative group on HNPCC. Gastroenterology 1999;116:1453–6. https://doi.org/10.1016/s0016-5085(99)70510-x.
4. Moreno V, Gemignani F, Landi S, Gioia-Patricola L, Chabrier A, Blanco I, et al. Polymorphisms in genes of nucleotide and base excision repair: risk and prognosis of colorectal cancer. Clin Cancer Res Off J Am Assoc Cancer Res 2006;12:2101–8. https://doi.org/10.1158/1078-0432.CCR-05-1363.

5. Mort R, Mo L, McEwan C, Melton DW. Lack of involvement of nucleotide excision repair gene polymorphisms in colorectal cancer. Br J Cancer 2003;89:333–7. https://doi.org/10.1038/sj.bjc.6601061.
6. Valko M, Rhodes CJ, Moncol J, Izakovic M, Mazur M. Free radicals, metals and antioxidants in oxidative stress-induced cancer. Chem Biol Interact 2006;160:1–40. https://doi.org/10.1016/j.cbi.2005.12.009.
7. Chang D, Wang F, Zhao Y-S, Pan H-Z. Evaluation of oxidative stress in colorectal cancer patients. Biomed Environ Sci BES 2008;21:286–9. https://doi.org/10.1016/S0895-3988(08)60043-4.
8. Obtulowicz T, Swoboda M, Speina E, Gackowski D, Rozalski R, Siomek A, et al. Oxidative stress and 8-oxoguanine repair are enhanced in colon adenoma and carcinoma patients. Mutagenesis 2010;25:463–71. https://doi.org/10.1093/mutage/geq028.
9. Paz-Elizur T, Ben-Yosef R, Elinger D, Vexler A, Krupsky M, Berrebi A, et al. Reduced repair of the oxidative 8-oxoguanine DNA damage and risk of head and neck cancer. Cancer Res 2006;66:11683–9. https://doi.org/10.1158/0008-5472.CAN-06-2294.
10. Park J, Chen L, Tockman MS, Elahi A, Lazarus P. The human 8-oxoguanine DNA N-glycosylase 1 (hOGG1) DNA repair enzyme and its association with lung cancer risk. Pharmacogenetics 2004;14:103–9. https://doi.org/10.1097/00008571-200402000-00004.
11. Aguiar PH, Furtado C, Repolês BM, Ribeiro GA, Mendes IC, Peloso EF, Gadelha FR, Macedo AM, Franco GR, Pena SD, Teixeira SM, Vieira LQ, Guarneri AA, Andrade LO, Machado CR. Oxidative stress and DNA lesions: the role of 8-oxoguanine lesions in Trypanosoma cruzi cell viability. PLoS Negl Trop Dis. 2013 Jun 13;7(6):e2279. https://doi.org/10.1371/journal.pntd.0002279.
12. Dianov G, Bischoff C, Piotrowski J, Bohr VA. Repair pathways for processing of 8-oxoguanine in DNA by mammalian cell extracts. J Biol Chem 1998;273:33811–6. https://doi.org/10.1074/jbc.273.50.33811.
13. Marsin S, Vidal AE, Sossou M, Ménissier-de Murcia J, Le Page F, Boiteux S, et al. Role of XRCC1 in the coordination and stimulation of oxidative DNA damage repair initiated by the DNA glycosylase hOGG1. J Biol Chem 2003;278:44068–74. https://doi.org/10.1074/jbc.M306160200.
14. Markkanen E, Dorn J, Hübscher U. MUTYH DNA glycosylase: the rationale for removing undamaged bases from the DNA. Front Genet 2013;4:18. https://doi.org/10.3389/fgene.2013.00018.
15. Ratnasinghe D, Yao SX, Tangrea JA, Qiao YL, Andersen MR, Barrett MJ, et al. Polymorphisms of the DNA repair gene XRCC1 and lung cancer risk. Cancer Epidemiol Biomark Prev Publ Am Assoc Cancer Res Cosponsored Am Soc Prev Oncol 2001;10:119–23.
16. Olshan AF, Watson MA, Weissler MC, Bell DA. XRCC1 polymorphisms and head and neck cancer. Cancer Lett 2002;178:181–6. https://doi.org/10.1016/s0304-3835(01)00822-9.
17. Thibodeau ML, Zhao EY, Reisle C, Ch'ng C, Wong H-L, Shen Y, et al. Base excision repair deficiency signatures implicate germline and somatic MUTYH aberrations in pancreatic ductal adenocarcinoma and breast cancer oncogenesis. Cold Spring Harb Mol Case Stud 2019;5:a003681. https://doi.org/10.1101/mcs.a003681.
18. Wu Z, Miao X, Zhang Y, Li D, Zou Q, Yuan Y, et al. XRCC1 Is a Promising Predictive Biomarker and Facilitates Chemo-Resistance in Gallbladder Cancer. Front Mol Biosci 2020;7:70. https://doi.org/10.3389/fmolb.2020.00070.
19. Canbay E, Cakmakoglu B, Zeybek U, Sozen S, Cacina C, Gulluoglu M, et al. Association of APE1 and hOGG1 polymorphisms with colorectal cancer risk in a Turkish population. Curr Med Res Opin 2011;27:1295–302. https://doi.org/10.1185/03007995.2011.573544.
20. Park H-W, Kim I-J, Kang HC, Jang S-G, Ahn S-A, Lee JS, et al. The hOGG1 Ser326Cys Polymorphism Is Not Associated with Colorectal Cancer Risk. J Epidemiol 2007;17:156–60. https://doi.org/10.2188/jea.17.156.
21. Hansen R, Saebø M, Skjelbred CF, Nexø BA, Hagen PC, Bock G, et al. GPX Pro198Leu and OGG1 Ser326Cys

polymorphisms and risk of development of colorectal adenomas and colorectal cancer. Cancer Lett 2005;229:85–91. https://doi.org/10.1016/j.canlet.2005.04.019.

22. Engin AB, Karahalil B, Karakaya AE, Engin A. Association between XRCC1 ARG399GLN and P53 ARG72PRO polymorphisms and the risk of gastric and colorectal cancer in Turkish population. Arh Hig Rada Toksikol 2011;62:207–14. https://doi.org/10.2478/10004-1254-62-2011-2098.
23. Gsur A, Bernhart K, Baierl A, Feik E, Führlinger G, Hofer P, et al. No association of XRCC1 polymorphisms Arg194Trp and Arg399Gln with colorectal cancer risk. Cancer Epidemiol 2011;35:e38-41. https://doi.org/10.1016/j.canep.2011.03.005.
24. Tao H, Shinmura K, Suzuki M, Kono S, Mibu R, Tanaka M, et al. Association between genetic polymorphisms of the base excision repair gene MUTYH and increased colorectal cancer risk in a Japanese population. Cancer Sci 2008;99:355–60. https://doi.org/10.1111/j.1349-7006.2007.00694.x.
25. Allgayer J, Kitsera N, von der Lippen C, Epe B, Khobta A. Modulation of base excision repair of 8-oxoguanine by the nucleotide sequence. Nucleic Acids Res 2013;41:8559–71. https://doi.org/10.1093/nar/gkt620.
26. Janssen K, Schlink K, Götte W, Hippler B, Kaina B, Oesch F. DNA repair activity of 8-oxoguanine DNA glycosylase 1 (OGG1) in human lymphocytes is not dependent on genetic polymorphism Ser326/Cys326. Mutat Res 2001;486:207–16. https://doi.org/10.1016/s0921-8777(01)00096-9.
27. Mahjabeen I, Kayani MA. Loss of Mitochondrial Tumor Suppressor Genes Expression Is Associated with Unfavorable Clinical Outcome in Head and Neck Squamous Cell Carcinoma: Data from Retrospective Study. PloS One 2016;11:e0146948. https://doi.org/10.1371/journal.pone.0146948.
28. Kohno Y, Yamamoto H, Hirahashi M, Kumagae Y, Nakamura M, Oki E, et al. Reduced MUTYH, MTH1, and OGG1 expression and TP53 mutation in diffuse-type adenocarcinoma of gastric cardia. Hum Pathol 2016;52:145–52. https://doi.org/10.1016/j.humpath.2016.01.006.
29. Jiang Z, Hu J, Li X, Jiang Y, Zhou W, Lu D. Expression analyses of 27 DNA repair genes in astrocytoma by TaqMan low-density array. Neurosci Lett 2006;409:112–7. https://doi.org/10.1016/j.neulet.2006.09.038.
30. Janik J, Swoboda M, Janowska B, Cieśla JM, Gackowski D, Kowalewski J, et al. 8-Oxoguanine incision activity is impaired in lung tissues of NSCLC patients with the polymorphism of OGG1 and XRCC1 genes. Mutat Res 2011;709–710:21–31. https://doi.org/10.1016/j.mrfmmm.2011.02.009.
31. Russo MT, De Luca G, Degan P, Bignami M. Different DNA repair strategies to combat the threat from 8-oxoguanine. Mutat Res 2007;614:69–76. https://doi.org/10.1016/j.mrfmmm.2006.03.007.