DOI: 10.4274/MMJ.galenos.2025.72708
Medeni Med J 2025;40:116-127

Original Article

PARP-1 rs1136410 Polymorphism and Gastrointestinal Cancer Risk: A Meta-Analysis of Cancer-Type and Ethnic-Specific Associations

PARP-1 rs1136410 Polimorfizmi ve Gastrointestinal Kanser Riski: Kanser Türü ve Etnik Spesifik İlişkilerin Meta Analizi

Amirhosein NASERI[1], Mohammad Hossein ANTIKCHI[2], Sepideh SOLEYMANI[3], Mehdi KHOSRAVI-MASHIZI[3], Rezvan NEZAMESLAMI[4], Alireza NEZAMESLAMI[5], Bahareh MEHDIKHANI[6], Ahmad SHIRINZADEH-DASTGIRI[3], Seyed Masoud HAGHIGHIKIAN[3], Mohammad VAKILI-OJAROOD[7], Amirhossein RAHMANI[8], Hossein NEAMATZADEH[9]

[1] AJA University of Medical Sciences, Imam Reza Hospital, Department of Colorectal Surgery, Tehran, Iran
[2]Islamic Azad University, Department of Internal Medicine, Yazd Branch, Yazd, Iran
[3]Iran University of Medical Sciences, School of Medicine, Department of General Surgery, Tehran, Iran
[4]Shahid Beheshti University of Medical Sciences, Imam Hossein Hospital, Department of Ophthalmology,, Tehran, Iran
[5]Tehran University of Medical Sciences, Farabi Hospital, Department of Ophthalmology, Tehran, Iran
[6]Iran University of Medical Sciences, School of Medicine, Department of Radiology, Tehran, Iran
[7]Ardabil University of Medical Sciences, School of Medicine,Department of Surgery, Ardabil, Iran
[8] Iranshahr University of Medical Sciences, School of Medicine, Department of Plastic Surgery, Iranshahr, Iran
[9]Shahid Sadoughi University of Medical Sciences, Hematology and Oncology Research Center, Yazd, Iran

ABSTRACT

Objective: Poly (ADP-ribose) polymerase-1 (*PARP-1*) is a key enzyme in DNA repair pathways and has been implicated in cancer susceptibility. The rs1136410 polymorphism in the *PARP-1* gene has shown inconsistent associations with gastrointestinal cancer risk across populations. This meta-analysis aimed to evaluate the association between *PARP-1* rs1136410 polymorphism and the risk of colorectal cancer (CRC) and gastric cancer (GC), with a focus on ethnic differences.

Methods: A systematic literature search was performed in PubMed, Scopus, EMBASE, Web of Science, Cochrane Library, BIOSIS, LILACS, CNKI, CBM, Wan Fang, and other regional databases up to February 1, 2025. Eligible case-control studies assessing the association between *PARP-1* rs1136410 polymorphism and CRC or GC were included. Pooled odds ratios (ORs) and 95% confidence intervals (CIs) were calculated under five genetic models using Comprehensive Meta-Analysis software.

Results: Thirteen case-control studies were included, comprising 3.591 patients and 5.433 controls. For GC (8 studies; 1,784 cases and 2,521 controls), significant associations were observed under multiple genetic models: allele comparison (C vs. T: OR=2.01, 95% CI 1.04-3.91, p=0.039), homozygous comparison (CC vs. TT: OR=1.77, 95% CI 1.24-2.52, p=0.002), heterozygous comparison (CT vs. TT: OR=1.36, 95% CI 1.18-1.57, p<0.001), and recessive comparison (CC vs. CT+TT: OR=1.54, 95% CI 1.08-2.20, p=0.017). No significant association was detected for CRC (5 studies; 1.807 cases and 2.912 controls). Ethnic subgroup analysis revealed a protective

ÖZ

Amaç: Poli (ADP-riboz) polimeraz-1 (*PARP-1*), DNA onarım yolaklarında önemli bir enzimdir ve kansere yatkınlıkla ilişkili olduğu düşünülmektedir. *PARP-1* genindeki rs1136410 polimorfizmi, farklı popülasyonlarda gastrointestinal kanser riski ile tutarsız ilişkiler göstermiştir. Bu meta-analiz, etnik farklılıklara odaklanarak *PARP-1* rs1136410 polimorfizmi ile kolorektal kanser (CRC) ve mide kanseri (GC) riski arasındaki ilişkiyi değerlendirmeyi amaçlamıştır.

Yöntemler: PubMed, Scopus, EMBASE, Web of Science, Cochrane Library, BIOSIS, LILACS, CNKI, CBM, Wan Fang ve diğer bölgesel veritabanlarında 1 Şubat 2025 tarihine kadar sistematik bir literatür taraması yapıldı. *PARP-1* rs1136410 polimorfizmi ile CRC veya GC arasındaki ilişkiyi değerlendiren uygun olgu-kontrol çalışmaları dahil edildi. Comprehensive Meta-Analysis yazılımı kullanılarak beş genetik model altında birleştirilmiş odds oranları (OR) ve %95 güven aralıkları (CI) hesaplandı.

Bulgular: 3.591 hasta ve 5.433 kontrolü içeren on üç olgu-kontrol çalışması dahil edildi. GC için (8 çalışma; 1.784 olgu ve 2.521 kontrol), çoklu genetik modeller altında anlamlı ilişkiler gözlemlenmiştir: alel karşılaştırması (C vs. T: OR=2,01, %95 CI 1,04-3,91, p=0,039), homozigot karşılaştırması (CC vs. TT: OR=1,77, %95 CI 1,24-2,52, p=0,002), heterozigot karşılaştırması (CT vs. TT: OR=1,36, %95 CI 1,18-1,57, p<0,001) ve resesif karşılaştırması (CC vs. CT+TT: OR=1,54, %95 CI 1,08-2,20, p=0,017). CRC için anlamlı bir ilişki tespit edilmemiştir (5 çalışma;

Address for Correspondence: M.H. Antikchi, Yazd Branch, Islamic Azad University, Department of Internal Medicine, Yazd, Iran
E-mail: mhantikchi.gastro@gmail.com **ORCID ID:** orcid.org/0000-0001-7781-5740

Received: 04 June 2025
Accepted: 28 August 2025
Published: 29 September 2025

Cite as: Naseri A, Antikchi MH, Soleymani S et al. PARP-1 rs1136410 polymorphism and gastrointestinal cancer risk: a meta-analysis of cancer-type and ethnic-specific associations. Medeni Med J. 2025;40:116-127

effect against CRC in Caucasians but increased susceptibility in Asians.

Conclusion: The *PARP-1* rs1136410 polymorphism is associated with elevated GC risk but not CRC, with ethnicity-dependent effects suggesting differential genetic susceptibility. These findings highlight the importance of considering population-specific genetic backgrounds in gastrointestinal cancer risk assessment, prevention, and precision medicine strategies.

Keywords: Colorectal cancer, Gastric cancer, *PARP-1*, rs1136410 polymorphism, meta-analysis, genetic susceptibility, ethnic variation

1.807 olgu ve 2.912 kontrol). Etnik alt grup analizi, Kafkasyalılarda CRC'ye karşı koruyucu bir etki olduğunu, ancak Asyalılarda duyarlılığın arttığını ortaya koymuştur.

Sonuçlar: *PARP-1* rs1136410 polimorfizmi, GC riskiyle ilişkili olmakla birlikte CRC ile ilişkili değildir ve etnik kökene bağlı etkiler, farklı genetik duyarlılığa işaret etmektedir. Bu bulgular, gastrointestinal kanser risk değerlendirmesi, önleme ve hassas tıp stratejilerinde popülasyona özgü genetik arka planların dikkate alınmasının önemini vurgulamaktadır.

Anahtar kelimeler: Kolorektal kanser, mide kanseri, *PARP-1*, rs1136410 polimorfizmi, meta-analiz, genetik duyarlılık, etnik varyasyon

INTRODUCTION

Gastrointestinal cancers, particularly colorectal cancer (CRC) and gastric cancer (GC), pose a significant global health challenge[1]. In the US, 2024 projections estimate 152,810 new CRC diagnoses (81.540 in males, 71.270 in females) and 53.010 deaths (28.700 men, 24.310 women)[2-4]. CRC incidence and mortality exhibit racial/ethnic disparities, with Black Americans experiencing the highest rates, followed by Native Americans. Hispanic and Asian American/Pacific Islander populations show lower incidence, with Hispanic populations having better outcomes than non-Hispanic Whites[5-7]. These disparities stem from complex interactions of genetics, environment, and social determinants. GC has a distinct profile, with approximately 26,890 new cases (16.160 in males, 10.730 in females) and 10.880 deaths projected for 2024. Unlike CRC, GC incidence is higher among the Asian and Hispanic populations, as well as non-Hispanic Black Americans[8-10]. GC etiology includes Helicobacter pylori infection, tobacco use, diet, and familial predisposition, highlighting gene-environment interactions[11,12]. Understanding these patterns is crucial for investigating genetic polymorphisms influencing cancer risk[13].

Poly (ADP-ribose) polymerase-1 (*PARP-1*), also known as ADPRT, PARP, and NAD(+)-glycohydrolase, is crucial in the DNA damage response and repair via poly (ADP-ribosyl)ation[14,15]. In CRC, PARP-1 has a dual role, inhibiting tumor initiation via its interaction with the DNA repair protein O6-methylguanine-DNA methyltransferase, and promoting tumor progression influenced by genetic and environmental factors[16,17]. Increased *PARP-1* mRNA and protein levels are associated with worse outcomes in CRC, particularly in tumors with mutated p53[18-20]. *PARP-1* might also contribute to the cancer stem cell phenotype, essential for tumor aggressiveness and recurrence[18,21]. In GC, high *PARP-1* expression is associated with aggressive tumor traits such as invasion and metastasis, with specific single nucleotide polymorphisms of the *PARP-1* gene linked to increased susceptibility and lymph node metastasis[22]. *PARP-1* activation is involved in GC pathogenesis, especially through its interaction with Helicobacter pylori, which can stimulate *PARP-1* activity and promote inflammatory responses that encourage tumor development[23,24]. Consequently, the use of PARP inhibitors as potential treatments for GC has become more appealing, as they may improve the efficacy of standard chemotherapies like cisplatin[25].

The *PARP-1* gene, located on chromosome 1q41-42 and containing 23 exons, features the extensively studied SNP rs1136410 (Val762Ala)[13,26]. This SNP, resulting from a single nucleotide change that potentially alters *PARP-1*'s role in DNA repair and cancer-related processes, has been linked to cancer risk, particularly colorectal and GCs. Meta-analyses suggest a significant association between the rs1136410 C > T polymorphism and increased cancer susceptibility, especially in GC. The C allele is associated with increased risk for thyroid and cervical cancers, and decreased risk for brain cancer[27]. The association with GC is particularly strong in East Asian populations[27,28]. However, conflicting results suggest that the rs1136410 polymorphism may be protective or exhibit no correlation in some demographics or cancer types[29], highlighting the complexity of genetic influences on cancer. These inconsistencies necessitate comprehensive meta-analyses to clarify genetic associations. This meta-analysis investigates the relationship between *PARP-1* rs1136410 and CRC/GC risk, aiming to provide insights for patient risk assessment and management, especially in population-specific genetic counseling and precision medicine, and to establish evidence-based recommendations for incorporating genetic polymorphism data into clinical decision-making for gastrointestinal cancer prevention and early detection.

MATERIALS and METHODS

Literature Search and Database Selection

This systematic review and meta-analysis did not require ethical approval because it did not involve primary data collection from human subjects. A comprehensive literature search was conducted across

multiple electronic databases through February 1, 2025, to ensure complete and up-to-date coverage of relevant studies examining the association between the *PARP-1* rs1136410 polymorphism and CRC or GC risk, including both English and non-English publications. The databases searched included PubMed/MEDLINE, Scopus, EMBASE, Web of Science, Cochrane Library, BIOSIS Citation Index, LILACS, the Cochrane Central Register of Controlled Trials, ClinicalTrials.gov, ProQuest Dissertations and Theses, Google Scholar, OpenGrey, and region-specific sources such as the China National Knowledge Infrastructure, Chinese Biomedical Database, Wan Fang Database, and VIP Information/Chinese Science and Technology Journal Database (VIP). The search strategy utilized a combination of Medical Subject Headings terms and free-text keywords, with cancer-related terms such as "colorectal cancer," "gastric cancer," "stomach cancer," "colon cancer," "rectal cancer," "digestive tract cancer," "gastrointestinal carcinoma," "gastric neoplasm," and "digestive system neoplasms"; *PARP-1* related terms including "poly (ADP-ribose) polymerase 1," "*PARP-1*," "NAD+ ADP-ribosyltransferase 1," "poly (ADP-ribose) synthase 1," and "DNA repair enzyme"; and polymorphism-specific terms such as "rs1136410," "Val762Ala," "V762A," "C>T," "single nucleotide polymorphism," "SNP," "genotype," "allele," "mutation," "variant," and "genetic susceptibility." Boolean operators (AND, OR, NOT), truncation, and proximity operators were applied to optimize retrieval. Reference lists of identified articles, relevant meta-analyses, and review papers were manually screened for additional studies. Ethical approval was not required for this systematic review and meta-analysis, as no primary data collection from human subjects was involved.

Study Selection Criteria

Studies were independently screened by two investigators using predefined inclusion and exclusion criteria. Inclusion criteria required: (1) case-control or cohort study design examining human subjects; (2) investigation of *PARP-1* rs1136410 polymorphism association with CRC or GC risk; (3) availability of sufficient genotype frequency data to calculate odds ratios (ORs) and 95% confidence intervals (CIs); (4) clearly defined case and control populations with appropriate diagnostic criteria. Exclusion criteria eliminated: (1) animal studies, in vitro experiments, or cell line investigations; (2) studies lacking complete genotype frequency data; (3) family-based or linkage studies involving related individuals; (4) abstracts, case reports, editorials, reviews, conference proceedings, or meta-analyses; (5) duplicate publications or overlapping study populations. When multiple publications reported on the same study population, only the most recent or largest study was included to prevent data duplication.

Data Extraction and Management

Two independent reviewers extracted data using standardized forms, with disagreements resolved through discussion or consultation with a third reviewer when necessary. Extracted variables included first author name and publication year; study design and geographic location; participant ethnicity categorized as Asian, Caucasian, African, Hispanic, or mixed populations; total sample sizes for cases and controls; genotype frequencies for *PARP-1* rs1136410 polymorphism in both cases and controls; genotyping methodology employed; Hardy-Weinberg equilibrium (HWE) test results in control groups; and minor allele frequencies in control groups. When data were unclear or missing, original study authors were contacted via email for clarification.

Quality Assessment

Study quality was evaluated using the Newcastle-Ottawa Scale (NOS), a validated tool for assessing the quality of non-randomized studies in meta-analyses[30,31]. The NOS evaluates three domains: selection of study groups (4 criteria), comparability of groups (1 criterion with 2 subcategories), and ascertainment of exposure or outcome (3 criteria). Each criterion awards one star except comparability, which can award up to two stars, resulting in a maximum score of nine stars. Studies scoring seven or more stars were classified as high quality, while those scoring five to six stars were considered of moderate quality and remained eligible for inclusion.

Statistical Analysis Methods

Meta-analysis was performed using Comprehensive Meta-Analysis software version 2.0. The association between *PARP-1* rs1136410 polymorphism and cancer risk was assessed using ORs with 95% CIs under five genetic inheritance models: allele comparison (C vs. T), homozygous comparison (CC vs. TT), heterozygous comparison (CT vs. TT), dominant model (CC+CT vs. TT), and recessive model (CC vs. CT+TT). HWE in control groups was evaluated using Fisher's exact test, with p-values <0.05 indicating deviation[32]. Between-study heterogeneity was assessed using Cochran's Q statistic and quantified using the I^2 statistic, which describes the percentage of total variation across studies due to heterogeneity rather than chance. I^2 values of 25%, 50%, and 75% were interpreted as low, moderate, and high heterogeneity, respectively.

When significant heterogeneity was detected (P<0.10 for Q statistic or I^2>50%), a random-effects model using the DerSimonian-Laird method was employed; otherwise, a fixed-effects model using the Mantel-Haenszel method was applied[33-35]. Predefined subgroup analyses were conducted by ethnicity, geographic region, control source (population-based vs. hospital-based), and genotyping method to explore potential sources of heterogeneity[36]. Sensitivity analyses were performed by sequentially excluding individual studies to assess the robustness of pooled estimates. Publication bias was evaluated using Begg's funnel plots and Egger's linear regression test, with p<0.05 indicating significant bias. When publication bias was detected, the trim-and-fill method was applied to adjust pooled estimates. All statistical tests were two-sided with significance set at p<0.05.

RESULTS

Study Selection and Characteristics

As shown in Figure 1, the initial literature search identified 420 articles, which were reduced to 203 unique articles after removing duplicates. Title and abstract screening excluded 113 studies, leaving 90 for full-text review. Ultimately, 13 case-control studies met all eligibility criteria, comprising 3,591 cancer patients and 5,433 healthy controls. These included five CRC studies (1.807 cases, 2.912 controls) [37-41] and eight GC studies (1.784 cases, 2.521 controls)[42-48]. Table 1 shows the characteristics of selected studies. Published between 2004 and 2023, the studies represented global geographic distribution, including the United States, Singapore, China, Saudi Arabia, South Korea, and Brazil, and consisted predominantly of Asian (10 studies), with Caucasian (3 studies) and mixed ethnicity representation, reflecting

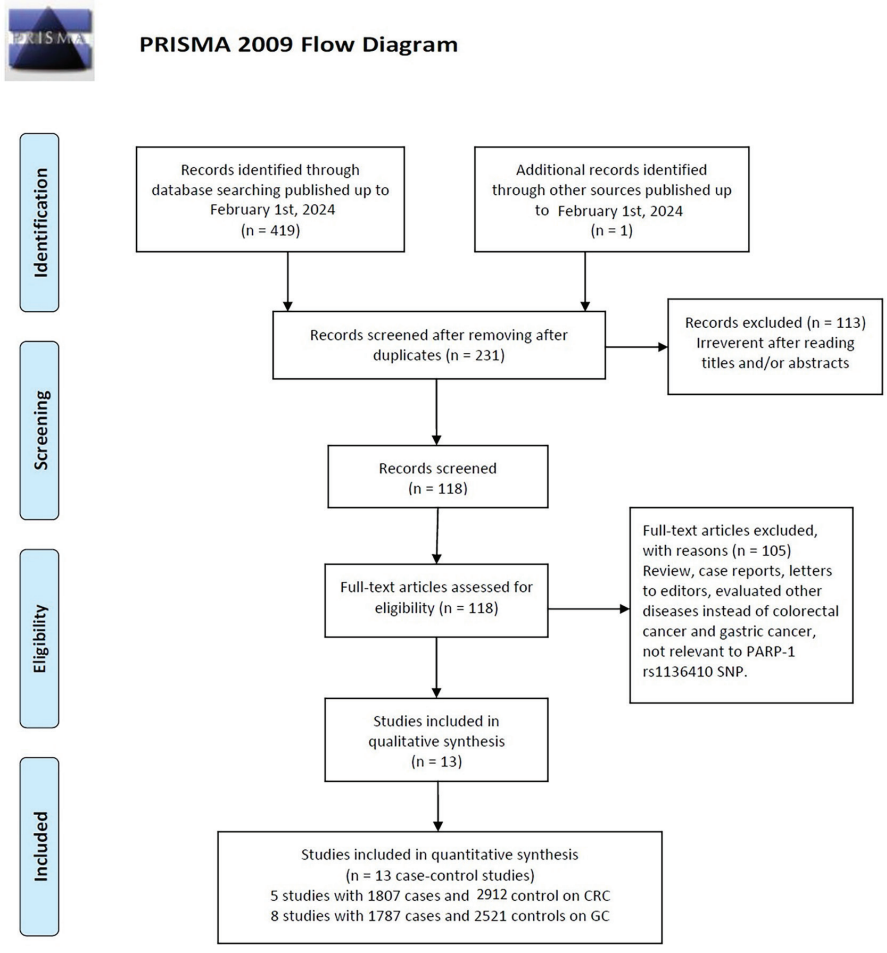

Figure 1. Flowchart depicting the selection process for eligible studies.

Illustrates the stepwise process used to identify and select studies meeting the inclusion criteria for this meta-analysis. It details the number of studies screened, assessed for eligibility, and included in the final analysis.

Table 1. Key features of the studies included in the meta-analysis.

Author/Year	Cancer type	Country (Ethnicity)	SOC	Genotype method	Case/ Control	Case					Control					HWE	MAF	NOS
						TT	TC	CC	T	C	TT	TC	CC	T	C			
Berndt[37]	CRC	USA(Caucasian)	PB	TaqMan	691/702	492	179	20	1163	219	488	183	31	1159	245	0.116	0.175	10
Stern[38]	CRC	Singapore(Asian)	PB	TaqMan	307/1173	93	150	64	336	278	381	564	228	1326	1020	0.456	0.435	11
Brevik[39]	CRC	USA(Caucasian)	FB	TaqMan	308/361	196	100	12	492	124	239	110	12	588	134	0.879	0.186	8
Li[40]	CRC	China(Asian)	HB	PCR-RFLP	451/626	134	228	89	496	406	222	319	85	763	489	0.078	0.391	8
Alshammari[41]	CRC	KSA(Asian)	HB	Sequence	50/50	47	2	1	96	4	49	1	0	99	1	0.943	0.010	8
Miao[42]	GC	China(Asian)	HB	PCR-RFLP	500/1000	150	257	93	557	443	396	492	112	1284	716	0.026	0.358	10
Zhang[47]	GC	China(Asian)	HB	PCR-RFLP	138/110	85	37	16	207	69	80	25	5	185	35	0.114	0.159	5
Zhang[43]	GC	China(Asian)	HB	PCR-RFLP	236/320	113	83	40	309	163	181	106	33	468	172	0.005	0.269	10
Kang[44]	GC	China(Asian)	PB	SNaPshot	150/152	70	67	13	207	93	88	50	14	226	78	0.089	0.257	5
Kim[45]	GC	Korea(Asian)	HB	GoldenGate	151/320	42	70	39	154	148	102	161	57	365	275	0.635	0.430	5
Wen[46]	GC	China(Asian)	HB	MassARRAY	307/307	96	154	57	346	268	105	132	70	342	272	0.024	0.443	5
Tang[25]	GC	China(Asian)	PB	PCR-RFLP	200/210	122	56	22	300	100	162	40	8	364	56	0.011	0.133	5
Dantas[48]	GC	Brazil(Mixed)	HB	AS-PCR	102/102	86	16	0	188	16	87	15	0	189	15	0.422	0.074	7

CRC: Colorectal cancer; GC: Gastric cancer; SOC: Source of controls, HB: Hospital based; PB, Population based, PCR-RFLP: Polymerase chain reaction-restriction fragment length polymorphism, AS: Allele-specific polymerase chain reaction, HWE, Hardy-Weinberg equilibrium, MAF: Minor allele frequency; NOS: Newcastle-Ottawa score

cancer prevalence and enabling ethnic subgroup analyses. State-of-the-art genotyping methodologies were employed, including restriction fragment length polymorphism (RFLP)- polymerase chain reaction (PCR), TaqMan assays, SNaPshot sequencing, Illumina GoldenGate assays, Sequenom MassARRAY, and AS-PCR. The NOS indicated generally high study quality, but four GC studies (Miao[42], Zhang[43], Wen[46], Tang[25]) exhibited deviations from HWE ($p<0.05$), potentially impacting those analyses.

Quantitative Synthesis of Genetic Associations

Colorectal Cancer Risk Analysis

A meta-analysis of five studies investigating CRC risk found no significant overall association between the PARP-1 rs1136410 polymorphism and CRC risk across all genetic models (Table 2). However, ethnic stratification revealed significant population-specific differences. In Caucasian populations, the *PARP-1* rs1136410 C allele demonstrated a significant protective effect against CRC development. The allele comparison model (C vs. T) showed a substantial risk reduction (OR=0.487, 95% CI 0.299-0.794, p=0.004), indicating that individuals carrying the C allele have approximately 51% lower odds of developing CRC compared to those with the T allele. This protective effect was consistent across multiple genetic models. Conversely, Asian populations exhibited a significantly increased CRC risk associated with the C allele. The allele comparison revealed a substantial risk elevation (C vs. T: OR=5.785, 95% CI 4.481-7.467, p≤0.001), indicating nearly six-fold increased odds of CRC development. The homozygous comparison (CC vs. TT: OR=1.413, 95% CI 1.094-1.824, p=0.008) and recessive model (CC vs. CT+TT: OR=1.302, 95% CI 1.040-1.629, p=0.021) further supported this increased risk pattern in Asian populations.

Gastric Cancer Risk Analysis

The meta-analysis of eight GC studies demonstrated consistent and statistically significant associations between the *PARP-1* rs1136410 polymorphism and increased GC risk across multiple genetic inheritance models, providing robust evidence for genetic susceptibility to GC. The allele comparison model (C vs. T) showed a significant association with GC risk (OR=2.012, 95% CI 1.035-3.911, p=0.039), indicating that the C allele approximately doubles the odds of GC development (Figure 2A). The homozygous comparison (CC vs. TT) revealed an even stronger association (OR=1.766, 95% CI 1.239-2.515, p=0.002), suggesting that individuals homozygous for the C allele face nearly 77% increased odds of developing

GC (Figure 2B). Heterozygous comparison (CT vs. TT: OR=1.359, 95% CI 1.180-1.565, p≤0.001) demonstrated significant risk elevation even in carriers of a single C allele (Figure 2C). The dominant model (CC+CT vs. TT: OR=0.649, 95% CI 0.455-0.927, p=0.017) (Figure 2D) and recessive model (CC vs. CT+TT: OR=1.541, 95% CI 1.079-2.200, p=0.017) (Figure 2E) provided additional evidence for the association. Ethnic subgroup analysis revealed that the association between *PARP-1* rs1136410 polymorphism and GC risk was particularly pronounced in Asian populations, where the majority of included studies were conducted. This finding aligns with the known higher prevalence of GC in East Asian countries and suggests potential gene-environment interactions specific to these populations.

Heterogeneity Test

Heterogeneity analysis of the PARP-1 rs1136410 polymorphism showed variable inconsistency across genetic models and cancer types. In CRC, the C versus T genotype comparison exhibited high heterogeneity (I^2=98.36%, pH ≤0.001), indicating significant variability in study outcomes. Moderate heterogeneity was observed for CC versus TT and CC+CT versus TT (I^2 = 54.43% and

Table 2. Results of the meta-analysis on the PARP-1 rs1136410 polymorphism regarding the risk of colorectal and gastric cancer.

	Genetic model	Type of model	Heterogeneity		Odds ratio (OR)				Publication bias	
			I^2 (%)	P_H	OR	95% CI	Z_{OR}	P_{OR}	P_{Beggs}	P_{Eggers}
Colorectal Cancer										
Overall	C vs. T	Random	98.36	≤0.001	1..660	0.435-6.331	0.742	0.458	0.462	0.595
	CC vs. TT	Fixed	54.43	0.067	1.239	0.990-1.551	1.869	0.062	0.806	0.865
	CT vs. TT	Fixed	0.00	0.827	1.077	0.937-1.237	1.043	0.297	0.462	0.331
	CC+CT vs. TT	Fixed	48.29	0.102	0.844	0.689-1.033	-1.644	0.100	0.806	0.852
	CC vs. CT+TT	Fixed	48.29	0.102	1.185	0.968-1.451	0.713	0.476	0.806	0.852
Ethnicity										
Caucasians	C vs. T	Random	82.14	0.018	0.487	0.299-0.794	-2.883	0.004	NA	NA
	CC vs. TT	Fixed	36.90	0.208	0.791	0.494-1.268	-0.973	0.331	NA	NA
	CT vs. TT	Fixed	0.00	0.523	1.016	0.836-1.235	1.235	0.162	NA	NA
	CC+CT vs. TT	Fixed	28.99	0.235	1.270	0.795-2.029	1.001	0.317	NA	NA
	CC vs. CT+TT	Fixed	28.99	0.235	0.787	0.493-1.258	-1.001	0.317	NA	NA
Asians	C vs. T	Fixed	0.00	0.448	5.785	4.481-7.467	13.474	≤0.001	0.296	0.138
	CC vs. TT	Fixed	26.10	0.258	1.413	1.094-1.824	2.652	0.008	1.000	0.798
	CT vs. TT	Fixed	0.00	0.817	1.143	0.938-1.394	1.323	0.186	1.000	0.474
	CC+CT vs. TT	Fixed	26.67	0.256	0.768	0.614-0.962	-2.302	0.021	1.000	0.772
	CC vs. CT+TT	Fixed	26.67	0.256	1.302	1.040-1.629	2.302	0.021	1.000	0.772
Gastric Cancer										
Overall	C vs. T	Random	93.67	≤0.001	2.012	1.035-3.911	2.063	0.039	0.173	0.472
	CC vs. TT	Random	61.65	0.016	1.766	1.239-2.515	3.149	0.002	0.763	0.752
	CT vs. TT	Fixed	0.00	0.742	1.359	1.180-1.565	4.266	≤0.001	0.710	0.944
	CC+CT vs. TT	Random	67.94	0.007	0.649	0.455-0.927	-2.380	0.017	0.548	0.667
	CC vs. CT+TT	Random	67.94	0.005	1.541	1.079-2.200	2.380	0.017	0.548	0.667
Ethnicity										
Asians	C vs. T	Random	93.36	≤0.001	2.494	1.290-4.819	2.718	0.007	0.367	0.827
	CC vs. TT	Random	61.65	0.016	1.766	1.239-2.515	3.149	0.002	0.763	0.752
	CT vs. TT	Fixed	0.00	0.682	1.370	1.187-1.581	4.303	≤0.001	1.000	0.715
	CC+CT vs. TT	Random	67.94	0.005	0.649	0.455-0.927	-2.380	0.017	0.548	0.667
	CC vs. CT+TT	Random	67.94	0.005	1.541	1.079-2.200	2.380	0.017	0.548	0.667

NA: Not applicable, H: Heterogeneity, Beggs: Begg's test, Eggers: Egger's test

48.29%, respectively), but the p-values did not indicate significant heterogeneity. Conversely, in the CT versus TT and CC versus CT+TT models, no heterogeneity was observed (I^2=0.00%). In GC, substantial heterogeneity was also found for C versus T (I^2=93.67%, p≤0.001) and CC versus TT (I^2=61.65%, p=0.016), while CT versus TT showed no variability (I^2=0.00%). Random effects models for specific comparisons in both CRC and GC revealed significant heterogeneity, especially among Asian populations, suggesting potential genetic or environmental influences on cancer risk across ethnicities. Overall, these heterogeneity findings highlight the complexity of interpreting associations between the *PARP-1* rs1136410 polymorphism and cancer risk.

Sensitivity Analyses

The sensitivity analysis, conducted to evaluate the influence of individual studies on the meta-analysis of the *PARP-1* rs1136410 polymorphism, demonstrated that no single study significantly altered the overall ORs across different genetic models, confirming the robustness of the findings. Exclusion of four studies deviating from HWE (Miao[42], Zhang[43], Wen[46], and Tang[25]) did not substantially change the pooled OR estimates. Specifically, for GC, after excluding the HWE-violating studies, significant associations were observed in the allele model (C vs. T: OR=1.89, 95% CI 1.12-3.21, p=0.018), homozygous model (CC vs. TT: OR=1.68, 95% CI 1.15-2.46, p=0.007), heterozygous model (CT vs. TT: OR=1.31, 95% CI 1.09-1.58, p=0.004), and recessive model (CC vs. CT+TT: OR=1.39,

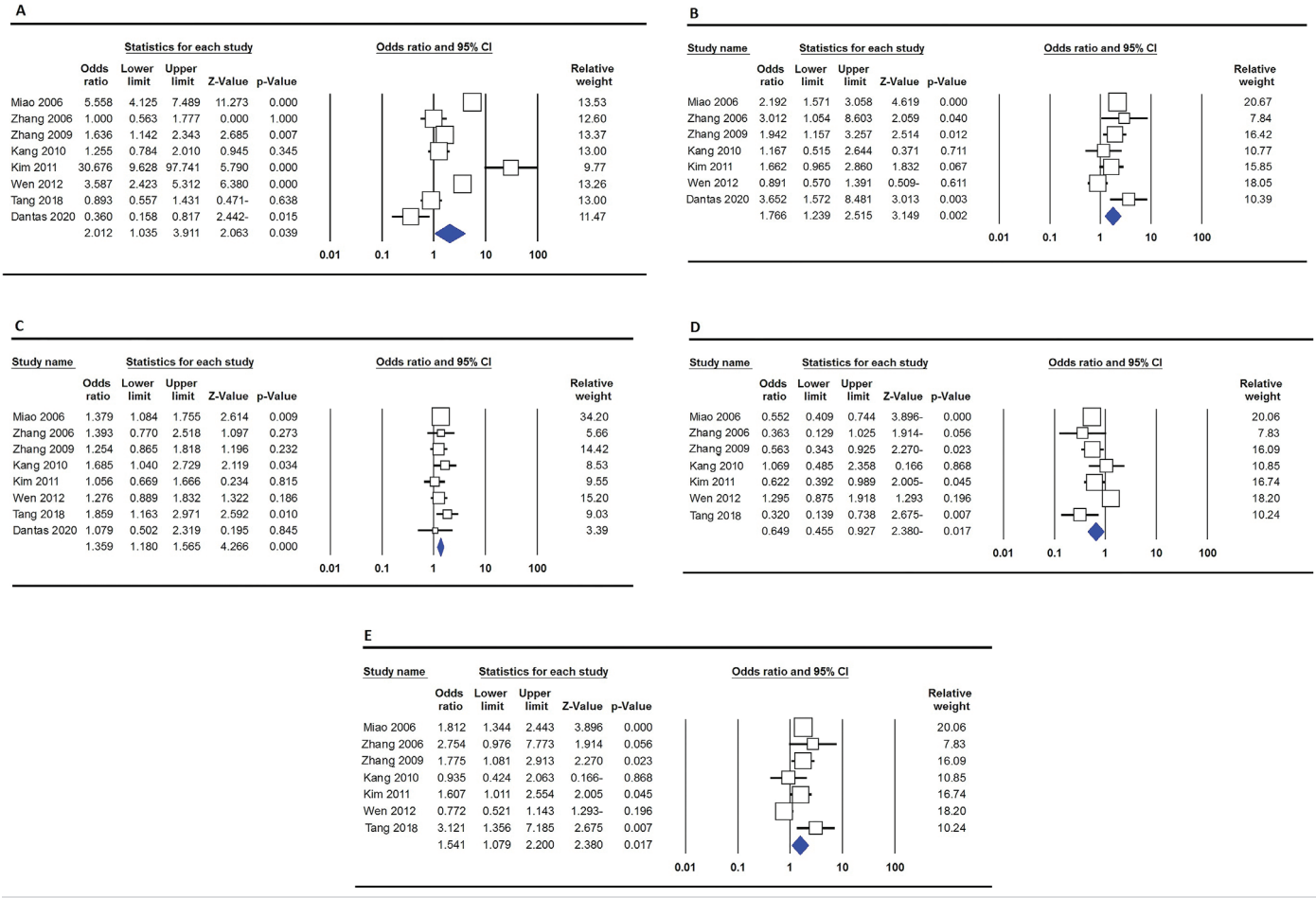

Figure 2. Forest plot illustrating the association between the *PARP-1* rs1136410 polymorphism and GC risk. **A)** allele (C vs. T). **B)** homozygote (CC vs. TT. **C)** heterozygote (CT vs. TT). **D)** dominant (CC+CT vs. TT). **E)** recessive (CC vs. CT+TT).

Presents a forest plot summarizing the meta-analysis results for the association between the *PARP-1* rs1136410 polymorphism and GC risk. Sub-figures A-E correspond to different genetic models (allele, homozygote, heterozygote, dominant, and recessive). The plot shows effect sizes (odds ratios) and 95% confidence intervals for individual studies and the overall pooled estimate.

95% CI 1.01-1.91, p=0.043), while the dominant model showed a borderline association (CC+CT vs. TT: OR=0.72, 95% CI 0.51-1.01, p=0.058). For CRC, all genetic models remained non-significant with effect sizes comparable to the main analysis, though ethnic-specific patterns -protective in Caucasians and risk-enhancing in Asians- persisted. Overall, these results reinforce the reliability of the meta-analysis conclusions and strengthen confidence in the observed association between the *PARP-1* rs1136410 polymorphism and cancer susceptibility, thereby enhancing the credibility of the study.

Publication Bias

The assessment of publication bias for the *PARP-1* rs1136410 polymorphism in relation to CRC and GC revealed varying results across different genetic models and ethnicities. Funnel plots (Figure 3A-E) indicate publication bias in the association between the PARP-1 rs1136410 polymorphism and the risks of CRC and GC. Begg's and Egger's tests indicated no significant publication bias for most genetic comparisons in CRC (p>0.05), including C vs. T, CC vs. TT, CT vs. TT, and CC+CT vs. TT models, and CC vs. CT+TT models (Begg's p=0.806;

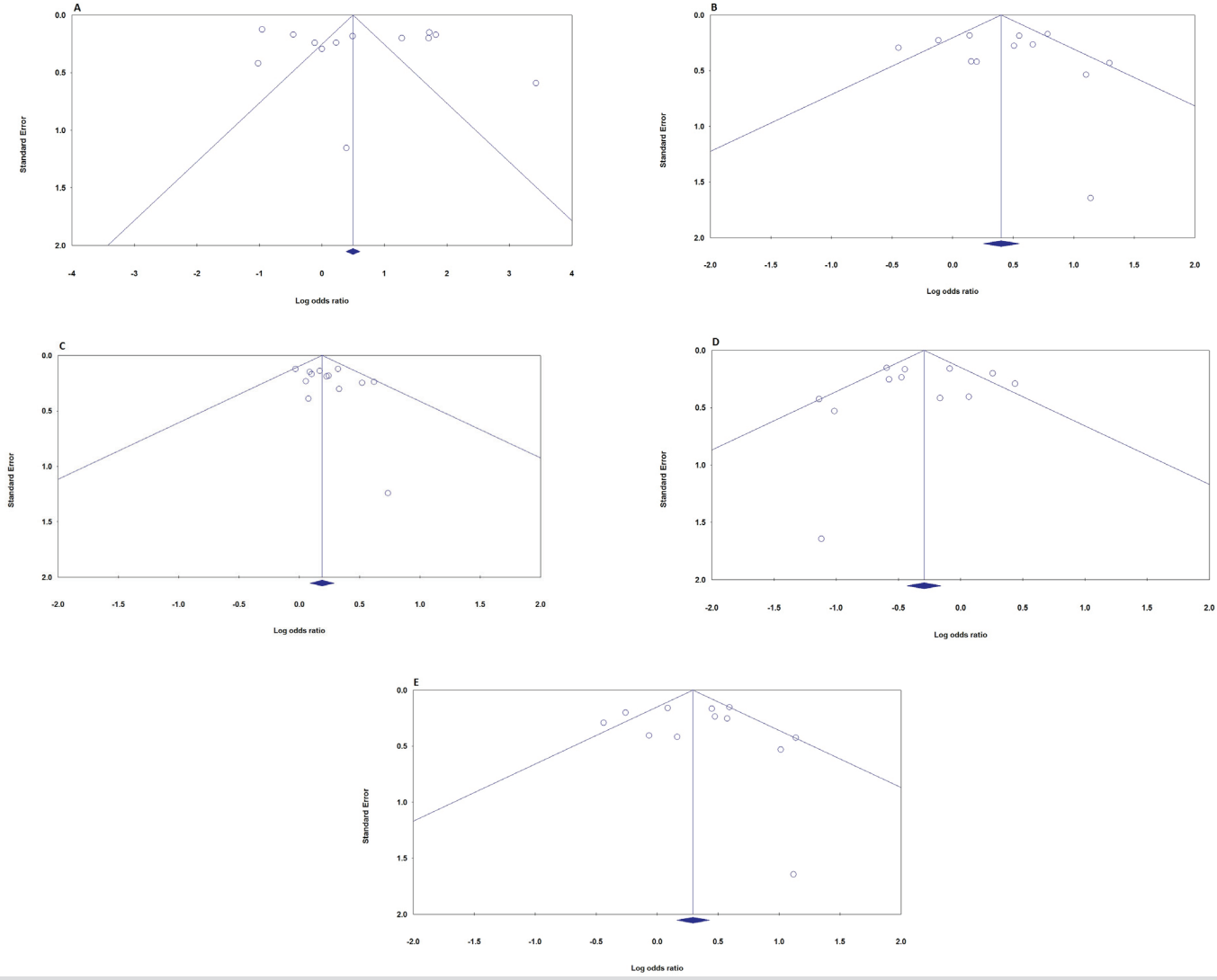

Figure 3. Funnel plots assessing publication bias for the association between the *PARP-1* rs1136410 polymorphism and CRC and GC risk. A) allele model (C vs. T). B) homozygote model (CC vs. TT). C) heterozygote model (CT vs. TT). D) dominant model (CC+CT vs. TT). E) recessive model (CC vs. CT+TT).

Displays funnel plots evaluating publication bias in the meta-analysis of PARP-1 rs1136410 and CRC/GC risk. Sub-figures A-E represent the same genetic models as in Figure 2. The funnel plot shapes indicate potential presence or absence of publication bias.

Egger's p=0.852). Similarly, among Asians, the C vs. T model showed no evidence of publication bias (Begg's p=0.296; Egger's p=0.138), while other comparisons exhibited limited variation, mostly indicating no bias (p≥0.050). For GC, assessment of publication bias also showed consistent results, with most comparisons displaying no significant bias, (C vs. T: Begg's p=0.173; Egger's p=0.472; CC vs. TT: Begg's p=0.763; Egger's p=0.752). These findings suggest a general absence of publication bias across the analyzed genetic models, reaffirming the robustness of the examined associations between the *PARP-1* rs1136410 polymorphism and cancer risk.

DISCUSSION

This meta-analysis provides strong evidence for a link between the *PARP-1* rs1136410 polymorphism and increased GC risk. This aligns with *PARP-1*'s role in gastric carcinogenesis. The C allele is associated with an approximate two-fold increase in GC odds (OR=2.012, 95% CI 1.035-3.911, p=0.039). Furthermore, individuals with two copies of the risk allele (CC vs. TT: OR=1.766, 95% CI 1.239-2.515, p=0.002) show a substantially elevated cancer susceptibility, suggesting a gene-dosage effect. Even a single copy of the variant allele (CT vs. TT: OR=1.359, 95% CI 1.180-1.565, p≤0.001) confers a measurable increased risk, indicating a dose-dependent influence on cancer development. The Val762Ala amino acid substitution encoded by rs1136410, located within the *PARP-1* catalytic domain, may affect enzyme activity and DNA repair. In GC, where *Helicobacter pylori* infection causes chronic inflammation and DNA damage, altered *PARP-1* function could impair cellular responses to genotoxic stress. Previous meta-analyses support this association, with Li et al.[26] suggesting a borderline significant increase in cancer risk associated with the C allele, particularly for GC. Qin et al.[28] found elevated risk for GC among Asian populations (OR=1.17, 95% CI 1.09-1.25). Hu et al.[29] also reported increased susceptibility to gastrointestinal cancers, especially within Asian populations.

In contrast to the GC findings, no overall association was found between the *PARP-1* rs1136410 polymorphism and CRC risk. This difference may reflect fundamental distinctions in the molecular pathways driving colorectal versus gastric carcinogenesis. Factors like distinct embryological origins, tissue microenvironments, and mutational signatures could lead to varying selective pressures on DNA repair mechanisms. The multistep nature of colorectal carcinogenesis, involving specific genetic alterations such as *Adenomatous Polyposis Coli* mutations and microsatellite or chromosomal instability, might overshadow the impact of *PARP-1* variants. Different roles of environmental factors in gastric and colorectal carcinogenesis may also modulate the penetrance of genetic susceptibility variants. The meta-analysis, encompassing five CRC studies (807 cases and 2.912 controls), provides sufficient statistical power to suggest that any association is likely small and clinically insignificant at the population level.

Ethnic Stratification and Population-Specific Risk Assessment

Ethnic stratification analysis reveals opposing effects of the *PARP-1* rs1136410 polymorphism on CRC risk in Caucasian and Asian populations. In Caucasians, the C allele demonstrates a protective effect, with approximately 51% risk reduction (OR=0.487, 95% CI 0.299-0.794, p=0.004), while in Asians, it is associated with a six-fold increase in CRC odds, (OR=5.785, 95% CI 4.481-7.467, p≤0.001). These differences likely reflect complex interactions between the rs1136410 variant and population-specific genetic backgrounds, including linkage disequilibrium patterns, modifier gene allele frequencies, and distinct evolutionary histories. The magnitude of these ethnic differences necessitates a fundamental reconsideration of how genetic risk factors are incorporated into clinical practice and public health strategies. For Caucasian populations, individuals carrying the C allele of rs1136410 may warrant less intensive CRC screening, while Asian individuals carrying this variant may benefit from enhanced surveillance. However, the implementation of such ethnicity-specific recommendations requires careful consideration of factors such as the accuracy of self-reported ethnicity, the increasing prevalence of mixed-ancestry individuals, and the potential to exacerbate healthcare disparities. Future research should prioritize identifying causal variants and developing polygenic risk scores that account for population-specific effect sizes and allele frequencies.

Methodological and Geographic Considerations

This meta-analysis identified HWE deviations in nine of the included studies (p<0.05), indicating potential issues in study design, population stratification, or genotyping quality. While excluding these studies in sensitivity analyses did not significantly change the overall findings, the frequency of HWE deviations suggests a need for more rigorous quality control in future research. Significant heterogeneity across studies, addressed using random-effects models, reflects the complexity of genetic associations across diverse populations, study designs, and environmental contexts. Quality assessment using the NOS indicated predominantly high-quality

studies,majority ≥7 stars, supporting the validity of the included research despite these challenges. Moreover, the global distribution of studies, including data from the United States, Singapore, China, Saudi Arabia, South Korea, and Brazil, strengthens the analysis by allowing for assessment of population-specific effects. However, the predominance of Asian studies (10 out of 13) may limit the generalizability of the findings and underscores the need for more research in underrepresented populations, particularly African and Hispanic populations. The temporal span of included studies (2004-2023) reflects advancements in genotyping technology, from RFLP-PCR to high-throughput platforms like TaqMan assays, Illumina GoldenGate, and Sequenom MassARRAY. The consistency of results across this technological timeline suggests that the observed associations represent genuine biological phenomena rather than platform-specific artifacts, although technological evolution likely contributes to some observed heterogeneity.

Clinical Implications and Translational Potential

This meta-analysis suggests that incorporating *PARP-1* rs1136410 genotyping into personalized gastrointestinal cancer risk assessment is warranted. In GC, the consistent association with the C allele across multiple genetic models indicates its potential contribution to polygenic risk scores for stratified screening, particularly in high-risk individuals or those with additional risk factors. The observed two-fold increased risk with the C allele is clinically relevant and could influence screening recommendations. For CRC, ethnic-specific effects (protective in Caucasians, increased risk in Asians) offer opportunities for ancestry-specific risk stratification, but require careful implementation in diverse healthcare systems. Future research should focus on clinical decision support tools integrating genetic information, traditional risk factors, and ancestry-specific effect sizes. The association between *PARP-1* rs1136410 and GC risk also has implications for PARP inhibitor therapy. Individuals with risk variants may exhibit differential responses due to altered baseline *PARP-1* activity or dependencies on PARP-mediated DNA repair. Genotype-associated tumor characteristics may guide patient selection for PARP inhibitor monotherapy or combination therapy with chemotherapeutics like cisplatin. Understanding the functional consequences of the Val762Ala substitution may reveal mechanisms of PARP inhibitor resistance and sensitivity, informing the development of improved PARP inhibitors. Ethnic-specific effects suggest potential pharmacogenomic considerations for optimizing PARP inhibitor dosing across diverse populations.

Limitations and Future Research Directions

Despite the rigorous methodology applied in this meta-analysis, several limitations should be acknowledged. These include reliance on retrospective case-control studies that limit causal inference and introduce potential selection bias, and significant heterogeneity across included studies likely reflects unmeasured confounders. Frequent deviations from HWE in control groups, particularly in GC studies, may suggest underlying biases, while the ethnic imbalance caused by the predominance of Asian populations constrains the generalizability of the findings. Additionally, variability in genotyping methods and incomplete adjustment for environmental exposures may have further influenced the results. Looking forward, future research should prioritize prospective cohort studies with robust phenotyping and environmental exposure assessment, alongside large-scale, multi-ethnic genome-wide association studies and polygenic risk scoring to improve predictive accuracy. Functional investigations are essential to clarify the biological consequences of the rs1136410 (Val762Ala) variant and its role in DNA repair, while Mendelian randomization could help establish causality. Integrating multi-omics approaches would provide a more comprehensive understanding of how *PARP-1* variants contribute to disease susceptibility, while pharmacogenomic studies linking rs1136410 genotype with PARP inhibitor response in clinical trials could yield immediate translational relevance. Ultimately, the development of ancestry-informed genetic risk calculators incorporating multiple variants alongside clinical and environmental risk factors represents an important step toward advancing precision medicine.

CONCLUSION

This meta-analysis provides compelling evidence for cancer-type and ethnicity-specific associations between *PARP-1* rs1136410 polymorphism and gastrointestinal cancer risk, with significant implications for personalized medicine approaches in oncology. The consistent association with increased GC risk across multiple genetic models, combined with the striking ethnic differences in CRC susceptibility, underscores the complexity of genetic influences on cancer development and the necessity of population-specific risk assessment strategies. These findings advance our understanding of the genetic architecture of gastrointestinal cancers and provide a foundation for developing more precise, ancestry-aware approaches to cancer screening, prevention, and treatment. Future research should focus on mechanistic studies, multi-ethnic validation, and

clinical implementation strategies to translate these genetic insights into improved patient outcomes and population health benefits.

Ethics

Ethics Committee Approval: This article does not contain any studies with human participants or animals performed by any of the authors.

Acknowledgments

The authors wish to extend their heartfelt appreciation to all the contributors of the articles incorporated in this meta-analysis. Their invaluable insights and efforts were crucial to the successful completion of this manuscript.

Footnotes

Author Contributions

Surgical and Medical Practices: A.N., Concept: M.H.A., A.N., S.M.H., H.N., Design: S.S., R.N., Data Collection and/or Processing: A.N., M.K.-M., B.M., M.V.I-O.,Analysis or Interpretation: A.S.-D., H.N., Literature Search: S.S., R.N., A.S.-D.,Writing: M.V.I-O., H.N.

Conflict of Interest: The authors have no conflict of interest to declare.

Financial Disclosure: The authors declared that this study has received no financial support.

REFERENCES

1. Antikchi MH, Asadian F, Dastgheib SA, et al. Cumulative evidence for association between IL-8 -251T>A and IL-18 -607C>A polymorphisms and colorectal cancer susceptibility: a systematic review and meta-analysis. J Gastrointest Cancer. 2021;52:31-40.
2. Siegel RL, Giaquinto AN, Jemal A. Cancer statistics, 2024. CA Cancer J Clin. 2024;74:12-49.
3. Ghelmani Y, Asadian F, Antikchi MH, et al. Association between the hOGG1 1245C>G (rs1052133) polymorphism and susceptibility to colorectal cancer: a meta-analysis based on 7010 cases and 10,674 controls. J Gastrointest Cancer. 2021;52:389-98.
4. Mollanoori H, Ghelmani Y, Hassani B, Dehghani M. Integrated whole transcriptome profiling revealed a convoluted circular RNA-based competing endogenous RNAs regulatory network in colorectal cancer. Sci Rep. 2024;14:91.
5. Carethers JM. Racial and ethnic disparities in colorectal cancer incidence and mortality. Adv Cancer Res. 2021;151:197-229.
6. Zavala VA, Bracci PM, Carethers JM, et al. Cancer health disparities in racial/ethnic minorities in the United States. Br J Cancer. 2020;124:315-32.
7. Antikchi MH, Neamatzadeh H, Ghelmani Y, et al. The Risk and prevalence of COVID-19 infection in colorectal cancer patients: a systematic review and meta-analysis. J Gastrointest Cancer. 2021;52:73-9.
8. Morgan E, Arnold M, Camargo MC, et al. The current and future incidence and mortality of gastric cancer in 185 countries, 2020-40: a population-based modelling study. EClinicalMedicine. 2022;47:101404.
9. Huang D, Song M, Abe SK, et al. Family history and gastric cancer incidence and mortality in Asia: a pooled analysis of more than half a million participants. Gastric Cancer. 2024;27:701-13.
10. Behboudi E, Charostad J, Nakhaie M, Khajouei A, Ghelmani Y. JNK Signaling pathways and oncoviruses. Iran J Med Microbiol. 2024;18:148-62.
11. Mamun TI, Younus S, Rahman MH. Gastric cancer-Epidemiology, modifiable and non-modifiable risk factors, challenges and opportunities: An updated review. Cancer Treat Res Commun. 2024;41:100845.
12. Farahani NN, Kalani BS, Monavari SH, et al. Therapeutic effects, immunogenicity and cytotoxicity of a cell penetrating peptide-peptide nucleic acid conjugate against caga of helicobacter pylori in cell culture and animal model. Iran J Microbiol. 2021;13:360-71.
13. Keshmiri F, Ghelmani Y. The effect of continuing interprofessional education on improving learners' self-efficacy and attitude toward interprofessional learning and collaboration. J Interprof Care. 2023;37:448-56.
14. Harrision D, Gravells P, Thompson R, Bryant HE. Poly(ADP-Ribose) glycohydrolase (PARG) vs. poly(ADP-Ribose) Polymerase (PARP) - Function in genome maintenance and relevance of inhibitors for anti-cancer therapy. Front Mol Biosci. 2020;7:191.
15. Montazer F, Alizadeh-Navaei R. Expression of GLUT1 in neoplastic cells of papillary thyroid cancer. Turk J Oncol. 2019;34:243-7.
16. Dörsam B, Seiwert N, Foersch S, et al. PARP-1 protects against colorectal tumor induction, but promotes inflammation-driven colorectal tumor progression. Proc Natl Acad Sci U S A. 2018;115:E4061-70.
17. Nakhaie M, Charostad J, Behboudi E, et al. Investigation of liver function test findings in COVID-19 patients considering the disease timeline. Jundishapur J Microbiol. 2024;17:e153763.
18. Puentes-Pardo JD, Moreno-SanJuan S, Casado J, et al. PARP-1 expression influences cancer stem cell phenotype in colorectal cancer depending on p53. Int J Mol Sci. 2023;24:4787.
19. Montazer F, Boozari B, Alizadeh-Navaei R. Evaluation of LGR5 cancer stem cell marker expression in breast cancer and its relationship with hormonal profile and clinical pathological features. Asian Pac J Cancer Prev. 2023;24:467-70.
20. Zekri A, Mesbahi Y, Boustanipour E, Sadr Z, Ghaffari SH. The potential contribution of microRNAs in anti-cancer effects of aurora kinase inhibitor (AZD1152-HQPA). J Mol Neurosci. 2018;65:444-55.
21. Demuth P, Thibol L, Lemsch A, et al. Targeting PARP-1 and DNA damage response defects in colorectal cancer chemotherapy with established and novel PARP inhibitors. Cancers (Basel). 2024;16:3441.
22. L Liu Y, Zhang Y, Zhao Y, Gao D, Xing J, Liu H. High PARP-1 expression is associated with tumor invasion and poor prognosis in gastric cancer. Oncol Lett. 2016;12:3825-35.
23. Allah MSABD, Kariem HMABD, Rashad HM. Evaluation of (PARP-1) Expression in Gastric Carcinoma by Immunohistochemistry and Quantitative Real-Time PCR and its Relation to HER2 Status. Med J Cairo Univ. 2020;88:1581-7.
24. Montazer F, Jahani Amiri K, Mofarrah R, Ahmadi A, Nouripour B, Mofarrah R. A first case of fixed drug eruption due to Tamsulosin. J Cosmet Dermatol. 2020;19:1143-5.
25. Tang W, Liu X, Qiu L, et al. Influence of hypoxia-related genetic polymorphisms on the prognosis of patients with metastatic gastric cancer treated with EOF. Oncol Lett. 2018;15:1334-42.

26. Li H, Zha Y, Du F, Liu J, Li X, Zhao X. Contributions of PARP-1 rs1136410 C>T polymorphism to the development of cancer. J Cell Mol Med. 2020;24:14639-44.
27. Xin Y, Yang L, Su M, Cheng X, Zhu L, Liu J. PARP1 rs1136410 Val762Ala contributes to an increased risk of overall cancer in the East Asian population: a meta-analysis. J Int Med Res. 2021;49:300060521992956
28. Qin Q, Lu J, Zhu H, et al. PARP-1 Val762Ala polymorphism and risk of cancer: a meta-analysis based on 39 case-control studies. PLoS One. 2014;9:e98022.
29. Hu Y, Zhou M, Li K, et al. Two DNA repair gene polymorphisms on the risk of gastrointestinal cancers: a meta-analysis. Tumour Biol. 2014;35:1715-25.
30. Gholami S, Hazar N, Bagheri-Fahraji B, et al. The Association between Metabolic Syndrome and the Consumption of some Supplements. J Nutr Food Secur. 2022;7(3):355-61.
31. Naderipour Z, Behnezhad F, Charostad J, et al. Assessment of Torque Teno Virus (TTV) frequency in healthy blood donors in the central region of Iran, Yazd. Int J Hematol Stem Cell Res. 2024;18:110-6.
32. Sadr Z, Rohani M, Jamali P, Alavi A. A case report of concurrent occurrence of two inherited axonopathies within a family: the benefit of whole-exome sequencing. Int J Neurosci. 2024;134:1282-7.
33. Habibi A, Talebi H, Bahrami R, et al. A comprehensive integration of data on the association of ITPKC polymorphisms with susceptibility to Kawasaki disease: a meta-analysis. BMC Med Genomics. 2025;18:56.
34. Vafapour M, Talebi H, Danaei M, et al. G Global and population-specific association of MTHFR polymorphisms with preterm birth risk: a consolidated analysis of 44 studies. BMC Pregnancy Childbirth. 2025;25:230.
35. Ghasemi A, Sadr Z, Babanejad M, Rohani M, Alavi A. Copy number variations in hereditary spastic paraplegia-related genes: evaluation of an Iranian hereditary spastic paraplegia cohort and literature review. Mol Syndromol. 2023;14:477-84.
36. Talebi H, Dastgheib SA, Vafapour M, et al. Association of SLCO1B1 genetic variants with neonatal hyperbilirubinemia: a consolidated analysis of 36 studies. BMC Pediatr. 2025;25:251.
37. Berndt SI, Huang WY, Fallin MD, et al. Genetic variation in base excision repair genes and the prevalence of advanced colorectal adenoma. Cancer Res. 2007;67:1395-404.
38. Stern MC, Conti DV, Siegmund KD, et al. DNA repair single-nucleotide polymorphisms in colorectal cancer and their role as modifiers of the effect of cigarette smoking and alcohol in the Singapore Chinese Health Study. Cancer Epidemiol Biomarkers Prev. 2007;16:2363-72.
39. Brevik A, Joshi AD, Corral R, et al. Polymorphisms in base excision repair genes as colorectal cancer risk factors and modifiers of the effect of diets high in red meat. Cancer Epidemiol Biomarkers Prev. 2010;19:3167-73.
40. Li Y, Li S, Wu Z, et al. Polymorphisms in genes of APE1, PARP1, and XRCC1: risk and prognosis of colorectal cancer in a northeast Chinese population. Med Oncol. 2013;30:505.
41. Alshammari AH, Shalaby MA, Alanazi MS, Saeed HM. Novel mutations of the PARP-1 gene associated with colorectal cancer in the Saudi population. Asian Pac J Cancer Prev. 2014;15:3667-73.
42. Miao X, Zhang X, Zhang L, et al. Adenosine diphosphate ribosyl transferase and x-ray repair cross-complementing 1 polymorphisms in gastric cardia cancer. Gastroenterology. 2006;131:420-7.
43. Zhang Q, Li Y, Li X, et al. PARP-1 Val762Ala polymorphism, CagA+ H. pylori infection and risk for gastric cancer in Han Chinese population. Mol Biol Rep. 2009;36:1461-7.
44. Kang SL, Li YM, He W, et al. Association between PARP-1 polymorphisms and susceptibility to gastric cancer. World Chin J Dig. 2010;18:1434-41.
45. Kim JH, Pyun JA, Lee KJ, Cho SW, Kwack KB. [Study on association between single nucleotide polymorphisms of MMP7, MMP8, MMP9 genes and development of gastric cancer and lymph node metastasis]. Korean J Gastroenterol. 2011;58:245-51.
46. Wen YY, Pan XF, Loh M, et al. ADPRT Val762Ala and XRCC1 Arg194Trp polymorphisms and risk of gastric cancer in Sichuan of China. Asian Pac J Cancer Prev. 2012;13:2139-2144.
47. Zhang Z, Miao XP, Tan W, Guo YL, Zhang XM, Lin DX. [Correlation of genetic polymorphisms in DNA repair genes ADPRT and XRCC1 to risk of gastric cancer]. Ai Zheng. 2006;25:7-10.
48. Dantas RN, Souza AM, Herrero SST, Kassab P, Malheiros CA, Lima EM. Association between PSCA, TNF-α, PARP1 and TP53 gene polymorphisms and gastric cancer susceptibility in the brazilian population. Asian Pac J Cancer Prev. 2020;21:43-8.