Association of the eIF4E (rs11723037) gene polymorphism and IL-23 levels with the risk of developing psoriasis

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Abstract. Psoriasis is a chronic inflammatory skin disease mediated by an immune mechanism and influenced by multiple genetic disorders. Despite extensive global research, the potential immunogenetic involvement of the eukaryotic translation initiation factor 4E (eIF4E) polymorphism (rs11723037) in psoriasis remains uninvestigated. To the best of our knowledge, this is the first study to evaluate the association between the eIF4E rs11723037 polymorphism and psoriasis in a specific population. While previous studies have demonstrated the biological and functional involvement of eIF4E in psoriasis, the potential contribution of this specific genetic variant to psoriasis susceptibility has not yet been adequately investigated. The present study included 87 individuals with clinically confirmed psoriasis and 80 healthy controls, in whom baseline characteristics, eIF4E genotypes and serum IL-23 concentrations were assessed. Genomic DNA was amplified by tetra-primer amplification refractory mutation system PCR to determine the eIF4E rs11723037 genotype, while IL-23 serum concentrations were quantified using ELISA. The present study revealed that patients with psoriasis exhibited significantly elevated serum levels of IL-23 and a higher frequency of the eIF4E rs11723037 genotype compared with the healthy controls. On the whole, these findings suggest that both Il-23 and the eIF4E rs11723037 polymorphism are associated with psoriasis susceptibility and may serve as complementary biomarkers.

Introduction

Psoriasis is a chronic inflammatory (immune-mediated) disorder of the skin characterized by rapid keratinocyte proliferation, leading to marked alterations in epidermal structure and the appearance of well-circumscribed, erythematous plaques covered with silvery scales (1). Although the underlying mechanisms of the condition remain obscure, it is accepted that genetic predisposition and environmental trigger(s) play a critical role in its development (2). Epidemiological studies indicate that psoriasis is distributed worldwide, with a prevalence of ~2-3% in numerous countries (3).

Psoriasis is an immune cell-mediated inflammatory skin disease. While recent studies have demonstrated that certain antimicrobial peptides are linked to the development of psoriasis, these mechanisms of action have not yet been fully understood (4). However, it is clear that the interleukin (IL)-23/IL-17 axis plays a crucial role in the development of psoriasis; the effectiveness of new biological treatments such as TNF-α, IL-23 and IL-17 inhibitors has verified these findings (5). It has been shown that immune-related cells, such as dendritic cells (DCs) and macrophages, are related to the development of psoriasis, in addition to other molecules, such as Toll-like receptors (TLRs) and various cytokines, including interferon (IFN)α, TNF-α, IL-12, IL-22, IL-23 and IL-17 (6).

TLRs are key pattern recognition receptors of the innate immune system that recognize pathogen-associated molecular patterns and damage-associated molecular patterns, thereby initiating a host immune response (7,8). Upon activation, TLRs trigger intracellular signaling pathways, particularly the NF-κB pathway, leading to the production and release of pro-inflammatory cytokines, including members of the IL family (9). The coordinated interaction between TLRs and ILs plays a critical role in regulating both innate and adaptive immune responses and maintaining immune homeostasis (10). Therefore, genetic differences within IL genes may influence cytokine expression and functional activity, thereby affecting the magnitude of inflammatory reactions and potentially explaining variations among individuals in their susceptibility to immune-related disorders and disease outcomes. Genetic polymorphisms in IL genes have attracted considerable attention as they can modify cytokine production and immune homeostasis, thereby playing a critical role in the susceptibility and progression of immune-mediated diseases (11).

Psoriasis develops through a multifaceted immune-mediated process characterized by a complex interaction among dendritic cells, lymphocytes and keratinocytes (12). Chronic

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immune dysfunction is a hallmark of psoriasis and leads to the abnormal hyperproliferation of epidermal keratinocytes. The underlying inflammatory response is mainly sustained by cytokines secreted by infiltrating immune cells, particularly DCs and pathogenic T-lymphocytes. IL-17 is considered one of the principal cytokines driving keratinocyte hyperproliferation and chronic cutaneous inflammation. Consequently, the Il-23/Il-17 signaling pathway is currently recognized as a central regulator of the molecular, cellular and histopathological features that characterize psoriasis (13,14).

Eukaryotic translation initiation factor 4E (eIF4E) functions as a key regulator of gene expression in the eukaryotic system and participates in several critical cellular processes, including proliferation, apoptosis and cellular differentiation (15). Evidence from previous research indicates that eIF4E and several eIF subunits are upregulated in psoriatic skin, indicating their role in psoriasis pathophysiology and highlighting their potential as direct targets for topical therapeutic intervention (16).

IL-23 is mainly secreted by antigen-presenting cells, while the receptor is found on numerous innate and adaptive immune cells, enabling these cells to amplify their immunological activity (17). External stimuli, such as tissue injury or infection, trigger the release of host-derived nucleotides, which subsequently interact with antimicrobial peptides produced by keratinocytes. Plasmacytoid DCs release type I IFNs, which subsequently activate myeloid dendritic cells to produce pro-inflammatory cytokines such as IL-23 and TNF-α (18). Recent studies have indicated that the activation of T-cells and DCs plays a central role in the development of psoriasis (19). The disease is largely driven by the IL-23 signaling pathway, which suggests that keratinocytes are capable of producing IL-23 themselves (18). IL-23 is likely to play a central role in the development of type 1 autoimmune and inflammatory diseases in humans (20). The aim of the present study was to examine whether the eIF4E (rs11723037) gene variant and circulating IL-23 levels are linked to the pathogenesis and severity of psoriasis.

Subjects and methods

Study design. The present research was performed in compliance with established ethical guidelines governing studies involving human participants. Baseline demographic and clinical characteristics and peripheral venous blood samples were collected from all participants at enrollment from October 20, 2024 to April 1, 2025. The study design received formal approval from the Ethics Committee of North Al-Nasiriyah Hospital (Nasiriyah, Iraq; ethical approval no. DV/NNH/24/045; October 15, 2024). Furthermore, the Scientific Research Ethics Committee of Al-Ayen Iraqi University (Nasiriyah, Iraq) covered the laboratory analysis of blood samples, data processing, and manuscript preparation (ethical approval no. 22 on January 5, 2025). The present study was conducted in accordance with the ethical standards of the Dhi-Qar Health Department, and written informed consent was obtained from all participants prior to patient enrollment. A total of 87 patients of both sexes newly diagnosed with psoriasis and who had not received any prior therapy were enrolled in the present study. The study was conducted on participants aged 18-70 years of age who presented to the Dermatology and Venereology Department of North Al-Nasiriyah Hospital. In addition, 80 healthy volunteers without a family history of psoriasis were selected as the control group. The overall workflow and sequential procedures followed in the present study are illustrated in Fig. 1.

Collection of blood samples. For the present study, ~6 ml venous blood were collected from each participant, with 1 ml transferred to an EDTA tube for genomic DNA extraction and the subsequent analysis of the rs11723037 polymorphism, while the remaining 5 ml were collected in a clot-activator tube for serum separation. Following centrifugation at 1,380 x g for 10 min at 25˚C, serum was stored at -20˚C until analysis, and serum IL-23 concentrations were quantified using a commercial ELISA kit (BT Lab; cat. no. E0074Hu) as previously described (21).

Inclusion and exclusion criteria. Participants were enrolled according to previously established inclusion and exclusion criteria (22). Healthy controls were recruited from the Clinical Dermatology Department (North Al-Nasiriyah Hospital, Dhi Qar Health Directorate, Ministry of Health, Iraq), while the psoriasis patient group consisted of treatment-naïve patients with newly diagnosed disease, minimizing the potential confounding effect of prior therapy on clinical, immunological and genetic findings. Special physiological (pregnancy) and medical conditions (chronic celiac disease and autoimmune illness) were excluded to reduce possible confounding variable. Furthermore, patients with a history of psoriasis treatment were not eligible for enrollment, ensuring that the study population consisted exclusively of treatment-naïve cases.

Human genomic DNA extraction. The extraction of genomic DNA from whole blood samples was carried out using the FavorPrep™ Blood/Cultured Cells Genomic DNA Extraction Mini kit (Favorgen Biotech Corp.) (23). DNA purity was subsequently measured using a NanoDrop 2000 microvolume UV/Visible spectrophotometer (Thermo Fisher Scientific, Inc.). Spectrophotometric measurements were performed using elution buffer as the blank, and the purity of the DNA samples was assessed by calculating the absorbance ratio at 260/280 nm. According to the manufacturer's protocol (Thermo Fisher Scientific, Inc.), DNA samples with an absorbance ratio close to 1.8 were considered pure, with concentrations ranging between 4 and 10 μg/ml.

Primer design. The eIF4E gene polymorphism evaluated in the present study was rs11723037, which was identified using the National Centre for Biotechnology Information (NCBI) database. The primer design process was performed *in silico* within a dry lab environment using available bioinformatics tools prior to experimental validation (24). Two specific primer sets were designed using the publicly available Primer1 tool (http://primer1.soton.ac.uk/primer.html) according to previously described protocols (24,25). The specificity and melting temperatures of the designed primers were assessed using BLAST analysis (http://www.ncbi.nlm.nih.gov/BLAST), and the primer sequences are presented in Table I.

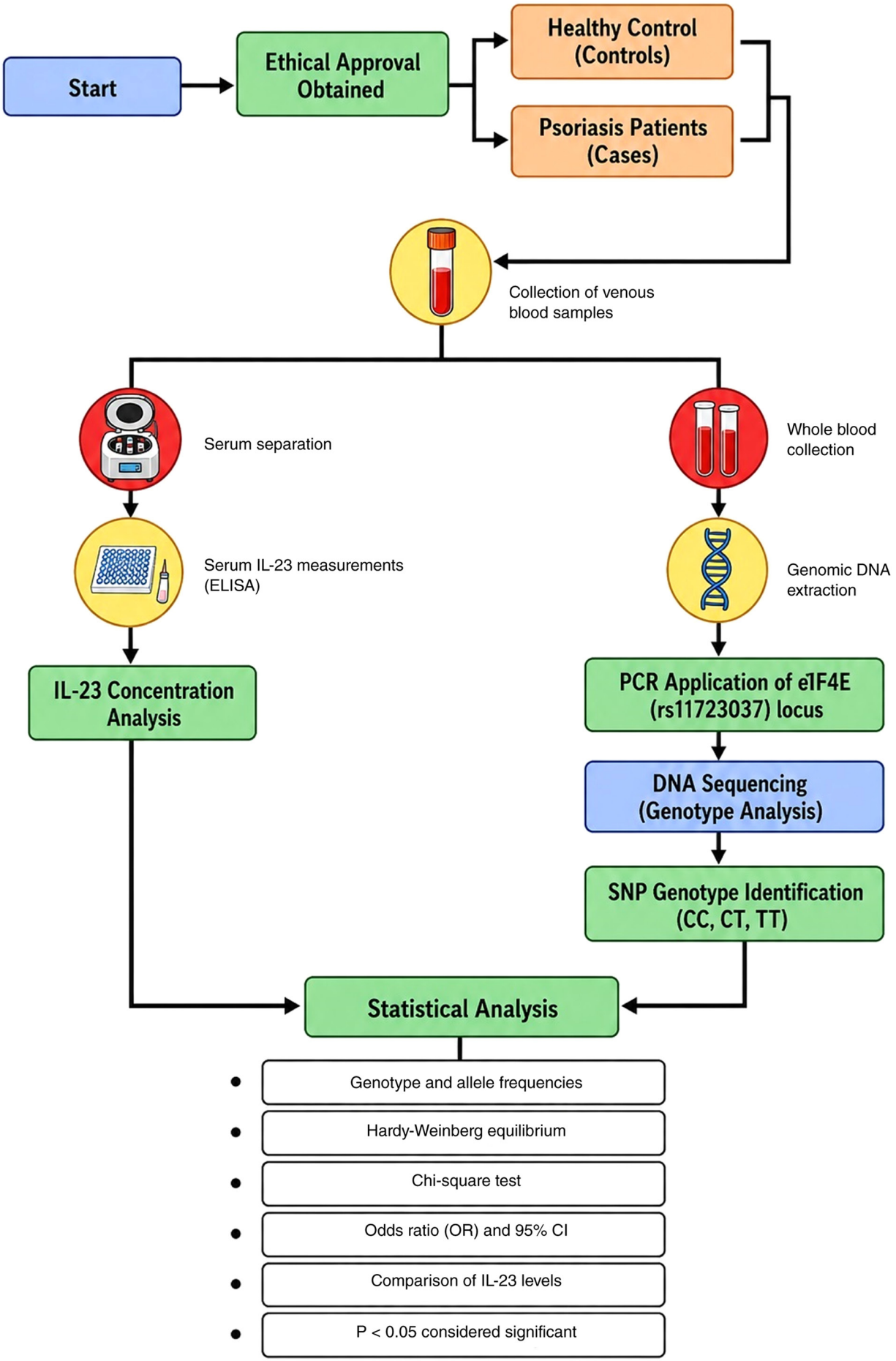

Figure 1. Diagram illustrating the overall workflow and sequential procedures followed in the methodology of the present study.

Table I. List of primers utilized in tetra-primer ARMS PCR for the genotyping of eIF4E polymorphisms.

SNP ID	Primer set	Temperature (˚C)	Product size
rs11723037	Forward inner primer: 923 GTCCGCGGGAGGTCAGGTCCAACATAAC 950	75	202 bp
(C allele)	Reverse inner primer: 976 ACTGTACCCCTTGCCGCCCCTTCCTCT 950	75	257 bp
(A allele)	Forward outer primer (5'-3'): *720 GGCCCTGCGCCTTCCTATCATGAAG ACA 747	75	404 bp
	Reverse outer primer (5'-3'): 1123 CCTTCTGGAGCGGTTGTGCGATCAG ATC 1096	75	

The numbers present before and after each sequence indicate the nucleotide positions of the primer sequences within the reference sequence.

Optimization steps of tetra-primer ARMS PCR. Critical factors in optimizing tetra-primer ARMS PCR included the determination of optimal outer- to-inner primer ratios and annealing temperature, aiming to minimize non-specific amplification. A gradient PCR approach, testing multiple annealing temperatures in a single run, combined with adjustment of primer ratios, was used to refine the protocol. The PCR reaction was assembled at 20 μl total volume, containing 10 μl KAPATaq 2X ready mix (Kapa Biosystems, Inc.). Optimized ratios of outer and inner primers (10 nm/μl each) and 1-3 μl genomic DNA (20-50 ng/μl) were used. DNA amplification was performed using a Bio-Rad C1000 thermocycler (Bio-Rad Laboratories, Inc.). The optimum outer-to-inner ratio for tetra-primer ARMS PCR for rs11723037 was determined to be 1:2.

The PCR protocol included an initial denaturation at 95˚C for 2 min, followed by 35 amplification cycles comprising denaturation at 95˚C for 30 sec, annealing at 56˚C for 30 sec, extension at 72˚C for 1 min, and a final extension step at 72˚C for 2 min (26). For result analysis, 5 μl PCR product was combined with 2 μl loading buffer and electrophoresed on a 3% agarose gel (1st BASE) pre-stained with ethidium bromide (molecular biology grade; cat. no. ETBC1001, MP Biomedicals). A 100-1500 bp DNA marker (1st BASE) served as the molecular size reference.

Immune assays. In the present case-control study, both patients with psoriasis and healthy subjects were examined to determine IL-23 levels using a commercial IL-23 ELISA kit (BT-Lab; cat. no. E0074Hu), in accordance with the manufacturer's guidelines (27). Cytokine concentrations were quantified for each group using an ELISA assay. All reagents were provided by BT Lab. Venous blood (5 ml) was collected with a sterile syringe, placed into gel tubes, and centrifuged at 1,380 x g for 20 min at 25˚C to separate the components. Serum specimens were preserved in 1.5-ml Eppendorf tubes at -20˚C until the analysis of all serological markers. The IL-23 levels in each sample were measured using an ELISA reader with an absorbance of 450 nm, in accordance with the manufacturer's guidelines (BT Lab).

Statistical analysis. Standard statistical tests were used to analyze the data. The Chi-squared test was used to compare categorical variables when the test's assumptions were satisfied. However, when expected cell counts were <5, Fisher's exact test was used instead. Furthermore, comparisons between two independent groups were performed using the independent samples t-test following the assessment of data normality using the Shapiro-Wilk test. Moreover, odds ratios (ORs) with 95% confidence intervals (CIs) were calculated to estimate the strength of the association between frequencies of genotypes and susceptibility to psoriasis (26). Data were analyzed with the Statistical Package for the Social Sciences (SPSS) program (version 20) (IBM Corp.) (28).

Results

Distribution of patients and controls

Age and sex. In the present study, the data demonstrated that of the 87 participants (patients with psoriasis) 63 (72.5%) were males and 24 (27.5%) and females. In addition, of the 80 healthy individuals, 60 (75%) were males and 20 (25%) were females. There were no significant differences in sex distribution between the patients with psoriasis and the healthy individuals (P-value=0.839; Table II).

The distribution of the patients with psoriasis and the healthy individual according to age is presented in Table III. As regards the patients with psoriasis 17 (19.5%) were between 30-40 years, 32 (36.8%) were between 41-50 years and 38 (43.7) were >50 years of age. As regards the healthy control group, 15 (18.75%) were between 30-40 years, 30 (37.50%) were between 41-50 years and 35 (43.75%) were >50 years of age. There were no significant differences (P-value=0.990) in age distribution between the patients with psoriasis and the healthy individuals (Table III).

Family history. The analysis of participant characteristics (demographic and clinical) between the patients with psoriasis and healthy controls revealed that a family history of psoriasis was significantly associated with the disease (P<0.001). A positive family history was confirmed by 40.2% (35/87) of the patients, whereas none of the controls had a similar history, suggesting a significant genetic predisposition. By contrast, the baseline characteristics did not differ significantly between the two groups. However, in the patient group the prevalence of smoking was slightly elevated (49.4%) compared with the controls (31.3%). Similarly, the distribution of patients according to residential area (urban/rural) was comparable to that of the controls. A statistically significant differences were observed between the patients and the

Table II. Comparison of sex distribution between the patients with psoriasis and the healthy controls.

Sex	Patients with psoriasis (n=87)	Healthy individuals	χ^2 value	P-value
Sex			0.041	0.839
Male	63 (72.4%)	60 (75.0%)		
Female	24 (27.6%)	20 (25.0%)		
Total	87 (100%)	80 (100%)		

Data are presented as number (n) and percentage (%). The P-value was calculated using the Chi-squared test. P<0.05 was considered to indicate a statistically significant difference.

Table III. Comparison of age distribution between the patients with psoriasis and the healthy controls.

Age, years	Patients with psoriasis (n=87)	Healthy controls (n=80)	P-value
Age group			0.990
30-40	17 (19.5%)	15 (18.75%)	
41-50	32 (36.8%)	30 (37.50%)	
>50	38 (43.7%)	35 (43.75%)	
Total	87 (100%)	80 (100%)	

Data are presented as number (n) and percentage (%). The P-value was calculated using the Chi-squared test (χ^2=0.019). P<0.05 was considered to indicate a statistically significant difference.

control group as regards alcohol consumption, with alcohol consumption reported in 10% (8/80) of the control group compared with nil (0/87) of the psoriasis patients (P<0.0029). Furthermore, no significant association was observed with respect to the existence of hypertension between the patients and controls (Table IV).

Immune markers. The serum level of IL-23 was significantly elevated in the patients with psoriasis (770.22±5.51 pg/ml) compared to the healthy individuals (395.44±9.77 pg/ml), with a highly significant difference (P<0.001; Table V).

Genotype and allele frequencies of the eIF4E (rs11723037) gene polymorphism. The results of PCR analysis of the eIF4E gene polymorphism are illustrated in Fig. 2. The present study revealed the presence of three bands at 404, 257 and 202 bp, which represented the genotyping pattern of psoriasis in the patients and control subjects. The samples that exhibited only a single band (404 bp) were classified as wild-type homozygous, while the samples that displayed two bands (257 and 202 bp) represented the allele. Furthermore, the presence of three bands in the same lane indicated the heterozygous genotype. These PCR detected results were subsequently confirmed by tetra-primer ARMS-PCR.

The results of the comparison of the genotype and allele frequencies of the eIF4E gene polymorphism (rs11723037) between the patients with psoriasis and the healthy individuals are presented in Table VI. The analysis of the genotype frequencies indicated that the AA genotype was predominant in both groups (patients with psoriasis and controls), with frequencies of 92% (80/87) and 100% (80/80), respectively. The AC genotype appeared only in the patient group (8%, 7/87), and was not observed among the controls, while the CC genotype was not detected in either group.

A significant variation in genotype distribution was observed between the two groups (χ^2=6.67, P=0.0098). Carriers of the AC genotype were found to have a substantially elevated risk of developing psoriasis, with an OR of 9.14 (95% CI, 1.08-77.10), relative to carriers of the AA genotype.

The analysis of the allele distribution revealed that the A allele was the predominant allele in both groups, accounting for 96% (167/174) among the patients with psoriasis and 100% (160/160) among the healthy individuals. The C allele was observed only in the patients with psoriasis, accounting for 4% (7/174) of alleles, while it was completely absent in the healthy controls. Allele distribution differed significantly between the groups (χ^2=7.02, P=0.008), and the C allele conferred an 8.04-fold increased susceptibility to psoriasis (OR=, 8.04; 95% CI, 1.00-64.7).

These findings suggest that both the C allele and the heterozygous AC genotype may play a role in enhancing susceptibility to psoriasis within the investigated population. The lack of both the C allele and the CC genotype among healthy controls provides additional support for a possible immunogenetic contribution of this polymorphism to disease pathogenesis.

Discussion

The present study investigated participant characteristics associated with psoriasis relative to healthy controls. Notably, the matching of the patients and controls by age and sex strengthened the internal validity of the study and minimized demographic confounding factors (29).

Males represent the predominant sex in both study groups, with no significant difference observed between the groups (30). Despite the observed male predominance, it has been reported that psoriasis occurs at comparable rates in males and females, suggesting that the distribution in the present study may reflect sampling bias or sociocultural influences rather than true sex-specific susceptibility (31).

In the present study, no significant differences were observed as regards age in both groups. Within the same

Table IV. Clinical characteristics of the patients with psoriasis and the healthy controls.

Characteristic	Psoriasis with patients (n=87)	Healthy controls (n=80)	P-value
Family history of psoriasis			
Yes	35 (40.2%)	0 (0.0%)	<0.001[a]
No	52 (59.8%)	80 (100.0%)	
Smoking			
Yes	43 (49.4%)	25 (31.3%)	0.070[a]
No	44 (50.6%)	55 (68.7%)	
Residence			
City	66 (75.9%)	60 (75.0%)	0.810[a]
Rural	21 (24.1%)	20 (25.0%)	
Alcohol consumption			
Yes	0 (0.0%)	8 (10.0%)	0.0029[b]
No	87 (100.0%)	72 (90.0%)	
Hypertension			
Yes	22 (25.3%)	17 (21.3%)	0.300[a]
No	65 (74.7%)	63 (78.7%)	

Data are presented as number (n) and percentage (%). P-values were calculated using [a]the Chi-squared test or [b]Fisher's exact test (where the expected counts were below the assumptions required for the Chi-squared test). P<0.05 was considered to indicate a statistically significant difference.

Table V. Comparison of serum IL-23 levels between the patients with psoriasis and the healthy controls.

Immune marker	Patients with psoriasis (n=87), mean ± SD	Healthy controls (n=80), mean ± SD	P-value
IL-23	770.22±5.51	395.44±9.77	<0.001

Data are presented as the mean ± standard deviation (SD). The difference between groups was analyzed using an independent samples t-test. P<0.05 was considered to indicate a statistically significant difference.

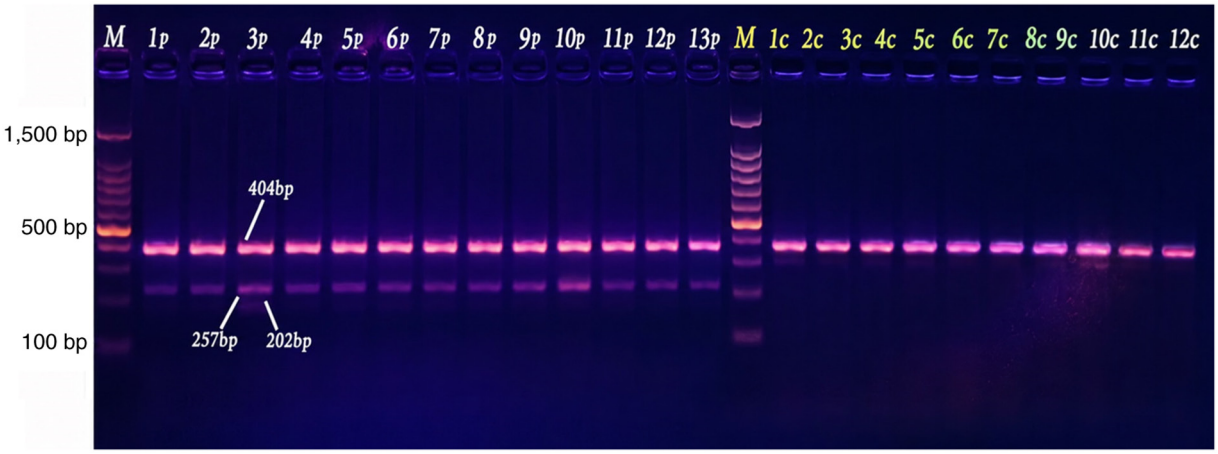

Figure 2. Agarose gel electrophoresis of the PCR product for genotyping the eIF4E rs11723037 polymorphism. M, 100 bp DNA ladder; p, patients with psoriasis; c, healthy control samples.

context, individuals >50 years of age represented the largest subgroup, followed by the 41-50-year age group. The observed predominance of older participants aligns with the well-documented second peak of psoriasis onset in adulthood.

The present study demonstrated a statistically positive associated between psoriasis and family history (P<0.001), as 40.2% of the patients reported having a family history, in contrast to no relation among the controls (32). This

Table VI. Genotype and allele distributions of the eIF4E rs11723037 polymorphism in the patients with psoriasis and the healthy controls.

A, Genotype

Variable genotype	Patients with psoriasis, n (%)	Healthy controls, n (%)	P-value[a]	OR (95% CI)[b]
AA (wild-type)	80 (92.0)	80 (100.0)	Reference	Reference
AC	7 (8.0)	0 (0.0)	0.0098	9.14 (1.08-77.10)
CC	0 (0.0)	0 (0.0)	-	Not estimable

B, Allele

Allele	Patients with psoriasis, n (%)	Healthy controls, n (%)	P-value[a]	OR (95% CI)[b]
	Frequency			
A	167 (96.0)	160 (100.0)	Reference	Reference
C	7 (4.0)	0 (0.0)	0.0080	8.04 (1.00-64.70)

Data are presented as number (n) and percentage (%). [a]P-values were calculated using Fisher's exact test as one or more expected cell counts were <5. [b]Odds ratios and 95% confidence intervals were calculated from 2x2 contingency tables using the AA genotype and A allele as the reference categories. OR, odds ratio; CI, confidence interval.

result revealed the role of hereditary factors in psoriasis and emphasizes the importance of familial susceptibility in its pathogenesis. No significant relation was observed between psoriasis and baseline characteristics, as also previously demonstrated (33). This suggests that genetic susceptibility may play a crucial role compared to the examined baseline characteristics or comorbidity factors in this cohort (34).

Strong statistical significance (P<0.001) was observed in serum IL-23 levels, which were detected at elevated levels in the patients with psoriasis (770.22±5.51 pg/ml) compared with the controls (395.44±9.77 pg/ml), as previously demonstrated in patients with systemic lupus erythematosus (35). This result reflects the involvement of the IL-23/Th17 axis in the pathogenesis of psoriasis (36). This finding may be explained by the fact that the IL-23/Th17 axis represents one of the principal immunological pathways that participate in the pathogenesis of psoriasis. Moreover, IL-23 regulates the survival/persistence of Th17 cells, which release IL-17 and IL-22, which play a role in the proliferation of keratinocytes and sustained skin inflammation (37). The marked elevation in IL-23 concentrations in patients compared to controls highlights its utility as a disease biomarker and supports the clinical strategy for IL-23 inhibition. These findings are in agreement with those of previous research, indicating that IL-23-inhibitors are effective in treating moderate to severe psoriasis (38).

A marked association (P<0.0098) has been observed between the risk of developing psoriasis and the eIF4E polymorphism (rs11723037) (39). In the present study, the AA genotype was the most dominant in both groups. By contrast, the heterozygous AC genotype was observed only among psoriasis patients (8%) and was linked to an almost 9-fold higher risk of developing psoriasis (OR, 9.14). In addition, the C allele was identified exclusively in 4% of patients with psoriasis, which represents an ~8-fold increase in the risk of developing psoriasis (P=0.008) (40).

The available literature demonstrated that the eIF4E protein is involved in controlling proliferation/regulating of cellular immune responses. Thus, dysregulation of eIF4E-dependent protein synthesis may lead to the proliferation of keratinocytes and amplification of inflammatory signaling, which are characteristic features of psoriasis. Therefore, the presence of the C allele may affect susceptibility to the disease by modifying the translational regulation of pathways involved in inflammation or cellular proliferation (41).

Nevertheless, the low frequency of the C allele observed in the present study may not accurately reflect the distribution among patients with psoriasis, as the relatively small sample size may have limited the precision of allele frequency estimates. Therefore, these findings should be interpreted with caution and confirmed in larger studies in the future (42,43).

The present study indicated a strong association between psoriasis and the eIF4E polymorphism, along with the marked activation of the IL-23 inflammatory pathway. By contrast, baseline characteristics did not reveal a significant effect on the distribution of the disease (13). These results underscore the role of immune dysregulation and genetic predisposition in psoriasis and support targeted therapeutic strategies (44). The eIF4E rs11723037 polymorphism and serum IL-23 levels may serve as potential biomarkers for psoriasis susceptibility in the Iraqi population, pending validation in a larger cohort.

In addition to the findings regarding the critical role of the eIF4E rs11723037 polymorphism and IL-23/IL-17 axis activity, other cytokines, including IL-12, IL-6, IL-1β and IL-18, contribute to inflammatory amplification, whereas IL-10 aids in the regulation of immune balance. Furthermore, TLR activation enhances dendritic cell activity and promotes

IL-23 and IL-12 production, linking innate and adaptive immunity (45). Understanding the IL and TLR pathways may provide key insight into the mechanisms of psoriasis and may identify potential therapeutic targets.

The present study has several limitations that should be considered when interpreting the findings. First, the study was conducted in a relatively small cohort from a single Iraqi population, which may limit the generalizability of the results to other ethnic groups. Second, although significant associations were observed between the eIF4E rs11723037 polymorphism, serum IL-23 levels, and psoriasis, these findings have not yet been validated in an independent cohort. Third, adjustment for potential confounding factors, including age, sex, smoking status and family history, was not performed. Consequently, the observed associations may have been influenced by these variables, and the independent contributions of the genetic polymorphism and serum IL-23 levels could not be fully assessed. In addition, a formal statistical power analysis and population stratification analysis were not conducted, which may affect the robustness and interpretation of the genetic association results. Therefore, the present findings should be considered preliminary and interpreted with caution. Future studies involving larger, multi-center cohorts with independent validation, multivariable logistic regression analyses, statistical power estimation, and the assessment of population structure are warranted to confirm and extend these observations.

In conclusion, in the present study, comparable age and sex distributions between patients and the control support appropriate group comparability, whereas a positive family history, elevated serum IL-23, and the eIF4E rs11723037 C allele/AC genotype were significantly associated with psoriasis susceptibility. Collectively, these findings underscore the combined contribution of genetic susceptibility and IL-23-mediated immune dysregulation to psoriasis pathogenesis and highlight their potential as complementary biomarkers and therapeutic targets.

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Availability of data and materials

The data generated in the present study may be requested from the corresponding author.

Authors' contributions

HAA and HAK conceived and designed the study. HAA and DYT performed the experiments and collected the data. HAK analyzed and interpreted the data. All authors (HAA, HAK and DYT) contributed to the writing, reviewing, and editing the manuscript. HAK and HAA confirm the authenticity of all raw data. All authors have read and approved the final version.

Ethics approval and consent to participate

The study design received formal approval from the Ethics Committee of North Al-Nasiriyah Hospital (under ethical approval no. DV/NNH/24/045 on October 15, 2024). Furthermore, the Scientific Research Ethics Committee of Al-Ayen Iraqi University covered the laboratory analysis of blood samples (ethical approval letter no. 22 on January 5, 2025).

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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