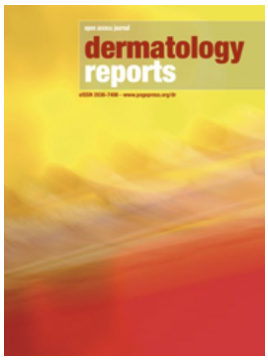

Dermatology Reports
https://journals.pagepress.net/dr

eISSN 2036-7406

Please cite this article as:

Chau NH, Le HT, Huynh PA, et al. Association of interleukin-6 rs1800796 polymorphism with keloid susceptibility and severity in a Vietnamese population: a case-control study. *Dermatol Rep 2026 [Epub Ahead of Print] doi: 10.4081/dr.2026.10835*

Received: 13 February 2026; Accepted: 14 August 2026.

Association of interleukin-6 rs1800796 polymorphism with keloid susceptibility and severity in a Vietnamese population: a case-control study

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Key words: keloid; interleukin-6; single nucleotide polymorphism; genetic susceptibility; scar severity.

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Conflict of interest: the authors declare no conflict of interest.

Ethics approval and consent to participate: the protocol of the study received approval from the Institutional Review Board of the University of Medicine and Pharmacy at HCMC, Ho Chi Minh City, Vietnam (IRB No. 24647 - ĐHYD) and adhered to the Declaration of Helsinki. All participants provided written informed consent before participation.
Availability of data and materials: all data generated or analyzed during this study are included in this published article.

Funding: this research was funded by the University of Medicine and Pharmacy at Ho Chi Minh City, Vietnam, under contract number 211/2024/HĐ-ĐHYD, dated August 22, 2024.

Acknowledgments: the authors are grateful to their colleagues at the Department of Dermatology and Skin Aesthetics, University Medical Center HCMC, Ho Chi Minh City, Vietnam, for their assistance.

Abstract

Keloids are fibroproliferative skin tumors characterized by excessive collagen deposition and persistent inflammation. Interleukin (IL)-6 plays a key role in wound healing and fibrosis, and promoter polymorphisms of the IL-6 gene have been implicated in keloid susceptibility in several populations. However, data on Vietnamese patients remain limited. We conducted a case-control study including 47 patients with clinically diagnosed keloids and 43 age- and sex-matched healthy controls to investigate the association between the IL-6 rs1800796 (−572 C>G) polymorphism and both keloid susceptibility and scar severity. Genotyping was performed using allele-specific oligonucleotide – polymerase chain reaction (ASO-PCR). Scar severity was assessed using the Vancouver Scar Scale (VSS). The CG genotype and G allele were significantly more frequent in patients with keloid than in controls. Carriers of the G allele demonstrated an increased risk of keloid formation and exhibited progressively higher VSS scores compared with CC homozygotes. These findings suggest that the IL-6 rs1800796 G allele is associated with increased susceptibility to keloids and greater scar severity in Vietnamese patients.

Key words: keloid; interleukin-6; single nucleotide polymorphism; genetic susceptibility; scar severity.

Introduction

Keloids are benign fibroproliferative tumors characterized by excessive collagen deposition beyond the original wound boundary with a low likelihood of spontaneous regression.[1,2] Keloids usually develop following skin trauma, namely acne, surgery, piercing, burns, lacerations, vaccinations, *etc.*, or may occur spontaneously.[3] Their pathogenesis involves chronic inflammation, persistent fibroblast activation, and extracellular matrix accumulation.[4] Prolonged inflammatory signaling stimulates dermal fibroblasts to produce collagen continuously, leading to unregulated fibrosis.[5] Despite extended research, their pathophysiology remains incompletely understood, contributing to a high rate of recurrence after treatment.[1]

Interestingly, immune cell infiltrates are commonly observed in keloid tissue, supporting its classification as an inflammatory fibrotic disorder.[6] Interleukin (IL)-6 is a pro-inflammatory cytokine central to wound healing and fibrogenesis. Normally, IL-6 promotes tissue repair during early healing phases, then subsides.[7] In keloids, however, IL-6 expression remains elevated, both in lesional fibroblasts and in circulation.[8] IL-6 drives fibroblast proliferation and collagen synthesis *via* the IL-6 receptor/gp130

signaling axis.[9,10] Experimental blockade of IL-6 or its receptor reduces collagen and fibronectin production, indicating IL-6's role in sustaining keloid fibrosis.[11]

Genetic predisposition also contributes to keloid formation.[12] The IL-6 promoter polymorphism rs1800796 (−572 C>G) has been associated with increased IL-6 expression and an increased risk of keloids in several populations. Studies in China, Japan, and Egypt have shown that the G allele is associated with elevated serum IL-6 levels and significantly increased odds of keloid development and severity.[13-15] These findings suggest a consistent association between the G allele and keloid susceptibility across diverse ethnic groups.

However, data on IL-6 polymorphisms in Vietnamese patients with keloid are lacking. Given ethnic variation in IL-6 allele frequencies and disease associations, the relevance of rs1800796 in Vietnam remains uncertain. This study aims to evaluate the association of IL-6 −572 C>G polymorphism with keloid susceptibility and severity in a Vietnamese cohort, addressing a gap in the literature and contributing to the understanding of population-specific genetic risk for keloids.

Materials and Methods

Study design and participants

This was a case-control study, conducted at the Department of Dermatology and Skin Aesthetics, University Medical Center HCMC, Ho Chi Minh City, Vietnam, from November 2024 to May 2025.

Consecutive adult patients (≥18 years) with clinically diagnosed keloids who attended the outpatient dermatology clinic during the study period and met the eligibility criteria were invited to participate. The healthy control group was recruited from hospital staff and volunteers who had no personal history of keloids. Each control participant was individually matched to a patient with keloid according to sex and age (±2 years).

Information was obtained from all participants, including age, gender, weight, height, medical history, age of onset, disease duration, family history, subjective symptoms and frequency, previous keloid treatment, and trigger factors.

Exclusion criteria for both groups consisted of pregnancy, chronic diseases (including diabetes, hypertension, asthma, autoimmune disorders, cardiovascular or renal disease, systemic vascular disease, and HIV/AIDS), and a history of keloid treatment within the past 6 months using local or systemic therapies. All participants provided written informed consent before participation.

The protocol of the study received approval from the Institutional Review Board of the University of Medicine and Pharmacy at HCMC, Ho Chi Minh City, Vietnam (IRB No. 24647 - ĐHYD) and adhered to the Declaration of Helsinki.

Assessment of keloid lesions

Keloids were diagnosed clinically based on the Japan Scar Workshop Scar Scale (JSS). The JSS is a standardized tool developed to assess and classify pathological scars, including keloids and hypertrophic scars. It evaluates key clinical features such as scar height, redness, hardness, itchiness, and pain, using a numerical scoring system to quantify severity. By systematically capturing both physical and symptomatic characteristics, the scale aids in distinguishing keloids from other scar types and tracking treatment response.[16] Patients were diagnosed with keloids if they had a total score ≥16.

Afterwards, keloid severity was determined *via* the Vancouver Scar Scale (VSS). The VSS is a widely used clinical tool for assessing scar characteristics. It evaluates four parameters: vascularity, pigmentation, pliability, and height, assigning a score to each to quantify overall scar severity: mild (0 to 3 points), moderate (4 to 7 points), and severe (8 to 13 points).[17]

Evaluation of IL-6 rs1800796 polymorphism

To assess the IL-6 single-nucleotide polymorphism rs1800796, allele-specific oligonucleotide – polymerase chain reaction (ASO-PCR) was performed following a standardized workflow. Peripheral venous blood (2 mL) was collected in ethylenediaminetetraacetic acid (EDTA)-containing tubes and stored at −80°C until analysis. Genomic DNA (gDNA) was extracted from whole blood using the GeneJET Whole Blood Genomic DNA Purification Mini Kit (Thermo Fisher Scientific, Waltham, MA, USA) according to the manufacturer's instructions. The concentration and purity of the extracted gDNA were evaluated using a NanoDrop 2000 spectrophotometer (Thermo Fisher Scientific), and DNA samples were stored at −20°C until PCR amplification.

Allele-specific primers targeting the rs1800796 polymorphic region of the IL-6 gene were designed using CLC Main Workbench v5.5 (Qiagen, Venlo, The Netherlands), based on the reference sequence available in public databases. Primer specificity and thermodynamic properties were verified using Primer-BLAST to ensure selective amplification of the target allele without cross-reactivity. PCR reactions were prepared in a final volume of 10 µL containing PCR Master Mix 5µL (Thermo Fisher Scientific) allele-specific forward and reverse primers (0.5µM), and approximately 50-100 ng of gDNA template. Amplification

was carried out with an initial denaturation at 98°C for 2 minutes, followed by 30 cycles of denaturation at 98°C for 15 seconds, annealing at 60°C for 1 minute, and extension at 72°C for 1 minute.

PCR products were resolved by electrophoresis on a 1.5% agarose gel prepared in 0.5× Tris-borate-EDTA (TBE) buffer and stained with ethidium bromide. A 1 kb DNA ladder was used as a molecular size marker to confirm amplicon size. Gels were visualized and documented using a GelDoc-It imaging system. The presence or absence of allele-specific amplification bands, compared with appropriate controls, was used to determine the IL-6 rs1800796 genotype for each sample, thereby enabling reliable single nucleotide polymorphism discrimination using the ASO-PCR approach.

Statistical analysis

All statistical analyses were performed using R software (version 4.3.1), and graphs were created with GraphPad Prism (version 10.2.2). Continuous variables are reported as mean ± standard deviation. Data normality was assessed to determine the appropriate statistical tests. For comparisons between two groups, independent *t*-tests were applied to normally distributed data, while the Mann-Whitney U test was used for nonparametric data. For comparisons among three groups, one-way analysis of variance (ANOVA) was used for parametric data, and the Kruskal-Wallis test for nonparametric data. Categorical variables were compared using the chi-square test or Fisher's exact test, depending on expected cell counts. For genotype distributions with three categories, pairwise comparisons were performed using univariable binary logistic regression, with the CC genotype as the reference category, to estimate odds ratios (ORs) and 95% confidence intervals (CIs). A two-sided p-value <0.05 was considered statistically significant.

Results

Baseline demographic characteristics of study participants

A total of 47 patients with keloids and 42 healthy controls were enrolled in this case-control study. The demographic characteristics of both groups are summarized in Table 1. There were no statistically significant differences between keloid patients and controls with respect to age, sex distribution, or body mass index. These findings indicate that the two groups were well matched for major demographic variables, minimizing potential confounding effects in subsequent genetic analyses.

Clinical characteristics of patients with keloid assessed by the Japan Scar Scale

Clinical features of keloid disease assessed using the JSS are presented in Table 2. The mean age of disease onset was 24.11±11.42 years, with a mean disease duration of 6.92±5.56 years. The most common chief complaints were aesthetic concerns (59.57%) and pruritus (51.06%), whereas pain was reported less frequently (10.64%). Subjective symptoms were highly prevalent, with itch reported by 89.36% of patients and pain by 23.40%.

Most patients experienced intermittent symptoms (70.21%), while 19.15% reported persistent symptoms. A positive family history of keloids was frequently observed (61.70%), involving siblings (21.28%), fathers (27.66%), and mothers (12.77%). Regarding lesion burden, nearly half of patients had 2-5 keloid lesions (48.94%), while 25.53% presented with more than 10 lesions.

Acne vulgaris (57.45%) and spontaneous occurrence (48.94%) were the most common triggers, followed by wounds (27.66%). Lesions were most frequently located on the anterior chest (65.96%) and scapular area (27.66%). Approximately half of the lesions exceeded 20 cm^2 in size. Notably, all patients were classified as having keloid-type scars (≥16 points) according to the JSS, confirming the clinical homogeneity of the keloid cohort.

Scar severity characteristics assessed by the Vancouver Scar Scale

Scar severity evaluated using the VSS is summarized in Table 3. Vascularity assessment revealed that most lesions were purple (44.68%) or red (34.04%). Hyperpigmentation was present in the vast majority of cases (93.62%). With respect to pliability, firm scars were most common (42.55%), followed by yielding (27.66%) and rope-like textures (19.15%). Scar height was predominantly between 2-5 mm (51.06%), with 31.91% exceeding 5 mm.

The mean total VSS score was 9.30±2.30, indicating overall moderate to severe scar involvement. Based on severity categorization, most patients fell within the moderate-to-severe range, further supporting the presence of clinically significant keloid disease in the study population.

Distribution of IL-6 rs1800796 genotypes and allele frequencies

The distribution of IL-6 rs1800796 genotypes and allele frequencies is shown in Figure 1 A-C. The CG genotype was significantly more frequent in patients with keloid compared with controls (19 *vs.* 8), conferring 3.14-fold increased odds of keloid formation relative to the CC genotype (OR=3.14, 95% CI: 1.21-8.70, p=0.02). Meanwhile, the GG genotype did not statistically increase the odds of keloid formation

compared with the CC genotype (OR=3.96, 95% CI: 0.48-82.71, p=0.25). When CG and GG genotypes were combined, carriers of the G allele exhibited significantly higher odds of keloids compared with CC homozygotes (OR=3.23, 95% CI: 1.25-7.75, p=0.01). Allelic analysis further demonstrated that the G allele was significantly overrepresented in keloid patients compared with controls (25 *vs.* 10), corresponding to a 2.68-fold increased odd of keloid formation (OR=2.68, 95% CI: 1.15-5.46, p=0.01). These findings suggest a strong association between the IL-6 rs1800796 G allele and keloid development.

Association between IL-6 rs1800796 genotype and scar severity

VSS scores increased progressively across IL-6 rs1800796 genotypes, with CC carriers exhibiting the lowest scores (median [interquartile range, IQR]: 8 [6-9.5]), followed by CG (median [IQR]: 11 [9-12]) and GG (median [IQR]: 13 [11-13]) carriers (Figure 1D). Statistically significant differences were observed between CC and CG ($p<0.001$) and between CC and GG ($p=0.003$), whereas no significant difference was detected between CG and GG genotypes ($p = 0.67$).

Figure 2 summarizes the study design and methods as well as the main results.

Discussion

This study provides preliminary evidence supporting an association between the IL-6 rs1800796 polymorphism and both keloid susceptibility and scar severity in a Vietnamese cohort of patients with keloids. The G allele was more frequent in keloid cases than in controls in our cohort, and carriers of this variant showed higher VSS scores, reflecting more severe scarring. This trend aligns with prior studies in Asian populations. For example, a Japanese study reported a significantly higher frequency of the –572G allele in patients with keloid (40.6%) than in controls (23.0%), corresponding to an OR of 2.34 for keloid risk.[13] A Chinese Han cohort similarly found that the IL-6 –572 GG genotype conferred about a two-fold increased keloid risk (OR=2.1) and the G allele frequency was modestly elevated in cases (35.9%) *vs.* controls (29.9%).[14] In contrast, an Egyptian study observed a dramatically higher G allele prevalence among patients with keloid (67.5% *vs.* 26.7% in controls) with a five-fold increased risk (OR approximately 5.1).[15] Interestingly, a study conducted in a Polish population reported no significant association between the IL-6 rs1800796 polymorphism and keloid susceptibility.[18] However, the interpretation of these findings warrants caution, as the control group consisted of newborns. Because keloids typically develop later in life following skin injury or inflammation, the use of neonates as controls may introduce misclassification bias, potentially underestimating true disease risk and attenuating

genotype-phenotype associations. Thus, the magnitude of risk associated with IL-6 –572G appears to vary by population – from none in the Polish sample, to modest in the Chinese and Japanese studies, to very strong in the Egyptian cohort – and our Vietnamese data seem to fall between these ranges. Notably, despite differences in allele frequency and OR, all these studies consistently identify the G allele as a risk factor for keloid formation, reinforcing the relevance of IL-6 –572 polymorphism across ethnicities. Moreover, the association of the G allele with higher scar severity (VSS score) in our patients is congruent with the Egyptian findings that GG genotype patients had significantly worse scar scores than CC genotype (mean VSS, 8.34 *vs.* 3.4).[15] Taken together, our study and previous reports suggest that while baseline G allele frequencies differ, the presence of the –572G variant consistently correlates with increased keloid risk and potentially greater scar severity.

The link between the G allele and elevated VSS scores can be interpreted in light of IL-6's known profibrotic and pro-inflammatory functions. Functional analyses have shown that the –572G variant enhances IL-6 expression: in the Chinese study, the G-allele promoter drove approximately 1.5-fold higher IL-6 transcriptional activity than the C-allele in luciferase assays, and patients with keloid with GG genotype had significantly higher serum IL-6 levels than those with CC.[14] Mechanistically, increased IL-6 production can directly contribute to exuberant scar formation by stimulating fibroblast activity and collagen synthesis. In detail, IL-6 signaling through the Janus kinase/signal transducer and activator of transcription 3 and extracellular signal-regulated kinase/mitogen-activated protein kinase pathways has been implicated in extracellular matrix overproduction in keloids.[19] Keloid fibroblasts show upregulated IL-6 and IL-6 receptor expression alongside increased collagen output, and blocking IL-6 or its receptor reduces collagen synthesis.[20] IL-6 also helps sustain chronic inflammation in wounds: it promotes a profibrotic feedback loop by inducing transforming growth factor (TGF)-β1 and other cytokines that perpetuate fibroblast activation.[19] Thus, carriers of the –572 G allele may have a genetically driven tendency to overproduce IL-6 in lesional tissue, which in turn prolongs inflammatory signaling and drives excess collagen deposition. This mechanism would explain why Vietnamese patients with keloid with the G allele experienced more severe scarring in our study. It is noteworthy that similar observations were made in other populations; for instance, Egyptian patients with keloid with GG genotypes not only had a higher risk of keloids but also exhibited higher IL-6 levels and more severe lesions.[15] Overall, the convergence of genetic association and biological evidence supports a model in which the IL-6 –572G variant exacerbates keloid pathogenesis by boosting IL-6-mediated fibroproliferative responses.

Despite the encouraging findings, our study has limitations that temper the interpretation of the IL-6 –572 C>G polymorphism's role in keloid disease. First, the sample size was relatively modest, which may limit statistical power and the precision of risk estimates. Smaller cohorts increase the chance of both false-negative results (if the effect is subtle) and inflated OR estimates in subgroup analyses. Thus, while we detected significant associations, these results should be confirmed in larger Vietnamese populations. Second, we did not obtain functional or expression data from the keloid lesions to directly support the genetic association. We lacked measurements of intralesional or serum IL-6 protein and mRNA levels in our patients. This omission makes it difficult to definitively link the G allele to a functional increase in IL-6 in our cohort. Without these data, our mechanistic explanation remains inferential, based on external studies rather than on direct evidence from our patients. Additionally, we focused on a single polymorphism and did not examine other IL-6 gene variants such as rs1800795 (−174 G>C) or rs1800797 (−597 G>A). The lack of a broader genetic analysis means we cannot determine whether the −572 C>G effect is independent or part of a haplotype with other IL-6 variants. Together, these limitations constrain our ability to draw firm mechanistic conclusions. Our findings establish a correlation, but the causative link between the IL-6 –572G allele and keloid biology needs further elucidation.

Looking ahead, future studies should evaluate IL-6 levels in keloid tissue or serum to determine its potential as a biomarker of disease activity or severity, particularly in individuals carrying the −572G allele, which may drive increased IL-6 expression. Establishing a clear genotype-phenotype correlation could support risk stratification and help monitor treatment response or recurrence. Given the role of IL-6 in promoting fibroblast activation and collagen synthesis, therapies targeting IL-6 signaling, such as tocilizumab, may offer clinical benefit, especially for patients with elevated IL-6 levels. Investigating such treatments in clinical trials or case studies, alone or alongside standard therapies, could open new therapeutic avenues. Additionally, expanding genetic studies in larger and more diverse Vietnamese populations, and including other IL-6 variants or fibrosis-related genes, may reveal broader patterns of susceptibility and inform personalized approaches to prevention and management.

Conclusions

This study demonstrates that the IL-6 −572 C>G polymorphism is significantly associated with both the risk and severity of keloids in a Vietnamese population. Carriage of the G allele confers an increased susceptibility to keloid formation and is linked to higher Vancouver Scar Scale scores, reflecting more severe clinical manifestations. These findings reinforce the role of IL-6-driven inflammatory and fibrotic

pathways in keloid pathogenesis and highlight IL-6 rs1800796 as a potential genetic marker for risk stratification. Future studies incorporating larger cohorts and functional analyses of IL-6 expression are warranted to further clarify the mechanistic and clinical implications of this polymorphism.

References

1. Chike-Obi CJ, Cole PD, Brissett AE. Keloids: pathogenesis, clinical features, and management. Semin Plast Surg 2009;23:178-84.
2. Knowles A, Glass DA, 2nd. Keloids and Hypertrophic Scars. Dermatol Clin 2023;41:509-17.
3. McGinty S, Siddiqui WJ. Keloid. Treasure Island (FL): StatPearls [Internet]; 2025 [updated 2023 Jul 17]. Available from: https://www.ncbi.nlm.nih.gov/books/NBK507899/.
4. Latoni DI, McDaniel DC, Tsao H, Tsao SS. Update on the Pathogenesis of Keloid Formation. JID Innov 2024;4:100299.
5. Wang ZC, Zhao WY, Cao Y, et al. The Roles of Inflammation in Keloid and Hypertrophic Scars. Front Immunol 2020;11:603187.
6. Nangole FW, Agak GW. Keloid pathophysiology: fibroblast or inflammatory disorders? JPRAS Open 2019;22:44-54.
7. Mahmoud NN, Hamad K, Al Shibitini A, et al. Investigating Inflammatory Markers in Wound Healing: Understanding Implications and Identifying Artifacts. ACS Pharmacol Transl Sci 2024;7:18-27.
8. Johnson BZ, Stevenson AW, Prele CM, et al. The Role of IL-6 in Skin Fibrosis and Cutaneous Wound Healing. Biomedicines 2020;8.
9. Ghazizadeh M. Essential role of IL-6 signaling pathway in keloid pathogenesis. J Nippon Med Sch 2007;74:11-22.
10. Ghazizadeh M, Tosa M, Shimizu H, et al. Functional implications of the IL-6 signaling pathway in keloid pathogenesis. J Invest Dermatol 2007;127:98-105.
11. Liu M. Cytokines, chemokines and growth factors involved in keloids pathogenesis. An Bras Dermatol 2025;100:300-7.
12. Liu S, Yang H, Song J, et al. Keloid: Genetic susceptibility and contributions of genetics and epigenetics to its pathogenesis. Exp Dermatol 2022;31:1665-75.
13. Tosa M, Watanabe A, Ghazizadeh M. IL-6 Polymorphism and Susceptibility to Keloid Formation in a Japanese Population. J Invest Dermatol 2016;136:1069-72.

14. Zhu XJ, Li WZ, Li H, et al. Association of interleukin-6 gene polymorphisms and circulating levels with keloid scars in a Chinese Han population. Genet Mol Res 2017;16:gmr16029110.
15. Allah AMKA, Mohammed KI, Farag AGA, et al. Interleukin-6 serum level and gene polymorphism in keloid patients. Cell Mol Biol 2019;65:43-8.
16. Ogawa R. Japan Scar Workshop (JSW) Scar Scale (JSS) for Assessing Keloids and Hypertrophic Scars. In: Teot L, Mustoe TA, Middelkoop E, Gauglitz GG, editors. Textbook on Scar Management: State of the Art Management and Emerging Technologies [Internet]. Springer; 2020. p. 133-40.
17. Sullivan T, Smith J, Kermode J, et al. Rating the burn scar. J Burn Care Rehabil 1990;11:256-60.
18. Dmytrzak A, Lewandowska K, Boron A, et al. No Association of Polymorphisms in the Genes Encoding Interleukin-6 and Interleukin-6 Receptor Subunit Alpha with the Risk of Keloids in Polish Patients. Int J Mol Sci 2024;25:5284.
19. Lee CC, Tsai CH, Chen CH, et al. An updated review of the immunological mechanisms of keloid scars. Front Immunol 2023;14:1117630.
20. Uitto J. IL-6 signaling pathway in keloids: a target for pharmacologic intervention? J Invest Dermatol 2007;127:6-8.

Table 1. Demographic characteristics of participants.

	Patients with keloids (n=47)	**Control** (n=42)	**p-value**
Age, years Median (IQR)	28 (23-34)	27 (26-30)	0.71[a]
Gender, n (%)			
Male	26 (55.32)	22 (52.38)	0.78[b]
Female	21 (44.68)	20 (47.62)	
BMI, kg/m^2 Mean±SD	22.62±2.58	23.07±2.52	0.37[c]

IQR, interquartile range; BMI, body mass index; SD, standard deviation.

[a]Comparison between groups using Mann-Whitney test; [b]comparison between groups using chi-square test or Fisher's exact test, depending on expected count; [c]comparison between groups using independent *t*-test.

Table 2. Clinical characteristics of patients with keloids and JSS assessment.

	Patients with keloids (n=47)
Age of onset, years	24.11±11.42
Disease duration, years	6.92±5.56
Chief complaint, n (%)	
Itch	24 (51.06)
Pain	5 (10.64)
Aesthetics	28 (59.57)
Worry about disease progression	8 (17.02)
Subjective symptoms, n (%)	
Itch	42 (89.36)
Pain	11 (23.4)
Frequency of symptoms, n (%)	
Never	5 (10.64)
Intermittent	33 (70.21)
Always exist	9 (19.15)
Family history of keloids, n (%)	
Present	29 (61.70)
Absent/unclear	18 (38.30)
Number of keloid lesions, n (%)	
1	12 (23.40)
2-5	23 (48.94)
6-10	1 (2.130)

>10	12 (25.53)
Triggers, n (%)	
Wound	13 (27.66)
Acne vulgaris	27 (57.45)
Surgery	5 (10.64)
Vaccination	2 (4.26)
Spontaneous	23 (48.94)
Site of lesions, n (%)	
Anterior chest	31 (65.96)
Breast	2 (4.26)
Deltoid area	4 (8.51)
Scapular area	13 (27.66)
Submandibular area	5 (10.64)
Auricle	2 (4.26)
Abdomen	6 (12.77)
Limbs	4 (8.51)
Suprapubic	1 (2.13)
Back	1 (2.13)
Size, n (%)	
Over 20 cm^2	23 (48.94)
Under 20cm^2	24 (51.06)
Vertical growth, n (%)	
Clearly exists	0 (0)
Not clearly	47 (100)
Horizontal growth, n (%)	
Clearly exists	4 (8.51)
Not clearly	43 (91.49)
Characteristic shape, n (%)	
Yes	21 (44.68)
Others	26 (55.32)
Erythema around scars, n (%)	
Clearly present	25 (53.19)
Not present	22 (46.8)
Classification by JSS, n (%)	
Similar to mature scar (0-5 points)	0 (0)
Similar to hypertrophic scar (6-15 points)	0 (0)
Similar to keloid scar (≥16 points)	47 (100)

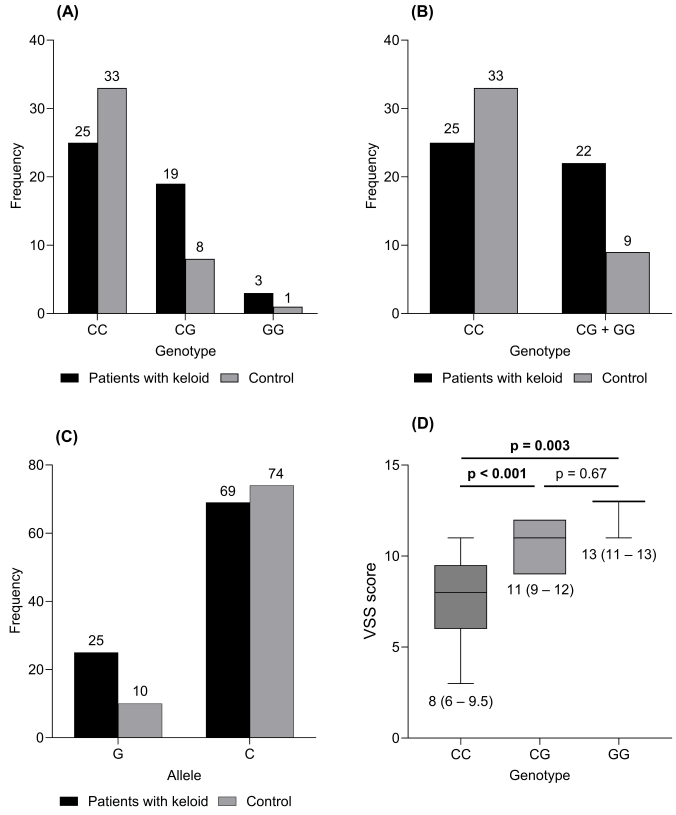
JSS, Japan Scar Workshop Scar Scale.

Table 3. Scar characteristics assessed using the VSS.

	Patients with keloids (n=47)
Vascularity, n (%)	
Normal	4 (8.51)
Pink	6 (12.77)
Red	16 (34.04)
Purple	21 (44.68)
Pigmentation, n (%)	
Normal	3 (6.38)
Hypopigmentation	0 (0)
Hyperpigmentation	44 (93.62)
Pliability, n (%)	
Normal	0 (0)
Supple	0 (0)
Yielding	13 (27.66)
Firm	20 (42.55)
Ropes	9 (19.15)
Contracture	5 (10.64)
Height, n (%)	
Flat	0 (0)
<2 mm	8 (17.02)
2-5 mm	24 (51.06)
>5 mm	15 (31.91)
VSS score Mean±SD	9.30±2.30
Severity, n (%)	
Mild (0-3 points)	1 (2.13)
Moderate (4-7 points)	8 (17.02)
Severe (8-13 points)	38 (80.85)

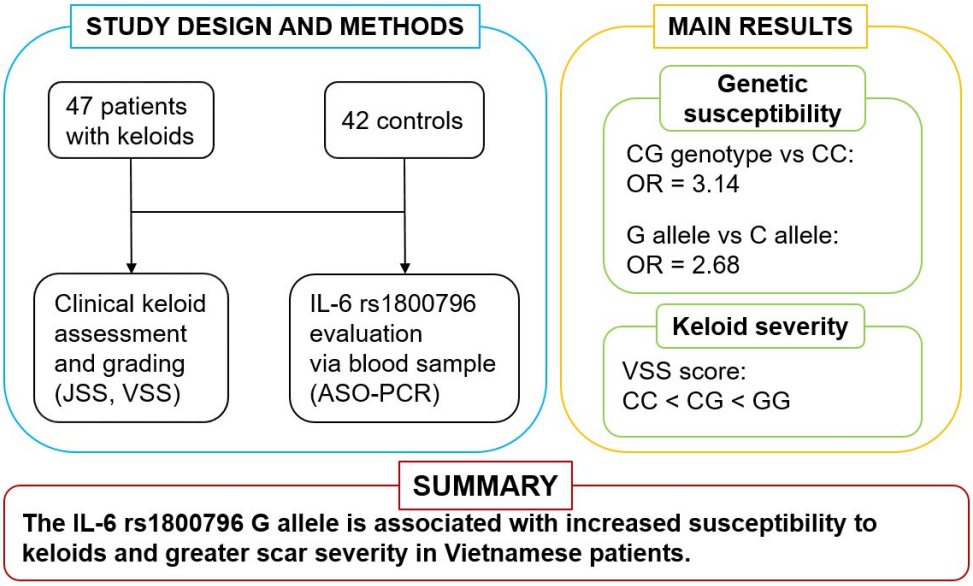
VSS, Vancouver Scar Scale; SD, standard deviation.

Figure 1. Distribution of the IL-6 rs1800796 genotypes and alleles in patients with keloids and healthy controls, and comparison of VSS scores among genotypes in patients with keloids. **A**) Distribution of the CC, CG, and GG genotypes. **B**) Distribution of the CC genotype *vs.* G allele carriers (CG+GG). **C**) Distribution of the C and G alleles. **D**) Comparison of VSS scores among the three genotype groups in patients with keloids.



Data are presented as frequency or median (IQR), as appropriate. VSS scores were compared using the Kruskal-Wallis test, followed by Dunn's *post hoc* test with Bonferroni correction for multiple comparisons. Statistically significant p-values are in bold.

Figure 2. Summary of the study design, methods and main results.



JSS, Japan Scar Workshop Scar Scale; VSS, Vancouver Scar Scale; ASO-PCR, allele-specific oligonucleotide – polymerase chain reaction.