

Correlation Analysis of Clinical Phenotypes, Inflammatory Molecular Markers, and Susceptibility Gene Polymorphisms in Acne Patients in Urumqi and Construction of Treatment Regimens

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Abstract

Objective: To investigate the correlation between clinical phenotypes, inflammatory molecular markers, and susceptibility gene polymorphisms in acne patients in Urumqi, and to construct targeted treatment regimens. **Methods:** A total of 80 acne patients admitted to our hospital from February 2025 to March 2026 were enrolled as the study group, and 40 healthy subjects who received physical examination in our hospital during the same period with normal results were enrolled as the control group. Fasting peripheral blood was collected from both groups for the detection of inflammatory molecular markers. Meanwhile, clinical phenotype evaluation and gene polymorphism analysis were performed on patients in the study group. The clinical phenotypes of acne patients in Urumqi were analyzed, and the levels of inflammatory molecular markers such as tumor necrosis factor- α (TNF- α), interleukin (IL)-6, IL-1 β , and IL-8 were compared between the two groups. The polymorphisms of the TNF- α gene and IL gene family, including TNF- α gene -308G>A polymorphism, IL-8 -251T>A polymorphism, and IL-4R Q551R A/G polymorphism, were analyzed between acne patients in Urumqi and healthy populations. The correlation between clinical phenotypes, inflammatory molecular markers, and gene polymorphisms in acne patients in Urumqi was also analyzed. **Results:** Among the 80 acne patients, as assessed by the modified Pillsbury classification, 21 cases (26.25%) were mild (grade I), 30 cases (37.50%) were moderate (grade II), 16 cases (20.00%) were moderate (grade III), and 13 cases (16.25%) were severe (grade IV). The serum levels of inflammatory molecular markers such as TNF- α , IL-6, IL-1 β , and IL-8 in the study group were significantly higher than those in the control group, with statistically significant differences ($P < 0.05$). For the TNF- α gene -308G>A polymorphism, the distribution of GG, GA, and AA genotype frequencies in acne patients was significantly different from that in the control group ($P < 0.05$), and carrying the A allele increased the risk of acne. For the IL-8 -251T>A polymorphism, the distribution of TT, TA, and AA genotype frequencies in acne patients was significantly different from that in the control group ($P < 0.05$), and carrying the T allele increased the risk of acne. For the IL-4R Q551R A/G polymorphism, the distribution of AA, AG, and GG genotype frequencies in acne patients was significantly different from that in the control group ($P < 0.05$), and carrying the G allele increased the risk of acne. Among the acne patients in Urumqi,

the levels of TNF- α , IL-6, IL-1 β , and IL-8 showed an upward trend with the increase of acne severity. The frequency of mutant genotypes increased with the aggravation of acne severity, and the difference was statistically significant ($P < 0.05$), suggesting that gene polymorphism is closely related to the severity of acne. **Conclusion:** Acne patients in Urumqi are mainly moderate acne, followed by mild acne, and the proportion of severe acne is relatively low. With the increase of acne severity, the levels of inflammatory molecular markers show an upward trend, and gene polymorphism is closely related to the severity of acne.

Keywords

Urumqi; Acne; Clinical phenotype; Inflammatory molecular marker; Susceptibility gene polymorphism; Correlation analysis; Treatment

Acne is a common dermatosis in modern populations, which mainly involves the pilosebaceous unit, with a particularly high incidence in adolescence. It is characterized by various skin lesions such as comedones, papules, pustules, nodules, and cysts [1]. Patients with this disease may suffer from impaired psychosocial function due to damage to skin barrier function. Urumqi is located in the Xinjiang Uygur Autonomous Region, with a unique geographical location, strong ultraviolet radiation, dry climate, and frequent wind and sand, which leads to unique regional and ethnic characteristics in the incidence of acne [2]. In recent years, with the gradual deepening of research in molecular biology, immunology, and other fields, there has been an increasing number of studies in the medical field on the role of inflammatory molecular markers and susceptibility gene polymorphisms in the pathogenesis of acne. Proinflammatory cytokines such as interleukin-6 (IL-6), interleukin-1 β (IL-1 β), and tumor necrosis factor- α (TNF- α) play important roles in the inflammatory response of acne [3]. Inflammatory factors can regulate the expression of a variety of proinflammatory genes by activating transcription factors, thus participating in the inflammatory response. Studies on gene polymorphisms have confirmed that the polymorphisms of the TNF- α gene, IL gene family, and androgen-related genes are closely related to the susceptibility to acne, which may affect individual susceptibility to acne by influencing protein function or protein expression [4]. This study, combined with actual clinical case data, aims to analyze the correlation between clinical phenotypic characteristics, inflammatory molecular marker levels, and susceptibility gene polymorphisms in acne patients in Urumqi and construct individualized treatment regimens for acne cases with different molecular phenotypes, so as to provide some ideas for the prevention and treatment of acne in the multi-ethnic population in Urumqi.

1. Materials and Methods

1.1 General Information

A total of 80 acne patients admitted to our hospital from February 2025 to March 2026 were enrolled as the study group, including 50 males and 30 females, aged 14 to 36 years, with a mean age of (24.39 ± 4.58) years. The course of acne ranged from 1 to 11 years, with a mean course of (6.10 ± 2.39) years. Meanwhile, 40 healthy subjects who received physical examination in our hospital during the same period with normal results were enrolled as the control group, including 24 males and 16 females, aged 13 to 37 years, with a mean age of (25.01 ± 4.29) years. Inclusion criteria: Local residents of Urumqi who have lived in the area for ≥ 5 years; Patients in the study group met the diagnostic criteria for acne and were confirmed diagnosed; Complete clinical data; Normal cognitive function; Voluntary participation in this study; The patients (healthy subjects) and their families signed the informed consent form. Exclusion criteria: Complicated with severe organic diseases; Concomitant infectious diseases; Mental disorders; Concomitant immune system dysfunction; Complicated with hematological system diseases. There was no statistically significant difference in general data, such as gender and age, between the two groups ($P > 0.05$), indicating comparability.

1.2 Methods

1.2.1 Detection of Inflammatory Molecular Markers

Peripheral venous blood (5 ml per subject) was collected from all subjects in the morning under fasting conditions, placed in EDTA anticoagulant tubes, centrifuged at 3000 r/min for 10 min to separate serum, and stored frozen for subsequent detection. The levels of inflammatory molecular markers, including TNF- α , IL-6, IL-1 β , and interleukin-8 (IL-8), were determined by enzyme-linked immunosorbent assay (ELISA).

1.2.2 Clinical Phenotype Assessment

The patients were assessed for skin lesion type, number of acne lesions, distribution area of acne, severity grading, and accompanying symptoms. The severity of acne in the study group was graded using the modified Pillsbury classification, which was divided into mild (grade I), moderate (grade II), moderate (grade III), and severe (grade IV).

1.2.3 Gene Polymorphism Analysis

The -308G>A (rs1800629) polymorphism in the promoter region of the TNF- α gene was detected by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP). The -251T>A (rs4073) polymorphism of the IL-8 gene and the Q551R A/G (rs1801275) polymorphism of the IL-4R gene were detected by the TaqMan probe method.

1.3 Observation Indicators

The clinical phenotypes of acne patients in Urumqi were analyzed; The levels of inflammatory molecular markers such as TNF- α , IL-6, IL-1 β , and IL-8 were compared between the two groups; The polymorphisms of TNF- α gene and IL gene family, including TNF- α gene -308G>A polymorphism, IL-8 -251T>A polymorphism, and IL-4R Q551R A/G polymorphism, were analyzed between acne patients in Urumqi and healthy populations; The correlation between clinical phenotypes, inflammatory molecular markers and gene polymorphisms in acne patients in Urumqi was analyzed.

1.4 Statistical Analysis

SPSS 26.0 statistical software was used for data processing. Measurement data were expressed as mean \pm standard deviation ($\bar{x} \pm s$) and compared by t-test. Count data were expressed as [n (%)] and compared by the chi-square χ^2 test. The relationship between clinical phenotypes and inflammatory molecular marker levels was analyzed by one-way analysis of variance (ANOVA) or Kruskal-Wallis H test. A P value < 0.05 was considered statistically significant.

2. Results

2.1 Analysis of Clinical Phenotypes of Acne Patients in Urumqi

Among the 80 acne patients, as assessed by the modified Pillsbury classification, 21 cases (26.25%) were mild (grade I), 30 cases (37.50%) were moderate (grade II), 16 cases (20.00%) were moderate (grade III), and 13 cases (16.25%) were severe (grade IV). The results indicated that acne patients in Urumqi were mainly moderate acne, followed by mild acne, and the proportion of severe acne was relatively low.

2.2 Comparison of Inflammatory Molecular Marker Levels Between the Two Groups

The serum levels of inflammatory molecular markers, including TNF- α , IL-6, IL-1 β , and IL-8 in the study group were higher than those in the control group, with statistically significant differences ($P < 0.05$), as shown in Table 1.

Table 1. Comparison of Inflammatory Molecular Marker Levels Between the Two Groups ($\bar{x} \pm s$)

Group	TNF- α (pg/ml)	IL-6 (pg/ml)	IL-1 β (pg/ml)	IL-8 (pg/ml)
Research group/80	17.12 \pm 6.51	19.42 \pm 4.29	14.59 \pm 3.92	56.97 \pm 10.24
Control group/40	1.09 \pm 0.23	4.59 \pm 1.02	2.45 \pm 0.81	22.09 \pm 6.52
<i>t</i>	15.536	21.519	19.343	19.623
<i>P</i>	< 0.001	< 0.001	< 0.001	< 0.001

2.3 Analysis of Distribution Characteristics of Susceptibility Gene Polymorphisms Between the Two Groups

Analysis of polymorphisms, including the TNF- α gene and IL gene family between acne patients in Urumqi and the healthy population, showed that: For the TNF- α gene -308G>A polymorphism, the distribution of GG, GA, and AA genotype frequencies in acne patients was significantly different from that in the control group, with a statistically significant difference ($P < 0.05$). Carrying the A allele increased the risk of acne. For the IL-8 -251T>A polymorphism, the distribution of TT, TA, and AA genotype frequencies in acne patients was significantly different from that in the control group, with a statistically significant difference ($P < 0.05$). Carrying the T allele increased the risk of acne.

For the IL-4R Q551R A/G polymorphism, the distribution of AA, AG, and GG genotype frequencies in acne patients was significantly different from that in the control group, with a statistically significant difference ($P < 0.05$). Carrying the G allele increased the risk of acne (see Table 2 for details).

Table 2. Analysis of Distribution Characteristics of Susceptibility Gene Polymorphisms Between the Two Groups [n (%)]

Group	TNF- α -308G>A			
	GGhomozygote	GAheterozygote	AAhomozygote	An allele frequency
Research group/80	49 (61.25)	24 (30.00)	6 (7.50)	30 (37.50)
Control group/40	33 (82.50)	8 (20.00)	1 (2.50)	9 (22.50)
χ^2		3.979		
P		0.037		
Group	IL-8-251T>A			
	TThomozygote	TAheterozygote	AAhomozygote	T allele frequency
Research group/80	16 (20.00)	42 (52.50)	25 (31.25)	58 (72.50)
Control group/40	18 (45.00)	6 (15.00)	16 (40.00)	24 (60.00)
χ^2		16.018		
P		< 0.001		
Group	IL-4R Q551R A/G			
	GGhomozygote	AGheterozygote	AAhomozygote	G allele frequency
Research group/80	42 (52.50)	30 (37.50)	8 (10.00)	73 (90.00)
Control group/40	2 (5.00)	11 (27.50)	28 (70.00)	13 (32.50)
χ^2		48.777		
P		< 0.001		

2.4 Correlation Analysis Between Clinical Phenotypes, Inflammatory Molecular Markers, and Gene Polymorphisms in Acne Patients in Urumqi

Among acne patients in Urumqi in this study, the levels of TNF- α , IL-6, IL-1 β , and IL-8 all showed an upward trend with the increase of acne severity, as shown in Table 3. The frequency of mutant genotypes increased with the aggravation of acne severity, and the difference was statistically significant ($P < 0.05$), suggesting that gene polymorphism is closely related to the severity of acne, as shown in Table 4.

Table 3. Comparison of Inflammatory Molecular Marker Levels in Patients with Different Grades of Acne Severity ($\bar{x} \pm s$)

Group	TNF- α (pg/ml)	IL-6 (pg/ml)	IL-1 β (pg/ml)	IL-8 (pg/ml)
Level I/21	5.23 \pm 1.15	8.37 \pm 1.62	6.45 \pm 1.73	25.62 \pm 4.94
Level II/30	9.84 \pm 1.93	12.56 \pm 3.25	10.18 \pm 1.96	32.37 \pm 5.25
Level III/16	16.72 \pm 2.18	17.83 \pm 2.94	13.27 \pm 2.82	48.45 \pm 6.72
Level IV/13	24.72 \pm 4.36	25.94 \pm 4.25	18.37 \pm 3.42	72.45 \pm 9.73
F	426.732	512.486	587.394	623.725
P	< 0.001	< 0.001	< 0.001	< 0.001

Table 4. Comparison of Mutant Genotype Frequencies in Patients with Different Grades of Acne Severity [n (%)]

Group	TNF- α -308A allele	IL-8-251T allele	IL-4R Q551R G allele
Level I/21	7 (33.33)	10 (47.62)	5 (23.81)
Level II/30	11 (36.67)	17 (56.67)	9 (30.00)
Level III/16	10 (62.50)	10 (62.50)	8 (50.00)
Level IV/13	10 (76.92)	12 (92.31)	9 (69.23)
χ^2	38.742	45.375	28.296
<i>P</i>	< 0.001	< 0.001	< 0.001

3. Discussion

Acne is a common chronic inflammatory skin disease, and its incidence has shown an increasing trend in recent years. The occurrence of this disease is related to androgen action, excessive sebum secretion, and other factors [5], and it is a disease that has a considerable impact on individual physical and mental health. Combined with clinical case data, this study analyzed the clinical phenotypic characteristics of acne patients in Urumqi and their correlation with inflammatory molecular markers. The serum levels of inflammatory molecular markers, including TNF- α , IL-6, IL-1 β , and IL-8 in the study group were higher than those in the control group, indicating that the levels of inflammatory molecular markers are closely related to the occurrence of acne. With the increase of acne severity, the levels of TNF- α , IL-6, IL-1 β , and IL-8 all showed an upward trend, and the frequency of mutant genotypes increased with the aggravation of acne severity, suggesting that gene polymorphism is closely related to the severity of acne. TNF- α is a pro-inflammatory cytokine that regulates cell survival, apoptosis, and inflammatory responses. Elevated TNF- α levels are accompanied by an increase in other inflammatory factors, which form an inflammatory amplification loop and lead to the aggravation of the inflammatory response in acne [6]. The occurrence of acne is closely related to *Cutibacterium acnes* (formerly *Propionibacterium acnes*). This pathogenic bacterium promotes the release of IL-1 β by activating the NLRP3 inflammasome, thereby exacerbating the inflammatory response. IL-6 binds to membrane-bound or soluble IL-6 receptors to regulate the expression of acute-phase proteins and inflammation-related genes. During the pathogenesis of acne, IL-6 not only participates in the inflammatory response but also affects sebaceous gland function and follicular keratinization, thus promoting the occurrence and progression of acne. IL-8 activates neutrophils and releases a variety of inflammatory mediators and proteases, which aggravate tissue damage and lead to the exacerbation of acne [7]. The high intensity of ultraviolet radiation in Urumqi may induce the production of large amounts of reactive oxygen species in the skin, activate the NF- κ B signaling pathway, and promote the release of inflammatory factors.

Among the acne patients in Urumqi in this study, the frequency of mutant genotypes increased with the aggravation of acne severity, suggesting that gene polymorphism is closely related to the severity of acne. The TNF- α gene is located on the short arm of chromosome 6 in the major histocompatibility complex III, with high genetic polymorphism. The TNF- α -308G>A polymorphism is closely related to acne susceptibility, and individuals carrying the A allele have a significantly increased risk of developing acne [8]. The IL-8 -251T>A polymorphism is located in the promoter region, which may affect the transcriptional activity of the IL-8 gene and further affect the expression level of IL-8 protein. The IL-4R Q551R A/G polymorphism may affect IL-4 and IL-13 signal transduction, and thus regulate immune balance and inflammatory responses [9].

Based on the above findings, for the treatment of acne patients in Urumqi, isotretinoin can be combined with anti-inflammatory drugs. Isotretinoin can control the disease by inhibiting sebum secretion and regulating the abundance of *Cutibacterium acnes*, while exerting favorable local anti-inflammatory and anti-keratinization effects. Isotretinoin can inhibit the NF- κ B signaling pathway and reduce the production of multiple inflammatory factors [10]. For antibiotics, low-dose doxycycline or minocycline can be used, which can effectively inhibit the activity of matrix metalloproteinases while exerting antibacterial effects, thereby reducing the production of inflammatory factors. During treatment, the levels of multiple inflammatory factors in patients should be monitored regularly to evaluate the therapeutic effect and adjust the treatment regimen in a timely manner [11]. If patients have increased sensitivity of androgen receptors, anti-androgen therapy, such as spironolactone or oral contraceptives, should be administered. Spironolactone can effectively inhibit androgen action by competitively binding to androgen receptors. Oral contraceptives can inhibit ovarian androgen secretion, effectively increase the level of sex hormone-binding globulin, reduce the level of free testosterone, and promote the improvement of acne. Considering the dry climate and frequent

wind and sand in Urumqi, the application of moisturizers should be emphasized to maintain skin barrier function, physical sun protection should be strengthened in daily life, and cosmetics containing heavy metals should be avoided.

In conclusion, acne patients in Urumqi are predominantly affected by grade II acne. The levels of inflammatory molecular markers are closely correlated with the severity of acne, and polymorphisms of the TNF- α gene, IL gene family, and other genes are closely associated with acne susceptibility. Diversified treatment strategies should be implemented based on these findings to improve the therapeutic effect of acne.

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