Polymorphisms in the cytochrome P-450 (CYP) 1A1 and 17 genes are not associated with acne vulgaris in the Polish population

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Abstract

Introduction: The pathogenesis of acne is complex, multifactorial and not well understood. The genetic background of this dermatosis is well documented.

Aim: To assess the frequency of –34 T>C single nucleotide polymorphism in the promoter of the CYP17 gene as well as m1 (+6,235 T>C) and m2 (+4,889 A>G) mutation in the coding region CYP1A1 gene patients from the Northern Polish population.

Material and methods: The study included 115 acne patients and 94 healthy controls (aged over 20) without acne in anamnesis. The CYP1A1 polymorphism was analyzed by polymerase chain reaction (PCR). The restriction fragment length polymorphism (RFLP) was used to analyze m2 mutation and allele-specific PCR in the case of m1 mutation. The CYP17 polymorphism was analyzed by RFLP. The results were evaluated by the Pearson’s χ² test.

Results: There were no statistically significant associations between allele and genotype frequencies between the acne and the control group.

Conclusions: We did not confirm the role of the CYP1A1 and CYP17 gene as predictor factors for acne development in the Polish population.

Key words: acne, genetic factors, cytochrome P-450, CYP1A1, CYP17, gene polymorphism.
The etiopathogenesis of acne vulgaris is multifactorial and associated with genetic and environmental aspects. The sebaceous gland function is regulated by various factors (hormones, cytokines, chemokines, growth factors) however vitamin A metabolites and androgens play a crucial role. Therefore, that might be the reason why CYP genes are possible acne gene candidates.
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Polymorphic variants of CYP family genes were associated with several inflammatory and neoplastic disorders but only few studies are concentrated on acne [13–15, 17].

The first molecular researches of genetic acne predisposition were performed at the end of the 20th century. In 1998, Paraskevaidis et al. [15] found a trend to an overexpression of CYP1A1 m1 alleles in acne patients and normal frequency of m2. Authors believed that the m1 mutation might define a marker for alterations on regulatory sites, the biological efficacy of natural retinoids could be greatly impaired by their rapid metabolism to inactive compounds. A deficit of active natural retinoids may be implicated with the development of acne in some patients, due to abnormal sebocyte differentiation and hyperkeratinization of the follicular canal. Our preliminary study on a smaller group showed a two times higher incidence of CYP1A1 m1 and m2 mutations in the acne group compared to controls [18]. We have not revealed any association between CYP1A1 gene polymorphisms and acne in this study in spite of including twice as many patients.

The relationship between the CYP17-34T>C gene polymorphism was first observed by He et al. [14]. Authors revealed that a CYP14-34C/Homozygote Chinese man had a significantly increased risk of developing severe acne. A subsequent Chinese report revealed that the presence of base substitution thymine to cytosine in −34 CYP17 increases the risk of post adolescent acne in female subjects with increased androgen levels [19, 20]. In our study, we did not confirm these results. Caputo et al. [13] evaluated CYP21 gene mutations in a selected group of women with papulopustular and comedonal acne refractory to treatment, irregular menses and hirsutism. Authors revealed several different point mutations and demonstrated that a cohort of patients resistant to acne therapy can be carriers of or affected by non-classical 21-hydroxylase deficiency (late onset). Yang et al. [17] analyzed the CAG repeat polymorphism in the androgen receptor gene and acne in the Chinese population. Their results indicate that polymorphism to be one of the candidate genetic markers for male acne susceptibility.

That inconsistent results suggest that genetic predisposition to acne is poligenetically coded and can be associated with the patient origin. Our and Romanian-Hungarian researches did not show any relationship between −308G>A TNF gene polymorphism and acne contrary to two Arabic studies. Also TNF-308G>A genotype frequencies of control individuals were different in Polish, Hungarian-Romanian and Turkish studies [7, 10, 20, 21].

Conclusions

Presented data did not confirm the role of the CYP1A1 and CYP17 gene as predictor factors for acne development in the Polish population. Results of our study as well as literature data indicate that genetic susceptibility to acne may vary in a different population. Further complex, multicenter investigations are strongly required.

Conflict of interest

The authors declare no conflict of interest.

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