Defensins are antimicrobial peptides expressed on mucosal surfaces. They function as part of the innate immune system. Palatine tonsils play important roles in innate immune system. However, our knowledge on the pathophysiology of chronic tonsils is limited. Eighty six patients with chronic tonsillitis and eighty controls without history of chronic tonsillitis were enrolled in this study. Genotypes were determined by restriction fragment length polymorphism analyses after polymerase chain reaction.

The aim of this study was to investigate the association between beta defensin 1 gene single nucleotide polymorphisms and chronic tonsillitis. Genotype and allele frequencies of the -20G/A (rs11362), -44C/G (rs1800972) and -52G/A (rs1799946) single nucleotide polymorphisms were not statistically different between patients and control groups (p > 0.05).

Our patient group was consisted of 86 consecutive patients with chronic tonsillitis; 44 were men and 42 were women (mean age 10.49 9.64 years). The control group was consisted of 80 healthy volunteers; 51 were men and 29 were women (mean age 27.11 16.03 years). There was a statistically significant difference in terms of age, between the study and control groups (p < 0.001).

When gender was considered, there was no statistically significant difference between the two groups (p = 0.572). The ethnicity of the patients and volunteers were the same, Turkish. DEFB1 genotype distributions and allele frequencies of the patients and controls are given in Table 1. The distribution of the -20G/A, -44C/G and -52G/A genotypes and the frequencies of the alleles did not differ between the patient and control groups (p > 0.05) (Table 1).

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Defensin induction needs more intense and prolonged microorganellar triggering. Our study suggests that DEFB1 SNPs at genomic positions -20G/A, -44C/G and -52G/A are not associated with chronic tonsillitis. Despite this disconnection, some limitations of our study might affect the results. First, it is a population-based study with a limited number of subjects. Although we only investigated three SNPs in the 5′ UTR of DEFB1, additional polymorphisms in different localizations have been described in the literature for DEFB1. In a population-based study with a limited number of subjects. Although we only investigated three SNPs in the 5′ UTR of DEFB1, additional polymorphisms in different localizations have been described in the literature for DEFB1. In general, hBDs are endogenous antibiotics against gram-negative bacteria, gram-positive bacteria, fungi, viruses and protozoa [6]. This protein was first isolated from hemorrhage [7]. Expression of hBD1 was shown in epithelial cells of the urinary tract, respiratory tract, and keratinocytes. Human beta defensin 1 expression is constitutive [8], but it was showed that microbial pathogens and cytokines stimulate the expression of beta defensins in oral epithelial cells during inflammation [9]. Thereafter, palatine tonsils are capable of producing proinflammatory molecules shaping the immune response. Beta defensins are a component of innate immune response. It was showed that the expression of hBD1 varies between individuals [18]. Therefore, our hypothesis was that individuals may exhibit increased susceptibility to chronic tonsillitis upon the differences in genotypes of beta defensin 1 (DEFB1) gene. However, as far as we know, there is no study investigating the association of DEFB1 genotypes with chronic tonsillitis. The aim of this study was to determine whether three coding single nucleotide polymorphisms (SNPs) (-20G/A -rs11362, -44C/G and -52G/A-rs1799946) located in 5′-untranslated region (UTR) of DEFB1 gene were related to susceptibility to chronic tonsillitis.

Beta defensins are a component of innate immune response. It was showed that the expression of hBD1 varies between individuals [18]. Our study is the first one to investigate the association between DEFB1 SNPs and chronic tonsillitis. We found no association between DEFB1 variants and chronic tonsillitis. Therefore we suggested that DEFB1 -20G/A, -44C/G and -52G/A SNPs are not associated with susceptibility of chronic tonsillitis in our population. The polymorphisms are different substitutions causing relatively conservative amino acid changes in the proteins. -20G/A, -44C/G and -52G/A SNPs are situated in the 5′ untranslated region of the DEFB1 gene. They are suggested as important for regulating gene expression [11].

Schwaab et al. [12] found that hBD1 to 3 were expressed at same concentration as in acute tonsillitis, hypertrophic tonsil and peritonsillar abscess. The authors attributed this condition to changed external circumstances as reduced number of macrophages, antigen presenting cells, dendritic cells and colonies in the biofilm. In accordance with this study, Wang et al. [13] showed that hBD1 was similar in the patients and the normal group, but hBD2 expressed significantly higher levels in chronic tonsillitis group. In another study, Claes et al. [3] demonstrated that there was strong hBD2 expression in tonsillar tissue, in with no (regardless of) significant difference between hypertrophic tonsillar disease and recurrent tonsillitis, compared with nasal-paranasal mucoa and adenoids. Therefore, the authors concluded that defensin induction needs more intense and prolonged microorganellar triggering.

Our study suggests that DEFB1 SNPs at genomic positions -20G/A, -44C/G and -52G/A are not associated with chronic tonsillitis. Despite this disconnection, some limitations of our study might affect the results. First, it is a population-based study with a limited number of subjects. Although we only investigated three SNPs in the 5′ UTR of DEFB1, additional polymorphisms in different localizations have been described in the literature for DEFB1. In this regard, it could be planned to compare the expression level of DEFB1 in tonsil tissues of patient with chronic tonsillitis and in those of control subjects and to characterize the cellular source of their mRNA expression. Besides this, further studies with larger groups are required to establish the role of the DEFB1 in chronic tonsillitis and its clinical consequences.

Conclusion

There are a lot of unknowns about processes underlying chronic tonsillitis. Therefore, determination of the innate immune system components in the palatine tonsils, will lead to be better informed about the role of the palatine tonsils in immune response. Beta defensins are a component of the innate immune response and we investigated SNPs of DEFB1 gene. This is the first report on the association of DEFB1 polymorphisms with chronic tonsillitis. We did not find any association, but changes in DEFB1 structure or function may lead to a modification of antimicrobial defense in the oral mucosa. So that, DEFB1 may still play a role in the pathophysiology of chronic tonsillitis.