Psoriasis vulgaris is an inflammatory, hyperproliferative disease of the skin, affecting 1–3% of Caucasians (Ikaheimo et al. 1996). Although the aetiology of the disease is still unknown, the genetic basis for psoriasis is beyond doubt. So far the strongest genetic association has been found for early onset psoriasis and major histocompatibility complex (MHC) genes, especially HLA-Cw6. There is also some evidence that psoriasis is a T-cell mediated autoimmune process. Activated lymphocytes, other immune accessory cells and lymphokines have been detected in psoriatic plaques (Elder et al. 1994; Henseler et al. 1998). T-cells accumulate early in psoriatic plaques and their cytokines induce abnormal keratinocyte proliferation. In addition to HLA genes, immune responses are dependent on several genes encoding molecules that generate and translocate antigenic peptides. The genes involved in class I and II antigen processing pathways include TAP, LMP, and HLA-DM, and may be considered as candidate genes for research on susceptibility to psoriasis. The TAP genes are located in the HLA class II region, between the DQB1 and DPAL loci, and exhibit genetic polymorphisms. The TAP genes consist of TAP1 and TAP2 genes, which encode a heterodimer molecule that forms a heterodimeric complex for delivering antigenic peptides to the endoplasmic reticulum prior to the assembly of class I heavy chain α2-microglobulin dimers (Pyo et al. 2003). Two polymorphic sites have been found in the TAP1 gene and four in the TAP2 gene. There are four allele combinations of polymorphism in TAP1 and eight combinations in TAP2 (Powis et al. 1993). TAP polymorphism has been investigated in several HLA-associated diseases in Caucasian patients (e.g. ankylosing spondylitis,
multiple sclerosis and insulin-dependent diabetes mellitus). The functional consequences of TAP polymorphism are still unknown. It has been suggested that psoriasis may be triggered by the direct activation of CD8 and/or NK T-cells bearing receptors for MHC class I molecules (Bos and De Rie 1999). Therefore the interaction of specific TAP molecules and peptides might cause altered activity of specific HLA-C, such as low expression on the cell surface, resulting in the activation of NK cell cytotoxicity to own cells in psoriasis patients, and the associated TAP alleles might play a role in the development of psoriasis (Pyo et al. 2003).

For this study we recruited 169 unrelated Caucasian psoriasis patients (n = 169; 63 females and 106 males) from the Department of Dermatology, Venereology and Allergology, Medical University of Gdańsk, Poland. Patients were divided according to positive family history and age of onset of psoriasis into two subgroups: type I psoriasis (onset before the age of 40 and positive family history, n = 138; 54 females and 84 males) and type II psoriasis (onset later than at the age of 40 and negative family history, n = 31; 9 females and 22 males). Healthy Polish volunteer blood donors formed the control group (n = 66; 21 females and 45 males). Genomic DNA was extracted from mononuclear cells of peripheral blood according to the enzymatic method of Blood DNA Prep Plus (A&A Biotechnology, Gdańsk, Poland). In our study we used the amplification refractory mutation system (ARMS) PCR method for analysing the TAP1 gene polymorphism, according to the procedure described by Powis et al. (1993). In each person the two dimorphic sites of the TAP1 gene encoding different amino acids in positions 333 and 637 were analysed. Each allele of the TAP1 gene was defined by the combination of polymorphisms at different positions, as follows: TAP1*A (Ile-333 and Asp-637), TAP1*B (Val-333 and Gly-637), TAP1*C (Val-333 and Asp-637) and TAP1*D (Ile-333 and Gly-637).

Frequencies of the TAP1 alleles for the psoriasis patients and the control group are shown in the Table 1. below. We found that TAP1*A was the most frequent allele in both groups. Its frequency in the patients was much lower than in healthy donors (66% vs. 82.6%).

There were no significant differences in frequencies of TAP1*B and TAP1*C alleles between the groups. The analysis also showed that the frequency of allele TAP1*D in psoriasis patients was significantly increased, as compared to the control (15.4% to 2.3%). There were no significant differences in the frequencies of TAP1 alleles for type I and type II psoriasis.

There have been several reports so far on the analysis of TAP alleles in patients with psoriasis. In Germany, Fakler et al. (1994) analysed the TAP2 gene polymorphism in psoriasis, and showed no significant difference in allele frequencies between the control group and psoriasis type I and/or type II. Two years later, Hohler et al. (1996) reported an increase in the TAP1*A allele in Caucasian patients with juvenile onset psoriasis and decrease in the frequency of the other TAP1 alleles. Ikaheimo et al. (1997) compared five dimorphic amino acid positions of TAP genes between the psoriasis and control group but there were no significant differences. A study of Japanese patients with psoriasis, performed by Saeki et al. (1998), showed a decrease in TAP2*E allele frequency, but the difference was not significant. They also compared the frequencies of TAP alleles between patients with early onset psoriasis (before the age of 30) and late onset psoriasis (after the age of 30), but did not find any differences. The most recent study of Pyo et al. (2003), on association of TAP genes with psoriasis in Koreans, showed that the frequency of TAP2*B was significantly increased, while TAP1*B and TAP2*A frequencies were decreased in psoriasis patients, compared with the control group. Our results indicate that psoriasis patients have more frequently the TAP1*D allele, which could lead to genetic

<table>
<thead>
<tr>
<th>TAP1 allele</th>
<th>Psoriasis (2n=338)</th>
<th>Type I (2n=274)</th>
<th>Type II (2n=64)</th>
<th>Control (2n=132)</th>
</tr>
</thead>
<tbody>
<tr>
<td>TAP1*A</td>
<td>223 (66.0%)*</td>
<td>181 (66.1%)</td>
<td>42 (65.6%)</td>
<td>109 (82.6%)</td>
</tr>
<tr>
<td>TAP1*B</td>
<td>51 (15.1%)</td>
<td>39 (14.2%)</td>
<td>39 (14.2%)</td>
<td>15 (11.3%)</td>
</tr>
<tr>
<td>TAP1*C</td>
<td>12 (3.5%)</td>
<td>9 (3.3%)</td>
<td>3 (4.7%)</td>
<td>5 (3.8%)</td>
</tr>
<tr>
<td>TAP1*D</td>
<td>52 (15.4%)*</td>
<td>45 (16.4%)</td>
<td>7 (11.0%)</td>
<td>3 (2.3%)</td>
</tr>
</tbody>
</table>

* p < 0.05
susceptibility toward psoriasis vulgaris in Poles. However, further investigations and a much deeper and refined statistical analysis of a larger data set are needed for a definitive conclusion.

REFERENCES


