Comparison of MHC class I risk haplotypes in Thai and Caucasian psoriatics shows locus heterogeneity at PSORS1

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Key words human genetics; human leukocyte antigens; major histocompatibility complex; psoriasis

Abstract

Earlier studies have shown that psoriasis in Japan and Thailand is associated with two different major histocompatibility complex (MHC) haplotypes – those bearing HLA-Cw6 and those bearing HLA-Cw1 and HLA-B46. In an independent case-control sample from Thailand, we confirmed the association of psoriasis with both haplotypes. No association was seen in Thai HLA-Cw1 haplotypes lacking HLA-B46, nor was HLA-Cw1 associated with psoriasis in a large Caucasian sample. To assess whether these risk haplotypes share a common origin, we sequenced genomic DNA from a Thai HLA-Cw1-B46 homozygote across the ∼300 kb MHC risk interval, and compared it with sequence of a HLA-Cw6-B57 risk haplotype. Three small regions of homology were found, but these regions share equivalent sequence similarity with one or more clearly non-risk haplotypes, and they contain no polymorphism alleles unique to all risk haplotypes. Differences in psoriasis phenotype were also observed, including lower risk of disease, greater nail involvement, and later age at onset in HLA-Cw1-B46 carriers compared with HLA-Cw6 carriers. These findings suggest locus heterogeneity at PSORS1 (psoriasis susceptibility 1), the major psoriasis susceptibility locus in the MHC, with HLA-Cw6 imparting risk in both Caucasians and Asians, and an allele other than HLA-Cw1 on the HLA-Cw1-B46 haplotype acting as an additional risk variant in East Asians.

Introduction

Human leukocyte antigen (HLA) associations with psoriasis have been known for nearly 40 years (1). Earlier studies localized the disease determinant to the class I end of the MHC (2, 3) and assigned the name PSORS1 [OMIM (Online Mendelian Inheritance in Man) # 177900] to this locus (4). Association with HLA-Cw6 is particularly strong in many different world populations (5), and recent sequencing and haplotype analyses of Caucasian and Chinese Han psoriatics have indicated that HLA-Cw6 itself is likely to be the susceptibility determinant on these chromosomes, rather than any of 10 nearby genes in the 300-kb PSORS1 candidate interval (6, 7). The prevalence of psoriasis differs markedly throughout the world (8). While it is unclear whether genetic or environmental factors are primarily responsible for this variation, it has been suggested that the rarity of psoriasis in Australian aborigines and several Amerindian populations is correlated with the absence of HLA haplotypes carrying HLA-Cw6 (8).

Several studies have documented a strong association between psoriasis and another HLA haplotype that is common in Japan and Thailand, but extremely rare in Caucasians (HLA-A*0207, -B*4601, -Cw*01) (9–13). This haplotype was associated with psoriasis when found in cis to any of three HLA class II haplotypes (10), suggesting that the disease determinant resides on the class I end of these haplotypes. Interestingly, all studies but one (9) found that the HLA-Cw1-B46 haplotype imparts considerably lower risk for psoriasis than does HLA-Cw6. There is also some evidence that this determinant produces a different clinical form of psoriasis as HLA-Cw1-B46 is equally associated with early or late-onset disease (9, 10), whereas HLA-Cw6 is much more strongly associated with early-onset psoriasis in both Thais (10) and Caucasians (14).
A major goal of this study was to determine whether the HLA-Cw1-B46 psoriasis risk haplotype found in Japanese (12, 13, 15) and Thai (9, 10) populations and the HLA-Cw6-bearing psoriasis risk haplotypes found in both Caucasians and Asians represent allelic or locus heterogeneity at the PSORS1 locus, or if they share a disease locus inherited identical by descent (IBD) from a common ancestor. To this end, we cloned and sequenced the PSORS1 candidate interval of the HLA-Cw1-B46 haplotype for comparison with sequences for the HLA-Cw6-B57 and HLA-Cw6-B50 risk haplotypes and nine non-risk MHC haplotypes that were derived by us (6) and the Sanger Centre (16). In addition, we looked for differences in associated relative risk and phenotype of the HLA-Cw1-B46 and HLA-Cw6-bearing haplotypes in a previously unreported sample of 206 Thai cases and 114 Thai controls. Finally, we compared the haplotype compositions and odds ratios (ORs) for association of HLA-Cw1 in our Caucasian and Thai samples. Together, these analyses confirm that HLA-Cw1-B46 is a psoriasis risk haplotype in the Thai population, demonstrate that HLA-Cw1 is unlikely to be a direct determinant of risk for psoriasis in the Caucasian or Thai populations, and strongly suggest that the disease determinants carried on these two ancestral haplotypes are not derived from a common ancestor.

**Materials and methods**

**Subjects**

Informed consent was obtained from all subjects under protocols adherent to the Declaration of Helsinki principles and approved by the Institutional Review Boards of the participating institutions. In the Caucasian sample, which consisted of 2438 cases and 2311 controls, most affected individuals were identified through the dermatology services of the University of Michigan Medical Center, the Ann Arbor Veterans Affairs Medical Center, and Henry Ford Hospital of Detroit. A few psoriatics were also provided by the National Psoriasis Foundation Tissue Bank. Individuals were defined as affected if chronic plaque or guttate psoriasis lesions covered more than 1% of the total body surface area (TBSA) or if at least two skin, scalp, nail or joint lesions were clinically diagnostic of psoriasis (17). Controls were recruited from the southeast Michigan area, and were required to be unrelated to each other or to any case, and to be free of a family history of psoriasis. For this study, only cases and controls of self-reported European Caucasian origin were analyzed. The Thai sample consisted of 206 psoriasis cases and 114 normal controls, all collected at the Institute of Dermatology in Bangkok, Thailand, using the same inclusion and exclusion criteria used for the Caucasian sample.

**DNA preparation**

Genomic DNA was prepared from heparinized whole blood using previously established methods (18). Blood samples collected in Bangkok were transported to Ann Arbor for DNA preparation within 4 days.

**Genotyping**

Eight single-nucleotide polymorphisms (SNPs) in exons 2 and 3 of the HLA-C gene were genotyped – rs1131151, rs28732105, rs1050409, rs1131123, rs1131118, rs1050384, rs17839985, and rs415474919 at positions 89, 213, 218, 341, 361, 387, 459, and 540 of the coding sequence. These SNPs allow absolute discrimination of HLA-C to a triallelic level (Cw1/Cw6/neither), even in the absence of external phasing information, for all known alleles in release 2.10.00 of the IMGT-HLA Sequence Database (19); URL: http://www.ebi.ac.uk/imgt/hla). Six SNPs in exons 2 and 3 of the HLA-B gene were also genotyped – rs713031, rs41562914, rs1131204, rs41553715, rs1071652, and rs2308466 at positions 142, 206, 277, 299, 362, and 560 of the coding sequence. These SNPs provide typing of HLA-B to a biallelic level (B46/other) in the absence of phasing information for all known alleles in release 2.16.00 of the IMGT-HLA database. All SNPs were typed by single-base primer extension, as implemented in the SnapShot assay protocol (Applied Biosystems, Foster City, CA), per the manufacturer’s instructions. Polymerase chain reaction (PCR) amplification and SnapShot extension primer sequences are provided in Table S1 (Supporting Information). Microsatellites were genotyped by PCR amplification using fluorescently labeled forward and unlabeled reverse primers followed by size determination by capillary electrophoresis on an Applied Biosystems 3100 Genetic Analyzer.

**Cloning and sequencing**

A Thai psoriatic who was homozygous for the HLA-Cw1-B46 haplotype throughout the 300-kb PSORS1 candidate region (31.129–31.429 Mb on build 36.3 of the human reference sequence for chromosome 6) was identified by genotyping HLA-C, HLA-B, and 10 microsatellite markers extending from MICA to telomeric of CDSN. A fosmid library was prepared from the genomic DNA of this individual and screened for the region of interest, as previously described (6). Thirteen overlapping fosmid clones that provided complete coverage of the risk interval were selected, with no attempt made to distinguish clones from the maternal or paternal chromosome. Inserts of each fosmid clone were subjected to shotgun sequencing, as described previously (6). High quality sequence coverage from at least two different plasmid subclones – and from both strands, whenever possible – was required for the entire fosmid insert, which resulted in a 22-fold average depth of coverage. The published sequence of the HLA-Cw7-B8 haplotype of the Cox homoygous cell line (20) was used as both a reference for sequence alignment and for the numbering of the coordinate system used in the
tables and figures of the present study, which starts at the first base of the 5′ primer (GCAAACCTTTCGTGCAATCCA) used to amplify microsatellite marker D6S273 and extends in the telomeric direction. Overlapping fosmid clone sequences were assembled into a single contig; the resulting 337.1 kb of HLA-Cw1-B46 haplotype sequence (spanning 31.105–31.446 Mb on human reference) has been deposited in Genbank (accession number GQ472773).

Association analysis

Single marker association was evaluated using a chi-squared contingency test of allelic counts; asymptotic P-values are reported. Haplotype inference and haplotype-based association tests were carried out with v1.07 of PLINK (21); http://pngu.mgh.harvard.edu/purcell/plink. For standard haplotype association, a logistic regression model with an allele dosage term was used, and P-values were determined with 1 million permutations of case-control status. For conditional haplotype-based association, a test of whether HLA-Cw1 has effects independent of HLA-B46 was constructed as a likelihood ratio test comparing an alternative model with separate effects for each of the three HLA-Cw1-B46 haplotypes to a null model which groups the Cw1+/B46− and Cw1−/B46− haplotypes together. An analogous conditional test for independent effect of HLA-B46 compares association of the Cw1+/B46+ and Cw1+/B46− haplotypes. Meta-analysis of disease associations in the two Thai studies used Cochran-Mantel-Haenszel test procedures. Power calculations were carried out with version 3.1 of G•POWER (22); http://wwwpsycho.uni-duesseldorf.de/aap/projects/gpower.

Sequence analysis

The HLA-Cw1-B46 sequence was aligned with the other 18 MHC haplotype sequences using SeqMan (DNASTAR, version 8.0.2); whenever necessary, sequence alignments were manually adjusted to yield the minimum possible number of polymorphisms. For each polymorphism, its location in the Cox HLA-Cw7-B8 reference sequence and its alleles for all 19 haplotypes were recorded. MHC haplotype sequences were then compared with that of the HLA-Cw6-B57 haplotype by determining the percentage difference of polymorphic alleles over 2.5-kb intervals. Regions of similarity between pairs of MHC haplotype sequences were delineated by a two-step approach (23). Rough bounds were first obtained using a moving window of 2.5 kb with a lag of 100 bp and a criterion of at least 80% identity of alleles for all included polymorphisms. Recursive entropic segmentation (24) with a stopping criterion based on the Bayesian information criterion (25) was then applied as a second-stage refinement. Version 0.97-600-1000 of the MNCOV program (26); (http://www.stanford.edu/group/molepi/free software.html) was used to search for minimal combinations of polymorphism alleles unique to risk haplotypes. MHC haplotype sequences within regions of homology were clustered using an average-distance agglomerative hierarchical method with a metric of percentage difference of polymorphism alleles. Multiple instances of a single MHC haplotype (viz., two HLA-Cw6-B57, two Cw7-B7, two Cw8-B65, three Cw7-B8, two Cw3-B62, and two Cw12-B38 haplotypes) were consolidated into a single representative consensus sequence before comparison of sequence similarity and combinatorial analysis. All 19 available MHC sequences were used for clustering.

Phenotype analysis

Five phenotypic aspects of psoriasis were measured at entry into the study: age at onset of disease, TBSA involvement of lesions, toenail involvement, fingernail involvement, and arthritis. All traits were compared for four different HLA-CB phenotypes (carriage of HLA-Cw1-B46 but no HLA-Cw6, carriage of HLA-Cw6 but no HLA-Cw1-B46, carriage of both HLA-Cw6 and HLA-Cw1-B46, carriage of neither HLA-Cw1-B46 nor HLA-Cw6), as well as all six possible HLA-CB genotypes involving these two alleles. Age at onset and TBSA were analyzed by one-way analysis of variance (ANOVA) after transforming the variables to approximate normality with the optimal Box–Cox power transformation (power of 0.8 for age at onset and 0.3 for TBSA); P-values were determined using 10,000 randomizations of the response variable observations. There were no significant departures from the assumption of homogeneity of variances for either of the transformed variables, as assessed by a randomization version of Levine’s test. Sheffe’s modified S-method (27, 28) was used for an unplanned comparison of mean age at onset of HLA-Cw6 carriers vs noncarriers; it controls the experimentwise error rate at the nominal level for all possible linear contrasts of the group means. Nail involvement and arthritis were analyzed by unordered two-way contingency tables, using Fisher’s exact test to determine the significance of association between phenotype variables and HLA-C status. Standardized Pearson residuals were examined to determine the relative contributions of different cells of the contingency table to the overall test result, and a 2 × 2 contingency table was used to analyze nail involvement for HLA-Cw1-B46 carriers vs noncarriers.

Results

Association analysis

As shown in Table 1, in our Thai sample, HLA-Cw6, HLA-Cw1 and HLA-B46 all are significantly associated with psoriasis (P = 3.2 × 10−6, 0.0011 and 0.0017, respectively). The associations with HLA-Cw1 and HLA-B46 are driven entirely by association with an underlying HLA-Cw1-B46 haplotype (P = 0.0016, Table 2). In this sample HLA-B46 is invariably linked with HLA-Cw1 (i.e. no HLA-Cw1−/B46+
Table 1  Single marker analysis of HLA-Cw1, HLA-Cw6, and HLA-B46 associations with psoriasis in Thais and Caucasians

<table>
<thead>
<tr>
<th>Allele</th>
<th>Frequency (proportion) in Thais</th>
<th>Frequency (proportion) in Caucasians</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Cases (proportion)</td>
<td>Controls (proportion)</td>
</tr>
<tr>
<td>HLA-Cw1</td>
<td>94 (0.2338)</td>
<td>26 (0.1238)</td>
</tr>
<tr>
<td>HLA-Cw6</td>
<td>71 (0.1766)</td>
<td>9 (0.0429)</td>
</tr>
<tr>
<td>HLA-B46</td>
<td>79 (0.1955)</td>
<td>22 (0.0991)</td>
</tr>
</tbody>
</table>

aOdds ratio and its 95% confidence interval for the allelic association test.
bGlobal P-value = 0.0036; all the P-values based on 1 million permutations.

Table 2  Association of HLA-Cw1-B46 haplotypes with psoriasis in Thais

<table>
<thead>
<tr>
<th>HLA haplotype</th>
<th>Frequency cases</th>
<th>Frequency controls</th>
<th>OR (95% CI)a</th>
<th>Pb</th>
</tr>
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<tbody>
<tr>
<td>Cw1 B46</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>+ +</td>
<td>0.1965</td>
<td>0.0991</td>
<td>2.25 (1.34, 3.80)</td>
<td>0.0016</td>
</tr>
<tr>
<td>+ –</td>
<td>0.0373</td>
<td>0.0283</td>
<td>1.34 (0.51, 3.57)</td>
<td>0.63</td>
</tr>
<tr>
<td>– +</td>
<td>0.0000</td>
<td>0.0000</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>– –</td>
<td>0.7662</td>
<td>0.8726</td>
<td>0.46 (0.28, 0.75)</td>
<td>0.0012</td>
</tr>
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</table>

aOdds ratio and its 95% confidence interval in logistic regression dosage model for association.

Sequence comparisons

In order to determine the DNA sequence of the PSORS1 risk region on the HLA-Cw1-B46 haplotype, an affected Thai individual homozygous for this haplotype was identified by HLA typing and microsatellite genotyping, and a fosmid library was prepared and screened as described in Methods. A total of 13 overlapping fosmid clones were isolated that provided complete coverage of a 337 kb region extending from 15 kb telomeric of HLA-B to 90 kb centromeric of CDSN. The sequenced interval fully includes a 298-kb candidate region for PSORS1 shared by all known HLA-Cw6 risk haplotypes (6). We then compared this sequence to a collection of genomic DNA sequences generated by ourselves (6) and by the MHC Haplotype Project (16). Besides providing new examples of haplotypes we previously sequenced (HLA-Cw7-B8, Cw7-B7, Cw3-B62, and Cw6-B57), inclusion of the MHC Haplotype Project sequences contributed sequences for four new haplotypes (HLA-Cw5-B18, Cw5-B44, Cw16-B44, and Cw3-B60) that all appear to be non-risk from our previous analysis (6). All together, 19 sequences were available, including those for 11 distinct MHC haplotypes that were complete enough for sequence comparison in the candidate interval.
Figure 1 Sequence comparison of 10 MHC class I haplotypes with the HLA-Cw6-B57 risk haplotype. Known genes and their direction of transcription, as well as a 9.7-kb indel are shown above the coordinate axis. Genes expressing non-coding RNA are colored cyan, and those expressing protein are colored red. Three delineations of the PSORS1 candidate region (6) are shown below the coordinate axis. The per cent disagreement of polymorphism alleles, when compared with the HLA-Cw6-B57 haplotype, is plotted for each haplotype using a moving 2.5-kb window with a 500-bp lag. The bottom panel plots the number of polymorphisms that are variable among all sequenced haplotypes; only these polymorphisms were considered when computing per cent disagreement. Regions of sequence homology at least 5 kb in length between the HLA-Cw1-B46 and HLA-Cw6-B57 haplotypes are mapped as five-numbered orange bars in the top panel; these bars are also shown on all other haplotypes sharing the same regions of homology.

As shown in Figure 1, the HLA-Cw1-B46 and HLA-Cw6-B57 haplotypes exhibit substantial allelic divergence for more than three-quarters of the sequenced interval. Nevertheless, within the 331 kb region encompassing most sequences, four of 7364 qualifying polymorphisms carry an allele common to all three psoriasis risk haplotypes (HLA-Cw6-B57, Cw6-B50, and Cw1-B46) that is not found on any of the eight non-risk haplotypes (Table 3). Furthermore, there are more than 59,000 two-way combinations and 2 billion three-way combinations of polymorphism alleles fulfilling this same criterion for a potential IBD disease locus. Progressively narrowing the region of comparison to each of three different PSORS1
Table 3 Polymorphism analysis of PSORS1 candidate regions and regions of sequence homology between HLA-Cw1-B46 and HLA-Cw6-B57

<table>
<thead>
<tr>
<th>Region</th>
<th>Length (kb)</th>
<th>No. of haplotypes</th>
<th>No. of polymorphisms</th>
<th>Per cent disagreement</th>
<th>No. of combinations of polymorphisms</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>SNPs and indels</td>
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<td>common and unique to risk haplotypes</td>
</tr>
<tr>
<td>1</td>
<td>8.3</td>
<td>11</td>
<td>218</td>
<td>4.1</td>
<td>3.7</td>
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<tr>
<td>2</td>
<td>55.5</td>
<td>10</td>
<td>915</td>
<td>4.5</td>
<td>4.0</td>
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<tr>
<td>3</td>
<td>12.8</td>
<td>11</td>
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<td>12.0</td>
<td>11.0</td>
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<tr>
<td>4</td>
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<td>10</td>
<td>159</td>
<td>5.0</td>
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<td>11</td>
<td>34</td>
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<td>12.1</td>
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<td>7364</td>
<td>44.7</td>
<td>44.1</td>
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<td>6608</td>
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<th>Per cent disagreement</th>
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</table>

 Candidate regions (298, 224, and 158 kb), which were delineated by previous work (6), only modestly reduces the number of potential disease loci (Table 3). However, if HLA-Cw6 and HLA-Cw1-B46 risk haplotypes are indeed descended from a common PSORS1-bearing ancestor, then the disease locus should occur within a region of sequence homology. Five such regions at least 5 kb in length, marked in orange in Figure 1, could be delineated. Two of these (regions 1 and 5) occur outside the 298-kb candidate interval that is the shortest region common to all known HLA-Cw6 risk haplotypes, and two of the remaining three (regions 3 and 4) are unpromising candidates for an IBD disease region as these short (12.8 and 12.0 kb, respectively) intervals bear no polymorphism alleles or combinations of alleles unique to the risk haplotypes. Furthermore, region 4 falls outside of a 224-kb PSORS1 candidate interval firmly established by ancestral recombinant haplotype analysis, and region 3 falls outside of a probable although not definitively established 158-kb candidate interval.

The final and largest region of homology, region 2, is a 55.5-kb interval between HLA-C and HCG27 with 95.5% allelic identity at all 915 variable polymorphisms and a 96.0% allelic identity among the 881 more stable SNPs and indels [i.e. excluding highly mutable poly-A/T and short tandem repeat (STR) variations]. Region 2 bears no single polymorphism with an allele restricted to risk haplotypes, but it does have 31 two-way and 13,272 three-way combinations of polymorphism alleles unique to risk. However, as can be seen in Figure 1, the three risk haplotypes share roughly equivalent levels of sequence similarity in region 2 with two clearly non-risk haplotypes (HLA-Cw7-B8 and Cw8-B65). This visual comparison is confirmed more rigorously by the clustering dendograms of Figure 2. For region 2, the clustering distance separating the non-risk HLA-Cw7-B8 haplotypes from any of the HLA-Cw6 risk haplotypes is substantially less than the distance between the HLA-Cw6 and HLA-Cw1-B46 risk haplotypes, and the former distance is actually slightly less than that between the two different HLA-Cw6 haplotypes, which are almost certainly IBD in this region. Furthermore, the non-risk HLA-Cw8-B65 haplotype is only slightly more different from HLA-Cw1-B46 in region 2 than is the latter haplotype from the HLA-Cw6 haplotypes. Figure 2 shows a similar situation for regions 3 and 4. Extended regions of sequence similarity where only a few common haplotypes are observed (haplotype blocks) are commonplace within the MHC (29) and elsewhere in the human genome (30), which makes it difficult to test for identity by descent among these risk haplotypes. The lack of any known expressed genes or single polymorphism alleles unique to risk in region 2 argues strongly against an IBD disease locus in this interval, but a risk-specific haplotype of an unknown gene or of an intergenic regulatory element within the 55 kb defined by region 2 could conceivably be common to all three risk haplotypes, as long as it spans at least 2.3 kb (the minimum interval encompassed by any of the two-way or three-way allelic combinations unique to risk haplotypes).

Phenotype comparisons

We next undertook a comparison of psoriasis phenotype of Thais carrying HLA-Cw1-B46 vs HLA-Cw6, under the hypothesis that if the two HLA risk haplotypes share a common causative variant, then the resulting disease phenotype should...
be similar in the same genetic population. As shown in Table 4, among the four HLA-CB phenotypes significant differences were observed for mean age at onset, toenail involvement, and fingernail involvement \((P = 0.043, 0.0048, \text{and } 0.0070, \text{respectively})\). No significant differences in TBSA involvement or arthritis were observed \((P = 0.098 \text{ and } 0.84, \text{respectively})\).

Inspection of group means in Table 4 shows that age at onset is about 6 years earlier in the two groups of HLA-Cw6 carriers (30.0 and 30.2 years) than for either the HLA-Cw1-B46 only carriers (36.9 years) or carriers of neither risk haplotype (35.3 years). The contrast of the average of the mean transformed age at onset for the two groups of HLA-Cw6 carriers compared with the average of the mean transformed onset for the two groups of HLA-Cw6 noncarriers is significant \((P = 0.037)\). Conversely, inspection of standardized Pearson residuals for the four HLA-CB phenotype groups indicates that greater nail involvement for the two groups of HLA-Cw1-B46 carriers (36.4% and 26.3% for toenail, 36.4% and 31.6% for fingernail) vs lesser involvement for either HLA-Cw6 only carriers (10.2% and 14.3% for toenail and fingernail) or carriers of neither risk haplotype (15.4% and 14.1% for toenail and fingernail) is largely responsible for the significant test findings of the 4 × 2 contingency table. Collapsing the contingency table to a 2 × 2 format based on HLA-Cw1-B46 carriage yields a strong positive association for both toenail involvement \((OR = 3.30, P = 0.0010)\) and fingernail involvement \((OR = 3.28, P = 0.00074)\). TBSA trends higher in HLA-Cw6 carriers (34.2% vs 25.5%), and the marginal lack of significance for variation among groups may be because of inadequate power of our Thai sample, as increased TBSA has been shown to be associated with HLA-Cw6 in Caucasians (31). The findings for arthritis have little meaning given the low incidence of this trait (1.5%) among Thai affecteds in the sample.

Differences of disease phenotype among HLA-CB genotypes were similar to those seen among HLA-CB phenotypes, with mean age at onset lower in all groups carrying one or more copies of HLA-Cw6, and toenail and fingernail involvement higher in all groups carrying one or more copies of HLA-Cw1-B46 (data not shown). However, only the differences in toenail and fingernail involvement were significant \((P = 0.018 \text{ and } 0.024, \text{respectively})\). The weaker significances for HLA-CB genotype compared with HLA-CB phenotype may be a simple outcome of subdividing a relatively small sample into six vs four categories with a concomitant reduction in power.

**Discussion**

Genome-wide linkage scans (17, 32) as well as more recent genome-wide association studies (33–36) have made it clear that the major genetic determinant of psoriasis resides within the MHC. We have identified HLA-Cw6 as the predominant PSORS1 disease allele in the Caucasian population (6), and
Table 4 Variation of disease phenotype in Thai psoriatics as a function of HLA-CB phenotype

<table>
<thead>
<tr>
<th>HLA-CB phenotypea</th>
<th>n</th>
<th>Age at onsetb</th>
<th>TBSAc</th>
<th>Per cent toenail involvementb</th>
<th>Per cent fingernail involvementb</th>
<th>Per cent arthritisb</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cw1-B46 only</td>
<td>55</td>
<td>36.9 ± 4.6</td>
<td>26.2 ± 2.4</td>
<td>36.4 ± 6.5</td>
<td>36.4 ± 6.5</td>
<td>1.8 ± 1.8</td>
</tr>
<tr>
<td>Cw6 only</td>
<td>49</td>
<td>30.0 ± 2.3</td>
<td>34.2 ± 4.3</td>
<td>10.2 ± 0.9</td>
<td>14.3 ± 5.0</td>
<td>0.0 ± 0.0</td>
</tr>
<tr>
<td>Cw6 + Cw1-B46</td>
<td>19</td>
<td>30.2 ± 3.2</td>
<td>34.2 ± 6.3</td>
<td>26.3 ± 10.1</td>
<td>31.6 ± 10.7</td>
<td>0.0 ± 0.0</td>
</tr>
<tr>
<td>Neither</td>
<td>78</td>
<td>35.3 ± 1.8</td>
<td>24.7 ± 2.1</td>
<td>15.4 ± 4.1</td>
<td>14.1 ± 3.9</td>
<td>2.6 ± 1.8</td>
</tr>
<tr>
<td>Missing</td>
<td>5</td>
<td>34.8 ± 8.3</td>
<td>28.2 ± 8.9</td>
<td>40.0 ± 21.9</td>
<td>40.0 ± 21.9</td>
<td>0.0 ± 0.0</td>
</tr>
<tr>
<td>Total</td>
<td>206</td>
<td>34.0 ± 1.1</td>
<td>28.3 ± 1.5</td>
<td>21.4 ± 2.9</td>
<td>22.3 ± 2.9</td>
<td>1.5 ± 0.8</td>
</tr>
<tr>
<td>P</td>
<td>0.043</td>
<td>0.098</td>
<td>0.0048</td>
<td>0.0070</td>
<td>0.84</td>
<td></td>
</tr>
</tbody>
</table>

aHLA-CB phenotype is based on the carriage of HLA-CB haplotypes by the individual, where HLA-C is typed to a Cw1/Cw6/neither level and HLA-B to a B46/other level; i.e. ‘Cw1-B46 only’ designates individuals with one or two copies of a HLA-Cw1-B46 haplotype but no copies of a HLA-Cw6 haplotype, ‘Cw6 only’ means carriage of one or two copies of HLA-Cw6 but no copies of HLA-Cw1-B46, ‘Cw6 + Cw1-B46’ means carriage of one HLA-Cw6 and one HLA-Cw1-B46 haplotype, ‘neither’ means carriage of neither a HLA-Cw6 nor a HLA-Cw1-B46 haplotype, and ‘missing’ means the HLA-CB haplotypes are unknown because of typing failures. In this sample, HLA-B46 haplotypes always carry HLA-Cw1 (see Table 3).
bNumber of individuals
cMean and standard error for raw variable values are shown, but before analysis data were transformed to approximate normality using the optimal Box–Cox power transformation (power of 0.8 for age at onset and 0.3 for TBSA).
dP-values for age at onset and TBSA are for one-way ANOVA, based on 10,000 random permutations of the response variable observations; P-values for toenail and fingernail involvement and arthritis are for Fisher’s exact test on an unordered two-way contingency table. All tests excluded individuals with a missing HLA-CB phenotype.

This has been confirmed in the Han Chinese (7). However, considerable evidence indicates that HLA-Cw6 is not the only psoriasis susceptibility allele in the MHC. Psoriatic arthritis has also repeatedly been associated with HLA-B38 and HLA-B39 (splits of HLA-B16) (37–43) and with HLA-B27, especially when axial involvement is present (39, 40, 42, 44). Moreover, we have recently shown that additional, albeit less genetically robust, association signals are present in the MHC class III region (35, 45). Together with the HLA-Cw1-B46 association, which is the focus of this study, these findings suggest that genetic heterogeneity is likely to be present at PSORS1, with various effects on the phenotype.

Our interest in the HLA-Cw1-B46 haplotype stemmed from several prior demonstrations of disease association in Asian populations (9, 10, 12, 13, 15, 46). Taking advantage of a collection of Thai psoriatic patients and normal controls independent of those collected previously, we were able to robustly confirm the association of psoriasis with HLA-Cw6, HLA-Cw1, HLA-B46, and the HLA-Cw1-B46 haplotype in our Thai sample (Table 1). In order to assess whether these associations might be a result of allelic heterogeneity at HLA-C, we tested for HLA-Cw1-specific associations with psoriasis in the Thai and Caucasian populations. In our Thai sample, haplotypes carrying HLA-Cw1 but lacking HLA-B46 showed no significant association with psoriasis (Table 2), but our sample lacks adequate power given the relatively low frequency of this haplotype. However, similar findings, in a Japanese study (11) where HLA-Cw1 not on HLA-B46 haplotypes trended toward negative association with psoriasis (OR = 0.45, P = 0.068) and in a Thai study (9) where the strength of association of HLA-B46 with psoriasis (OR = 4.23, P = 1.4 × 10^{-6}) was much greater than that for HLA-Cw1 (OR = 1.70, P = 0.083), increase the likelihood that HLA-Cw1 is not a direct determinant of psoriasis in East Asians.

In our Caucasian sample, which showed highly significant evidence for association with HLA-Cw6, we found no evidence for association with HLA-Cw1 despite >99% power to detect an association of the strength observed in the Thai population. No occurrences of the HLA-B46 allele were seen for a large genotyped subset of our Caucasian sample, which includes all HLA-Cw1 carriers, confirming the specificity of HLA-Cw1-B46 for Asian populations. While two small studies have reported association of HLA-Cw1 with psoriatic arthritis (47, 48), this may reflect the fact that HLA-Cw1 is in linkage disequilibrium with HLA-B27 in Caucasian populations. However, HLA-Cw1 was clearly unassociated with 493 psoriatic arthritis cases in our own much larger Caucasian sample (P = 0.38), with an effect size nearly identical to that seen for 1,549 purely cutaneous psoriasis cases in the same sample (OR = 0.84 vs 0.85, respectively). One other study of 50 pediatric Kuwaiti psoriatics and 120 controls yielded a positive association with HLA-Cw1, but no association with HLA-Cw6 (49). Whether this divergent finding is the result of small sample size, different ethnicity (predominantly Arab), very early onset (<12 years), or the presence of arthritis (which was not reported) remains to be determined. Overall, it appears highly unlikely that HLA-Cw1 itself is a psoriasis risk determinant in either Thais or Caucasians. Hence another MHC locus, perhaps HLA-B46 itself, is driving the observed associations with the HLA-Cw1-B46 haplotype.

Consistent with data presented by others, we noted that HLA-Cw6 appears to be more strongly associated with psoriasis than is HLA-Cw1-B46 in the Thai population. While the 95% CI for the two ORs estimated from our sample...
overlapped (Table 1), the greater strength of the HLA-Cw6 association could be statistically established after combining our study with the only other relevant Thai study with allele-based HLA genotyping (10). In addition, three out of four of the older serological studies (11–13) corroborate the greater risk of disease imparted by HLA-Cw6 compared with HLA-Cw1-B46 in Asian populations. To our knowledge there is no evidence for an association between guttate psoriasis and the HLA-Cw1-B46 haplotype, in contrast to its strong association with HLA-Cw6 (50). It is also notable that the HLA-Cw1-B46 haplotype has been associated with other autoimmune diseases, including myasthenia gravis and Graves disease (51), whereas HLA-Cw6 has not. Moreover, Romphruk et al. reported that HLA-Cw1-B46 is equally associated with early and late-onset disease in Thai psoriasis, whereas HLA-Cw6 is more strongly associated with early-onset disease (46). Taken together with the aforementioned difference in strength of association, these findings suggested that the psoriasis susceptibility determinants carried on these two haplotypes are different. We tested this hypothesis in two ways: by performing a sequence analysis of the two haplotypes, and by comparing the phenotypes of known carriers of each haplotype.

Detailed sequence comparison with eight non-risk haplotypes (Figure 1 and Table 3) found no single variants unique to the HLA-Cw1-B46 and HLA-Cw6 risk haplotypes within potential IBD regions of homology in the PSORS1 candidate interval. Although two-way and three-way combinations of variants unique to these two risk haplotypes do exist, they are confined to a 55 kb region that contains no known genes and that has equivalent similarity with two non-risk haplotypes (Figure 2). Nevertheless, based on sequence analysis alone, we cannot completely exclude the possibility that this region contains a variant that is IBD within a regulatory element or a novel expressed gene.

Phenotypic analysis provided additional support for the hypothesis of genetic heterogeneity, although its conclusions must be tempered by sample size considerations. We found that Thai psoriatics carrying HLA-Cw1-B46 have a later age at onset and greater nail involvement than do carriers of the HLA-Cw6 risk haplotype (Table 4). However, it is important to note that age at onset correlates with the presence or absence of HLA-Cw6 but not of HLA-Cw1-B46, and likelihood of nail involvement with the presence or absence of HLA-Cw1-B46 but not of HLA-Cw6. Together, the weight of evidence from these sequencing and phenotype comparisons strongly favors the hypothesis that the HLA-Cw1-B46 and HLA-Cw6 risk haplotypes do not derive from a common ancestral risk chromosome.

Given these findings in support of genetic heterogeneity, the evolutionary history of HLA-B46 is of interest. In 1992, Parham and colleagues dissected a complicated serological determinant known as Cw1x3 antigen (also called Cw11, CwB, Cx46, Cw1+3, C-Bangkok, and CSH1). In doing so, they showed that the HLA-B46 allele is the result of an unusual gene conversion event in which a 31-bp segment of HLA-Cw1 encoding residues 66–76 of the α1 helix replaced the corresponding sequences of the HLA-B62 allele (52). Haplotype containing HLA-B62 and HLA-Cw1 are not uncommon in Asian populations (53), supporting the notion of a gene conversion event rather than recombination. HLA-B62 has a worldwide distribution, whereas HLA-B46 is specific for Asian populations, showing that HLA-B62 is the ancestral allele and that the gene conversion occurred in an individual of Asian descent. HLA-B46 is a common allele in Asian populations, suggesting that this event was followed by marked expansion in the population. Whether this expansion reflects positive selection for pathogen resistance, analogous to the postulated selection for HLA-Cw6 in resistance to Streptococcal pneumonia (54), is unknown.

The 11 amino acids transferred from HLA-Cw1 to HLA-B62 by gene conversion differ from the corresponding residues of HLA-Cw6 only at amino acid residue 73 (threonine in HLA-Cw1 vs alanine in HLA-Cw6). Because we have shown here that HLA-Cw1 is not disease-associated, on the (unproven) hypothesis that this specific segment of HLA-C confers disease susceptibility, we could infer that alanine residue 73 is unlikely to be of critical importance, as previously suggested (55). However, there are many other possible explanations for the observed HLA-B46 association. HLA-B and HLA-C are very similar to each other, reflecting a relatively recent gene duplication (56). As MHC class I genes, both HLA-B and HLA-C are involved in the presentation of peptides to CD8+ T cells, whose emigration into the epidermis appears to be necessary for the development of epidermal hyperplastic response (57). One possibility would be that the two alleles could be presenting different antigens. Alternatively, another nearby gene in the MHC class III region could be the causative agent on the HLA-Cw1-B46 haplotype. Several of these genes are strong functional candidates. For instance, MICA and MICB are nonclassical MHC genes that participate in the regulation of CD8+ T cells and natural killer (NK) cells (58), and the tumor necrosis factor and lymphotoxin genes encode proteins whose blockade is highly therapeutically effective (59). While our earlier studies of recombinant ancestral haplotypes argue strongly against a primary role for MHC class III genes as the drivers of the HLA-Cw6 association signal (6, 60), no comparable mapping studies exist as yet for the HLA-Cw1-B46 disease association in Asians. Thus, at this stage it is premature to speculate that the genetic heterogeneity suggested by our data must involve HLA-B46 itself, although it is certainly possible.

In conclusion, we have presented several lines of evidence for a distinct PSORS1 locus in the Thai population. Future genetic studies of this allele in Asian populations should focus on increasing sample size and high-density genotyping of HLA-B, its flanking sequences, and the MHC class III region.
Acknowledgments

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References


**Supporting Information**

The following supporting information is available for this article:

Table S1. Amplification and single base extension primers for HLA-C and HLA-B SNPs.

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