Primate DRB6 pseudogenes: clue to the evolutionary origin of the HLA-DR2 haplotype

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Abstract. The HLA-DR2 haplotype contains three β-chain encoding DRB genes and one α-chain encoding DRA gene. Of the three DRB genes, two are presumably functional (HLA-DRB1 and HLA-DRB5), whereas the third (HLA-DRBVI) is a pseudogene. A pseudogene closely related to HLA-DRBVI is present in the chimpanzee (Patr-DRB6) and in the gorilla (Gogo-DRB6). We sequenced the HLA-DRBVI and Patr-DRB6 pseudogenes (all exons and most of the introns), and compared the sequence to that of the Gogo-DRB6 gene (of which only the exon sequence is available). All three pseudogenes seem to lack exon 1 and contain other deletions responsible for shifts in the translational reading frame. At least the HLA-DRBVI pseudogene, however, seems to be transcribed nevertheless. The chimpanzee pseudogene contains two inserts in intron 2, one of which is an Alu repeat belonging to the Sb subfamily, while the other remains unidentified. These inserts are lacking in the human gene. A comparison with sequences published by other investigators revealed the presence of the HLA-DRBVI pseudogene also in the DR1 and DRw10 haplotypes. Measurements of genetic distances indicate DRB6 to be closely related to the DRB2 pseudogene and to the HLA-DRB4 functional gene. In humans, gorillas, and chimpanzees, the DRB6 pseudogene is associated with the same functional gene (DRB5) indicating that this linkage disequilibrium is at least six million years old and that DR2 is one of the oldest DR haplotypes in higher primates.

Introduction

The class II (D) region of the HLA complex, the human major histocompatibility complex (Mhc), is divided into five subregions: DP, DN, DO, DQ, and DR (Klein 1986; Carson and Trowsdale 1986). The DP and DQ subregions each contain two A loci coding for the α chain of the class II αβ heterodimer, and two B loci coding for the β chain. The DR subregion contains one A locus and one or more B loci. In the DN subregion only an A locus has been identified thus far; in the DO subregion only one B locus appears to exist. The DR subregion of the HLA complex displays two kinds of polymorphism — allelic and haplotype. Extensive allelic DR polymorphism is restricted largely to one locus in this subregion — the DRB1 locus; the DR4 locus and the extra DRB loci (if present) show only limited intraspecies variability (Dupont 1989). The haplotype polymorphism is manifested in different cis combinations of alleles at different DRB loci and in different organization and number of DRB genes borne by a single chromosome. Five haplotype groups have been identified. Haplotypes of the DR1 group (DR1, DRw10) contain two loci, DRB1 and an as yet unidentified second locus (Böhme et al. 1985). The DR2 haplotype contains three loci — two presumably functional and polymorphic loci (DRB1 and DRB5), and one pseudogene [DRBVI (Kawai et al. 1989). Of the human DRB pseudogenes, only one (DRB2) has thus far been given an official designation. For the remaining pseudogenes, we use here tentative designations based on Roman rather than Arabic numerals]. Up until now, four alleles have been recognized officially at each of the two functional loci: HLA-DRB1*1501, *1502, *1601, *1602, HLA-DRB5*0101, *0102, *0201, *0202 (The WHO Nomenclature Committee for factors of the HLA System 1991). Haplotypes of the DR3 group (DR3, DR5, DRw6) also contain three loci (Rollini et al. 1985) — the polymorphic DRB1 locus, the DRB2 pseudogene, and the oligomorphic DRB3 locus. The DRB3 gene codes for the supertypic, serologically detectable DRw52 determinant characteristic of this haplotype group (Dupont 1989). The DRw8 haplotype, which contains only one DRB gene, is probably derived from a DR3-like haplotype by the fusion of the 5' end of the DRB1 gene with the 3' part of the DRB3.
gene and a deletion of the intervening segment (Gorski 1989; Jonsson et al. 1989). The DRB3-derived portion of the single DRw8 haplotype gene encodes the DRw52 supertypic determinant. Finally, chromosomes in the DR4 haplotype group (DR4, DR7, DR9) each contain four DRB genes, the highly polymorphic and functional DRB1, the DRBVII and DRBVIII pseudogenes, and the oligomorphic DRB4 gene (Andersson et al. 1987; Spies et al. 1985).

Both the allelic and the haplotype polymorphism evolve in a trans-specific manner in which the divergence of allelic and haplotype lineages often predated speciation. Evidence for trans-species evolution of DRB alleles was provided by Fan and co-workers (Fan et al. 1989); indications of trans-species evolution of DRB haplotypes are emerging from the studies of Brändle and co-workers (1991) and Kasahara and co-workers (Kasahara et al. 1990, 1991). The high allelic polymorphism and the trans-specific mode of evolution complicate the interpretation of the relationships between individual DRB haplotypes, which may be important for understanding the association of certain haplotypes with disease susceptibility (Dawkins et al. 1983). To avoid these complications, we have focused our efforts on deciphering the relationships between the HLA pseudogenes which are presumably largely unaffected by the selection pressures acting on the functional DRB loci (Hughes and Nei 1989). Moreover, we have approached the question of haplotype interrelationship from a historical perspective by studying the pseudogenes in the nearest human relatives, the gorilla and the chimpanzee (Klein et al. 1991; Vincek et al. 1991). In the present communication we describe how this approach helps to understand the origin of the human DR2, DR1, and DRw10 haplotypes.

Materials and methods

Isolation of cosmid clones containing the HLA-DRBVI pseudogene. Genomic library prepared from the DNA of the chimpanzee (Pan troglodytes) B-cell line Hugo, as reported elsewhere (Brändle et al. 1991), and screened with the chimpanzee cDNA probe C4-2 which covers almost the entire coding sequence of the Patr-DRB1 gene (Fan et al. 1989). Hybridizing cosmid clones were isolated and their restriction maps constructed (for details, see Brändle et al. 1991). Hybridizations of four overlapping cosmid clones with exon-specific probes revealed the presence of a truncated DRB gene which, like the human HLA-DRBVI, lacked exon 1 but had all the remaining exons. In preparation for sequencing, three Eco R1 fragments were isolated from the cosmid 2.12: 1 a 3.7 kb long fragment encompassing exon 2 and the flanking introns; a 2.5 kb long fragment encompassing exons 3 and the flanking introns; and a 2.8 kb long fragment containing the rest of the gene including the 3' UT region. All three fragments were subcloned in the Bluescript SKII vector.

DNA sequencing. Single- or double-stranded DNAs were prepared and sequenced by the dideoxy chain-termination method (Sanger et al. 1977) using the Sequenase version 2.0 DNA sequencing kit (US Biochemicals, Cleveland, OH). The sequencing strategy for both DRB genes is depicted in Figure 1. To prepare single-stranded DNA, bacterial cultures were grown overnight in the presence of a helper phage (Stratagene). The cultures were then spun down for 20 min at 11 000 g and the DNA was precipitated from the supernatant in 4% polyethylene glycol (PEG). The DNA was resuspended in 400 μl of Tris EDTA (TE; 10 mM Tris-HCl, pH 8.0, 1 mM ethylenediaminetetraacetic acid, EDTA), extracted four times with phenol and once with chloroform, and precipitated with absolute ethanol. One microgram of single-stranded DNA was used in each sequencing reaction. Double-stranded DNA was prepared by the standard Trizol-lysozyme method (Davis et al. 1986). Five micrograms of DNA were denatured in 0.2 M NaOH, 0.2 mM EDTA for 30 min at 37 °C, and then ethanol-precipitated in the presence of 0.3 M sodium acetate, pH 6.0. The DNA was dissolved in 7 μl of distilled water at 37 °C and sequenced. The reactions were run in 6% Accugel (National Diagnostics, Manville, NJ) at a constant 65 W current. Synthetic oligonucleotides corresponding to specific sequences along the DRB gene were synthesized in the GenAssembler Plus Synthesizer (Pharmacia LKB, Freiburg, FRG) and used as primers together with the -20 and reverse M13 primers (Table 1 and Fig. 1).

Construction of dendrograms. Genetic distances were calculated by Kimura's two-parameter method (Kimura 1980) and phylogenetic trees were drawn using the neighbor-joining method (Saitou and Nei 1987).

Results

While the sequences of the DRBl*15, DRBl*16, and the DRB5 genes of the HLA-DR2 haplotype are known (Lee et al. 1987; Wu et al. 1987; Hurley et al. 1988; Liu et al. 1988), the sequence of the DR2 haplotype pseudogene has not been available. Since it is the pseudogene in particular that can shed light on the origin of the DR2 haplotype and its relationship to other HLA-DR haplotypes, we resolved to sequence it. Furthermore, during our search for the evolutionary origins of the human DR2 haplotype, we discovered a gene in the chimpanzee Hugo which, superficially at least, resembled the HLA-DRBVI pseudogene in that both genes seemed to lack exon 1. Expecting information on the chimpanzee gene to help in the interpretation of the phylogenetic relationships be-