

HLA AND LEUKEMIA: Is it a Simple Allelic Association?*

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The first association between a disease and MHC antigens was established for viral leukemogenesis in mice. Since then, numerous studies in humans have been carried out and the data obtained suggest that Cw3 and Cw4 may be markers for leukemia susceptibility genes. Given the relatively weak relevance of HLA-C locus antigens in immune response, unrecognized properties of Cw3 and Cw4 should be considered to explain this association. Family studies have consistently revealed limited heterogeneity of HLA antigens in those families, increased parental HLA antigen sharing resulting in increased homozygosity among offspring and high frequency of recombinations within the MHC. Furthermore, the HLA genotype of leukemic patients was found more frequently among their siblings than the anticipated 25 percent. Another significant deviation from the Mendelian expectation was increased HLA-DR identity of offspring to that of their mother in those families. These and other observations imply that in leukemia families unknown MHC-linked recessive factors linked to Cw3 and Cw4 alleles may be susceptibility genes which also cause segregation distortion of HLA genes and probably developmental errors. *Key words:* HLA antigens, acute lymphoblastic leukemia, segregation, family, chromosome 6.

The existence of a major histocompatibility complex (MHC) linked susceptibility factor has long been postulated from the well-known role of H-2 haplotypes and virus-induced leukemogenesis in mice¹. The resistance loci for the Friend, Gross and Moloney murine leukemia viruses have all been mapped in the H-2 region²⁻⁴. To date, the strongest associations have been established in humans between HLA-Cw3, Cw4, A30, B17, DPw2 and DPw5 and acute leukemias whereas HLA-Aw19, B14, DR7 and DPw1 have been found to be decreased in leukemia patients⁵⁻¹². Most other antigens reported to be increased in leukemia patients are indeed in strong linkage disequilibrium with Cw3 and Cw4¹³. The HLA-Cw3, Cw4 and HLA-DP association is most significant in acute lymphoblastic leukemia (ALL) patients⁵⁻⁹. In a family study, two of four sibs with ALL had the HLA haplotype "Aw31, Cw3, Bw61, DR5"¹⁴. In a subgroup of adult ALL patients of whom 45.5 percent had at least one close relative with familial leukemia, HLA-Cw3 was consistently positive along with high transcortin levels⁷. A strong association of the acute type of adult T-cell leukemia with "HLA-A26, Bw62,

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Cw3" haplotype has recently been reported¹⁵. Survival following bone marrow transplantation is good for individuals bearing a DRw52 haplotype and poor for those bearing a DRw53 haplotype¹³. The strong positive association of Cw3 and Cw4 with leukemia supports the possibility that the genes encoding them are, or are closely linked with, putative leukemia susceptibility gene(s)⁶.

In a survey of 194 families of patients with acute leukemia, Chan et al¹⁶ found that a genotypically HLA-identical sibling was available for 35 percent of leukemic patients although 25 percent had been anticipated. In a different series of ALL patients, more than 25 percent HLA identity was reported in sibs of patients¹⁷. A striking excess of identical antigens (especially HLA-DR) among the parents of leukemic patients has been reported by a number of authors^{6,16,18,19}. Limited heterogeneity of HLA antigens has also been reported in parents of children with Down's syndrome which is associated with an increased risk of acute leukemia²⁰.

In the study of Carpentier et al¹⁸, the HLA genotype was determined in 73 unrelated patients with acute myeloblastic leukemia (AML) and also in their first degree relatives. A significant finding was the presence of a clear genetic distortion favoring HLA homozygosity in the affected offspring. In offspring with leukemia of such families, there is a significant deviation from the Mendelian expectation of the number of patients homozygous for DR alleles shared by parents but not in healthy sibships. Von Vliedner et al¹⁹ reported a two-fold increase in the number of homozygotes among patients compared to the expected value in families where parents shared a B or DR antigen, and significantly more heterozygotes for the shared antigens among the healthy siblings. In the same patient population of Carpentier et al¹⁸. The distribution of DR antigens shared by parents markedly favored phenotypic HLA identity of patients with their mothers as compared with their fathers. Obviously, this is possible only if the parental shared haplotype has a high transmission ratio as compared to the homologous haplotype (Fig. 1).

On the other hand, in a very large data set of non-diseased families, parental sharing of one or two HLA class-I antigens did not result in altered allele segregation among the 2569 healthy offspring tested²¹. In the same study, homozygous children of HLA-sharing couples and children histocompatible with their mothers were observed with frequencies close to that envisaged. In another comprehensive survey, no evidence was obtained for segregation distortion of MHC in non-diseased families²².

The possible implications of these studies are: the segment of chromosome 6 carrying the HLA genes also carry the recessive gene(s) influencing leukemogenesis and thus the HLA alleles per se are not the critical genes; haplotypes including shared antigens should also bear a gene or genes which confer(s) the ability of preferential (male-specific) gametic transmission to those haplotypes, and if there

is a leukemia susceptibility locus on chromosome 6, it is likely linked to the MHC, as in the case of mice¹.

As mentioned above, in general, more unaffected sibs than anticipated are found to have the same HLA genotypes as their sibs with ALL, which conforms with segregation distortion. However, the subgroup of ALL patients with both HLA-Cw3 and high transcortin levels and familial tendency reacts in the opposite way. Instead of more HLA-identical sibs, fewer are found, suggesting fetal wastage of the latter combination²³.

If one can explain the association of certain HLA antigens with leukemia along with segregation distortion and relevance of homozygosity to expression of leukemic phenotype, this may well be a major step towards understanding the mysteries of leukemogenesis. The same explanation should clarify the typical maternal reproductive history of childhood leukemia seen with recurrent abortions or fetal wastage²⁴, and how paternal but not maternal preconceptional accumulated doses of radiation may confer a risk for leukemia in offspring²⁵. Another observation which is yet unexplained is the high recombination frequency within MHC in leukemic families^{26,27}.

It is a well-known phenomenon that couples experiencing recurrent abortions share HLA antigens more frequently than control couples²⁸. Not only recurrent abortions and leukemia but also aplastic anemia²⁹, gestational trophoblastic tumors³⁰ and anencephaly³¹ seem to be associated with parental sharing of HLA antigens. The properties of the HLA system are not sufficient to rationalize these associations, but some HLA-linked factors influencing embryogenesis, as well as carcinogenesis may be responsible. Previously, these associations have been interpreted from the point of view that increased maternal-fetal HLA compatibility may somehow cause defects in embryogenesis and recurrent abortions. However, in cases of HLA antigen sharing between parents, repetitive maternal-fetal HLA compatibility is possible only if male transmission distortion exists.

The oncogene *pim-1* (located at 6p21 adjacent to the MHC)³² and the *myb* oncogene (located at "6q22-q24")³³ have been reported to be over-expressed in acute leukemias. There are even more oncogenes at or beyond 6q21, such as *mas-1*, *fyn*, *syn*, and *ros-1*³⁴. A Friend murine leukemia virus integration site (*fim-1*) was recently mapped onto the human chromosome 6p23³⁵. This retroviral integration region is known to be involved in mouse myeloblastic leukemias. Furthermore, there are six fragile sites on chromosome 6, three of which are located within 6p22.2-p25.1³⁶. Various translocations involving 6p23 or 6q27, and more frequently (particularly in ALL) deletions at 6q15, 6q21 and 6q23 have been reported at considerable frequencies in acute leukemias³⁴. Accumulation of oncogenes and fragile sites at two regions on the same chromosome with MHC may have some implications regarding the relevance of chromosome 6 in leukemogenesis in humans.

Considering the current hypothesis³⁷ regarding the development of childhood ALL, the first developmental error initiating a preleukemic clone in utero might be homozygosity of putative lethal factors linked to the MHC, and rearrangements on chromosome 6, such as deletions in the long arm may fit this hypothesis as a subsequent genetic error. In conclusion, investigators attempting to establish an association between HLA and leukemia should consider the entire chromosome 6 along with the genetic evolution of this particular region of the human genome.

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