Association between the Epidemic Form of Hemolytic-Uremic Syndrome and HLA-B 40 in the Netherlands and Flanders

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Dear Sir,

Evidence for an autosomal recessive or autosomal dominant mode of inheritance is present in a small minority of patients with hemolytic-uremic syndrome (HUS) [1].

In one report of a familial relapsing autosomal dominant form, the disease was associated with HLA-A3, B7 haplotype [2]. In the Netherlands and the Flemish part of Belgium, the epidemic or classical form is most frequently observed. An infection by verocytotoxin-producing *Escherichia coli* was a proven frequent cause of this epidemic form during recent years [unpubl. study]. Not all infants and children infected by verocytotoxin-producing *E. coli* develop HUS. In one outbreak of *E. coli* 0157 only 3 (8.3%) of the 36 symptomatic children developed HUS. In another outbreak, HUS became evident in 3 (7%) of 42 symptomatic children [3]. A genetic predisposition was suspected.

Sheth et al. [4] evaluated HLA-A, B, C, DR, DQ, antigens in 31 children, who had classical HUS previously. They reported a relative risk of 5 of developing HUS with the presence of HLA-B 40 alone. The severity of HUS was not related to the genetic predisposition.

The distribution of HLA-A, B and DR antigen was studied in 31 patients with chronic renal failure due to the epidemic form of HUS. All patients were on dialysis or transplanted. One patient was excluded because he was of Turkish origin. All other patients were of Dutch or Flemish origin and were cared for in six transplantation centres.

Compared with the control population, there was no significant difference in the distribution of HLA-A, B, DR antigens with one exception.

An odds ratio of 2.5 (X², *p* = 0.039) could be calculated in our group of patients for HLA-B 40, (table 1).

In contrast to Sheth et al. [4], who found that all their 31 patients had at least one of the following HLA-B types:

Table 1. Comparison of HLA frequencies in Sheth's study compared with our study

Study of Sheth (n = 31) Our study (n = 31)

patients random population patients random population
 % n % % n %

40,13,7,44, which share a distinct amino acid sequence of the <X> domain, this was found in only 23 of our 31 patients (4 patients had more than 1 of the 4 HLA-B types).

We may conclude that in the severe form of epidemic HUS, as seen in the six transplantation centres there is a significant association with HLA-B 40.

References

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