THE +874 T/A POLYMORPHISM OF THE IFNG GENE AS A MARKER OF SUSCEPTIBILITY TO A RECURRING COURSE OF HERPES SIMPLEX INFECTION

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Relevance. Patients infected with the same virus experience markedly different disease courses: some have one or two recurrences a year, others as many as one a month. Part of this variation is attributable to the hereditary characteristics of the genes that regulate the immune response. Interferon-gamma is the central mediator of cell-mediated antiviral defence, and the +874 T/A polymorphism (rs2430561) located in the first intron of the IFNG gene is one of the principal determinants of its production level.

Objective. To determine the distribution of alleles and genotypes of the +874 T/A polymorphism of the IFNG gene in patients with recurrent herpes simplex infection (RHSI) and to assess their role in susceptibility to the disease.

Materials and Methods. The study was carried out at the Bukhara Regional Infectious Diseases Hospital. Genotyping included 137 patients with laboratory-confirmed RHSI (main group) and 38 apparently healthy individuals (control group). Genomic DNA was extracted from the leukocyte fraction of peripheral venous blood, and genotyping was performed by allele-specific amplification. Statistical processing included Pearson's χ^2 test, odds ratios (OR) and their 95% confidence intervals.

Results. The two groups differed markedly in allele distribution (Table 1).

Table 1

Distribution of alleles and genotypes of the IFNG +874 T/A polymorphism

Allele / genotype	Main group, n=137	Control group, n=38	p	OR (95% CI)
A allele	153 (55.8%)	19 (25.0%)	<0.001	3.79 (2.14–6.72)
T allele	121 (44.2%)	57 (75.0%)	<0.001	0.26 (0.15–0.47)
AA genotype	42 (30.7%)	4 (10.5%)	0.013	3.76 (1.25–11.27)
AT genotype	69 (50.4%)	11 (28.9%)	0.019	2.49 (1.15–5.42)
TT genotype	26 (19.0%)	23 (60.5%)	<0.001	0.15 (0.07–0.33)

In the main group the A allele accounted for 55.8% against 25.0% in the control group (χ^2=22.64; p<0.001). The AA genotype was identified in 30.7% of patients and in only 10.5% of controls. Conversely, the TT genotype accounted for 60.5% among controls, more than three times the figure in the main group (19.0%), with an odds ratio well below unity (OR=0.15).

These findings are biologically coherent. The T allele is associated with a higher level of interferon-gamma production, so carriers of the TT genotype mount a stronger cell-mediated antiviral response and restrict viral reactivation more effectively. The A allele, by contrast, is linked to lower production, leaving carriers of the AA genotype with weaker local defence and more frequent recurrences.

One limitation should be noted: the control group was relatively small (n=38), which widened the confidence intervals calculated for individual genotypes. Confirmation in a larger independent sample is therefore required.

Conclusion. The A allele and the AA genotype of the IFNG +874 polymorphism may be regarded as factors increasing susceptibility to a recurring course of herpes simplex infection, whereas the T allele and the TT genotype appear protective. Genotyping results may serve as an additional criterion for identifying risk groups and individualising dispensary follow-up.