

Distribution of Adenosine Deaminase (EC 3.5.4.4) Phenotypes in a Series of HIV-Seropositive Patients

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INTRODUCTION

Adenosine deaminase (ADA) takes its role in physiological pathway in deamination of adenosine to inosine. The enzyme was found in human erythrocytes and tissues. Three common phenotypes - ADA*1, ADA*2-1, ADA*2 - can be separated by electrophoresis. Rarer alleles (ADA⁰, ADA³, ADA⁴, ADA⁵, ADA⁶) have also been described. The ADA* polymorphism is coded by chromosome 20. This enzyme seems to be of interest for immunology, too. The homocygous ADA0 type is associated with the SCID syndrome (severe combined immune deficiency) (8,9). Several authors reported on increased ADA levels in HIV-infected patients (1,2,3,4,7,13, 14).

MATERIAL & METHODS

Blood samples were taken from 226 HIV-seropositive patients treated in the Institute of Blood Coagulation and Transfusions Medicine at the Heinrich-Heine-University. This series thus includes individuals that were only HIV-seropositive, patients with ARC (AIDS related complex), with full blown AIDS and with Kaposi-sarcoma. We compared this group with obviously healthy persons spot checked otherwise..

Electrophoresis was carried out on Cellogel electrophoresis membranes using electrophoresis buffer Biotest (dilution 1:10): 250 Volt, 15 mA, 50 min. Staining was performed with 15mg Adenosine, 5 mg MTT, 5 mg PMS, 25 µl nucleoside and 25 µl xanthine oxidase.

RESULTS & DISCUSSION

The ADA system takes a role in immunological reactions. The silent ADA gene ADA 0 is associated with the SCID syndrome. Several authors reported increased ADA levels in HIV-infected patients (1,2,3,4,7,13,14). For this study we examined the distribution of the ADA*phenotypes in a series of 226 HIV-infected persons. The distribution found is shown in table 1. We observed only the common three phenotypes ADA*1, ADA*2-1 and ADA*2. The results provide a satisfactory correlation to the Hardy-Weinberg-equilibrium (Chi²: 0.045<3.841;df=1;a=0.05).

In table 2 the results of other studies on ADA*polymorphism in Germany are listed. Small differences between the gene frequencies may be due to the small volume and to the heterogeneity of the HIV-group - large clinical catchment area.

The differences are not significant and there is no association between the ADA*system and HIV-infection detectable.

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TAB.1 ADA-PHENOTYPES IN HIV-SEROPOSITIVE PATIENTS

Phenotype	observed		expected	
	n	%	n*	%*
1-1	195	86.28	194.21	85.93
2-1	29	12.83	30.63	13.55
2-2	2	0.89	1.21	0.54
total	226	100	226	100

* values rounded up

gene frequencies: ADA1 : 0.9269 ; ADA2 : 0.0731

TAB.2 OTHER STUDIES ON ADA-POLYMORPHISM IN GERMANY

Country	ADA*1	ADA*2	n	Reference
Lower Rhine region	0.9447	0.0553	262	Scheil et al.
Düsseldorf region	0.9366	0.0634	500	Scheil et al.
South Western	0.9238	0.0762	302	Tariwerdian et al.
Hamburg	0.9355	0.0645	861	Goedde et al.
Hessen	0.9499	0.0501	579	Renninger et al.
Berlin	0.9420	0.0580	500	Lefevre and Niebuhr
This study	0.9269	0.0731	226	

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