SERUM PROTEIN POLYMORPHISMS IN PATIENTS WITH PROSTATIC CANCER

SOENKE ARPS[1], ALEXANDER RODEWALD[1], GEORGETA CARDOS[1, 2]

The distribution of phenotypes of Hp, Tf, Pi and Gc was determined in 109 patients with prostatic cancer. The statistical analysis of our findings in comparison with healthy control groups revealed no associations between particular Tf and Gc phenotypes and the disease. On the other hand statistical significant associations were found in Hp and Pi. Our study showed a significant decrease of Hp2-2 and increase of Hp 2-1 phenotypes in the patient group. Furthermore a significant increase of the M1-Z and decrease of the M1-1 phenotype in Pi was found in the patients.

INTRODUCTION

While little is known about the factors involved in the pathogenesis, some epidemiological observations suggest the involvement of a genetic component in the etiology of prostatic cancer. First of all, the incidence of prostatic cancer shows great variation in different ethnic groups (Zaridze and Boyle, 1987) and secondly, is observed more frequently in the male relatives of index patients than in controls (Steinberg *et al.*, 1990).

In recent years several polymorphic serum proteins have attracted interest as genetic markers in the investigation of disorders, where gene-environment interactions are likely to be of etiological importance. Several associations between particular phenotypes of a given polymorphism and different forms of malignancy have been reported (Mourant *et al.*, 1978).

In present study, we have determined the phenotypes of alpha-1-antitrypsin (Pi), transferrin (Tf), group specific component (Gc) and haptoglobin (Hp) in 109 patients with prostatic cancer to examine similar associations which could corroborate the pathogenesis of this disease.

MATERIAL AND METHODS

Serum samples were obtained from 109 consecutive patients with prostatic carcinoma. Hp phenotypes were determined by horizontal polyacrylamide gel

ANN. ROUM. ANTHROPOL., **42**, P. 133–136, BUCAREST, 2005