GENETIC POLYMORPHISM OF PROPERDIN FACTOR B (BF) IN CHINESE PATIENTS WITH TWO TYPES OF DIABETES MELLITUS

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Summary The distribution of phenotypes for properdin factor B (BF) has been investigated in 50 IDDM patients and 52 NIDDM patients living in Guangzhou, southern China, using high voltage agarose gel electrophoresis followed by immunofixation. A significant decrease in the frequency of BF F positive patients ($p < 0.01$) and an increase in the gene frequency of BF^*S ($p < 0.005$) were found in IDDM as compared to 259 normal controls. The relative risk for the BF F positive patients in IDDM was 0.15. On the other hand, no significant association was observed between BF types and NIDDM.

INTRODUCTION

It is known that genetic factors play a predominant role in the pathogenesis of insulin dependent and non-insulin dependent diabetes mellitus (IDDM and NIDDM). Since the association between the HLA antigens and IDDM was found (Nerup *et al.*, 1974), the interest has been extended to investigate the relationship between HLA-linked complement markers and IDDM. Certain alleles of factor B (BF), second component (C2), and fourth component (C4) have been shown to be associated with IDDM in Caucasoid populations (Raum *et al.*, 1979; Kirk *et al.*, 1980; de Mouzon *et al.*, 1979; Bertrams *et al.*, 1982). However, only a few reports have been published thus far on Mongoloid populations. The present paper is

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the first report concerning the distribution of BF phenotypes in Chinese patients with IDDM and NIDDM.

MATERIALS AND METHODS

Blood samples for BF typing were obtained from 50 IDDM and 52 NIDDM patients living in Guangzhou. All the patients have attended the Diabetic Clinic at the First Affiliated Hospital of Sun Yat-sen University of Medical Sciences. Samples for normal controls were obtained from 259 unrelated healthy persons attending routine antenatal clinic for genetic counselling at the same hospital. BF allotypes were examined using high voltage agarose gel electrophoresis and subsequent immunofixation according to Alper *et al.* (1972) with slight modifications (Tokunaga *et al.*, 1982a).

RESULTS AND DISCUSSION

The results of BF typing in the IDDM and NIDDM patients and in the controls are shown in Table 1. Both in the IDDM and NIDDM groups the observed numbers of phenotypes were in agreement with those expected on the Hardy-Weinberg's law ($p > 0.3$). A significant decrease in the frequency of BF F positive patients was found in IDDM when compared with controls ($\chi^2 = 7.17$, $p < 0.01$). Corresponding to the decrease, significant differences in the gene frequencies of *BF*S* and *BF*F* between IDDM patients and controls were also observed ($p < 0.005$). The relative risk for BF F positive individuals was calculated to be 0.15. In NIDDM patients, in contrast, no association with BF types was found.

The significantly increased frequencies of BF F1 and/or S07 (S1) in the patients with IDDM have been reported in many Caucasoid populations (Raum *et al.*, 1979; Kirk *et al.*, 1979b; Bertrams *et al.*, 1979a; Deschamps *et al.*, 1979; de Mouzon *et al.*, 1979). An increased frequency of BF F1 and a decreased frequency of BF F were also observed in American Negroid (Budowle *et al.*, 1982). Moreover, a strong age relationship in the association of BF F1 with IDDM has been found. The BF F1 was significantly associated with the early-onset IDDM (Kirk *et al.*,

Table 1. BF types and allele frequencies in Chinese diabetics and normal controls.

	No. tested	BF types No. (%)			Allele frequencies			
		S+ve	F+ve	S07+ve	<i>BF*S</i>	<i>BF*F</i>	<i>BF*S07</i>	Others
IDDM	50	50 (100.0)	2 (4.0) ^a	0 (0.0)	.980 ^b	.020 ^c	.000	.000
NIDDM	52	52 (100.0)	11 (21.2)	0 (0.0)	.894	.106	.000	.000
Controls	259	252 (97.3)	55 (21.2)	4 (1.5)	.867	.120	.008	.005

^a $p < 0.01$, ^b $p < 0.005$, ^c $p < 0.005$.

1979a; Barbosa *et al.*, 1979; Bertrams *et al.*, 1979b). A similar conclusion was obtained in a combined analysis using data on several Caucasoid populations (Budowle *et al.*, 1983).

As for Asian populations, a positive association between a rare variant BF FT (F075) and IDDM was suggested in the Japanese population (Tokunaga *et al.*, 1981, 1982b). A strong association between BF S07 and IDDM was reported in north India (Kirk *et al.*, 1982), while in south India BF F was strongly associated with IDDM (Kirk *et al.*, 1983).

We found no BF S07 positive diabetics in the present study, although four individuals out of 259 normal controls were S07 positive. On the other hand, the frequency of BF F positive IDDM patients was significantly decreased. These differences in the BF-IDDM associations among various ethnic groups may reflect the differences in the linkage disequilibria between BF alleles and the susceptibility gene(s) to IDDM.

As we expected, there was no difference in the distribution of BF types between NIDDM patients and normal controls, which again demonstrates genetic heterogeneity of diabetes mellitus.

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