Table 1

Genotype and Allele Frequencies in NIDDM Patients with (CHD+) and without (CHD−) Coronary Heart Disease

	CHD+	CHD−
	No. (%)	
Genotype:		
AA	86 (44.6)	188 (41.3)
AV	84 (43.5)	195 (42.9)
VV	23 (11.9)	73 (16.0)
	Frequency	
Allele:		
A	.663	.626
V	.337	.373

should, however, be taken into account. The most important is nutritional status, because folate deficiency may be necessary for the clinical consequences of the mutation to manifest (Jacques et al. 1996). Plasma folate levels were not measured in the present study, but diabetic patients pay particular attention to diet, which should minimize nutritional deficiencies. A corollary is that, in patients with poor metabolic control, which may partly reflect dietary noncompliance, the mutation could be of greater clinical significance. A larger study, stratifying patients by metabolic control, would be necessary to address this question. Also to be considered is the far greater susceptibility of diabetic patients to vascular disease. The higher risk profile may mask the impact of raised homocysteine levels. Again, a larger study may be required to demonstrate statistically the influence of mild hyperhomocysteinemia. In conclusion, our data suggest that the polymorphism giving rise to a thermolabile form of the enzyme MTHFR cannot be employed independently as a genetic risk factor for coronary heart disease in NIDDM patients.

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Differences in Methylenetetrahydrofolate Reductase Genotype Frequencies, between Whites and Blacks

To the Editor:

In a recent invited editorial in the *Journal,* Motulsky (1996) discussed the variation in frequency of homozygosity in the 677C→T variant of the 5,10 methylenetetrahydrofolate reductase (MTHFR) gene in different populations. Homozygosity for this polymorphism has been shown to be a predisposing factor for neural tube defects (van der Put et al. 1995; Whitehead et al. 1995; Ou et al. 1996). Motulsky referred to unpublished observations of lower frequencies of homozygotes in African Americans and to the known lower incidence of neural tube defects among Blacks.

We have investigated the frequency of the 677C→T mutation in the two major subpopulations in South Carolina: White (69% of the population, 60% of births) and Black (30% of the population, 39% of births).

Table 1

Prevalence of the 677C→T MTHFR Mutation in Whites and Blacks in South Carolina, and Comparison with Prevalence in Other Populations

Location (Reference)	Total No. Studied	No. (%) Heterozygous	No. (%) Homozygous
Quebec (Frosst et al. 1995)	57	29 (51)	7 (12)
Holland (van der Put et al. 1995)	207	86 (42)	10 (5)
Italy (de Franchis et al. 1995)	289	No data	47 (16)
Ireland (Whitehead et al. 1995)	99	43 (43)	6 (6)
Georgia (Ou et al. 1996)	109	36 (33)	5 (5)
South Carolina:			
White	151	65 (43)	20 (13)
Black	146	31 (21)	0

Twenty of 151 consecutively born White infants were homozygous for the 677C→T mutations, and 65 were heterozygous (table 1). Among consecutive Black newborns, 0 of 146 were homozygous, and 31 were heterozygous. The estimated allele frequency of the mutation was .35 among White newborns (95% confidence interval .28–.40) and .11 among Black newborns (95% confidence interval .08–.16).

It is of interest that the prevalence of neural tube defects in South Carolina is 16/10,000 pregnancies in Whites and 10/10,000 pregnancies in Blacks (W. Allen and R. Stevenson, unpublished observations). It is therefore very plausible, as suggested by Motulsky, that the 677C→T MTHFR mutation might contribute to the differences in neural tube defect prevalence in these populations.

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Prevalence and Parental Origin of De Novo 1.5-Mb Duplication in Charcot-Marie-Tooth Disease Type 1A

To the Editor:

Charcot-Marie-Tooth disease (CMT) is the most common inherited peripheral neuropathy. The most frequent form of the disorder, Charcot-Marie-Tooth disease type 1A (CMT1A), is associated with a 1.5-Mb tandem duplication on chromosome 17p11.2 (Lupski et al. 1991; Raeymaekers et al. 1991) that is found in 70% of Charcot-Marie-Tooth disease type 1 (CMT1) unrelated patients (Nelis et al. 1996). CMT1 is usually presented as an autosomal dominant trait; however, sporadic cases have been reported, many of them carrying the CMT1A duplication as the pathogenic mutation (Hoogendijk et al. 1992). A recent survey from a large number of European countries estimates a prevalence of the duplication in genetically sporadic CMT1 cases of 76.5% (Nelis et al. 1996).

In the March 1996 issue of the *Journal,* Blair et al. (1996) reported the prevalence of the de novo CMT1A