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Prevalence of Molecular Risk Factors FV Leiden, FV HR2, FII 20210G>A and MTHFR 677C>T in Different Populations and Ethnic Groups of Germany, Costa Rica and India

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ABSTRACT The prevalences of the molecular risk factors FVLeiden, FVHis1299Arg (R2), FII 20210G>A and MTHFR 677C>T were studied in blood donors from NE Germany, India (Punjab), San José (Costa Rica), and from two tribes (Chorotegas, Bribri) of Indians and Blacks from Costa Rica. The prevalences of FVL heterozygotes in blood donors from Germany, Costa Rica and India are 6.5, 2 and 1.2% resp. Heterozygosity of R2 allele of FVHR2 was found in 15.5 % in Germany, 13.3% in India. None of the Indians and Blacks of Costa Rica carried FVL, but heterozygotes R1R2 were extremely frequent found in both Indian tribes (44,7% and 50,6%,resp.); homozygosity for R2R2 was 11%. In Blacks the rare R3 polymorphism was found. The FII 20210G>A polymorphism is missing in the Chorotegas Indians and Blacks of Costa Rica and in the population from India. Concerning MTHFR the prevalence of the homozygous mutant genotype is 7.7% in Germany, 5.3% among the Blacks of Costa Rica and 2.7% in India. In the Indian tribes of Costa Rica the prevalence of homozygotes are extremely high: 31.6 % in Chorotegas and 46.7 % in Bribri Indians. The prevalence of genetic risk factors in various populations and ethnic groups is discussed.

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