

Frequency of CCR5 Gene 32-Basepair Deletion in Croatian Normal Population

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Abstract A 32-basepair deletion polymorphism in the CCR5 chemokine receptor gene (CCR5 Δ 32) could increase the resistance to HIV-1 infection or delayed progression to AIDS. This mutant allele is common among Caucasians of Western European descent, but has not been observed in people of African or Asian ancestry. Genetic studies provided in European countries have shown a highest prevalence in Nordic countries and the lowest in the Southern European and Mediterranean populations. We genotyped 303 randomly selected healthy Croatians for the prevalence of CCR5 Δ 32 mutation. CCR5 Δ 32 allele frequency in Croatia of 7.1% fits in the observed European north/south gradient. This first report of CCR5 Δ 32 mutation in Croatian population provides additional information on its frequency and geographical distribution in Slavic populations in South-Eastern Europe. Moreover, our data may have important implications for the prediction and prevention of HIV/AIDS in a tourist country such as Croatia.

The chemokine receptor CCR5 appears to be the major co-receptor for the macrophage-tropic strains of HIV-1. Recent data suggest that the 32-basepair deletion in the CCR5 gene (CCR5 Δ 32) prevents HIV transmission and delays the onset of AIDS (1). This allele is common in healthy Caucasians, but has not been found in people of African or Asian ancestry. Genetic studies provided in 34 European countries showed that the mean frequency of the mutant allele was about 8% (2). However, CCR5 Δ 32 is not distributed equally among the European population: the highest frequencies were found in Nordic countries (approximately 13%) (2-4) and the lowest in the Southern European and Mediterranean populations (2-6%) (4-10). Despite the greatest incidence rate of AIDS cases in Eastern European countries (11), data on CCR5 Δ 32 mutation prevalence in the populations of Slavic origin have been rather scarce (12).

In Croatia, both a central European and Mediterranean country, 218 patients with AIDS

have been reported from 1986 to 2004, yielding a low incidence rate of about 4 cases per million population (11). However, in our country there is one great potential risk factor during summer season in Croatia, when large number of tourists comes from all parts of Europe.

In order to assess the genetic susceptibility of Croatians, as a part of the Slavic population, to HIV-infection, we examined the allelic frequency of CCR5 Δ 32 in healthy Croatian population.

Methods and Results

A total of 303 unrelated blood donors originated from different part of Croatia were enrolled in our study. Genotyping of CCR5 polymorphism was performed using one-step polymerase chain reaction (PCR) method with primers flanking the region containing 32-bp deletion (13). The PCR products were analyzed by 3% agarose gel electrophoresis. The normal allele was detected as a 137bp fragment and the CCR5 Δ 32 allele was de-

tected as a 105bp fragment. The study was approved by the institutional ethics committee and informed consent was obtained from all volunteers.

The frequency of the CCR5 Δ 32 allele was 7.1% with the following distribution of CCR5 genotypes: 263 (86.8%) wt/wt, 37 (12.2%) wt/CCR5 Δ 32, and 3 (1%) CCR5 Δ 32/CCR5 Δ 32.

Comment

This is the first report on the prevalence of CCR5 Δ 32 mutation in Croatian population. Our results indicate that, in relation with the geographic position in Europe, CCR5 Δ 32 allele frequency in Croatia fits well in the observed European north/south gradient. The same trend has recently been shown in the distribution of the C282Y mutation of the hemochromatosis gene (14), as well as for the most common mutations of cytochrome P-450 genes (CYP2C9, CYP2C19, and CYP2D6) (15) in Croatia. The prevalence observed herein is much lower from that found in Northern European populations (9.2-15.8%) (2-5,12) and similar to those reported for Hungarians (8.5%) (4), Turks (6.2%) (4), and Italians (4.7-8.6%) (5-7). Lower prevalence was found in Southern European countries, ie, in Greece (4.2%) (8), Sevilla-Spain (3.8%) (9), Cyprus (2.8%) (10). The lowest allelic frequencies have been found in population with isolated genetic pools: Sardinians (2.1%) (6), Basques (1.8%) (2), and Corsicans (0.9%) (2).

In conclusion, our study provides the evidence for the prevalence of the CCR5 Δ 32 mutation in Croatia and provides additional information on its frequency in European populations of Slavic origin. Moreover, our data may have important implications for the prediction and prevention of HIV/AIDS in our country where the extensive contacts between high risk European populations and general Croatian population during the summer tourist season regularly occurs.

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