JAIDS Journal of Acquired Immune Deficiency Syndromes
26:298–301 © 2001 Lippincott Williams & Wilkins, Inc., Philadelphia

Letters to the Editor

Contrasting Frequencies of *CCR5Δ32* and *CCR2-64I* Alleles in the Tunisian Population

To the Editor: The human CC-chemokine receptor 5 (*CCR5*) is the major coreceptor on $CD4^+$ cells for most of the transmitting strains of HIV-1 (1,2). The complete absence of the *CCR5* protein expression on the surface of $CD4^+$ T cells in approximately 2% of the white population, due to homozygosity for a 32-nucleotide long deletion in the CCR5 coding region (*CCR5Δ32* allele), has been shown to be a protective mechanism against HIV-1 transmission in a number of HIV-1–exposed but uninfected individuals (3–6). Furthermore, *CCR5Δ32* heterozygotes were shown to progress more slowly in several AIDS study cohorts (5,6). Furthermore, a conservative substitution of a valine for an isoleucine at position 64 in the coding region of the CCR2 (*CCR264I*), was also shown to be protective against disease progression (7). Interestingly, *CCR264I* was found to be in strong linkage disequilibrium with *CCR5-59653T*, a mutation in the CCR5 regulatory region (8). More recently, it has been reported that infected individuals homozygous for a multisite haplotype of the CCR5 regulatory region containing the promoter allele *CCR5P1* progress to AIDS more rapidly than those with other CCR5 promoter genotypes (9).

We have studied the frequencies of the *CCR5-Δ32*, *CCR2-64I*, and *CCR5-59653T* alleles in 145 healthy HIV-1 uninfected Tunisian individuals by the spectral genotyping assay (10). We found that the *CCR5-Δ32* allele is significantly less frequent (Fisher exact test p value <.0001) compared with previous studies on white populations (8). The genotype distribution is in equilibrium as predicted by the Hardy-Weinberg equation (p = .8998) showing that no strong selection process is currently affecting the population (Table 1). In contrast to the *CCR5-Δ32* allele, the *CCR2-64I* allele is significantly more frequent in the Tunisian population (Fisher exact test p value = .0108). Furthermore, the *CCR-59653T* mutant allele is in complete linkage disequilibrium with *CCR2-64I* as previously reported (8).

TABLE 1. *Percentages of CCR5 and CCR2 genotypes*

Genotype	Number	Frequency (%)	HWE[a] χ^2	HWE[a] (p-value)
CCR5				
Total	145	1.03	0.0158	.8998
CCR5-$^{+/+}$	143			
CCR5-$^{+}$/Δ32	3			
CCR5-Δ32/Δ32	0			
CCR2				
Total	145	19.31	1.9101	.1670
CCR2-$^{+/+}$	97			
CCR2-$^{+}$/64I	40			
CCR2-64I/64I	8			

[a]Hardy-Weinberg equilibrium; the value of χ^2, with the associated p value for significant departures.

Our results of the *CCR5Δ32* and *CCR264I/CCR5-59653T* allele frequency obtained in the Tunisian population are consistent with results from previously published studies indicating that *CCR5Δ32* allele frequencies decrease in their frequency from Northern European to sub-Saharan populations (3–6,11) with intermediate values found in Mediterranean populations (12–14). In contrast, the *CCR264I* mutation, which is in complete linkage disequilibrium with the *CCR5-59653T*, shows an inverse gradient, with higher values in the south and lower values in the north (15). The reason for the differences in *CCR5Δ32* and *CCR264I* alleles frequencies observed in the Tunisian population compared with other white populations from Central or Northern Europe is unknown (15). One possible explanation, however, is that the modern Tunisian population is a mosaic resulting from the melding, through 3,000 years of history, of several populations such as Berber, Phoenician, Roman, Vandalic, Arabian, Black African, Spanish, Turkish, French, and other populations.

Acknowledgment: This work was funded by the National Institutes of Health under RO1A143868.

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