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SHORT REPORT

Absence of the HIV-1 protective Δ*ccr5* allele in most ethnic populations of India

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Recent epidemiological data and projections indicate that HIV infection will spread rapidly in India. An allele Δ*ccr5* of the β-chemokine receptor gene *CCR5* has been found to confer protection against HIV-1. We find that this protective allele is absent in most ethnic populations of India, except some populations of the northern and western regions where this allele may have been introduced by Caucasian gene flow. The implications of this finding are discussed in the light of increasing HIV prevalence in India. *European Journal of Human Genetics* (2001) **9**, 794–796.

Keywords: tribe; caste; HIV resistance

Introduction

WHO estimates indicate that the fastest spread of HIV infection is occurring in Asia.[1] Recent projections[2] indicate an alarming rate of increase of HIV infection in India, which may not be restricted to high-risk groups, but will spread rapidly to the general population through heterosexual transmission.[3] Certain members of the chemokine family of receptors serve as critical portals for the entry of HIV-1 into target cells. A mutant allele (Δ*ccr5*) of the β-chemokine receptor gene *CCR5* carrying a 32 base-pair deletion prevents cell invasion by the primary transmitting strain of HIV-1. Individuals who are homozygous for the Δ*ccr5* allele are highly resistant to HIV-1 infection; the heterozygote state does not protect against HIV-1 infection, although heterozygotes have been found to have significantly lower viral loads.[4] Early reports indicated that the Δ*ccr5* allele may be absent in indigenous non-European populations. However, a more recent global survey indicated that the Δ*ccr5* allele is not confined to people of European descent, but is found at frequencies of 2–5% throughout Europe, the Middle East and the Indian subcontinent.[5] In this survey, a limited (primarily the northern and western) geographical region of the Indian subcontinent was surveyed, where the frequency of the Δ*ccr5* allele was found to range from 1.47% to 4.69%. The surveyed regions of the Indian subcontinent are known to have had admixture with Caucasians, and the relatively high frequency of this allele in this region may be due to Caucasian gene flow.

Since the epidemiology of HIV in India may critically depend on the frequency of the Δ*ccr5* allele in ethnic populations, which remain largely maritally isolated, we undertook a study to estimate the frequency of the Δ*ccr5* allele in various ethnic populations of India, both tribal and non-tribal, covering primarily those regions of India that were not covered in the earlier global survey.

Materials and methods

Samples were collected from 1436 individuals, unrelated at least to the second cousin level, belonging to 40 ethnic groups. Ethnicity, as reported by the participant, was used. Reported ethnicity of a participant was cross-checked with other participants who reported as belonging to the same ethnic group. From each participant, 5–10 ml of blood was collected by venipuncture, with informed consent. Genomic DNA was isolated from each sample, and genotyping carried out by PCR amplification followed by agarose-gel electrophoresis. Established protocols and primers[5] were used in laboratory analyses of DNA samples for detecting the Δ*ccr5* allele.

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Results

Names of ethnic populations and other relevant information are provided in Table 1 along with the results of our analyses of screening the *CCR5* locus. We find that the Δ*ccr5* allele is absent in most ethnic populations inhabiting eastern, north-eastern, southern and central regions of India. In populations where sporadic presence of this allele was found, no homozygotes were detected. The maximum frequency (5.36%) of the Δ*ccr5* was found among Muslims of North India.

Discussion

HIV and SIV use chemokine receptors to gain entry into a susceptible cell. Although a large number of chemokine receptors are known, CCR5 is possibly the most important one for HIV infection. Our results show that the genetic protection conferred by the Δ*ccr5* allele against HIV-1 is largely absent in Indian populations. All individuals who possessed the Δ*ccr5* allele were heterozygous, and therefore are not protected against HIV infection. It is known that Caucasoid migrants from central Asia and western Eurasia had entered India about 8000–10 000 years ago. The Δ*ccr5* allele may have been introduced by these migrants. Our observation of a higher prevalence of the Δ*ccr5* allele in northern and western India is consistent with this historical fact. However, our finding of no intrinsic genetic resistance to HIV in most ethnic populations of India is alarming in view of the increased spread of HIV infection in India. This finding calls for additional efforts to contain the outbreak of a HIV epidemic in India.

Table 1 Distribution of Δ*ccr5* in 40 ethnic groups of India

Geographical region	*Name of ethnic group*	*Social status*	*No. of individuals tested (No. of CCR5/Δccr5 heterozygotes)*	*% Frequency ± s.d. of Δccr5 allele*
North-east	Tripuri	Tribe	50	0
	Riang	Tribe	50	0
	Jamatia	Tribe	55	0
	Mog	Tribe	25	0
	Mizo	Tribe	16	0
	Chakma	Tribe	10	0
East	Toto	Tribe	30	0
	Oraon	Tribe	51	0
	Santal	Tribe	20	0
	Munda	Tribe	7	0
	Lodha	Tribe	32	0
	Ho	Tribe	54	0
	Agharia	Caste	24	0
	Mahishya	Caste	34 (1)	1.47 ± 1.46
	Gaud	Caste	12	0
	Tanti	Caste	16	0
	Brahmin	Caste	23 (1)	2.17 ± 2.15
	Bagdi	Caste	31	0
South	Badaga	Tribe	40	0
	Kota	Tribe	44	0
	Irula	Tribe	50	0
	Toda	Tribe	32	0
	Kurumba	Tribe	52 (1)	0.96 ± 0.96
	Iyer	Caste	50 (1)	1.00 ± 0.99
	Iyengar	Caste	51	0
	Ambalakarer	Caste	50 (1)	1.00 ± 0.99
	Vanniyar	Caste	50 (1)	1.00 ± 0.99
	Veedakodi Vellalar	Caste	43	0
	Padmasaliyar	Caste	49	0
	Pallan	Caste	24	0
	Kamma Naidu	Caste	43	0
Central	Muria	Tribe	22	0
	Halba	Tribe	47	0
	Kamar	Tribe	57	0
	Chinda Bhunjia	Tribe	26	0
	Chaukhutia Bhunjia	Tribe	37	0
North	Rajput	Caste	51	0
	Brahmin	Caste	27 (1)	1.85 ± 1.32
	Chamar	Caste	25	0
	Muslim	Religious community	28 (3)	5.36 ± 3.01

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References

1 World Health Organisation: *Current and Future Dimensions of the HIV/AIDS Pandemic: A Capsule Summary*. Geneva: World Health Organisation, 1990.

2 Basu A, Basu S, Chakraborty MS, Dewanji A, Ghosh JK, Majumder PP: Projection of HIV infection in Calcutta. *Indian J Med Res* 1998; **107**: 159–172.

3 Lal S, Thakur BB: The problem of HIV and AIDS in India. *Curr Sci* 1995; **69**: 833–834.

4 Huang Y, Paxton WA, Wolinsky SM *et al*: The role of a mutant CCR5 allele in HIV-1 transmission and disease progression. *Nature Med* 1996; **2**: 1240–1243.

5 Martinson J, Chapman NH, Rees DC, Liu Y-T, Clegg JB: Global distribution of the CCR5 gene 32-basepair deletion. *Nature Genet* 1997; **16**: 100–103.