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Sequence Note

HIV Type 1 Sequences with GGC Substitution in Injecting Drug Users in Greece

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IT WAS SHOWN that subtype B variants of human immunodeficiency virus type 1 (HIV-1) from intravenous drug users (IDUs) differ from the variants of homosexual men in several genomic regions, including *vpu*, *vpr*, and sequences encoding the gp120 V3 loop.[1,2] The most conserved was found to be a synonymous nucleotide substitution in the second glycine codon at the tip of the gp120 V3 loop (GGC).[1] Several epidemiological studies were done among the different risk groups in various European countries and the United States. GGC viruses have been found in 85% of IDUs in northern Europe and in 45% of U.S. IDUs.[3] The GGC pattern was not found in V3 sequences obtained from homosexual men in various European countries and the United States.[3]

No epidemiological data on this topic had been gathered in Greece, where the majority of HIV-1 infections are observed among individuals infected sexually and only 4.3% of the cases are observed among IDUs. The predominant HIV-1 subtype in Greece is subtype B.[4] To investigate the situation in Greece, we obtained sequences of HIV-1 RNA encoding the V3 region of the envelope glycoprotein gp120 from 18 individuals infected between 1991 and 1997. Seven of them were IDUs, five were homosexuals, three were heterosexuals, two were bisexuals and for one the root of transmission was unknown. Nested polymerase chain reaction (PCR), direct sequencing, and phylogenetic analysis were performed as described earlier.[4]

It was found that five of the seven (71.4%) IDUs had GGC viruses, whereas the other two had non-GGC viruses (Fig. 1). None of the individuals in the other risk groups carried GGC viruses (data not shown). In addition, four of the seven Greek IDUs (57%) had a synonymous nucleotide substitution (TCC) at *env* position 837, like this Dutch IDUs[3] (Fig. 1). All of the individuals in the other risk groups presented a TCT pattern. Moreover, it was shown that a risk group-associated amino acid signature pattern was observed at *env* codon 288, where 90% of the sequences from homosexual Dutch men had a threonine residue (ACC) compared with 25% of the sequences from Dutch IDUs.[3] From our results it was found that four of five (80%) homosexual men carried sequences with this signature pattern compared with one of seven (14%) IDUs (Fig. 1).

These data may indicate that the HIV-1 epidemic among IDUs was established from a different source than in individuals of other risk groups, perhaps originating from IDUs of other European countries or from the United States. The GGC pattern has been observed among 41% of subtype B sequences from heterosexuals in The Netherlands, suggesting that a number of heterosexuals were infected from IDUs.[5] Further studies are needed to understand the epidemiology of HIV-1 in Greece.

Genbank accession numbers of the sequences described in this article are as follows: AJ224947–AJ224949, AJ224951–AJ224956, and AF094522–AF094530.

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The first and the second author contributed the same to this work.

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                 (1)                             (2)
NE IDU     GTAATTAGAT CCGACAATTT CACGGACAAT GCTAAAATCA TAATAGTACA
greek187   ---------- ---C------ ---------- ---------G ----------
greek71    ---N------ -N-------- ---A------ -------C-- ----------
greek175   ---N------ --TNG----- -TTN------ ---G------ -N--------
greek50    ---------- --A-A----- ---A------ ---C---A-- ----------
greek138   --------G- -TG-A----- ---------- -CTG------ ----------
greek64    --C-----G- -T--A----- ---A-A---- -------G-- ----------
greek94    ---C------ -T-C------ -T-------- N---G--A-- -GG-N-----

           GCTGAACCAA TCTGTAGAAA TTAATTGTAC AAGACCCAAC AACAATACAA
           ------TA-G ---------- ---------- ---------- ----------
           ------GGC- ---------- ---------- ---------- ----------
           ------TG-- ---------G ---------- ---------- ----------
           ------TGC- A-----A-C- ---C------ ---------- ----------
           ------TG-- ---------C ---------- ---------- ----------
           ------TG-- -----G-T-- ---------- ---------- --------G-
           ------TGT- ---------- ---------- T--------- ----------
                                   (3)
           GAAAAAGTAT ACATATAGGA CCAGGCAGAG CATTTTATAC AACAGGAGAA
           ---------- --------C- --------G- ----C---G- ----------
           ---------- --CC------ ---------- ---------- ---------C
           -T-G------ --C---G--- ---------- --------GG -------AG-
           -G-G------ ------G--- ---------T ---------- C--------T
           ---G------ --C------- -----G---- --------G- ---------C
           ---G------ -TT------- ---C-T--C- -----AT-G- ----A--A-C
           ---G---A-- -ACCT-G--- ---------- T--A------ -------C-G

           ATAATAGGAG ATATAAGACA AGCACATTGT AACCTTAGTA GAGCAAAATG
           --T------- ---------- ---C------ TT------CN --N--N----
           ---------- ---------- ---------- ---------- ----------
           ---------- ---------- ---------- N-TA-N---- -----NC---
           ---------- ---------- ---------- ---A------ --T--GC---
           ---------- ---------- ---------- G-TA----NC -----N-T--
           ---------- ---------- ---------- ---------- -----C----
           G--------- --------A- ----T----- --TG------ -----GG---

           GAATGACACT TTA
           -------N-- ---
           ---------- ---
           -NGG------ ---
           ---------- ---
           -G-CN----- ---
           ----A----- ---
           -G-CA--G-- ---
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FIG. 1. Nucleotide sequences of seven Greek HIV-1-positive IDU individuals. NEIDU: consensus sequence of IDU populations in northern Europe.[2] (1) C in IDUs, T in homosexuals; (2) T in IDUs, C in homosexuals; (3) C in IDUs, G in homosexuals.

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