West Nile virus (WNV), a member of the flavivirus family, is a reemerging pathogen maintained primarily between mosquitoes and birds, with humans representing one of several incidental hosts. First isolated in Uganda in 1937, WNV outbreaks have subsequently been reported in the Middle East, Africa, Western Asia, Australia, and, most recently, in the US, where it has rapidly spread westward and into Latin America and the Caribbean since arriving in New York City in 1999 (1–4).

Clinical manifestations of WNV infection can be quite variable. Epidemiologic studies indicate that although ~80% of infections remain subclinical, ~20% progress to a febrile illness (3). Of these, >30% of cases in the US progress to neuroinvasive disease, including meningitis, encephalitis, and/or flaccid paralysis. Survivors of severe disease typically require prolonged rehabilitation for chronic neurologic sequelae (5). To date, no specific treatments or vaccines for WNV disease have been approved by the U.S. Food and Drug Administration.

In the US, there were 16,577 laboratory-confirmed cases of WNV reported to the Centers for Disease Control and Prevention from 2001 to 2004, of which 648 were fatal (3.9%; references 6–9). Elderly and immunocompromised individuals have increased susceptibility to WNV (2, 6, 10, 11), but genetic risk factors and immunologic control mechanisms have not been fully delineated. We have recently identified the monocyte and T lymphocyte chemokine receptor CCR5 as a key factor in viral clearance and survival in a mouse model of WNV encephalitis, in which the mechanism involved trafficking of leukocytes into the infected brain (12). Consistent with this, WNV induces expression of CCR5 ligands in WNV-infected mouse brain (12, 13).
In the present study, we attempted to translate this finding to man by analyzing the distribution of the defective CCR5 allele CCR5Δ32 in two independent cohorts of symptomatic WNV-seropositive individuals from the US. CCR5Δ32 contains a 32-bp deletion within the CCR5 coding sequence and encodes a truncated protein that fails to traffic to the plasma membrane (14). CCR5Δ32 originated in Northern Europe and is found in homozygous form in 1% of Caucasians in the US (15, 16). These individuals completely lack CCR5 function, but appear healthy, suggesting that any important homeostatic functions are compensated for by other leukocyte chemoattractant receptors. In addition to regulating monocyte and T cell trafficking, CCR5 functions pathologically as a major HIV coreceptor (16). Accordingly, CCR5Δ32 homozygosity is strongly associated with resistance to HIV—one of the strongest genetic susceptibility factors known in infectious disease (15, 17). Similarly, the hypothesis that CCR5 plays an important role in WNV pathogenesis in man predicts that the distribution of CCR5Δ32 among symptomatic patients may be strongly skewed relative to its distribution in the general population. Here, we test this prediction.

RESULTS AND DISCUSSION

Three cohorts of patients, the Colorado WNV-seropositive cohort, the Arizona WNV-seropositive cohort, and the Arizona WNV-seronegative cohort, were identified that had symptomatic illness in which WNV was considered in the differential diagnosis. Inclusion criteria for patients in these cohorts are defined in the Materials and methods section and the clinical characteristics are given in Table I. Genotypes were defined for 247 of the 261 WNV-seropositive Arizona cases (94.6%); for 148 of the 155 WNV-seropositive Colorado cases (95.5%); for 143 of 152 and 72 of 74 of the self-reporting Caucasian subsets of the Arizona and Colorado WNV-seropositive cohorts, respectively; for all WNV-seronegative random blood donors (n = 1,318); and for 145 of 154 WNV-seronegative subjects from Arizona (94.2%).

Table I. Characteristics of study subjects

| Characteristics          | All racial groups | Caucasians only |
|--------------------------|-------------------|-----------------|
|                          | Arizona           | Colorado        | Combined       |
|                          | n = 247           | n = 148         | n = 395        | Arizona           | Colorado        | Combined       |
|                          |                   |                 |               | n = 143           | n = 72           | n = 72         |
| Mean age (y)             | 53 ± 19           | 50 ± 18         | 52 ± 19       | 45 ± 20           | 57 ± 18          | 50 ± 18        | 54 ± 18       |
| Male sex (%)             | 55.6              | 48.6            | 52.8          | 44.3              | 53.8             | 41.7           | 49.8          |
| Caucasian (%)            | 57.9              | 48.6            | 54.4          | 13.1              | 100              | 100            | 100           |
| Hispanic (%)             | 10.1              | 11.5            | 10.6          | 2.8               | N/A              | N/A            | N/A           |
| Asian/Pacific Islander (%)| 2.0               | 0.0             | 1.3           | 0.7               | N/A              | N/A            | N/A           |
| Native American (%)      | 2.4               | 0.0             | 1.5           | 2.1               | N/A              | N/A            | N/A           |
| Black (%)                | 0.0               | 0.7             | 0.3           | 0.7               | N/A              | N/A            | N/A           |
| Not specified (%)        | 27.5              | 39.2            | 31.9          | 80.7              | N/A              | N/A            | N/A           |
| Fever (%)a               | 26.7              | 24.3            | 25.8          | N/A               | 34.3             | 22.2           | 30.2          |
| Meningitis (%)a          | 25.9              | 39.9            | 31.1          | N/A               | 30.8             | 43.1           | 34.9          |
| Encephalitis (%)a        | 24.7              | 35.8            | 28.9          | N/A               | 31.5             | 34.7           | 32.6          |
| Not specified (%)        | 22.7              | 0.0             | 14.2          | N/A               | 3.5              | 0              | 2.3           |
| % Mortality (n)          | 3.2 (8)           | 7.4 (11)        | 4.8 (19)      | N/A               | 4.9 (7)          | 1.4 (1)        | 3.7 (8)       |

Arizona and Colorado refer to cohorts of patients with symptomatic seropositive WNV infection. Ariz WNV− refers to a second Arizona cohort of symptomatic patients in whom WNV was considered as the diagnosis but ruled out. Data pooled from the WNV+ Arizona and Colorado cohorts are also shown (Combined).

a Patients were classified into one of the four indicated disease categories by physician interview. N/A, not available or applicable.

Table II. Association of the CCR5Δ32 allele with symptomatic WNV infection in Arizona and Colorado

| CCR5Δ32 Genotype, n (%) | All racial groups | Self-reporting Caucasians |
|-------------------------|-------------------|--------------------------|
|                         | +/+               | +/Δ32                    | Δ32/Δ32      | +/+               | +/Δ32                    | Δ32/Δ32      |
| Arizona WNV+            | 205 (83.0)        | 31 (12.6)                | 11 (4.5)     | 115 (80.4)        | 22 (15.4)                | 6 (4.2)      |
| Colorado WNV+           | 111 (75.0)        | 31 (20.9)                | 6 (4.1)      | 49 (68.1)         | 17 (23.6)                | 6 (8.3)      |
| Combined WNV+           | 316 (80.0)        | 62 (15.7)                | 17 (4.3)     | 164 (76.3)        | 39 (18.1)                | 12 (5.6)     |
| Arizona WNV−            | 125 (86.2)        | 19 (13.1)                | 1 (0.7)      | 16 (84.2)         | 3 (15.8)                 | 0 (0)        |
| RBD                     | N/A               | N/A                      | N/A          | 1102 (83.6)       | 203 (15.4)               | 13 (1.0)     |

All patients from Arizona and Colorado had symptoms for which WNV infection was considered as the underlying cause. WNV+, WNV seropositive; WNV−, WNV seronegative; +, wild-type CCR5 allele; Δ32, CCR5Δ32 allele; RBD, random blood donors; N/A, not applicable.
The genotype distribution observed for the combined Arizona and Colorado WNV-seropositive cohorts deviated strongly from Hardy-Weinberg equilibrium (P = 0.013), mainly because of increased frequency of CCR5Δ32 homozygotes. 17 (4.3%) of the 395 informative cases in the combined Arizona and Colorado seropositive cohorts unstratified by race were CCR5Δ32 homozygotes (Table II). This value greatly exceeds the percentage of CCR5Δ32 homozygotes reported for the general US Caucasian population (0.8–1.1%; reference 18). To quantify the significance of this genotype–disease association, we have used as a reference the group of 1,318 healthy Caucasian random blood donors from the US, in which 1.0% were CCR5Δ32 homozygotes. Compared with this value, the increased frequency of CCR5Δ32 homozygotes in both the Arizona and Colorado WNV-seropositive cohorts was highly statistically significant (Table III). When all genotyped WNV-seropositive cases unstratified by race were compared with the US random blood donors, the odds ratios (OR) for this genetic factor were 4.7 for the Arizona cohort (95% confidence interval [CI], 2.1–10.6, P < 0.0001) and 4.2 for the Colorado cohort (95% CI, 1.6–11.3, P = 0.0018). It is important to note that this is a conservative analysis because the frequency of CCR5Δ32 homozygotes is certain to be lower in non-Caucasian racial groups from these cohorts (Table I).

Consistent with this, when the data were stratified to include only self-reporting Caucasians in both the WNV-seropositive cohorts (n = 215), the strength of the association increased by 30% (12 CCR5Δ32 homozygotes, 5.6%). When the self-reporting Caucasian portions of the two WNV-seropositive cohorts were compared separately to the random blood donor benchmark, the OR was 4.4 in the Arizona cohort (95% CI, 1.6–11.8, P = 0.0013), and 9.1 in the Colorado cohort (95% CI, 3.4–24.8, P < 0.0001).

Although unlikely, it is possible that the large increase in frequency of CCR5Δ32 homozygotes in these cohorts may be caused by an atypical geographic distribution of this allele in the general population of Arizona and Colorado. To directly address this possibility, we analyzed the distribution of CCR5Δ32 in a symptomatic Arizona WNV-seronegative cohort (n = 145). Because the CCR5Δ32 allele frequency in this cohort (7.2%) is only slightly lower than in the Arizona WNV-seropositive cohort (10.7%) and the US Caucasian random blood donors (8.7%), it is likely that this cohort contains only a slightly smaller percentage of Caucasians than the other two. Thus, given the size of the Arizona WNV-seronegative group, there is sufficient power at this allele frequency to meaningfully analyze the distribution of genotypes. Only one CCR5Δ32 homozygote was identified in the cohort (0.7%). Moreover, unlike the WNV-seropositive cohort, the observed CCR5Δ32 genotypic frequencies in the WNV-seronegative cohort did not deviate from Hardy-Weinberg equilibrium (P > 0.99). This strongly suggests that the general population in Arizona does not have an anomalous genetic structure with regard to the CCR5 locus, with a skewed increase in CCR5Δ32 homozygotes that could account for the high frequencies we observed in the WNV-seropositive cohorts. When the CCR5Δ32 homozygote genotype frequency was compared between the race-unstratified Arizona WNV-seronegative and -seropositive cohorts, an OR of 6.7 was determined (95% CI, 0.86–52.6, P = 0.07).

With regard to the distribution of CCR5 genotypes in symptomatic WNV-seropositive cases as a function of clinical outcome, no significant differences were observed compared with the distribution in the overall combined group (Table IV) or in the Arizona or Colorado WNV-seropositive cohorts considered separately (not depicted), with the exception of death (Fig. 1). A total of 19 of 395 individuals in the two cohorts died from WNV neuroinvasive disease (4.8%), which is similar to the national average of mortality reported for WNV cases from the past three years: 2002 (4,156 cases, 284 deaths, 6.8%); 2003 (9,862 cases, 264 deaths, 2.7%); and 2004 (2,539 cases from the past three years: 2002 (4,156 cases, 284 deaths, 6.8%); 2003 (9,862 cases, 264 deaths, 2.7%); and 2004 (2,539 cases from the past three years: 2002 (4,156 cases, 284 deaths, 6.8%); 2003 (9,862 cases, 264 deaths, 2.7%); and 2004 (2,539

### Table III. CCR5Δ32 homozygotes have increased risk of symptomatic WNV infection

| Cohort     | All racial groups OR 95% CI P | Self-reporting Caucasians OR 95% CI P |
|------------|------------------------------|---------------------------------------|
| Arizona    | 4.7 2.1–10.6 <0.0001          | 4.4 1.6–11.8 0.0013                   |
| Colorado   | 4.2 1.6–11.3 0.0018           | 9.1 3.4–24.8 0.0001                   |
| Combined   | 4.5 2.2–9.4 0.0001            | 5.9 2.7–13.2 0.0001                   |

Values were calculated in comparison to the CCR5Δ32 homozygous genotype frequency in 1,318 North American Caucasian random blood donors.

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Figure 1. CCR5 deficiency is associated with increased risk of death from WNV infection. Data presented are from the Arizona WNV-seropositive cohort and demonstrate that CCR5Δ32 homozygosity is associated with fatal outcome in both the race-unstratified (OR = 8.5 [95% CI, 1.5–48.2], P = 0.04) and self-reporting Caucasian (OR = 13.2 [95% CI, 1.9–89.9], P = 0.03) groups.
The present study provides the first evidence that the defective CCR5 allele CCR5∆32 is a risk factor for symptomatic WNV infection, the first genetic risk factor identified for this disease. The association was restricted to CCR5∆32 homozygotes and was very strong, similar in magnitude to the association we and others have previously reported for CCR5∆32 in the Arizona cohort (4.5 and 4.2%, respectively), and the differences are statistically significant: OR = 8.5 (95% CI, 1.5–48.2), P = 0.04, and OR = 13.2 (95% CI, 1.9–89.9), P = 0.03, respectively (Fig. 1). This association was not observed in the Colorado cohort. When Caucasians from both cohorts were analyzed together, the association test gave an OR of 6.6 (95% CI, 1.2–37), P = 0.07.

Another limitation of our study was the incomplete information about the racial background of cases (Table I), which is needed to more precisely quantitate risk because CCR5∆32 is primarily found in Caucasians. We have addressed this by consistently applying a conservative analysis of the data that includes close monitoring of AIDS patients treated with antagonists now in advanced stages of development targeting the HIV coreceptor activity of CCR5. Such agents are intended to imitate the homozygous CCR5∆32 genetic defect and involvement of CCR5 in regulating leukocyte migration to the brains of infected patients (19, 20). Fifth, WNV infection of mice induces expression of the CCR5 ligand CCL5 and accumulation of CCR5+ leukocytes in the brain (12, 13). Sixth, WNV infection in CCR5−/− mice is uniformly fatal (12).

Together these results imply that wild-type CCR5 functions as a host defense factor in WNV infection in man. CCR5 could potentially restrict WNV infection at the level of initial infection. This is not addressed by our retrospective study design and may not be feasible to resolve prospectively by measuring the association of CCR5∆32 homozygosity with asymptomatic WNV infection because this genotype and WNV infection are both uncommon in the general population. More likely, CCR5 restricts disease progression after initial infection so that its absence results in an increased likelihood of an infected patient coming to medical attention as a symptomatic case. Our data are consistent with this interpretation, and even suggest that a fatal outcome is more likely in the absence of CCR5 (Fig. 1). Additional work will be needed to more critically address the latter point because the positive association we observed between CCR5 deficiency and death in the Arizona cohort, although statistically significant, was based on only two cases, and could not be detected in the Colorado cohort, possibly because of its smaller size.

Table IV. Distribution of CCR5∆32 allele as a function of clinical outcome in WNV-seropositive patients

| Clinical outcome | All racial groups | Self-reporting Caucasians |
|------------------|-------------------|---------------------------|
|                  | +/+               | +/∆32                     | ∆32/∆32           | +/+                | +/∆32                     | ∆32/∆32           |
| Fever            | 85 (83.3)         | 12 (11.8)                 | 5 (4.9)           | 52 (80.0)          | 9 (13.8)                  | 4 (6.2)           |
| Meningitis       | 100 (81.3)        | 19 (15.4)                 | 4 (3.3)           | 59 (78.7)          | 13 (17.3)                 | 3 (4.0)           |
| Encephalitis     | 82 (71.9)         | 27 (23.7)                 | 5 (4.4)           | 48 (68.6)          | 17 (24.3)                 | 5 (7.1)           |
| Not Specified    | 49 (87.5)         | 4 (7.1)                   | 3 (5.4)           | 5 (100.0)          | 0 (0)                     | 0 (0)             |
| Death            | 13 (68.4)         | 4 (21.1)                  | 2 (10.5)          | 6 (75.0)           | 0 (0)                     | 2 (25.0)          |
| Total            | 316 (80.0)        | 62 (15.7)                 | 17 (4.3)          | 164 (76.3)         | 39 (18.1)                 | 12 (5.6)          |

Data were pooled from the Arizona and Colorado cohorts.

*Patients were classified into one of the four indicated disease categories by interview with the referring physician. +, wild-type CCR5 allele; ∆32, CCR5∆32 allele.
could render AIDS patients particularly vulnerable to severe and possibly fatal WNV infection.

In summary, we have established that homozygous CCR5Δ32 is a strong host genetic risk factor for symptomatic laboratory-confirmed WNV infection, the first one identified for this disease. In contrast, the homozygous CCR5Δ32 genotype has previously been strongly associated with resistance to HIV. These genetic data imply that CCR5 plays opposite roles in HIV and WNV infection, facilitating the former and restricting the latter. Our results have important implications regarding the potential safety of CCR5-blocking agents now under development for the treatment of HIV/AIDS. Clinical care of individuals taking these medicines while residing in WNV-endemic areas may mandate strict measures to limit mosquito exposure and a high index of suspicion for symptoms consistent with WNV.

MATERIALS AND METHODS

Study populations. The study was approved by the Office of Human Subjects Research of the US National Institutes of Health. Four patient groups were defined: (a) healthy North American Caucasian random blood donors from the National Institutes of Health Department of Transfusion Medicine (n = 1,318) previously collected under an IRB approved protocol; (b) the Arizona WNV-seropositive cohort (n = 261), defined as patients presenting with acute illness in Arizona who tested positive for WNV but negative for St. Louis encephalitis virus (SLE) by specific IgM ELISA of serum or cerebrospinal fluid (CSF) at the Arizona Department of Health Services between 5/26/04 and 10/2/04, the dates for receipt by the Department of the first and last patient samples during mosquito season in the state of Arizona in 2004; (c) the Colorado WNV-seropositive cohort (n = 155), defined as patients presenting with acute illness to a physician in Colorado who tested positive for WNV but negative for SLE by specific IgM ELISA of serum or CSF at the Colorado Department of Public Health and Environment between 7/20/03 and 9/30/03, the dates for receipt by the Department of the first and last patient samples for 2003; (d) the Arizona WNV-seronegative cohort (n = 261), defined as patients presenting with acute illness in Arizona who were defned as patients presenting with acute illness to a physician in Arizona who whom WNV and SLE had been considered in the differential diagnosis but ruled out by serological testing at the Arizona Department of Health Services between 5/26/04 and 10/2/04, the dates for receipt by the Department of the first and last patient samples during mosquito season in the state of Arizona in 2004; (e) the Colorado WNV-seronegative cohort (n = 154), defined as patients presenting with acute illness to a physician in Arizona in whom WNV and SLE had been considered in the differential diagnosis but ruled out by serological testing at the Arizona Department of Health Services between 5/26/04 and 10/2/04. In the Arizona WNV-seropositive cohort, only 89% of the samples collected were available and all of these were analyzed. In the Colorado WNV-seropositive cohort, only 164 samples remained that had a sufficient volume for purification of DNA and all of these samples were analyzed. This represented 14% of all Colorado samples originally collected. The following information was requested from the medical provider during case investigation by local health department communicable disease staff: age, sex, self-reported racial group, and clinical presentation based on the Centers for Disease Control-defined clinical parameters of disease; i.e., fever, meningitis, encephalitis, and death (Table I). At the time of data collection each symptomatic patient was classified into one of the three disease categories: fever, meningitis, or encephalitis. Follow-up data on disease course and the maximal severity of symptommatic disease in each patient were not available. All fatal cases were caused by complications of WNV neuroinvasive disease. Study investigators were blinded to unique patient identifiers.

DNA isolation. 100 μl of serum or CSF was thawed for genomic DNA purification using a QIAamp 96 DNA Blood kit according to the manufacturer’s instructions (QIAGEN). Purified DNA was eluted into 100 μl of the recommended buffer and stored at 4°C until further use. DNA from random blood donors was isolated as previously described (15).

CCR5Δ32 genotyping. Genotyping was performed by standard methods described previously (21). In brief, 2 μl of patient DNA was amplified by PCR using primers that flank the site of the 32-bp deletion: 5′-GTCTT-CATTACACCTGCAAGTCTC-3′ and 5′-GTCCAACCTGTATAGC-TAATGC-3′. PCR products were analyzed by electrophoresis on a 3% agarose/TBE gel with known wild-type CCR5 and CCR5Δ32 ampiclon controls (233 and 201 bp, respectively) and visualized with Gelstar (Cambrex) DNA staining. Each sample was tested in two independent PCR reactions, and results were concordant, as determined by two independent investigators.

Statistical analysis. OR and 95% confidence limits were calculated using a recessive genetic model (i.e., CCR5Δ12 homozygotes compared with the combination of wild-type CCR5 and CCR5Δ32 heterozygotes) by cross-tabulation. With the exception of the death data, significance was determined by χ2 tests using a two-sided P value and Yates’ continuity correction, and 95% CIs were estimated using the approximation of Woolf as implemented in the Prism statistics program version 4 (GraphPad Software). Association of CCR5Δ32 homozygosity with death, due to small numbers, was analyzed by Fisher’s exact test. Tests of Hardy-Weinberg equilibrium were performed using a χ2 test and two degrees of freedom after using the Hardy-Weinberg equation (p2 + 2pq + q2 = 1, where p and q represent the frequency of the two alleles) to calculate expected frequencies of each of the three genotypes.

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REFERENCES

1. Lanciotti, R.S., J.T. Roehrig, V. Deubel, J. Smith, M. Parker, K. Steele, B. Crise, K.E. Volpe, M.B. Crabtree, J.H. Scherret, et al. 1999. Origin of the West Nile virus responsible for an outbreak of encephalitis in the northeastern United States. Science. 286:2333–2337.
2. Hubalek, Z., and J. Halouzka. 1999. West Nile fever—a reemerging tropic virus isolated from the blood of a native of Uganda. Am. J. Trop. Med. Hyg. 20:471–492.
3. Klee, A.L., B. Maidin, B. Edwin, I. Poshni, F. Mostashari, A. Fine, M. Layton, and D. Nash. 2004. Long-term prognosis for clinical West Nile virus infection. Emerg. Infect. Dis. 10:1405–1411.
4. Annis, D.S., R. Conetta, G. Waldman, and A.A. Teixeira. 2001. The West Nile virus encephalitis outbreak in the United States (1999–2000); from Flushing, New York, to beyond its borders. Ann. NY Acad. Sci. 951:161–171.
5. Centers for Disease Control and Prevention. 2004. West Nile virus activity–United States, October 6–12, 2004. MMWR Morb. Mortal. Wkly. Rep. 53:950–951.
6. Centers for Disease Control and Prevention. 2005. West Nile virus activity–United States, November 20–25, 2003. MMWR Morb. Mortal. Wkly. Rep. 52:1160.
7. Centers for Disease Control and Prevention. 2002. West Nile virus activity–United States, November 14–20, 2002, and Missouri, January 1–November 9, 2002. MMWR Morb. Mortal. Wkly. Rep. 51:1049–1051.
8. Tsai, T.F., F. Poppovica, C. Cernescu, G.L. Campbell, and N.I. Nedelevu. 1998. West Nile encephalitis epidemic in southeastern Romania. Lancet. 352:767–771.
11. Asnis, D.S., R. Conetta, A.A. Teixeira, G. Waldman, and B.A. Sampson. 2000. The West Nile Virus outbreak of 1999 in New York: the flushing Hospital experience. Clin. Infect. Dis. 30:413–418.
12. Glass, W.G., J.K. Lim, R. Cholera, A.G. Pletnev, J.L. Gao, and P.M. Murphy. 2005. Chemokine receptor CCR5 promotes leukocyte trafficking to the brain and survival in West Nile virus infection. J. Exp. Med. 202:1087–1098.
13. Shirato, K., T. Kimura, T. Mizutani, H. Kariwa, and I. Takashima. 2004. Different chemokine expression in lethal and non-lethal murine West Nile virus infection. J. Med. Virol. 74:507–513.
14. Liu, R., W.A. Paxton, S. Choe, D. Ceradini, S.R. Martin, R. Horuk, M.E. MacDonald, H. Stuhlmann, R.A. Koup, and N.R. Landau. 1996. Homozygous defect in HIV-1 coreceptor accounts for resistance of some multiply-exposed individuals to HIV-1 infection. Cell. 86:367–377.
15. Zimmerman, P.A., A. Buckler-White, G. Alkhatib, T. Spalding, J. Kubočík, C. Combadiere, D. Weissman, O. Cohen, A. Rubbert, G. Lam, et al. 1997. Inherited resistance to HIV-1 conferred by an inactivating mutation in CC chemokine receptor 5: studies in populations with contrasting clinical phenotypes, defined racial background, and quantified risk. Mol. Med. 3:23–36.
16. Berger, E.A., P.M. Murphy, and J.M. Farber. 1999. Chemokine receptors as HIV-1 coreceptors: roles in viral entry, tropism, and disease. Annu. Rev. Immunol. 17:657–700.
17. Hill, A.V. 1998. The immunogenetics of human infectious diseases. Annu. Rev. Immunol. 16:593–617.
18. Martinson, J.J., N.H. Chapman, D.C. Rees, Y.T. Liu, and J.B. Clegg. 1997. Global distribution of the CCR5 gene 32-basepair deletion. Nat. Genet. 16:100–103.
19. Omalu, B.I., A.A. Shakir, G. Wang, W.I. Lipkin, and C.A. Wiley. 2003. Fatal fulminant pan-meningo-polioencephalitis due to West Nile virus. Brain Pathol. 13:465–472.
20. Yang, J.S., J.J. Kim, D. Hwang, A.Y. Choo, K. Dang, H. Maguire, S. Kudchodkar, M.P. Ramanathan, and D.B. Weiner. 2001. Induction of potent Th1-type immune responses from a novel DNA vaccine for West Nile virus New York isolate (WNV-NY1999). J. Infect. Dis. 184:809–816.
21. Abdi, R., T.B. Tran, A. Sahagun-Ruiz, P.M. Murphy, B.M. Brenner, E.L. Milford, and D.H. McDermott. 2002. Chemokine receptor polymorphism and risk of acute rejection in human renal transplantation. J. Am. Soc. Nephrol. 13:754–758.