It is possible that in the study by McAdam et al. [4], the likelihood of active disease developing among IDUs was related to their HIV status. However, these data were not provided in their paper, and it is just as possible that many of the TB patients who were not IDUs in that study were also HIV-infected. Hence, one can speculate to make either conclusion. The study by Reichman et al. [5] that we referenced was done before the beginning of the HIV epidemic; hence, there should have been no influence of the HIV serostatus on the disease outcome among purified protein derivative (PPD)–positive persons in that study. We felt that it was reasonable to reference two papers from New York City that provided data about the likelihood of active disease development among PPD–positive IDUs to speculate about a conclusion supportive of our hypothesis. Hence, this is not an error but an inference based on data provided by two relevant papers.

We did not present the analysis adjusting the odds ratios for residence in a shelter by injection drug use because the numbers became too small to make a meaningful conclusion, and we were not interested in stratifying a variable that was associated only with a cluster pattern. The point of this paper was to identify factors associated with infection with the C strain, not infection with a cluster pattern strain. The second control group was included to prevent confounding that may result from a factor associated with any cluster pattern strain of \( M. \) tuberculosis.

Nevertheless, we appreciate the attention paid by Munsiff and Driver to the details of our analysis. The point remains, however, that the drug-susceptible C strain was found to have particular epidemiologic and microbiologic characteristics which need further study.


Department of Medicine, Cornell University Medical College, Bellevue Hospital Center, New York University, Department of Medicine, Beth Israel Medical Center, Tuberculosis Center, Public Health Research Institute, and Department of Medicine, St. Barnabas Medical Center, New York, New York

Follow-up Study of Verocytotoxigenic Escherichia coli Infection in Dairy Farm Families

To the Editor—Between July 1992 and May 1993, evidence of verocytotoxigenic \( Escherichia \) coli (VTEC) was found in stool cultures of 24 (27.3%) of 88 healthy family members residing on 16 Ontario dairy farms [1]. Four of nine serotypes of VTEC isolated from these dairy farm family members were also isolated from cattle on their farms. Here we report on a follow-up study in which these 16 farms were revisited after 5–13 months to investigate the frequency and possible persistence of VTEC infection in these families and their dairy cattle.

All family members on the 16 dairy farms were asked to submit a stool specimen. A rectal swab sample was obtained from all calves <3 months of age on each farm. Similar samples were obtained from all cows in the milking herd (5 farms) or a random sample of the milking herd consisting of 25% of the herd or a minimum of 10 cows (11 farms). Human and bovine fecal samples were cultured and tested for the presence of VTEC by polymerase chain reaction (PCR) amplification of VT gene sequences as described previously [1–3]. Cultures positive by PCR were processed further to isolate VTEC [1].

Among the 89 dairy farm family members on the 16 dairy farms, 57 from 14 farms provided stool samples (compliance, 64%). Seventeen of those submitting samples were among the 24 who had evidence of VTEC in their stools in the initial study (compliance for retesting, 71%). Compliance for cattle testing was 100%, with a total of 409 samples (274 from cows and 135 from calves). Thirty-nine percent of the cows sampled had been tested in the initial study. All the calves, being <3 months of age, had not been tested in the initial study conducted 5–13 months previously.

Stool cultures from 3 (5.3%) dairy farm family members, each living on a different farm, were positive for VT genes by PCR (table 1). VTEC of serotype O26:H11 was isolated from 1 PCR-positive culture. None of the 17 family members with evidence of VTEC in their stool in the initial study tested positive in the follow-up study.

Evidence of VTEC by PCR was found in cattle on 16 farms (100%) and in 58 (21.2%) of 274 cows and 68 (50.4%) of 135 calves. VTEC were isolated from cattle on 14 (87.5%) of 16 farms at overall rates of 7.7% (21/274) from cows and 20.7% (28/135) from calves. VTEC serotype O26:H11 was isolated from 2 calves on the same farm as the dairy farm family member shedding this serotype. On 12 farms, between one and four VTEC serotypes present in cattle on the farms in the initial study were reisolated but not from any of the 107 cows retested. VTEC O103:H2, isolated from a dairy farm family member and cattle on the same farm in the initial study, was again isolated from cattle on the farm in the follow-up study. \( E. \) coli O157:H7 was reisolated from a calf on 1 of 5 previously \( E. \) coli O157:H7–positive farms, but the isolate belonged to a different phage type [3].

Asymptomatic carriage of VTEC by dairy farm family members did not persist for long periods, as evidenced by the failure to find VTEC in the 17 previously positive dairy farm family members who were retested after 5–13 months. Furthermore, the rate of VTEC carriage by family members on these farms at follow-up (5.3%) was lower than on the first sampling of the initial study (21/88, 23.9%) and approximated the overall rate of VTEC shed-
### Table 1

Microbiologic findings from fecal cultures from 3 verocytotoxigenic (VTEC)–positive members of 3 dairy farm families in follow-up testing of 14 farms previously having ≥1 VTEC-positive family members.

<table>
<thead>
<tr>
<th>Farm no.</th>
<th>Person code</th>
<th>Age (years) at initial study</th>
<th>VTEC status Initial study</th>
<th>Interval from last test (month)</th>
<th>Serotype isolated</th>
<th>Serotype present concurrently in cattle</th>
</tr>
</thead>
<tbody>
<tr>
<td>25</td>
<td>H1</td>
<td>28</td>
<td>Negative</td>
<td>Positive</td>
<td>O26:H11</td>
<td>Yes</td>
</tr>
<tr>
<td>66</td>
<td>H5</td>
<td>13</td>
<td>Negative</td>
<td>Positive</td>
<td>NI</td>
<td>ND</td>
</tr>
<tr>
<td>114</td>
<td>H5</td>
<td>7</td>
<td>Negative</td>
<td>Positive</td>
<td>NI</td>
<td>ND</td>
</tr>
</tbody>
</table>

**NOTE.** Persons were all male and were classified as VTEC-positive if their stool cultures were positive by polymerase chain reaction (PCR) for verocytotoxin genes. Stool cultures from additional 54 members of families on 14 farms, including 17 who had previously been VTEC-positive, were negative for VTEC by PCR. NI, no VTEC isolated; ND, not determined (because VTEC was not isolated from VTEC-positive human stool culture).

There were, however, 3 previously VTEC-negative family members on one farm, VTEC O26:H11, a known human pathogen, was isolated from a family member and from calves. Notably, this serotype was the only VTEC isolated on the dairy farm and had not been found in cattle or family members on the farm in the initial study, providing additional evidence that humans may acquire VTEC infection from cattle or the farm environment [1, 4–6]. VTEC carriage by cattle also appeared to be transient but some serotypes, including *E. coli* O157:H7, may persist in herds for several months. However, since subtyping revealed that *E. coli* O157:H7 strains from 1 farm over time were different [3], a similar approach would be required to determine if non–O157 VTEC serotypes isolated from the same farms over the two studies represented persistent or new infections.

### References


### Erratum

There are 2 errors in an article in the July 1997 issue of *JID*: Smith IL, Cherrington JM, Jiles RE, Fuller MD, Freeman WR, Spector SA. High-level resistance of cytomegalovirus to ganciclovir is associated with alterations in both the UL97 and DNA polymerase genes. J Infect Dis 1997;176:69–77. Polymerase alterations in table 1 for isolate 20 should read ‘‘T726V’’ (not ‘‘T722V’’) and for isolate 27 should read ‘‘D588N’’ (not ‘‘D588E’’) and ‘‘A1154P’’ (not ‘‘P1154A’’). The full table appears on the next page, with the corrected lines in bold type.