Human anthrax, which can include cutaneous, gastrointestinal, and inhalation forms, is caused by *Bacillus anthracis*. The type of anthrax is directly related to the route of infection. Inhalation anthrax, which was historically associated with textile mill workers and most recently with bioterrorism, occurs upon inhaling spores. Cutaneous anthrax is generally the result of infection via a skin abrasion while handling contaminated animal products, while gastrointestinal anthrax occurs upon eating contaminated meat. Human anthrax is very rare worldwide, and only three cases have been reported in Hong Kong in the last 20 years.

On 27 May 2003, a 2-year-old boy, who was in apparent good health prior to this illness, became ill with fever and anorexia as main symptoms. His condition rapidly deteriorated 3 days after admission to a hospital. *B. anthracis* was isolated from both cerebrospinal fluid and blood. Postmortem examination revealed the presence of gram-positive rods in mesenteric lymph nodes and brain tissues. Although pathological findings suggested an oral route of transmission, an extensive epidemiological investigation and culturing of food and environmental samples from the victim’s home, nursery, playgrounds, restaurants, supermarkets, and meat suppliers that might have been linked to the victim’s activities were all negative for *B. anthracis*.

We used multiple-locus variable-number tandem repeat analysis (MLVA) and *pagA* sequencing to genotype a *Bacillus anthracis* isolate from a fatal case of human anthrax in Hong Kong. The isolate has a unique MLVA genotype, is related to the Sterne and Ames strains, and is consistent with genotypes identified in China.

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FIG. 1. MLVA-based dendrogram generated using unweighted-pair group method arithmetic average cluster analysis of raw genotype scores of 88 diverse *B. anthracis* strains (2) and the Hong Kong isolate. Genotype numbers are listed as reported by Keim et al. (2). Note that genotype 25 is not present since reanalysis of the isolate indicated that it was missing the pXO2 virulence plasmid. We have indicated the locations of the Sterne strain, the Ames strain, and all Chinese strains. Included next to the Chinese strains are the provinces where the strains were isolated.
of PA genotype I. This PA genotype is the same as that of the Sterne and Ames strains of \textit{B. anthracis} (3).

MLVA and \textit{pagA} sequencing of the isolate causing this rare case of anthrax revealed that the isolate is closely related to strains such as Sterne and Ames and is consistent with genotypes previously identified in China. In fact, the isolate differs from genotype 59, a Chinese strain isolated from soil in the Guangxi province, by a single nucleotide addition in the pX02 locus (Fig. 2) (2). This is particularly interesting considering the geographic proximity of these two regions, the inland waterways that link them, and the extensive trade between Hong Kong and Guangxi. While the genotype of this isolate appears consistent with this region, the proximal source of the \textit{B. anthracis} isolate that caused this case remains unknown. In the future, if more extensive databases of subtyped \textit{B. anthracis} strains from this region become available, it may be possible to determine the origin of this strain with greater confidence.

\textbf{REFERENCES}


