Antigenic Divergence between \textit{Bordetella pertussis} Clinical Isolates from Moscow, Russia, and Vaccine Strains\(^{\text{\textregistered}}\)

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Received 20 August 2006/Returned for modification 19 October 2006/Accepted 20 December 2006

We analyzed temporal changes in the frequencies of the \textit{ptxA}, \textit{prn}, \textit{fim}2, and \textit{fim}3 alleles in \textit{Bordetella pertussis} strains isolated from pertussis patients in Moscow, Russia, from 1948 to 2004. The three strains used for the whole-cell vaccine harbored the alleles \textit{ptxA}2, \textit{ptxA}4, \textit{prn}1, \textit{fim}2-1, and \textit{fim}3A. Vaccine-type alleles of \textit{ptxA} (\textit{ptxA}2 and \textit{ptxA}4) were characteristic for all prevaccination strains and for 96% of the strains isolated in the 1960s and 1970s. At the beginning of the 1970s, \textit{ptxA}2 and \textit{ptxA}4 were replaced by the \textit{ptxA}1 allele. In the 1980s and to the present, strains with \textit{ptxA}1 were predominant in the \textit{B. pertussis} population. All prevaccination strains harbored the \textit{prn}1 allele, which corresponds to the vaccine-type allele. In subsequent years, the proportion of strains with the \textit{prn}1 allele decreased and the proportion of \textit{prn}3 and \textit{prn}2 alleles increased. From 2002 to 2004 strains with \textit{prn}2 or \textit{prn}3 were predominant in the \textit{B. pertussis} population. The vaccine-type alleles \textit{fim}2-1 and \textit{fim}3A were found in all prevaccination strains and in 92% of the strains isolated from 1960 to 1989. The \textit{fim}2-2 and \textit{fim}3B alleles were first observed at the beginning of the 1980s. In subsequent years, these strains became predominant. Together with waning immunity, the antigenic divergence between vaccine strains and clinical isolates observed in the Moscow area may explain the persistence of pertussis, despite the high rates of vaccine coverage. The results demonstrate that the selection of \textit{B. pertussis} strains for vaccine manufacturing must be based on a thorough study of the \textit{B. pertussis} population.

In the past few years, the pertussis epidemiological situation in Russia has been unfavorable. Regardless of the high rates of vaccination coverage for pertussis, we have registered an increase in the incidence of pertussis among school-aged children, along with persistently high incidences among infants under 12 months of age. In addition, some cases of pertussis have been registered among vaccinated children (8, 23). Similar trends have been observed in many other countries (1, 2, 5, 6, 10). Researchers point to many reasons for the increased incidence of pertussis, including improved surveillance, waning immunity, and pathogen adaptation. The last possibility is supported by the fact that divergence in the protective antigens pertussis toxin (Ptx) and pertactin (Prn) has been observed between vaccine strains and the strains circulating in many countries (2, 7, 9, 12, 13, 17, 18, 20, 24, 31–33). In general, it was found that “non-vaccine-type” alleles of \textit{ptxA} and \textit{prn} (i.e., \textit{ptxA}1, \textit{ptxA}2, and \textit{prn}3) have gradually replaced the “vaccine-type” alleles (i.e., \textit{ptxA}2, \textit{ptxA}4, and \textit{prn}1) that were in circulation earlier. Analysis of strains isolated in Russia (Moscow and St. Petersburg) from 1998 to 2002 also revealed that strains with the \textit{ptxA}1 and the \textit{prn}2 or \textit{prn}3 alleles prevailed in circulation (12, 14). Possible variations in nucleotide sequences in 15 other genes encoding surface-exposed proteins have also been studied. Polymorphisms were found in the \textit{bipA}, \textit{fhuB}, \textit{fim}2, \textit{fim}3, \textit{ompQ}, \textit{ptxA}S3, \textit{tcf}A, and \textit{vag8} genes; but they are especially manifest in \textit{ptxA}, \textit{prn}, and \textit{tcf}A (20, 27, 30, 31).

Here we present data on the polymorphisms in four genes, \textit{ptxA}, \textit{prn}, \textit{fim}2, and \textit{fim}3, among \textit{Bordetella pertussis} strains isolated before and after the introduction of vaccination in

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Moscow. Clinical isolates were compared with the strains used for vaccine production in Russia.

MATERIALS AND METHODS

Bacterial strains and culture conditions. We studied 62 B. pertussis strains isolated in Moscow from 2002 to 2004, as well as 96 B. pertussis strains isolated from 1948 to 1999 (from the collection of Gabrichevsky Institute of Epidemiology and Microbiology, Moscow, Russia) and the three vaccine strains currently used to manufacture the DPT vaccine in Russia (Table 1). The strains were grown on casein-charcoal agar with 10% sheep blood for 3 to 5 days at 36°C. Serotyping was performed with polyclonal rabbit antisera to agglutinogens 1, 2, and 3 (Gamelei Institute of Epidemiology and Microbiology, Moscow, Russia) and the three vaccine strains currently used to manufacture the DPT vaccine in Russia (Table 1).

Genotyping. DNA isolation, ptxA gene amplification, and sequencing of the B. pertussis strains were done as described previously (16, 18). Polymorphism in the prn gene was studied by PCR-based methods (19), and prn gene sequencing was done as described previously (16). The coordinates of the primers are based on the published genome sequence of the Tohama I strain (GenBank accession number NC_002929). The sequencing of the fim2 and fim3 genes of the B. pertussis strains was performed as follows. PCR amplification and sequencing of chromosomal DNA or bacterial lysate were performed by adding 1 μl DNA or lysate to 19 μl of a PCR mixture. For fim2, the PCR mixture consisted of 50% HotStarTaq Mastermix (QIAGEN), 4 μl 5 M betain (Sigma-Aldrich), 10 pmol PCR primer F (GGGCCGGGCGGAGCTTGATGCAC; coordinates 1176626 to 1176607), 10 pmol of primer R (GGGGGGTTGGCGATTTCCAGTTTCTC; coordinates 1176541 to 1176560), and 3 μl H2O. Thermal cycling for fim2 was as follows: 15 min at 95°C and 30 cycles of 30 s at 95°C, 30 s at 56°C, and 1 min at 72°C. A final extension was performed for 10 min at 72°C. For fim3, the PCR mixture consisted of 50% HotStarTaq Mastermix (QIAGEN), 5% dimethyl sulfoxide (ICN), 10 pmol PCR primer F (GACCTGATATTCTGATGCCG; coordinates 1647541 to 1647560), 10 pmol of primer R (GGGGGGTTGGCGATTTCCAGTTTCTC; coordinates 1170431 to 1170406), and 3 μl H2O. Thermal cycling for fim3 was as follows: 15 min at 95°C and 30 cycles of 30 s at 95°C, 30 s at 65°C, and 1 min at 72°C. A final extension was performed for 10 min at 72°C. The fim2 and fim3 PCR products were purified with ExoSap-IT (U.S. Biochemicals, Cleveland, OH) and sequenced with the same forward and reverse primers used for amplification. The sequencing reactions were performed with an ABI Prism BigDye Terminator reaction kit, and the reaction products were analyzed with a model 3700 ABI DNA sequencer (Perkin-Elmer Applied Biosystems). Sequence trace data were analyzed using the Kodon program (Applied Maths, Sint-Martens-Latem, Belgium). The nucleotide sequences of the alleles in the ptxA, prn, fim2, and fim3 genes of the B. pertussis strains were compared with sequences in the EMBL/GenBank database.

![FIG. 1. Vaccination coverage (lines) and pertussis incidence rates (columns) in Moscow from 1958 to 2004. Vaccination was introduced in 1958.](http://cvi.asm.org/Downloaded from http://cvl.asm.org/)
RESULTS AND DISCUSSION

Epidemiology of pertussis in Moscow. The area of Moscow studied encompasses 1,081 square kilometers and harbors a population of approximately 11 million people. The incidence rate (IR) of pertussis per 100,000 persons was 574 in the year that vaccination was introduced (Fig. 1). After the introduction of pertussis vaccination, IRs decreased, although in the first 9 years of mass immunization, some sharp increases in IRs were observed (IRs, 152 and 153 in 1961 and 1966, respectively), as were sharp decreases (IRs, 36 and 35 in 1963 and 1964, respectively). Between 1970 and 1979, IRs of pertussis infection stabilized (IRs, 53 and 19 in 1976 and 1978, respectively). This period was characterized by a slow decrease in IRs, with periodic peaks every 2 years. It is important to mention that the decreased IRs in the 1970s in Moscow were occurring against a backdrop of reduced vaccine coverage. An increase in IRs was observed in the 1980s, presumably an effect of the decreased vaccine coverage mentioned earlier (8, 23, 25) (Fig. 1).
In the 1980s, high IRs were registered in 1985 and 1988 (IRs, 186 and 140, respectively). Epidemics in the middle and late 1990s were less intense than those in the early and mid-1980s (4). Periodic peaks and troughs in the incidence of pertussis were then occurring against the backdrop of a sufficiently high rate of vaccination (DPT vaccine) coverage among 6- to 12-month-old children (Fig. 1). In the 1990s and 2000s, the rate of vaccine coverage increased from 33% in 1991 to 96% in 2004. In 2004, the percentage of children who had received a booster for pertussis by the age of 4 years was 96%. The booster at 18 months of age was given on time for 95% of the cases. Despite the high vaccine coverage rate, the average IR for the years 2000 to 2004 was 35 (Fig. 1). We studied 158 cases of pertussis from Moscow, where the high vaccine coverage rate, the average IR for the years 2000 to 2004 was 35 (Fig. 1). We studied 158 B. pertussis strains isolated from pertussis patients. Of these, 13 strains were isolated from patients in prevaccination periods (1948 to 1959), 20 strains were isolated from 1960 to 1969, 28 strains were isolated from 1970 to 1979, 27 strains were isolated from 1980 to 1989, 8 strains were isolated from 1990 to 1999, and 62 strains were isolated from 2002 to 2004 (Table 1).

Temporal trends in serotype frequencies. The three B. pertussis vaccine strains were of serotypes 2, 3, and 2; i.e., they expressed Fim2 and Fim3, Fim3 only, or Fim2 only, respectively. Serotyping with polyclonal sera showed that all B. pertussis strains isolated during the prevaccination period belonged to serotype 2.3 (Fig. 2). After the introduction of vaccination, serotype 2.3 strains were gradually replaced by serotype 3 strains. The frequencies of the serotype 3 strains were 35%, 82%, 81%, 50%, and 76% in the periods 1960 to 1969, 1970 to 1979, 1980 to 1989, 1990 to 1999, and 2000 to 2004, respectively. The increase in the frequency of serotype 3 after the introduction of vaccination has been described before and has been attributed to the lower immunogenicity of Fim3 and to the higher level of cross-reacting antibodies induced by Fim3 than by Fim2 (21, 22). Serotypes 0 and 2 were found at low frequencies (0% to 13%) throughout the whole period.

Temporal trends in frequencies of ptxA, prn, fim2, and fim3 alleles. Among the B. pertussis strains that we studied, ptxA gene sequencing yielded three allelic variants identified previously, ptxA1, ptxA2, and ptxA4 (16). The vaccine strains harbored the alleles ptxA2 and ptxA4. The presence of the ptxA2 or the ptxA4 allele was characteristic of B. pertussis strains isolated in the prevaccination period (1948 to 1959), when they were found at frequencies of 38% and 62%, respectively (Fig. 2). The ptxA1 allele was first detected from 1970 to 1979 (frequency, 11%), and the frequency of detection increased to 100% from 1980 to 1989 and subsequent periods.

Three prn alleles were identified in this study: prn1, prn2, and prn3 (16). The vaccine strains harbored the prn1 allele. The prn1 allele was found at a frequency of 100% in 1948 and from 1960 to 1969 (Fig. 2). In subsequent periods it gradually decreased in frequency to the low level of 2% from 2000 to 2004. The prn3 allele was first observed from 1970 to 1979 (frequency, 7%). In the subsequent periods, 1980 to 1989, 1990 to 1999, and 2000 to 2004, it was found at frequencies of 19%, 38%, and 29%, respectively. The prn2 allele was first detected from 1980 to 1989 (frequency, 11%) and increased in frequency in the periods from 1990 to 1999 (25%) and 2000 to 2004 (70%).

The characteristics of B. pertussis strains isolated in Moscow with respect to serotype and the ptxA and prn alleles agree with the data obtained from the analysis of B. pertussis strains isolated in St. Petersburg, Russia (12, 29).

There is a paucity of data on polymorphisms in the serotype and 3 fimbral genes, although the levels of antibodies against fimbriae have been implicated in protective immunity (3, 15, 26). Two fim2 alleles (fim2-1 and fim2-2) and two fim3 alleles (fim3A and fim3B) have been identified in B. pertussis populations (27, 31). The Russian vaccine strains were found to harbor fim2-1 and fim3A. These alleles were found at frequencies of 100% from 1948 to 1959. In the subsequent period, 1960 to 1989, fim2-2 and fim3B were found at low frequencies (8% for both alleles). In the next period analyzed, 1990 to 1994, fim2-2 and fim3B rose to predominance (frequencies, 89% and 64%, respectively). Shifts in fim2 alleles have been observed in the United Kingdom (20). When 80 strains isolated in the United Kingdom between 1920 and 2002 were studied, 75% were found to harbor fim2-1 and 25% were found to harbor fim2-2. The United Kingdom vaccine strains harbored fim2-1, and the fim2-2 allele was not found in isolates prior to 1998. Temporal trends in the frequencies of the fim3 alleles have been studied in Canada, where fim3B was detected in 1994, although isolates from earlier periods were not analyzed (27, 28).

Despite a high vaccination coverage rate in Moscow of 87% to 96% from 2000 to 2004, the average IRs were 35 and 224 for all age categories and those 0 to 14 years old, respectively. The antigenic divergence between vaccine strains and circulating strains may have contributed to the persistence of pertussis in Moscow, despite high rates of vaccine coverage. The mismatch between vaccine strains and clinical isolates raises the possibility that the current vaccine can be improved by the use of modern strains. However, it should be noted that waning immunity may also be an important cause for the reemergence of pertussis in Moscow, and pertussis vaccines which induce long-term immunity could reduce the pertussis burden significantly. The results obtained by us clearly demonstrate that the process of selection of B. pertussis strains for vaccine manufacture must be based on a thorough study of the B. pertussis population. Analyses of polymorphisms in B. pertussis genes other than those investigated here remain an important area of research. Such analyses will allow the identification of the evolutionary changes in B. pertussis which allow it to persist in immunized populations.

REFERENCES