INTRODUCTION

Mumps, an infection caused by the mumps virus (MuV), is best known as a moderate to highly contagious common childhood viral disease. MuV utilizes humans as the sole natural host, and it is transmitted by direct contact, droplet spread, or contaminated objects (1,2). The hallmark of mumps is the swelling of the parotid glands, accompanied by fever and pain (1). Although it is generally a mild, self-limiting disease, some patients may develop serious complications, including pancreatitis, deafness, encephalitis, aseptic meningitis, and orchitis (3). Encephalitis and deafness are rare complications, while aseptic meningitis and orchitis are relatively common in adults (4). Mumps is contagious from about 2 days before and up to 9 days after the onset of the swelling of the parotid glands (4).

The MuV is an enveloped, non-segmented, negative-strand RNA virus. Its genome contains approximately 15,384 nucleotides (nt) that include 7 tandem-linked transcription units: nucleocapsid (N), phosphoprotein (P), matrix (M), fusion (F), small hydrophobic (SH), hemagglutinin-neuraminidase (HN), and polymerase or large (L) protein genes (5,6). Each gene encodes a single protein, except for the P gene that encodes V, P, and I proteins having the same N-terminal segment but different C-terminal regions (6,7). Among these transcription units, the number of nucleotide sequence variations in the putative membrane-associated SH gene is the greatest in the entire genome; thus, the SH gene (316 nt) is used to define the MuV genotypes (8). When an ambiguous result is generated by the entire SH gene or a new lineage is suspected, the HN gene (1749 nt) should be used to define MuV genotypes (9). Twelve MuV genotypes have been identified and named from the letters “A” to “N,” excluding “E” and “M” (9). In mainland China, the genotype F has been the predominant MuV genotype since 1995 (3,10,11).

Mumps became a vaccine-preventable disease after the approval of its vaccine in 1967 (12). One dose of the attenuated mumps vaccine for children aged 18–24 months was introduced into the Expanded Program on Immunization in mainland China in 2008 (3). Both domestic and imported mumps-containing vaccines (MuCVs), which are mainly combined as measles–mumps–rubella (MMR) vaccine, have been utilized in mainland China. The imported and domestic MuCV strains are composed of the Jeryl Lynn strain (genotype A) and the S79 strain, respectively. The S79 strain has originated from the Jeryl Lynn strain (3). Since the implementation of the mumps vaccine as part of the national immunization program, the incidence of
mumps has decreased, though not significantly, from a reported incidence of 23.52 per 100,000 people in 2008 to 21.43 per 100,000 in 2019. Similarly, in the Henan Province, the reported incidence decreased from 17.96 per 100,000 people in 2008 to 15.54 per 100,000 people in 2019, which was not a significant change.

Viral sequence data and phylogenetic analysis can help understand the spread of infectious diseases in near real time, contribute to finding out outbreak origins and tracing the transmission routes (13,14) and aid in the development of more effective vaccines (15). This has been shown to be more helpful when integrated with epidemiological data. Epidemiological studies can provide strong evidence regarding the patterns of mumps cases, and thus promote the development of prevention and control measures that can be rapidly implemented. In this study, we conducted epidemiological and phylogenetic analysis of MuVs circulating in the Henan Province to elucidate the transmission pattern and circulating MuV genotypes and provide data for mumps control and prevention.

MATERIALS AND METHODS

Case definition, specimens, and data collection: Patients with clinical presentation or ultrasound features indicative of parotitis or those with an epidemic linkage to other patients with mumps were defined as suspected mumps cases; only those patients with positive polymerase chain reaction (PCR) results for MuV were defined as MuV-positive cases in this study. Between December 12, 2016 and December 30, 2019, 426 buccal swab samples were collected from suspected mumps patients admitted to The Sixth People’s Hospital of Zhengzhou and immediately transferred to the laboratory for detection of MuV. All of the suspected cases were assessed by interviewing the patients or their guardians. Medical records regarding clinical signs and symptoms, age, sex, mumps vaccination history, and exposure history were collected. In total, 153 mumps cases confirmed by PCR were selected for further analysis.

Reverse transcription (RT)-PCR and SH gene sequencing: Viral RNA was extracted from the buccal swab samples using a viral RNA extraction kit (Liferiver, Shanghai, China) according to the manufacturer’s protocol. Complementary DNA (cDNA) was reverse-transcribed using a RevertAid First Strand cDNA Synthesis Kit (Thermo Fisher Scientific, MA, USA). The entire SH gene was amplified using nested RT-PCR with previously reported primer pairs (16). The same amplification conditions for outer and inner PCR were used as follows: 94°C for 4 min, followed by 35 cycles of 94°C for 30 s, 55°C for 40 s, and 72°C for 40 s, and a final extension at 72°C for 10 min. The PCR products were gel-extracted and Sanger-sequenced (Sangon Biotech, Shanghai, China). The Editsiq program incorporated in the DNASTAR software (version 7.1) was used to edit the raw sequence data to obtain the 316 nt of full-length SH gene sequences.

Multiple sequence alignment and phylogenetic analysis: Due to the presence of many identical sequences, the identical sequences were collapsed together where possible. These groups were represented by the first isolated strain (number of sequences). Phylogenetic analysis was performed for full-length SH nucleotide sequences of 153 MuV strains isolated in this study, 32 genotype F representative sequences from other provinces of China, and 27 World Health Organization (WHO) reference sequences of different genotypes downloaded from GenBank. These full-length SH gene (316 nt) sequences were aligned using ClustalX as incorporated in Molecular Evolutionary Genetics Analysis (MEGA) software (version X), and parameter values for the best-fit substitution model were determined using the Kimura two-parameter model incorporating gamma distribution (K2+G) (17). A phylogenetic tree was inferred using the maximum likelihood method as implemented in the MEGA software (version X) based on the K2+G with a bootstrap value of 1,000 replicates (17). The determined SH sequences in this study were submitted to GenBank under the accession numbers MT232075–MT232227.

Statistical analysis: Statistical analysis was conducted using Statistical Package for the Social Sciences version 22.0. The categorical variables were represented as numbers. Crosstab in descriptive statistics was employed to compare differences among groups with categorical variables. P-values less than 0.05 were considered statistically significant.

Ethical approval: This study was approved by the Institutional Ethics Committee of The Sixth People’s Hospital of Zhengzhou, China. All participants or their guardians provided written informed consent.

RESULTS

Epidemiological and clinical characteristics: Of the total 426 patients suspected of MuV infection, 153 patients were confirmed by a positive result in the RT-PCR analysis. Among these positive cases, 152 came from 15 municipalities of the Henan Province and one from a municipality of Anhui, a neighboring province of Henan (Fig. 1). Furthermore, 58 of the MuV-positive patients had a history of exposure to patients with parotitis or mumps (Table 1), including 11 family cluster cases. The male-to-female ratio was 3:1 (115 vs. 38), and the median age of males and females was 9 years (range: 1–38) and 10.5 years (range: 6–41), respectively. The majority of the population included children and adolescents, and MuV-positive cases in the age groups of <5 years, 5–9, 10–15, 16–19, and ≥20 years accounted for 1%, 17%, 12%, 1%, and 12%, respectively. The majority of the population included children and adolescents, and MuV-positive cases in the age groups of <5 years, 5–9, 10–15, 16–19, and ≥20 years accounted for 1%, 17%, 12%, 2%, and 4% of the total number of suspected mumps cases, respectively. Fourteen male patients had orchitis, accounting for 12% of all MuV-positive male patients.

The difference in the demographic characteristics, clinical features, exposure history, and vaccination history of the male and female MuV-positive patients were not statistically significant, except for one of the clinical features. Swollen parotid glands lasting for more than 5 days was more frequently observed in male patients as compared to the female patients (P < 0.05, Table 1). In contrast, most female patients with swollen parotid glands had parotid gland enlargement lasting less than 5 days. The proportion of MMR vaccination in the age groups of <5 years, 5–9 years, 10–15 years, 16–19 years, and ≥20 years was 80%, 100%, 45%, 0%, 188
and 0%, respectively (Table 2).

**Sequence characteristics:** In this study, 153 full-length \( SH \) gene sequences were obtained. All of the sequences were named according to the WHO proposition in 2005 for systematic nomenclature of MuV (9). The \( SH \) gene sequences from these 153 MuV isolates were aligned and then realigned to the 27 WHO MuV reference sequences of different genotypes. Sequence alignment indicated that the \( SH \) gene (316 nt) of the 53 MuV isolates exhibited similarity ranging from 92.4% to 100% at the nucleotide level and 80.7% to 100% at the amino acid level. The greatest amount of nucleotide variation (7.6%, 24/316) of the \( SH \) gene was observed between a MuVs/Henan.CHN/9.18/1[F] strain from Zhumadian and a MuVs/Henan.CHN/29.18/4[F] strain from Zhengzhou or a

Fig 1. (Color online) Geographic distribution of mumps virus-positive cases in this study. n, number of MuV-positive cases.

Table 1. Demographic and clinical features, exposure history and vaccination history among 153 mumps virus-positive cases

| Variable                                      | Male (\( n = 115 \)) | Female (\( n = 38 \)) | \( P \) value |
|-----------------------------------------------|----------------------|------------------------|---------------|
| Age, median years                             | 9                    | 10.5                   | NA            |
| Age groups, \( n \) (%)                       | < 5                  | 5(4)                   | 0(0)          | NA            |
|                                               | 5-9                  | 55(48)                 | 15(39)        | 0.370         |
|                                               | 10-15                | 37(32)                 | 14(37)        | 0.597         |
|                                               | 16-19                | 8(7)                   | 2(5)          | 0.714         |
|                                               | ≥ 20                 | 10(9)                  | 7(18)         | 0.098         |
| Clinical features, \( n \) (%)               |                      |                        |               |
| Fever                                         | 99(86)               | 31(82)                 | 0.500         |
| Subauricular or periauricular swelling        | 115(100)             | 38(100)                | NA            |
| ≤ 5 days after parotitis onset                 | 84(73)               | 34(89)                 | 0.037         |
| > 5 days after parotitis onset                 | 31(27)               | 4(11)                  | 0.037         |
| Cough                                         | 3(3)                 | 3(8)                   | 0.146         |
| Abdominal pain                                | 19(17)               | 4(11)                  | 0.370         |
| Vomiting                                      | 56(49)               | 14(37)                 | 0.204         |
| Headache                                      | 45(39)               | 15(39)                 | 0.970         |
| Testicular swelling                           | 14(12)               | NA                     | NA            |
| Unilateral parotitis                          | 33(29)               | 10(26)                 | 0.777         |
| Bilateral parotitis                           | 81(70)               | 28(74)                 | 0.701         |
| Exposure history, \( n \) (%)                |                      |                        |               |
| Aware of others with parotitis/mumps          | 42(37)               | 16(42)                 | 0.539         |
| Vaccination history, \( n \) (%)             |                      |                        |               |
| 0 MMR vaccine                                 | 44(38)               | 12(32)                 | 0.458         |
| 1 MMR vaccine                                 | 71(62)               | 26(68)                 | 0.458         |

NA, not applicable; \( n \), number of MuV-positive cases.
MuVs/Henan.CHN/33.19/2[F] strain from Kaifeng. The greatest amount of amino acid variation was observed (19.3%, 11/57) between a MuVs/Henan.CHN/3.18[F] strain and a MuVs/Henan.CHN/23.18/3[F] strain, both from Zhengzhou. Compared with the MuV reference sequences of other genotypes, the lowest similarity in nucleotide sequence (83.2%) was observed between a MuVs/Henan.CHN/9.18/1[F] or MuVs/Henan.CHN/12.18[F] strain and a genotype A strain, MuVi/Pennsylvania,USA/13.63[A] (Jeryl-Lynn, vaccine strain). The lowest similarity in amino acid sequences (66.7%) was observed between the MuVs/Henan.CHN/23.18/3[F] strain and a genotype K strain, MuVi/Stockholm,SWE/26.83[K]. These new isolates were more closely related to genotype N (89.2%–92.7%) at the nucleotide level and unclassified MuVi/Tokyo.JPN/0.93 (78.9%–89.5%) strains at the amino acid level.

**Chronological and geographical characteristics of MuV isolates:** Sequence alignment of the SH gene of our isolates showed that there were 53 unique sequences and two-sequences and multi-sequences identical sequences. Detailed analysis indicated that isolates with identical sequences were often from the same or adjacent municipalities, but could also rarely originate from non-adjacent municipalities. For example, the SH gene sequence of a MuVs/Henan.CHN/51.16[F] strain exhibited 100% sequence similarity with 42 other strains that were isolated from the cities of Zhengzhou (n = 35), Jiyuan (n = 2), Zhoukou (n = 2), Xinxiang (n = 1), Zhumadian (n = 1), and Xinyang (n = 1), whereas the sequence of a MuVs/Henan.CHN/18.18/2[F] strain exhibited 100% sequence similarity with 13 other strains that were all isolated from Zhengzhou. In this study, the SH gene sequences within each family cluster case were the same. When the 53 unique MuV sequences obtained in our study were “BLASTed” using the Basic Local Alignment Search Tool (BLAST; https://blast.ncbi.nlm.nih.gov/blast.cgi), identical sequences were found with those strains isolated from other provinces or cities at the same or different time points. For example, the SH gene sequences between a MuVs/Henan.CHN/50.17/2[F] strain from Xuchang municipality of the Henan Province and a MuVi/Guangdong.CHN/8.12[F] strain from Guangdong Province and those between a MuVs/Henan.CHN/4.18/2[F] strain from Puyang or a MuVs/Henan.CHN/30.19[F] strain from Xinyang and MuVs/HongKong.CHN/30.19[F] were identical.

**Phylogenetic analysis:** Based on the phylogenetic analysis, the diversity of the 153 SH sequences was moderate, with 93 (61%) aligning identically to one of five groups. Each group included 5 or more identical sequences. The analysis with the epidemiological data suggested that identical sequences in these 5 groups might be from different mumps outbreaks. Phylogenetic analysis indicated that multiple transmission chains had been observed in the Henan Province during this period, and all of the isolates were of genotype F, which was in conformity with other reports that genotype F is the predominant genotype in China (Fig. 2). Multiple subclusters were identified for genotype F, and isolates in the same subcluster tended to be derived from the same community or municipalities.

**DISCUSSION**

Since before the vaccination era, children have been the most commonly affected by mumps, and its incidence has significantly decreased since the large-scale immunization with mumps vaccine conducted in several developed countries (18–20). In China, the proportion of mumps cases in children aged 5–9 years has remained high every year since 2008, as observed in this study. As vaccination certificate examination before the admission of children to kindergarten and primary school is strictly implemented, at least 97% of these children are administered the one-dose MMR vaccine (21), and our study results showed that 100% of MuV-positive cases in this age group had been vaccinated. It was unlikely that the high incidence of mumps in this age group was due to low vaccination coverage. Recent outbreaks of mumps in vaccinated communities have been a worldwide phenomenon, and no conclusive cause has been found (22). However, based on previous studies and on epidemiological, clinical, and molecular data, the waning immunity and immune escape might be the most important contributors in addition to other factors such as low vaccine coverage and primary vaccine failure.

Multiple studies have shown that waning immunity to either genotype G or genotype F might be the most plausible explanation for mumps resurgence (23–29). Their conclusions are based on the following evidences: first, mathematical modeling based on retrospective and prospective cohort studies suggests that an increasing proportion of immunized individuals will lose immunity over time (23,26); second, a continuous change in the age distribution of susceptible groups has been observed following one-dose and two-dose mumps vaccine immunization (19,28); and third, waning immunity to mumps in terms of seropositivity and geometric antibody levels does occur in kindergarten and primary school children with time (27,29). However, some studies have not demonstrated waning immunity as a cause for mumps, and waning humoral immunity does not mean loss of protection against mumps (30,31). Although vaccine-induced waning immunity occurs with time, one-dose MuCV immunization can still protect children from apparent infection (27).
The herd immunity threshold for mumps has been estimated to be within the range of 70%–90% (37). Therefore, achievement and maintenance of herd immunity with one dose might not be possible. The first dose is usually given to children at the age of 12–18 months, and most children receive the second dose when they enter primary school (about 6 years of age) (4). In China, each province can modify its immunization plan for mumps according to the regional characteristics (3). In fact, the mumps incidence rates of economically developed municipalities or provinces such as Beijing, Shanghai, Tianjin, and Zhejiang have gradually decreased each year after the implementation of the two-dose MuCV regimen, and they are significantly lower than those of other provinces (38). Children and adolescents in China have greatly benefited from the overall reduction in infectious diseases such as mumps in the past three decades; however, rapid demographic, epidemiological, and nutritional transitions have raised a pressing need to track infectious diseases in children and adolescents (39). Epidemiological and viral molecular surveillance are crucial and necessary for mumps control. Our results and analyses showed that phylogenetic analysis when combined with epidemiological data might help find the causes of outbreak. Furthermore, they suggest that there may have undetected and continuous circulation of mumps locally, including multiple independent introductions into the Henan Province and individual communities. When compared to the whole genome phylogeny, the SH gene does not always provide enough resolution (40). However, the higher costs of obtaining the whole genome sequence may be an obstacle in routine mumps surveillance. The SH gene is a small and convenient target for rapid identifying and sequencing (8), which makes it suitable for epidemiological surveillance and management of mumps outbreaks.

Our study had several limitations. First, because the sample size was not large enough and the geographical effects of vaccine-induced waning of immunity on mumps resurgences should be further investigated.

Immune escape has been suggested as another important contributor to mumps resurgence based on the mismatch between the strains that cause outbreaks and the strain used for vaccine production (genotype A). Phylogenetically, MuV of different genotypes exhibit distinct clusters as shown in this study. In silico analysis of immunoeptopes of different genotypes also showed antigenic variations that could potentially lead to varied immune responses (32,33). There is only one serotype of MuV; however, our isolates exhibited the highest heterogeneity in SH gene sequence with genotype A, to which the vaccine strain belongs, and in vivo and in vitro studies suggest that cross-neutralization between genotypes might be reduced (34,35). Cui et al. found that in healthy infants who received one dose of the MMR vaccine, only 33.3% of them could effectively produce MuV neutralizing antibodies for genotype F MuV wild-type strain even though the concentrations of MuV-specific immunoglobulin G in their sera were all positively detected by enzyme-linked immunosorbent assay (36). It is possible that the low levels of neutralizing antibody in the individuals would contribute to sporadic cases or some outbreaks.

Our study had several limitations. First, because the sample size was not large enough and the geographical effects of vaccine-induced waning of immunity on mumps resurgences should be further investigated.
distribution of the sample was uneven, this data set may not fully represent the true diversity of the gene sequences circulating in the Henan Province during 2016–2019. Cases were reported in all municipalities, but sequences were only obtained from the specimens collected from some municipalities. Additionally, several specimens were sequenced from Zhengzhou. This surveillance bias could lead to under-representation of sequences from sporadic cases from other municipalities. Second, we failed to collect travel history of the patients.

In conclusion, the incidence of mumps in the Henan Province was found to be high. The data from this study might promote further research in the clarification of the specific cause of mumps outbreaks, which can facilitate the implementation of effective prevention and control measures.

Conflict of interest None to declare.

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