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Phylogenetic Analysis Reveals a Correlation between the Expansion of Very Virulent Infectious Bursal Disease Virus and Reassortment of Its Genome Segment B

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Infectious bursal disease virus (IBDV) is a birnavirus causing immunosuppressive disease in chickens. Emergence of the very virulent form of IBDV (vvIBDV) in the late 1980s dramatically changed the epidemiology of the disease. In this study, we investigated the phylogenetic origins of its genome segments and estimated the time of emergence of their most recent common ancestors. Moreover, with recently developed coalescence techniques, we reconstructed the past population dynamics of vvIBDV and timed the onset of its expansion to the late 1980s. Our analysis suggests that genome segment A of vvIBDV emerged at least 20 years before its expansion, which argues against the hypothesis that mutation of genome segment A is the major contributing factor in the emergence and expansion of vvIBDV. Alternatively, the phylogeny of genome segment B suggests a possible reassortment event estimated to have taken place around the mid-1980s, which seems to coincide with its expansion within approximately 5 years. We therefore hypothesize that the reassortment of genome segment B initiated vvIBDV expansion in the late 1980s, possibly by enhancing the virulence of the virus synergistically with its existing genome segment A. This report reveals the possible mechanisms leading to the emergence and expansion of vvIBDV, which would certainly provide insights into the scope of surveillance and prevention efforts regarding the disease.

Infectious bursal disease (IBD) is an immunosuppressive disease of young chickens that causes considerable economic loss to the poultry industry worldwide. The causative agent of IBD is a bisegmented, double-stranded RNA virus of the Birnaviridae family named IBD virus (IBDV). IBD was firstly reported in 1957 in broilers of the Delmarva Peninsula of the United States. It had spread rapidly throughout the United States by 1965 but was effectively controlled by vaccinations in the mid-1970s (23). In 1986, vaccination failures were reported and IBDV isolates with enhanced virulence were identified and characterized (18). These new isolates, named very virulent IBDV (vvIBDV), were then described by Chettle and coworkers (4) as the causative agents of the first reported cases of severe and acute IBD in Europe. These very virulent strains have rapidly spread all over Asia and other parts of the world (11) in an explosive manner (42), following their introduction into Japan in the early 1990s (30).

The epidemiological event leading to the emergence and expansion of vvIBDV is an open question. Phylogenetic analyses have revealed independent evolutionary histories of the two genome segments (17, 44), suggesting that a reassortment event may have played a role in the emergence of vvIBDV. Previous reports suggested that both the major capsid protein (VP2) and the RNA-dependent RNA polymerase (VP1), which are located on genome segments A and B, respectively, contribute to the virulence of IBDV (1–3, 26, 43). Questions have been raised regarding the phylogenetic origins and roles of the unique mutations of the two genome segments in relation to the expansion of vvIBDV.

Temporally spaced sequence data from rapidly evolving RNA viruses provide opportunities to address problems regarding their evolutionary behaviors, e.g., past population dynamics and evolutionary rates (7, 9, 10). Here we investigated the phylogenetic origins and demographic behavior of vvIBDV, as well as the time of emergence of the most recent common ancestor (TM RCA) of its genomes. Several approaches, including linear regression (LR), maximum likelihood (ML), and Bayesian Monte Carlo Markov chain (BMCMC), under the assumption of both strict and relaxed molecular clocks, were employed for TM RCA estimations. An alternative technique for estimating the TM RCA of the VP1 data set, site-stripping clock detection (SSCD) (24), was also used, in an attempt to accommodate deviations from the molecular clock. Comparison of TMRCAs inferred with these approaches provides comprehensive estimations of the time of emergence of both genome segments of vvIBDV. The past population dynamics of vvIBDV were reconstructed by using coalescence approaches in both the ML and BMCMC frameworks (10, 35), allowing us to estimate the time of onset of vvIBDV expansion. By reconstructing the chronological order of these epidemiological events, this report provides insights into the possible mechanism leading to the emergence and expansion of vvIBDV.

METHODS AND MATERIALS
Identification of vvIBDV clades in phylogenies of both genome segments. For genome segment A, all available nonidentical serotype I IBDV nucleotide sequences containing the VP2 region, excluding all known tissue culture-adapted
strains, were retrieved from the GenBank database (http://www.ncbi.nlm.nih.gov) of at least 0.85.

Molecular clock analysis and SSCD. The sampling years of taxa in vvIBDV clades were obtained from references or personal communication with the authors. The alignments are available on request. The phylogenies of the vvVP1, vvVP2, and vvVP1 clades were reestimated with PAUP* (Sinauer Associates, Inc.) using an ML heuristic search with a tree bisection-reconnection branchswapping algorithm under the nucleotide substitution models suggested by MEGA (14). For the majority consensus tree summarized across four independent MCMC chains.

Inference of past population dynamics. To evaluate the possible biases of the SSCD procedure on TMRCA estimations, we used in order to assess the influence of priors on posterior distribution. The posterior distribution of the TMRCA was summarized across four independent MCMC chains.

Phylogenetic origins of both vvIBDV genome segments. The BMCmc phylogeny of the full-length VP2 data set (pVP2) revealed five major clades with BP support greater than 0.85; these were designated the classical 1, classical 2, classical 3, variant, and very virulent (vvVP2) clades, according to the typical classification of IBDV strains (42). These clades formed a monophyletic lineage, designated the major IBDV lineage, with 0.99 BP support, excluding the Australian strain, suggesting that these clades, contributing to the major world epidemics, evolved from the same TMRCA (16). Analysis of the partial VP2 data set (pVP2) resulted similar phylogeny, with well-supported major IBDV lineage and the very virulent clade (vvVP2), except that classical and variant clades were no longer supported by high BP (data not shown). In contrast, in the BMCmc phylogeny of VP1, the vvIBDV clade (vvVP1) was excluded from the lineage containing all other serotype I and II IBDV strains (0.87 BP support) (16), revealing an independent phylogenetic origin of vvVP1 that agreed with previous reports (17).

RESULTS

Phylogenetic origins of both vvIBDV genome segments. The BMCmc phylogeny of the full-length VP2 data set (pVP2) revealed five major clades with BP support greater than 0.85; these were designated the classical 1, classical 2, classical 3, variant, and very virulent (vvVP2) clades, according to the typical classification of IBDV strains (42). These clades formed a monophyletic lineage, designated the major IBDV lineage, with 0.99 BP support, excluding the Australian strain, suggesting that these clades, contributing to the major world epidemics, evolved from the same TMRCA (16). Analysis of the partial VP2 data set (pVP2) resulted similar phylogeny, with well-supported major IBDV lineage and the very virulent clade (vvVP2), except that classical and variant clades were no longer supported by high BP (data not shown). In contrast, in the BMCmc phylogeny of VP1, the vvIBDV clade (vvVP1) was excluded from the lineage containing all other serotype I and II IBDV strains (0.87 BP support) (16), revealing an independent phylogenetic origin of vvVP1 that agreed with previous reports (17).
Molecular clock analysis and TMRCA of vvIBDV genomes. An LRT showed that M0 (no-clock model) does not fit the vvfVP2 data set significantly better than M1 (global-clock model) ($P = 0.118$), allowing us to time the vvfVP2 TMRCA under the assumption of a strict global molecular clock. With the ML, BMCMC, and LR approaches, TMRCA of vvfVP2 was consistently estimated to be around the 1960s (Table 1). It is noted that LR, ML, and BMCMC estimated the evolutionary rate for the clocklike data set vvfVP2 to be $0.64 \times 10^{-3}$, $0.60 \times 10^{-3}$, and $0.67 \times 10^{-3}$ nucleotide substitutions per site per year, respectively, which is comparable to the capsid or envelope proteins of other RNA viruses (20). Comparable results were obtained with the vvpVP2 data set by the BMCMC and LR approaches (Table 1), although the molecular clock was significantly rejected in this case ($P = 0.003$), suggesting that nonclocklike substitution rates may still be reliable indicators of the average substitution rate if the data set is large enough (20).

Substitution rate variation among sites or lineages causing nonclocklike behavior is a common observation in RNA viruses (20), presenting standard dating applications with uncertainties and perhaps leading to strong dating biases (24), particularly in data sets with limited number of taxa. Although the vvVP1 data set violated the molecular clock ($P = 0.03$), its clocklike behavior was recovered by stripping 15 sites according to the SSCD procedure (Fig. 2A). The TMRCA of the site-stripped vvVP1 data set was then estimated to be in the early to mid-1980s by the LR, ML, and BMCMC approaches (Fig. 2B and Table 1). Initial dating efforts with the nonclocklike vvVP1 data set generally yielded TMRCA estimations comparable to that of the site-stripped vvVP1 data set, although the confidence intervals (CIs) are relatively large or unable to be estimated (Table 1). The possible biases of SSCD procedures were assessed by reestimating the TMRCA under a relaxed-clock model implemented in MULTIDIVTIME (22). The posterior distribution of the TMRCA of the original vvVP1 data set estimated under the relaxed clock generally overlapped with that of the site-stripped vvVP1 data set, although the confidence intervals (CIs) are relatively large or unable to be estimated (Table 1). The consistency of TMRCA estimations from different approaches indicates the robustness of our estimates, and the effect of evolutionary rate variation may be limited in this case. For clarity, LR and ML TMRCA

<table>
<thead>
<tr>
<th>Genome segment</th>
<th>Length (bp)</th>
<th>No. of taxa</th>
<th>lnL$^a$ M0</th>
<th>lnL$^a$ M1</th>
<th>LRT ($P$) (clock rejection)$^b$</th>
<th>Yr of TMRCA (range)$^c$</th>
</tr>
</thead>
<tbody>
<tr>
<td>vvfVP2</td>
<td>1,323</td>
<td>24</td>
<td>$-2,813.171$</td>
<td>$-2,828.190$</td>
<td>0.118 (no)</td>
<td>1960 (1942–1969)</td>
</tr>
<tr>
<td>vvpVP2</td>
<td>330</td>
<td>153</td>
<td>$-3,257.785$</td>
<td>$-3,361.408$</td>
<td>0.003 (yes)</td>
<td>1968 (1943–1977)</td>
</tr>
<tr>
<td>vvVP1</td>
<td>2,322</td>
<td>9</td>
<td>$-4,291.567$</td>
<td>$-4,299.338$</td>
<td>0.03 (yes)</td>
<td>1981 (NA–1989)</td>
</tr>
<tr>
<td>Site-stripped vvVP1</td>
<td>2,307</td>
<td>9</td>
<td>$-4,115.234$</td>
<td>$-4,120.421$</td>
<td>0.168 (no)</td>
<td>1984 (1972–1988)</td>
</tr>
</tbody>
</table>

$^a$ lnL represents the natural log likelihood of the global-clock (M1) and no-clock (M0) models calculated in PAML under the Hasegawa-Kishino-Yano nucleotide substitution model.

$^b$ The molecular clock is rejected when $P < 0.05$ under the LRT.

$^c$ The BMCMC TMRCA refers to the TMRCA estimated with BEAST under the assumption of a molecular clock. TMRCA estimated based on the corresponding approaches are presented as the best fit (for LR and ML) or mean (for BMCMC) value, with the 95% CI (for LR and ML) or high-probability density (for BMCMC) in parentheses. NA, not applicable.
estimations of only the clocklike data sets, i.e., vvVP2 and site-stripped vvVP1, are presented in Fig. 3.

Estimation of parameters of vvIBDV expansion. The BSP of the vvVP2 data set suggests a sudden exponential population growth in the late 1980s, followed by a sharp population drop around the mid-1990s (Fig. 4). Only the vvVP2 data set was used for demographic behavior estimations, because data sets of less than 25 taxa are unlikely to give reliable coalescence estimates (16). Based on the BSP, none of the existing parametric models adequately describes the sophisticated demographic signals of the vvVP2 data set. Use of incorrect demographic models will lead to biased and invalid estimates of demographic history (36). In order to describe the sudden exponential population growth with parametric models, the demographic signals of the vvVP2 data set were simplified by discarding taxa sampled after the estimated sharp population drop at 1995 (designated vvVP2-95; \( n \)). The time-scaled ML genealogy of the vvVP2-95 data set was then reconstructed with PAUP and PAML (45), and the goodness-of-fit of five demographic models was evaluated with GENIE (35). The piecewise expansion model, i.e., constant population size followed by exponential growth, best describes the vvVP2-95 ML genealogy in terms of likelihood, and the exponential model was rejected in favor of the piecewise expansion model \( (P < 0.01) \). According to model definition, the exponential growth phase start time, i.e., the onset of expansion, is defined as \(- \ln(\alpha)/r\), where \( r \) is the exponential growth rate and \( \alpha \) is the population size prior to change, as a proportion of the population size at present (Fig. 5A). It is noted that the piecewise expansion demographic model is not implemented in BEAST, version 1.3, and the codes for this particular model were developed by the authors; they are available on request. Superimposing the ML and Bayesian parametric estimates under the piecewise expansion model onto their nonparametric skyline plots revealed a good fit to the demographic signal within the vvVP2-95 data set (Fig. 5B and C). The ML estimation of exponential growth phase start time is 1983 (1970 to 1987), while the BMCMC estimation yielded consistent results with more precise CIs, i.e., 1988 (1986 to 1990). Although ML estimation of demographic parameters based on a single genealogy ignores possible phylogenetic errors, overlapping results were produced with the BMCMC estimation, which takes phylogenetic uncertainty into account (10), reflecting the reliability of our estimations of the onset of vvIBDV expansion.

DISCUSSION

Coalescence tools for the selection of parameter-rich demographic models allowed us to estimate the onset of vvIBDV expansion at around the late 1980s, which seems to be consistent with its documented explosive transmission pattern. The first documented case of vvIBDV was described by Chettle and coworkers in 1989 (4). In 1995, during the 63rd General Session of the Office International des Epizooties, about 80% of its member countries worldwide reported the occurrence of vvIBDV (11), reflecting the rapid spread of vvIBDV during the early 1990s.

The epidemiological events related to the initiation of vvIBDV expansion have not been investigated systematically.
While most of the interest regarding virulence and attenuation of the virus was focused on genome segment A, as it encodes neutralizing epitopes and the putative receptor binding protein (43), our estimations of the vvfVP2 TMRCA indicate that genome segment A of vvIBDV emerged more than 20 years before the first documented case of vvIBDV, suggesting that the vvIBDV expansion may not be directly initiated by the emergence of vvVP2. This observation argues against the hy-
hypothesis that mutation of genome segment A is the major contributing factor in the emergence and expansion of vvIBDV (33). Alternatively, the vvVP1 TMRCA was estimated to around the early to mid-1980s, which coincides with the estimated onset of IBDV expansion in a period of approximately 5 years, suggesting a possible role of vvVP1 in the initiation of vvIBDV expansion. The origin of vvVP1 is unknown, but its phylogenetic independence from all other known IBDV strains suggests that it may be reassorted from an unidentified reservoir. A serotype II IBDV strain was successfully isolated from African black-footed penguins (Spheniscus demersus) (19), implying the presence of other possible natural hosts of IBDV. Moreover, serological surveys of aquatic fowl (12, 15) and free-living wild birds (13, 31) suggested that several migratory and sedentary avian species, including cattle egrets (Ardea ibis), pigeons (Columba livia), carrion crows (Corvus corone), and Antarctic penguins (Pygoscelis adeliae), etc., may also be carriers or reservoirs of IBDV based on their seroprevalence.

A number of reports have demonstrated the drastic effects of mutations of VP2 residues on attenuation of the virulence of vvIBDV (3, 43); these residues were proposed to be related to the protein’s receptor binding efficiency (5), but they are not the sole determinants of virulence (2). On the other hand, VP1 was also demonstrated to be a determinant of virulence in vivo, possibly by altering the replication efficiency (1, 26). A recent study reported the isolation of a naturally reassorted IBDV with genome segment A of very virulent origin but genome segment B of non-very virulent origin; this isolate showed significantly reduced pathogenicity compared with typical vvIBDVs (25), demonstrating that the determinants on genome segment A may not be enough to induce the hypervirulence of typical vvIBDVs. These observations suggest that the hypervirulence of vvIBDV may be a synergistic effect of mutations on both of its genome segments, although experimental evidence is needed for further elucidation. In addition, examples of hypervirulence of other RNA viruses caused by mutations on their polymerase genes are well documented (6, 21, 27, 41). Taken together with our date estimates, the phylogenetic origin of vvIBDV genomes, the possible roles of both VP1 and VP2 in hypervirulence, and the reported evidence of the existence of possible reservoirs, we hypothesize that vvIBDV expansion may have been initiated by the reassortment of its genome segment B with a mutant VP2 background, which caused a sudden increase in virulence and hence expansion in the mid-1980s, rather than being directly related to the emergence of vvVP2 in the 1960s, as vvVP2 alone may not be enough to induce the hypervirulence of vvIBDV (25). The presence of rare IBDV isolates carrying vvVP2 and non-vvVP1 further supports this hypothesis (25), as these isolates can be considered the descendants of those rare “ancient” vvIBDVs that appeared after the estimated TMRCA of vvVP2 in the mid-1960s but before the estimated reassortment of vvVP1 and the expansion of vvIBDV in the mid-1980s.

Genome reassortment of multisegmented RNA viruses plays important roles in the emergence or expansion of new virus strains with altered antigenicity or pathogenicity (29, 32, 37), best demonstrated by the devastating pandemics of influenza A (39). Investigations of possible evolutionary mechanisms leading to the emergence and expansion of novel pathogenic virus strains would certainly provide insight into the
scope of surveillance and prevention efforts (14, 28). In the case of IBDV, while most of the sequencing efforts have been focused on genome segment A of viruses in chickens, largescale surveillance in other avian species and more sequence data on genome segment B would certainly provide important clues toward the understanding of the diversity and origin, as well as the evolutionary epidemiology, of IBDV.

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