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The identification of a new genotype of avian paramyxovirus type I in West-Africa provides new outcomes for phylogeny reconstruction

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INTRODUCTION

Newcastle disease (ND) is one of the most severe infectious diseases of birds, particularly poultry, and has been the cause of serious economic losses worldwide. Newcastle disease virus (NDV) or avian paramyxovirus type 1 (APMV-1) are divided in two clades (class I and class II) according to the genome size as well as sequence of the F and L genes. Virulent strains are found in the class II. There is no clear consensus for the NDV class II taxonomy since some authors use genotypes [1] whereas others use lineages, both covering distinct isolate clusters. Ten genotypes were traditionally considered for class II but a 11th genotype was recently proposed by our group. Auldous et al. [2] proposed 6 phylogenetic lineages based on the topology of the maximum likelihood tree of the 358bp of the F gene and of the F gene (further subdivided into 13 sublineages) to replace the genotype nomenclature previously adopted [1].

In many parts of Africa, ND is considered as endemic but only few data are available on the variants involved. In West Africa, new subgenotypes VII, VIII and IX were recently described [3] and integrated into the lineage S described by Auldous et al. [2]. Based on phylogenetic analyses of a partial F coding sequence of NDV isolates recovered from apparently healthy poultries in Mali in 2007 and 2008, we previously proposed a new subgenotype VII [4]. Cattoli et al. [5] have also described new strains that were clustered into a new lineage 7 and four new sublineages, 7a, 7b, 7c and 7d, corresponding to our subgenotypes VIIb, VIIIb and VIIc, respectively. Therefore, we suggest to limit the genotype VII to the subgenotype VIIb which is considered as the first appeared in the evolutionary model and to group subgenotypes VIIa, c, d, e in a new genotype XIII.

In this study we present and describe a new NDV detected in West-Africa. Sequences from these viruses and others publicly available were included in an extensive phylogeny reconstruction with different methods. We propose a refined taxonomy for NDV genotyping allowing better consistency than the former lineage nomenclature. Particularly, we introduce two new genotypes, XIII and XII using the analyses of the full length amino acids sequence of F and HN proteins.

MATERIALS AND METHODS

RESULTS

Figure 1. Schematic organisation of Newcastle disease virus genome and viral particle.

Figure 2. Complete procedure for new NDV strains analysis.

In this study, we show the phylogeny of 85 complete F and HN protein sequences of APMV-1. Trees were constructed using the maximum likelihood method with 1000 resampling for the bootstrap analysis. All class I strains were used as an outgroup. The F and HN trees were identical. Thus, only the F tree is represented. Within avian, branch support values for NH are indicated after the F bootstrap values. Sequences generated by our group are indicated with a parallelogram.

REFERENCES


Figure 3. Phylogenetic analysis of 85 complete F and HN protein sequences of APMV-1. Trees were constructed using the maximum likelihood method with 1000 resampling for the bootstrap analysis. A class I strain was used as an outgroup. The F and HN trees were identical. Thus, only the F tree is represented. Within avian, branch support values for NH are indicated after the F bootstrap values. Sequences generated by our group are indicated with a parallelogram.

DISCUSSION AND CONCLUSION

In this study, a comprehensive phylogenetic reconstruction of NDV was carried out. The data sets used and the comparison of different methods for tree reconstruction on the F and HN proteins allow to refine the ND classification. We consider that the genotype nomenclature proposed by Ballagyi-Pordanj [1] is more appropriate to describe phylogenetic relationships between isolates, including the new isolates from West-Africa or Madagascar. Indeed, the clustering of the different genotypes supported by the analyses of the minimal distances between and within genotypes (not shown) do not match with the lineage nomenclature proposed by Auldous et al [2] and adopted by others [3, 5, 6].

Our conclusion is supported by the agreement in the phylogeny reconstruction obtained by four different methods on the complete F protein sequence. The resulting trees were all very similar but statistical analysis clearly shows that the ML and Bayesian methods are more robust.

From our work, the subgenotype VIIb proposed by Herzeg [7] forms a distinct cluster in the branch including subgenotypes VIIa, c, d, e. Therefore, we propose to limit the genotype VII to the subgenotype VIIb which is considered as the first appeared in the evolutionary model and to group subgenotypes VIIa, c, d, e in a new genotype XIII.

Similarly, our five Malian strains form a new cluster containing other strains from West Africa described by Snook et al [3] and Cattoli et al [5]. Snook et al [3] described three new subgenotypes (g, h, i) of lineage 5 (genotype V) circulating in West Africa. Our Malian strains c_ML007_08 and c_ML025_07 clustered in two of these subgenotypes (VIIb and VIIIb, respectively). However, the other Malian strains g_ML018_07 and c_ML025_08 are distant enough to constitute a new clade corresponding to the lineage 7a proposed by Cattoli et al. [5]. We propose to introduce a new lineage 7a.

In this study, we propose that genotype XII emerged from a common ancestor with genotype VII (previously named subgenotype VIIb) and XII (before described as genotype XII) but in a different direction than described earlier [3, 5]. This suggests that an original strain older than genotype VII, probably linked to genotype VI was introduced in West Africa and since then has evolved in an independent manner to give genotypes VII and XIII whereas another lineage led to subgenotypes XII mainly found in Asia.