Short Reports

PERSPECTIVES OF MONITORING FOR NEWCASTLE DISEASE

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Wild birds are considered to be the natural reservoir of the Newcastle disease virus (NDV; avian paramyxovirus-1) causing Newcastle disease, and are often suspected to be involved in outbreaks in domesticated birds. To evaluation the epidemiologic status of nucleic acids of environmental samples were sequenced by shotgun technology. It is shown simultaneous circulation of lentogenic, mesogenic and velogenic virus variants it provides a basis for new insights into monitoring system for Newcastle disease. Metagenomics can become an essential tool for the characterization of the epizootic situation in wild birds or poultry to develop the options and reduce the possibility of Newcastle disease outbreaks in poultry industry.

Infection of birds with virulent strains of Newcastle disease virus (NDV) causes one of the most important infectious diseases of poultry, 123 countries reported ND in domestic species to the World Organization for Animal Health (OIE). In 2016 there were about 35 such countries (http://www.oie.int/wahis_2/public/wahid.php/Diseaseinformation/WI) and many countries have endemic NDV, with outbreaks occurring year after year [1]. Although all NDV strains belong to a single serotype, they are nevertheless genetically highly diverse. Based on the complete fusion gene sequences, NDV strains are divided into two classes, I and II. In the latter, at least 18 genotypes and multiple subgenotypes have been defined [2–4], but the diversity continues to increase as surveillance improves. NDV has a spacious diapason of host, including approximately 241 species of 27 orders, of the known 50 orders of birds [1]. More commonly species include chickens, turkeys, ducks, pigeons, guinea fowl, Japanese quail and many wild birds of all ages [5]. The most susceptible avian species to this disease are chickens and also some mammals like humans, cats and dogs [6]. The disease transmits through droppings and secretions from the nose, mouth and eyes of infected birds. The disease spreads by contaminated water, feed and transport. Airborne transmission of the virus is also an important route of transmission for ND [7]. Mechanical transfer of infected faeces occurs by rodents, insects, dogs, fleas, or scavenging animals [7]. Infection takes place by virus inhalation, ingestion or by contact with conjunctiva.

The disease is characterized by respiratory, nervous system impairment, gastrointestinal and reproductive problems. ND causes huge economic losses to the commercial poultry farmers round the world [2]. Wild aquatic birds are considered as reservoir hosts for NDVs and may act as vectors for transferring these viruses to poultry, causing outbreaks of disease. However Newcastle disease in wild birds occurs without clinical signs, which makes it difficult diagnose of the disease. The isolation of virus strains is possible in a small number of investigated samples. The number of positive samples does not exceed 10%. This feature of the diagnosis and the possibility of simultaneous circulation of the various genetic types of the disease make it difficult to restrictive actions against the outbreak.

Therefore the aim of the our investigation was to use the NGS for detection of NDV at environmental samples. Nucleic acids of environmental samples were sequenced by a shotgun technologies (HiSeq, Illumina). Paired-end sequence reads generated from the Illumina HiSeq were assembled into contigs using standalone Edena software, freely available under the General Public License (GPLv3) at www.genomic.ch/edena.php. This tool is all publicly available, and currently often used to assemble short reads generated by next-generation sequencing platforms, such as Illumina Genome Analyzer (read length = 35–150 bp). As a source of benchmark sequences (viral genomes) we used a standalone version of the NCBI nucleotide database, comprising 6079 complete genomes of viruses. It was found that environmental samples contain sequences of several genetic lines of the Newcastle disease virus. It is shown simultaneous circulation of lentogenic, mesogenic and velogenic virus variants and it provides a basis for new insights into monitoring system for Newcastle disease. This fact requires to carry out a vaccination program based on the possibility of circulation different viruses. Metagenomics could become an essential tool for the characterization of the epizootic situation in wild birds or poultry to develop the options and reduce the possibility of Newcastle disease outbreaks in poultry industry.

References

1. Alexander D., Senne D. Newcastle disease, other avian paramyxoviruses, and pneumovirus infections. In: Diseases of poultry. – 12th ed. – Ames: Blackwell Publishing, 2008. – P. 75–98

2. Aldous E.W., Mynn J.K., Banks J., et al. A molecular epidemiological study of avian paramyxovirus type 1 (Newcastle disease virus) isolates by phylogenetic analysis of a partial nucleotide sequence of the fusion protein gene Avian Pathol. – 2003. – Vol. 32. – P. 239–256.

3. Liu M., Shen X., Cheng X.., Li J., Dai Y. Characterization and Sequencing of a Genotype VIId Newcastle Disease Virus Isolated from Laying Ducks in Jiangsu, China // Genome Announc. – 2015. – № 3(6). – P. e01412–e01415.

4. Miller P.J., Haddas R., Simanov L., Lublin A., Rehmani S.F., Wajid A., Bibi T., Khan T.A., Yaqub T., Setiyaningsih S., Afonso C.L. Identification of new sub-genotypes of virulent Newcastle disease virus with potential panzootic features // Infect Genet Evol. – 2015. – Vol. 29. – P. 216–229.

5. Miller P.J., Estevez C., Yu Q., Suarez D.L., King D.J. Comparison of viral shedding following vaccination with inactivated and live Newcastle disease vaccines formulated with wild type and recombinant viruses // Avian Dis. – 2009. – Vol. 53. – P. 39–49.

6. Nanthakumar T., Kataria R.S., Tiwari A.K., Butchaiah G., Kataria J.M. Pathotyping of newcastle disease viruses by RT-PCR and restriction enzyme analysis // J. Vet. Res. Commun. – 2000. – Vol. 24. – P. 275–286.

7. Ullah S., Ashfaque M., Rahman S.U., Akhtar M., Rehman A. Newcastle disease virus in the intestinal contents of broilers and layers // Pak. Vet. J. – 2004. – № 24(1). – P. 28–30.