

Research Article

Occurrence of West Nile Virus Antibodies in Wild Birds, Horses, and Humans in Poland

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Serum samples of 474 wild birds, 378 horses, and 42 humans with meningitis and lymphocytic meningitis were collected between 2010 and 2014 from different areas of Poland. West Nile virus (WNV) antibodies were detected using competition enzyme linked immunosorbent assays: ELISA-1 ID Screen West Nile Competition, IDvet, ELISA-2 ID Screen West Nile IgM Capture, and ELISA-3 Ingezim West Nile Compac. The antibodies were found in 63 (13.29%) out of 474 wild bird serum samples and in one (0.26%) out of 378 horse serum samples. Fourteen (33.33%) out of 42 sera from patients were positive against WNV antigen and one serum was doubtful. Positive samples obtained in birds were next retested with virus microneutralisation test to confirm positive results and cross-reactions with other antigens of the Japanese encephalitis complex. We suspect that positive serological results in humans, birds, and horses indicate that WNV can be somehow closely related with the ecosystem in Poland.

1. Introduction

West Nile virus (WNV) can affect a wide range of bird species, horses, and humans. The virus is an emerging agent responsible for diseases in these animals and humans worldwide. The main vectors of WNV are several species of the blood sucking insects, which can transmit the virus to birds, horses, and humans [1].

The infections are characterised by high pyrexia, paralysis, and morbidity caused by the factors so far acknowledged as pathogenic only for the animals. More often infections are characterised by mild clinical signs [2].

WNV is on the list of the World Organization for Animal Health (OIE) as the neurotropic factor causing the disease under the obligation to notify. West Nile Fever (WNF) caused by the virus is a zoonosis, which is the major public health problem in USA [3].

WNV is an arbovirus belonging to the Flaviviridae family, genus *Flavivirus* included in Japanese encephalitis antigenic complex induced by related antigenically Japanese encephalitis virus (JEV), St. Louis encephalitis virus (SLEV), Murray Valley encephalitis virus (MVEV), and Usutu virus (USUV). The ssRNA+ genome of the virus contains a single open reading frame from 11.000 to 12.000 nucleotides. The genome of the virus consists of seven nonstructural proteins, NS1, NS2a, NS2b, NS3, NS4a, NS4b, and NS5, and three structural proteins: glycoprotein E, core protein C, and premembrane protein prM [4].

Tropical and migratory birds, which belong to different species, are the main reservoir of the virus [5]. Lineage 1 of WNV is a lineage isolated over the world, but lineage 2 was only isolated in Africa and Madagascar, until Hungarian outbreaks of WNV, which was caused by a novel lineage 2,