

## Case report

## West Nile virus lineage 2 infection in a blood donor from Vienna, Austria, August 2014



C. Jungbauer<sup>a,\*</sup>, M.K. Hourfar<sup>b</sup>, K. Stiasny<sup>c</sup>, S.W. Aberle<sup>c</sup>, D. Cadar<sup>d</sup>,  
J. Schmidt-Chanasit<sup>d,e,1</sup>, W.R. Mayr<sup>a,1</sup>

<sup>a</sup> Austrian Red Cross, Blood Service for Vienna, Lower Austria and Burgenland, 1040 Vienna, Austria

<sup>b</sup> German Red Cross, Blood Service for Baden-Württemberg-Hessen, Frankfurt, Germany

<sup>c</sup> Department of Virology, Medical University of Vienna, Vienna, Austria

<sup>d</sup> Bernhard Nocht Institute for Tropical Medicine, WHO Collaborating Centre for Arbovirus and Haemorrhagic Fever Reference and Research, Hamburg, Germany

<sup>e</sup> German Centre for Infection Research (DZIF), partner site Hamburg-Luebeck-Borstel, Hamburg, Germany

## ARTICLE INFO

## Article history:

Received 18 November 2014

Received in revised form

28 December 2014

Accepted 2 January 2015

## Keywords:

West Nile virus

Full-length genome

Phylogeny

Austria

Blood donor

## ABSTRACT

Eastern Austria is neighbouring regions with ongoing West Nile virus (WNV) transmissions. Three human WNV infections had been diagnosed during the past decade in Austria. The Austrian Red Cross Blood Service (ARC-BS) started a first voluntary screening for WNV in blood donors from Eastern Austria by Nucleic Acid Testing (NAT) in June 2014. This is also the most extensive WNV surveillance programme in humans in Austria so far. In August 2014, one autochthonous WNV infection was detected in a blood donor from Vienna. By now, one in 67,800 whole blood donations was found to be positive for WNV RNA.

© 2015 Published by Elsevier B.V.

### 1. Why this case is important

West Nile virus (WNV) is a mosquito-borne, single-stranded RNA virus that belongs to the Japanese encephalitis virus group within the family *Flaviviridae* [1–3]. WNV can cause West Nile fever (WNF) in humans which occurs in 20% of WNV infections and is characterized as a febrile syndrome with flu-like symptoms [4]. Less than 1% of WNV infections are manifested as West Nile neuroinvasive disease (WNND). However, the majority of WNV infections in humans are asymptomatic [4]. In 1999, WNV emerged in North America. By 2013, ≈2 million persons had become infected, with 39,557 reported cases of WNF and WNND including 1668 deaths [5].

WNV was first recognized in Europe in the 1960s and then, in 1996, when a large outbreak occurred in Romania [6]. WNV of lineage 1 (LN1) was identified first in Europe, but infections of birds with WNV of lineage 2 (LN2) have been reported in Europe since 2003 [7]. The last notable outbreak of WNV infection occurred in Greece in 2010 with 197 cases of which 33 died [8].

Increasing titers of antibodies to WNV have been found in immunoglobulin lots produced from plasma collected in Austria, Germany and the Czech Republic [9]. Although the presence of WNV in mosquitoes and birds had been noticed in Austria or at its borders [10,11], the only confirmed autochthonous human WNV infections were observed in 2009 and 2010. No viral isolates or WNV-RNA were available from these samples [12].

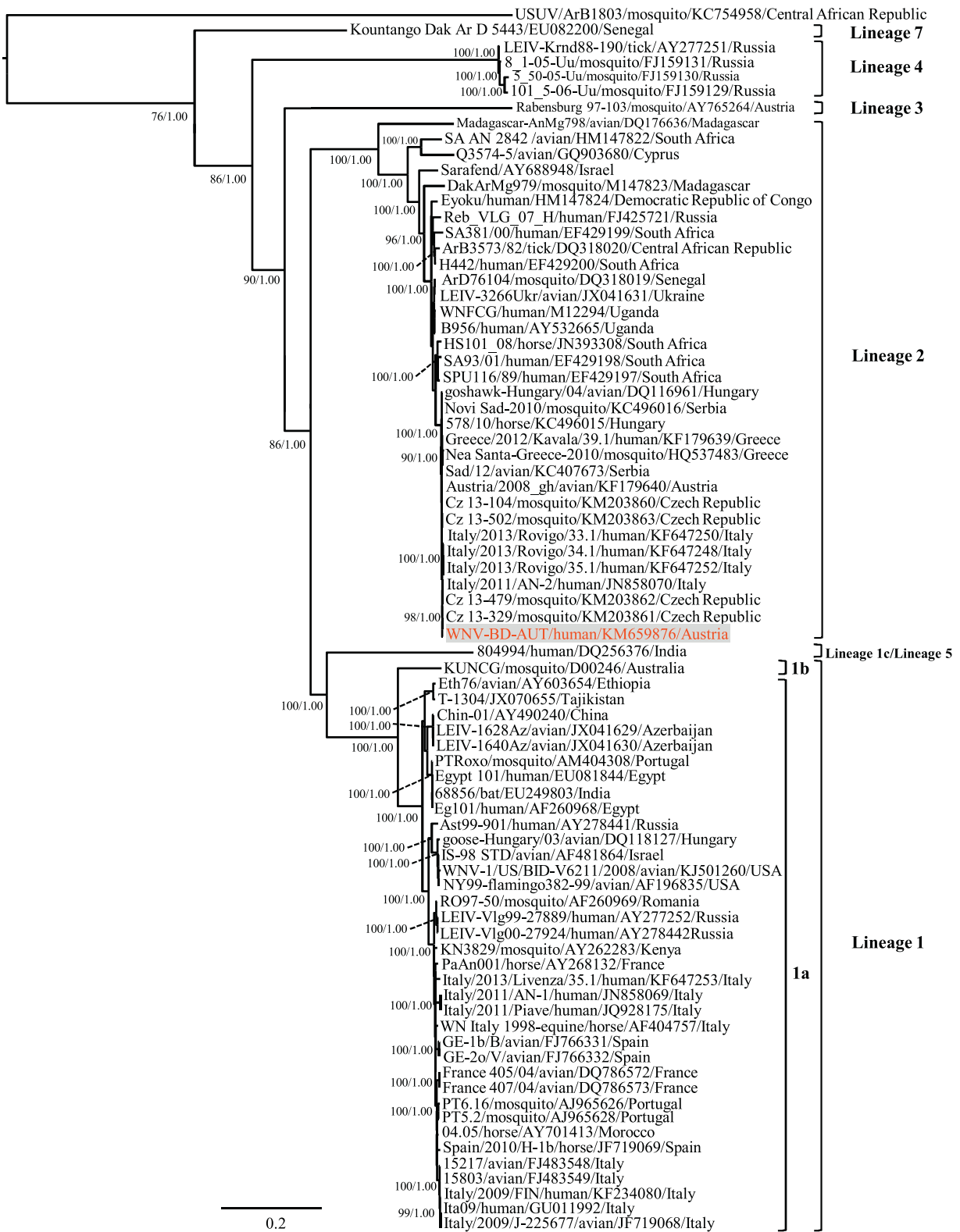
In response to the emergence of WNV, many countries adopted regulations regarding blood safety in blood products for direct transfusion. In the USA, WNV RNA screening was introduced in 2003 [13]. In Europe, the Commission Directive 2004/33/EC introduced a temporary 28 days deferral of donors after leaving an area with ongoing transmission of WNV to humans. Alternatively, blood donations can be screened by WNV NAT [14].

Eastern Austria is neighbouring regions with ongoing WNV transmissions to humans [15]. The ARC-BS started screening for WNV in all blood donations from Vienna, Lower Austria and Burgenland on a voluntary basis by NAT in pools of 24 (DRK WNV-PCR-kit, DRK-Blutspendedienst Baden-Württemberg-Hessen, Frankfurt, Germany; sensitivity >= 250 cop/ml) from June 2014. By now, 67,800 blood donations have been tested, representing ≈40% of total blood donations in Austria from this period. The screening was unveiling WNV-RNA in one donation.

\* Corresponding author. Tel.: +43 1 58900 402.

E-mail address: [jungbauer@redcross.at](mailto:jungbauer@redcross.at) (C. Jungbauer).

<sup>1</sup> Contributed equally to this article.



**Fig. 1.** Bayesian phylogenetic tree based on complete genome nucleotide sequences of the WNV-BD-AUT (KM659876) strain and representatives of all West Nile lineages. The General-Time-Reversible model of sequence evolution with gamma-distributed rate variation among sites (GTR+I+ $\Gamma$ 4) and proportion of invariable sites were used as the best model. Statistical support of grouping from Bayesian posterior probabilities (clade credibilities  $\geq 90$ ) and 1,000 parallel maximum likelihood bootstrap replicates ( $\geq 70\%$ ) is indicated at the nodes. Usutu virus strain ArB1803 (GenBank accession number KC754958) was chosen as an out-group. Taxon information includes the name, source of isolation, GenBank accession number, and country of origin. The West Nile virus strain generated during this study is marked in red and bold. The scale bar represents nucleotide substitutions per site.

Download English Version:

<https://daneshyari.com/en/article/6120273>

Download Persian Version:

<https://daneshyari.com/article/6120273>

[Daneshyari.com](https://daneshyari.com)