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Genomic epidemiology of West Nile virus in Europe

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ABSTRACT

West Nile virus is one of the most widespread mosquito-borne zoonotic viruses, with unique transmission dynamics in various parts of the world. Genomic surveillance has provided important insights in the global patterns of West Nile virus emergence and spread. In Europe, multiple West Nile virus lineages have been isolated, with lineage 1a and 2 being the main lineages responsible for human infections. In contrast to North America, where a single introduction of lineage 1a resulted in the virus establishing itself in a new continent, at least 13 introductions of lineages 1a and 2 have occurred into Europe, which is likely a vast underestimation of the true number of introductions. Historically, lineage 1a was the main lineage circulating in Europe, but since the emergence of lineage 2 in the early 2000s, the latter has become the predominant lineage. This shift in West Nile virus lineage prevalence has been broadly linked to the expansion of the virus into northerly temperate regions, where autochthonous cases in animals and humans have been reported in Germany and The Netherlands. Here, we discuss how genomic analysis has increased our understanding of the epidemiology of West Nile virus in Europe, and we present a global Nextstrain build consisting of publicly available West Nile virus genomes (https://nextstrain.org/community/grubaughlab/WNV-Global). Our results elucidate recent insights in West Nile virus lineage dynamics in Europe, and discuss how expanded programs can fill current genomic surveillance gaps.

1. Introduction

West Nile virus (Family: *Flaviviridae*, Genus: *Flavivirus*) is a globally dispersed mosquito-borne zoonotic virus consisting of at least 9 previously defined lineages (Fig. 1) [1–4]. Of these, lineages 1a and 2 are responsible for the majority of reported human cases and will be the main focus of this paper. An estimated 80% of human cases are thought to be asymptomatic, and < 1% of cases can develop a serious form of the disease known as West Nile neuroinvasive disease, which can lead to encephalitis and death [5,6]. West Nile virus is maintained in a complex enzootic cycle between mosquitoes and birds, with >60 mosquito species and over 300 bird species that have been implicated as potential vectors and hosts [7]. West Nile virus infection can have a significant negative impact on avian host populations [8]. Although humans and other mammals, such as horses, can develop disease, which may be fatal, they generally do not develop sufficient viremia to contribute to the transmission cycle, and are therefore considered "dead-end" hosts.

Despite recent progress in understanding the complex transmission dynamics and ecology of West Nile virus, prevention and control remain challenging. Particularly in Europe, West Nile virus continues to pose a threat to public health with yearly recurring outbreaks of which the largest outbreak to date reported in 2018, co-circulation of lineages 1 and 2, and recent emergence outside its endemic regions into more northern parts of the continent [9,10]. Consequently, understanding the patterns of West Nile virus emergence and spread in Europe is key to informing animal and public health responses and could provide valuable insights for regions with comparable ecology and lineages.

Virus genomic surveillance can provide additional insights by informing patterns of virus transmission and the role virus genetics and evolution may be playing in causing morbidity and mortality [11–14].

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Genomic surveillance of West Nile virus demonstrated its importance when the virus was introduced and subsequently became endemic in the United States [15]. Here, we discuss the complex ecology and dynamics of West Nile virus in Europe, where multiple lineages are circulating and frequent introductions happen from sub-Saharan Africa and the Middle-East through bird migration. To complement the review of existing literature on genomic surveillance, we developed a global Nextstrain build (https://nextstrain.org/community/grubaughlab/WNV-Global; Fig. 1) [16]. The Nextstrain build contains publicly available genomes belonging to eight different lineages, for which near-complete genomes (7700 base pairs or greater) were publicly available, and whose lineages were determined using the West Nile virus typing tool through Genome Detective [17]. Geographical resolution for the samples was done at the country level for all samples. State/province resolution was provided when available using the centroid of the geographical area. Samples without geographical information were removed from this analysis. Time resolution was to the day, samples that provided a year but no day were given June 1st of the provided year as the day. Samples without date information were excluded from this analysis. This build provides context for West Nile virus strains that are circulating in Europe and other parts of the world and can be used as a tool to explore West Nile virus genomic data discussed in the paper.

2. History of West Nile outbreaks

West Nile virus is believed to have originated in Africa, with its first discovery in Uganda in 1937 and subsequent phylogenetic analyses suggest it emerged in the 16th or 17th century [1,18,19]. While few known outbreaks have been reported in Africa since, recent studies have shown that it is likely underreported and an underestimated threat to animal and human health on the African continent [2,20–22]. Initially, West Nile virus was assumed to cause only rare and mild disease in humans until serosurveys confirmed the first widespread human outbreaks in Israel and Egypt in 1951 (later determined to be lineage 1a)

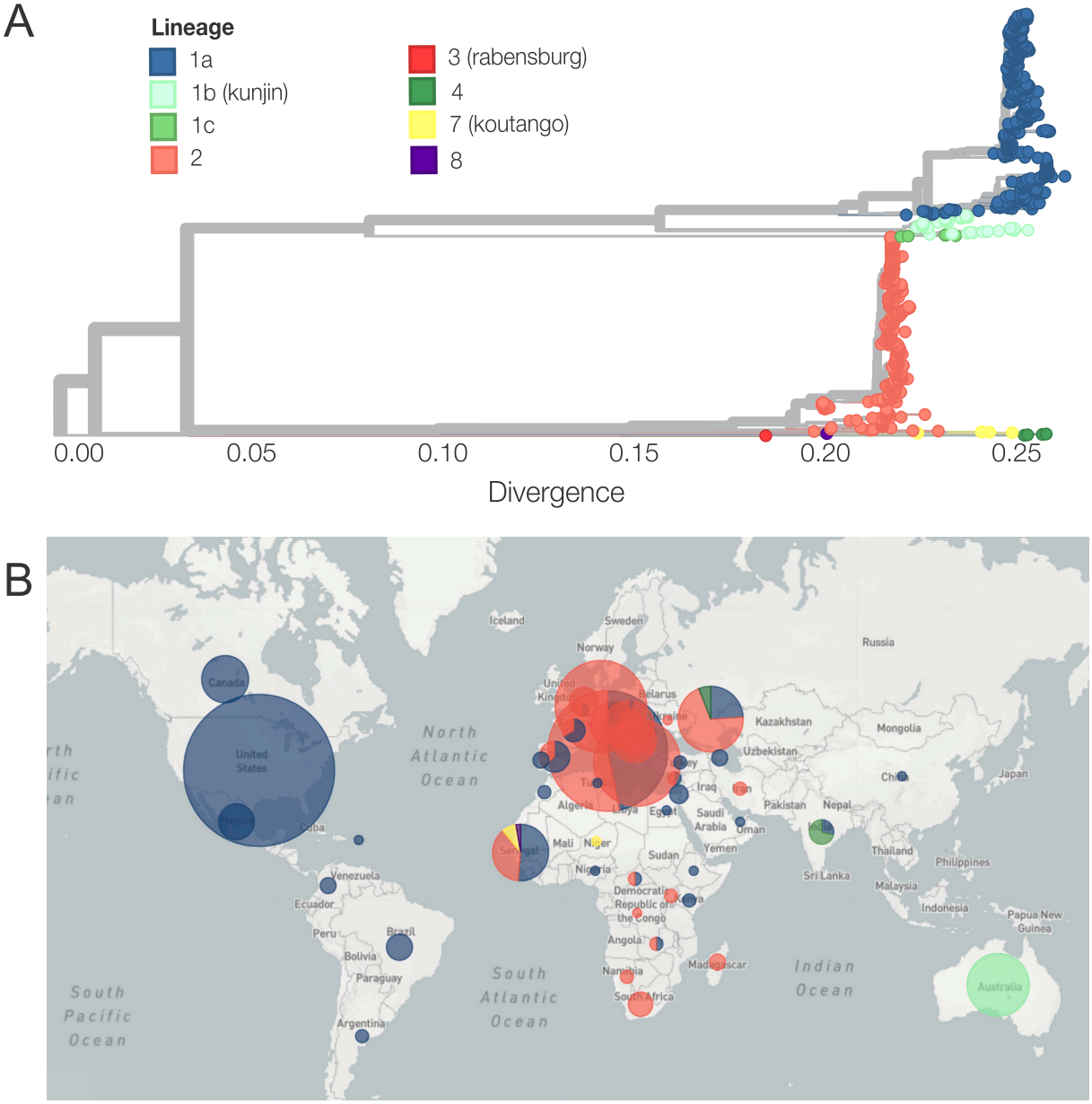

Fig. 1. Global phylogeny of West Nile virus lineages. A) Phylogenetic tree of all available whole genome sequences available on GenBank (USA downsampled). B) Geographic map of all sequences included in the phylogenetic tree. Missing metadata was supplemented from various sources please see GitHub repository for more details: https://github.com/grubaughlab/WNV-global.

[23,24]. West Nile virus was first detected in Europe during serosurveys conducted in Albania in 1958 and France in 1962 [25,26]. During the following decades, West Nile virus was not reported until 1996, when an unusually virulent outbreak occurred in Romania, with 393 human cases and an estimated case fatality rate in humans of roughly 4% [27,28]. Three years later an even more virulent outbreak occurred in Russia in 1999 with an estimated 480 human cases and a case fatality of nearly 10% [29]. Also in 1999, on the other side of the globe, West Nile virus was reported for the first time in the Americas, in New York City [30,31]. Once in the United States, West Nile virus rapidly spread across the continent reaching California by 2003 and causing a total of 55,442 human cases and 2683 deaths in 2022 since its introduction [15,32,33].

The outbreaks in Romania and Russia in the 1990's were harbingers of what was to come in Europe. Further outbreaks of West Nile virus occurred in the early 2000s due to lineage 1 circulation in southern Europe. A dramatic shift occurred in 2004 with the detection of lineage 2 in Hungary in a northern goshawk (*Accipiter gentilis*) [34]. This lineage spread rapidly to other southern European countries, with a notable outbreak involving large numbers of human cases in Greece in 2010 [35]. After the introduction of lineage 2 and a rise in human infections, the European Centre for Disease Prevention and Control began reporting horse, bird, and human outbreaks annually using a dedicated website since 2010 (Fig. 2) [36]. West Nile virus surveillance programs then emerged across the continent collecting and testing mosquito vectors and bird hosts, in addition to symptomatic human cases and horses with neurological signs [37]. The outbreak peaked in 2018, culminating in nearly 1800 human cases, more than the previous four years combined [36]. In 2019, West Nile virus expanded northward where the first locally acquired human cases were reported in Germany, followed by The Netherlands in 2020 [38,39]. Thus, over the past three decades the landscape of West Nile virus epidemiology in Europe has changed with continued heterogeneous transmission in southern and central regions as well as more favorable environmental conditions that have sustained transmission and enabled overwintering in Northwestern regions.

3. State of genomic surveillance in Europe

Compared to traditional surveillance, which constitutes detecting the presence of West Nile virus specific IgM antibodies for history of infection or viral load via qPCR for active infection from serum or cerebrospinal fluid [41,42]; genomic surveillance entails sequencing the pathogen genome from active infections to characterize genetic patterns [43]. For West Nile virus, genomic surveillance typically targets positive mosquito or bird samples, as these samples generally have sufficient virus concentrations needed for successful sequencing [41]. Sequences are available from humans and horses (blood, urine, or neurological tissue from fatal cases), but in non-fatal cases the virus is typically cleared by the time a case is diagnosed [41]. The intensity of different surveillance programs coupled with fluctuations in West Nile virus activity across Europe has resulted in heterogeneous genomic surveillance efforts, with certain countries contributing a large proportion of the sequencing [16]. For example, Italy, a country with high circulation of West Nile virus, initiated a genomic surveillance program in 2001 (three years after the first recent evidence of cases in horses in 1998) [37,44]. The Italian program is conducted through both research universities and government agencies, and samples are acquired through a national program in residential and sentinel chickens, sentinel horses, and resident and wild birds [45]. With West Nile virus circulation in nearby countries, Germany also initiated a mosquito surveillance program in 2007 and bird surveillance in 2011 [37,46,47]. Eleven years after Germany's surveillance efforts began, the first equine cases of West Nile virus were identified in 2018. The proactive genomic surveillance of West Nile virus provides health officials with better understanding of how and when West Nile virus was introduced into the country, confirm virus overwintering, and can inform targeted control strategies [39,48,49].

Different strategies for West Nile virus genomic surveillance are being used across Europe, depending on the purpose. The West Nile virus genome is typically ~11 kilobase pairs in length. For example, the West Nile virus lineage 2 strain Nea-Santa Greece 2010 virus consists of a genome of 11,028 base pairs (GenBank Accession number HQ573483). The vast majority of this sequence, 10,401 base pairs, encodes the virus polyprotein that is post-translationally cleaved into the virus structural (capsid, membrane, and envelope proteins) and non-structural protein (NS1, NS2b, NS2b, NS3, NS4a, NS4b, NS5). If lineage characterization is the main purpose, then sequencing specific genome regions, such as the coding-sequence for the envelope (E) or the non-structural protein 5 (NS5), is adequate as these regions contain sufficient phylogenetic signal to delineate lineages. Consequently, the majority of publicly available sequences from Europe are partial genomes (~60.4%; Fig. 3). However,

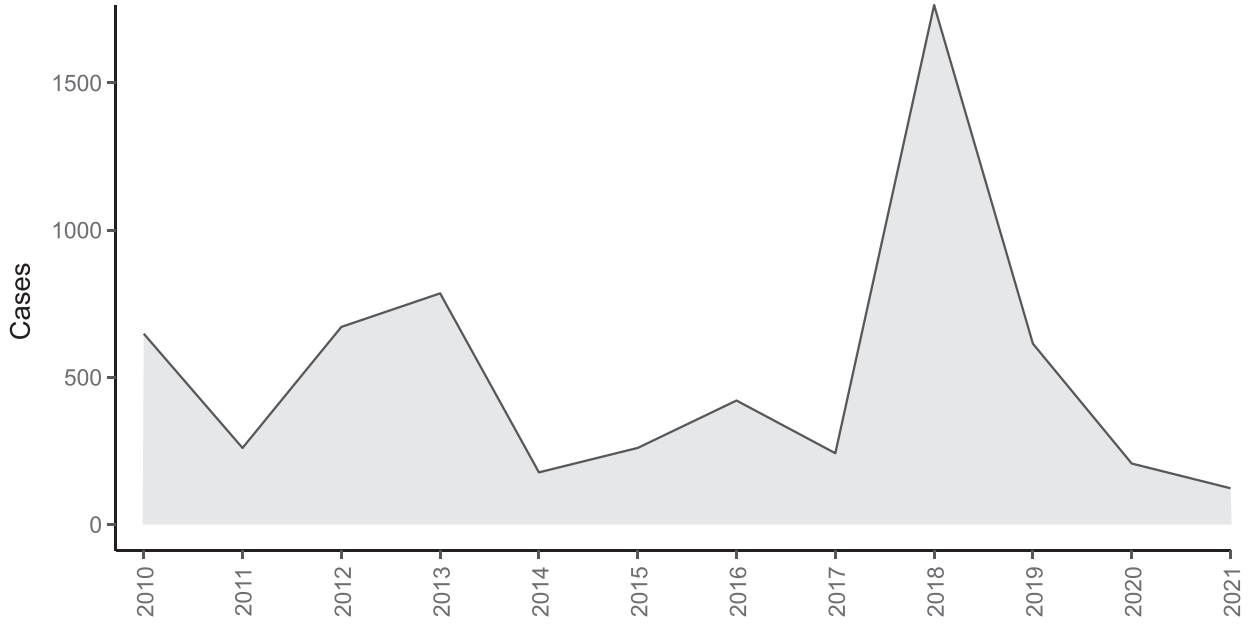

Fig. 2. Temporal trends in reported human cases of West Nile virus in Europe. Yearly West Nile cases in Europe as reported by the European Centre for Disease Prevention and Control (ECDC) [40]. Only confirmed human cases based on laboratory tests for case confirmation are shown.

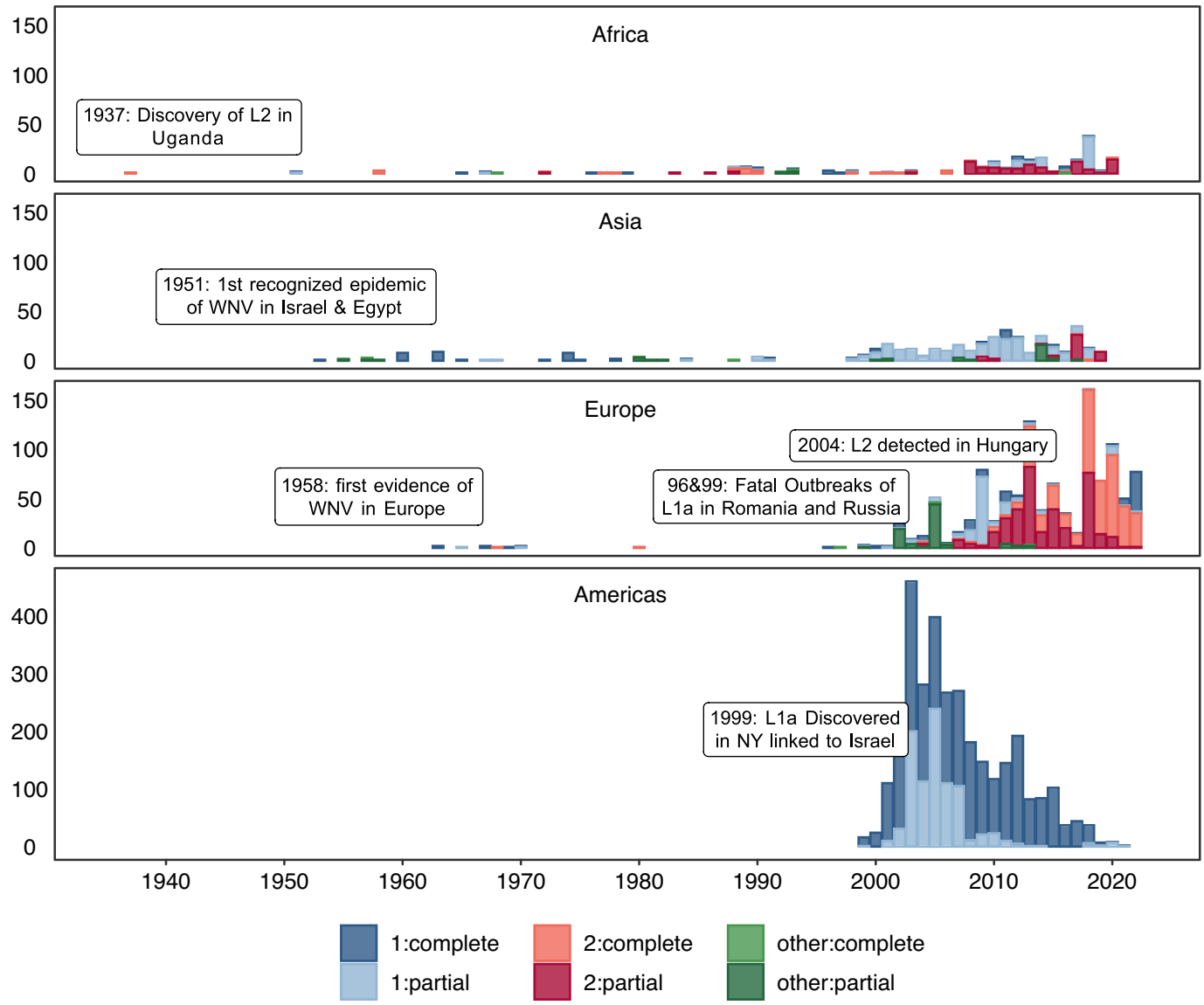

Fig. 3. Global sequencing of West Nile virus over time. We used GenBank to download all partial (e.g. Envelope and NS5 <7700 base pairs) and near-complete genomes (>7700 base pairs (i.e. >70% genome completeness)) from Africa, Asia, the Americas, and Europe from 1937 to 2022. The Americas includes South and North America and Asia includes Australia. Russia is counted in Europe as most cases occur in the Volgograd region near the Ukrainian border. The Genome Detective West Nile virus typing tool was used to assign lineages. "Other" samples include lineage 3 (Rabensburg), lineage 4, lineage 7 (Koutango), and lineage 8.

these partial genomes are less reliable for more advanced phylogenetic analyses, as they do not provide the same level of temporal resolution as whole genomes [50]. Moreover, partial genome sequencing might miss important regions of the genome that may be associated with differences in virus transmissibility or virulence [35,51]. Fortunately, in recent years the use of whole genome sequencing for understanding disease epidemiology has increased in Europe (Fig. 3), likely an outcome of the COVID-19 pandemic where robust genomic surveillance was critical for detecting variants of concern.

4. Introductions of West Nile virus in Europe

Global spread of mosquito-borne viruses is typically driven by movement of infected mosquito vectors or vertebrate hosts. Travel of infected humans is one of the primary modes of dispersal for mosquito-borne viruses such as dengue virus and Zika virus for which humans serve as reservoir hosts [52,53]. With humans considered as dead-end hosts for West Nile virus, virus spread is mostly driven by dispersal of infected birds and mosquitoes [54]. Land cover, landscape structure, and bird migration routes are, therefore, important determinants of intercontinental movement of West Nile virus [55,56]. The emergence of West Nile virus lineage 1a in North America was due to a single introduction that was estimated to have happened in New York in 1998, a year before the virus was first detected in 1999 [57,58]. This introduction was likely due to the importation of an infected bird or mosquito from the Middle East [19,58–60], as there are no major bird migration routes that connect North America with the Middle East. While lineage 1a is the only West Nile virus lineage that has been detected in North America to date, multiple introductions of lineages 1a and 2 have been detected in Europe (Fig. 4). Moreover, four additional lineages (lineages 3, 4, 8, and 9) have been detected in Europe as well [61]. The proximity of Europe to Africa and the Middle East along with several major bird migration routes create opportunities for frequent introductions between continents. Indeed, well documented avian migration routes into Europe from sub-Saharan Africa, that cross wetland areas where birds congregate and encounter abundant mosquito vectors, have been implicated as a main driver of West Nile virus introduction into southern Europe [22,62].

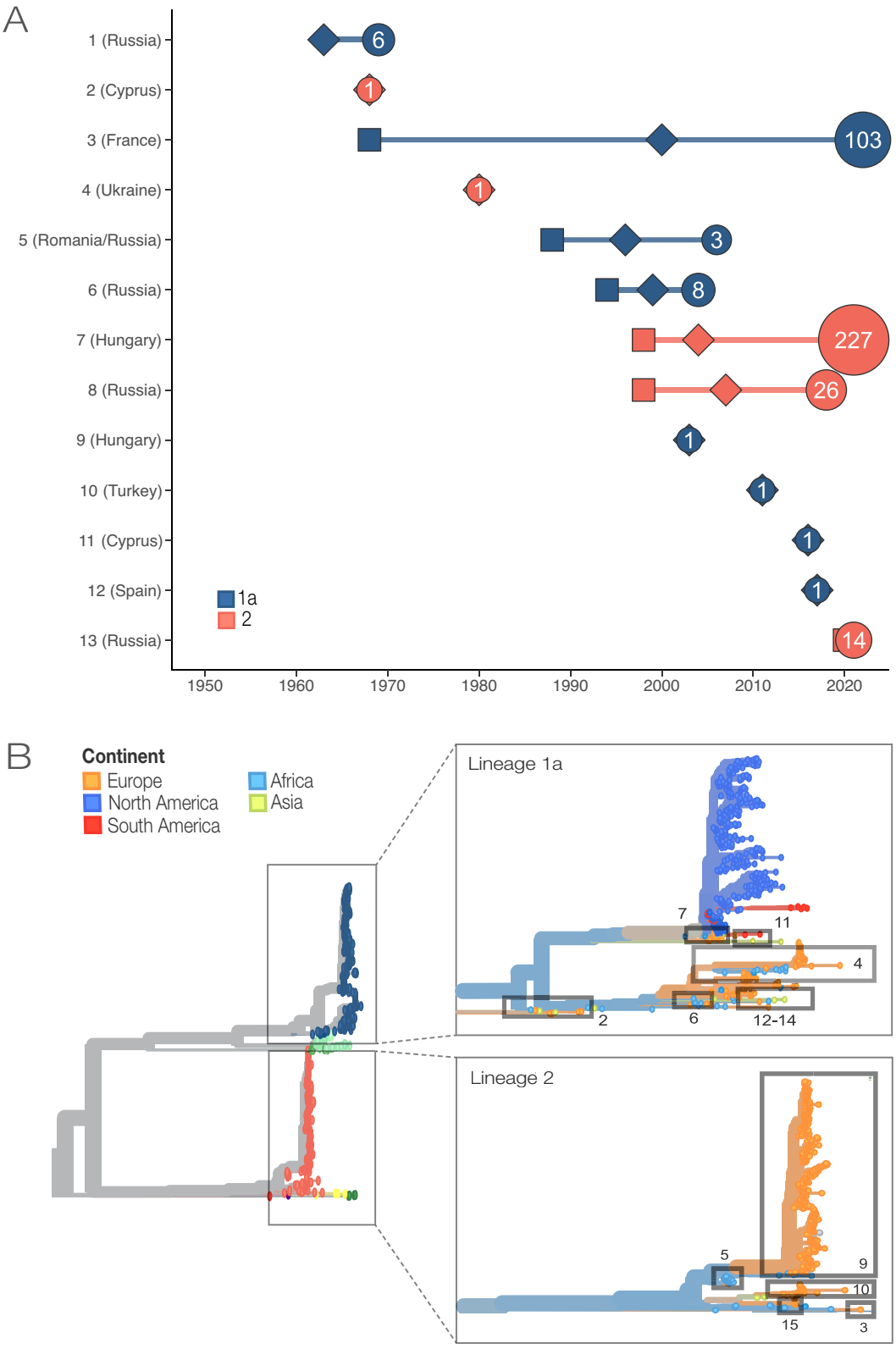

Fig. 4. West Nile virus intercontinental introductions into Europe. A) Time series of West Nile virus introductions into Europe. Introductions were identified in the Nexstrain build and verified with previous research. Lineages were assigned using the Genome Detective West Nile virus typing tool, with lineage 1a in blue and lineage 2 in pink. Square shaped points indicate the inferred introduction year, diamond shaped points indicate the first sample sequenced in the clade, and circle indicates the last sequenced sample from that clade. Y-axis labels indicate the country of introduction, and the size of the circles and number within the circles indicates the number of whole genome sequences identified within each clade. B) Lineages 1 and 2 phylogenetic trees with corresponding introductions labeled from A. Virus clades can be visualized on Nextstrain https://nextstrain.org/community/grubaughlab/WNV-Global. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

To characterize the frequency of new and/or repeated lineage introductions of West Nile virus into Europe, we used the phylogenetic framework of our Nextstrain build and compared our results with previous studies [19,59,63–67]. We used the West Nile virus typing tool developed by Genome Detective to assign lineages. Based on the currently available genomic dataset and lineage system, we identified at least thirteen distinct West Nile virus introductions of lineage 1a (8 introductions) and lineage 2 (5 introductions) into Europe, with evidence of sustained, multi-year persistence and transmission for seven (Fig. 4). However, these estimates could be a significant undercount of the true number of introductions into Europe due to paucity of sampling, potentially multiple reintroduction events to and from the continent within the clades, and introductions whose effective population size never reaches detectable levels. Despite these limitations, the frequent introductions of multiple lineages into Europe, through natural and frequent events i.e. bird migration, in contrast to the single introduction of lineage 1a into North America, which was almost certainly mediated by human activity, illustrates the differences in West Nile virus intercontinental spread that are detected by current surveillance efforts in different parts of the world.

The majority of the early West Nile virus introductions into Europe belonged to lineage 1a, with the first sequences from France (partial genome from 1965) [68] and Portugal (whole genome from 1969; GenBank accession: AM404308; Fig. 4, introduction 1) [69]. The genome from Portugal was genetically related to genomes from Egypt, Israel, and Russia that were collected in the 1950's and 1960's, and likely originated from northwestern Africa in the early 1900s [22]. This revealed that West Nile virus was more widespread across Europe during this time period than the documented outbreaks in nearby countries such as Egypt and Israel. For a period of 26 years, no additional lineage 1a genomes were sequenced from Europe until two new introductions occurred, which led to the outbreaks in Romania and Russia in 1996 and 1999 (Fig. 4, introductions 5 and 6) [27,29]. Around the same time, lineage 1a was detected in the western Mediterranean resulting in outbreaks in Morocco in 1996 (GenBank accession: AY701412) and in France in 2000 (GenBank accession: AY268132; Fig. 4, introduction 3) [70]. Most outbreaks within this clade have since occurred in Italy where viruses continued to persist through at least to 2022, but this clade has also spread to neighboring Spain and as far as Senegal [71–73].

The first evidence of West Nile virus lineage 2 introductions into Europe comes from whole genomes from Cyprus in 1968 (GenBank accession: GQ903680) and Ukraine in 1980 (GenBank accession: JX041631; Fig. 4, introductions 2 and 4). Both of these introductions consist of a single virus isolate and neither were associated with additional clusters [65,66]. More than two decades passed until the next known introduction of lineage 2 was detected in Hungary in 2004, when sequencing samples from sick goshawks (GenBank accession: DQ116961 and MZ605382; Fig. 4, introduction 7). This introduction led to the subsequent spread of the virus that formed the predominant clades that are currently circulating in Europe [61,66]. Recent studies indicate that the Hungarian introduction of lineage 2 had likely been introduced sometime between 1996 and 2004 from South Africa [22,61,66]. The detection of lineage 2 in Hungary was not the only introduction of West Nile virus lineage 2 into Europe at that time, as evidenced by partial genomes that were sequenced from clinical specimens from two West Nile fever patients in the Rostov region in Russia in 2004 (introductions not shown because genomes are partial) [74,75]. Additional West Nile virus lineage 2 outbreaks have happened in the Volgograd region in Russia in 2007, 2010, and more recently in 2021 [76], which were caused by at least two separate introductions of lineage 2 viruses (Fig. 4, introductions 8 and 13) [77]. Based on currently available West Nile virus genomic surveillance data it is clear that frequent introductions of West Nile virus lineage 1a and 2 have happened over the past decades, and that both lineages are currently co-circulating in Europe.

5. Intracontinental transmission dynamics

Historically, West Nile virus lineage 1a was the main lineage in Europe causing outbreaks, but after the introduction of lineage 2, the dynamics shifted across Europe. Most notably, in the last decade two major events changed the intracontinental transmission dynamics of West Nile virus in Europe, with 1) a shift from lineage 1a to lineage 2 being the predominant lineage, and 2) emergence into more northern regions. Since the introduction of lineage 2 starting in the early 2000s, cases have steadily risen across Europe, but with dramatic fluctuations between years [36]. Although this may be partly due to improved testing and mandatory reporting [78], this also coincides with the emergence of lineage 2 in Europe and the impact of climate change that has made northern regions of Europe more permissive for mosquito-borne virus transmission. The majority of human cases are typically not characterized to lineage level, but sequencing of mosquito and bird samples during outbreaks confirmed that lineage 2 has been responsible for most European outbreaks between 2010 and 2020 (Fig. 5A).

Since the West Nile virus lineage 2 introduction in Hungary, the virus quickly bifurcated into two clades sometime around 2002, and continued to spread across Europe [61]. One virus clade spread southward towards neighboring countries such as Serbia and Greece, and the other clade spread westward towards countries such as Austria and Italy. Phylogenetic analysis of the southern clade suggests that continued transmission was sustained in Greece with spillover into neighboring countries [61]. The other clade has continued to sustain in several countries, including Italy, where both lineage 1a and lineage 2 are currently co-circulating [71,79]. In Italy, a country with longitudinal sequencing data, the lineage shift is particularly clear with lineage 2 largely replacing lineage 1a (Fig. 5B). However, recent surveillance shows that lineage 1a has re-emerged in Italy (Fig. 4 Introduction 3). Eight years after the last human infections with lineage 1a were reported in Italy, two patients were diagnosed with lineage 1a infection in 2021 in the Padova province, with the virus spreading to a larger geographic area the year after and has shown evidence of increased risk for neuroinvasive disease [71,80]. There are two possible explanations for the re-emergence of lineage 1a, the virus has either continued to circulate unnoticed in the Mediterranean or it may be a new introduction. The co-circulation of both lineages raises concerns for public health, as concurrent outbreaks of lineage 1a and 2 could happen in the future.

With the emergence of lineage 2 in Europe, there was not only an increase in the number of West Nile cases, but also an expansion of its geographical distribution [36]. Prior to the emergence of lineage 2, West Nile virus was primarily circulating in southern and central Europe (Fig. 5). This changed in 2018, when West Nile virus was detected for the first time in birds and horses in Germany [39], followed by the first locally acquired human case in 2019 [81]. Phylogenetic reconstructions showed that the virus had likely been introduced in 2016 from the Czech Republic [82]. This clade maintained year-over-year transmission, with genomes being sequenced every year from 2018 to 2021, indicating that the virus is likely overwintering locally [39]. Following a similar pattern to Germany, The Netherlands first detected West Nile virus in a common whitethroat (*Curruca communis*) and two mosquito pools in 2020 [83], prior to the first autochthonous human cases in the same year [38]. West Nile virus was again detected in a grey heron (*Ardea cinerea*) in 2022 in The Netherlands [84], but no human cases have been reported since 2020. Global warming has been implicated as one of the possible drivers of the northward spread of West Nile virus in Europe, with higher spring and summer temperatures, winter warming, and lower water availability creating suitable conditions for transmission cycles to establish [10,85–90]. Expanded genomic surveillance will be critical to understand how West Nile virus will continue to expand its geographic distribution in Europe, and whether future outbreaks are caused by locally overwintering viruses or new introductions from other regions.

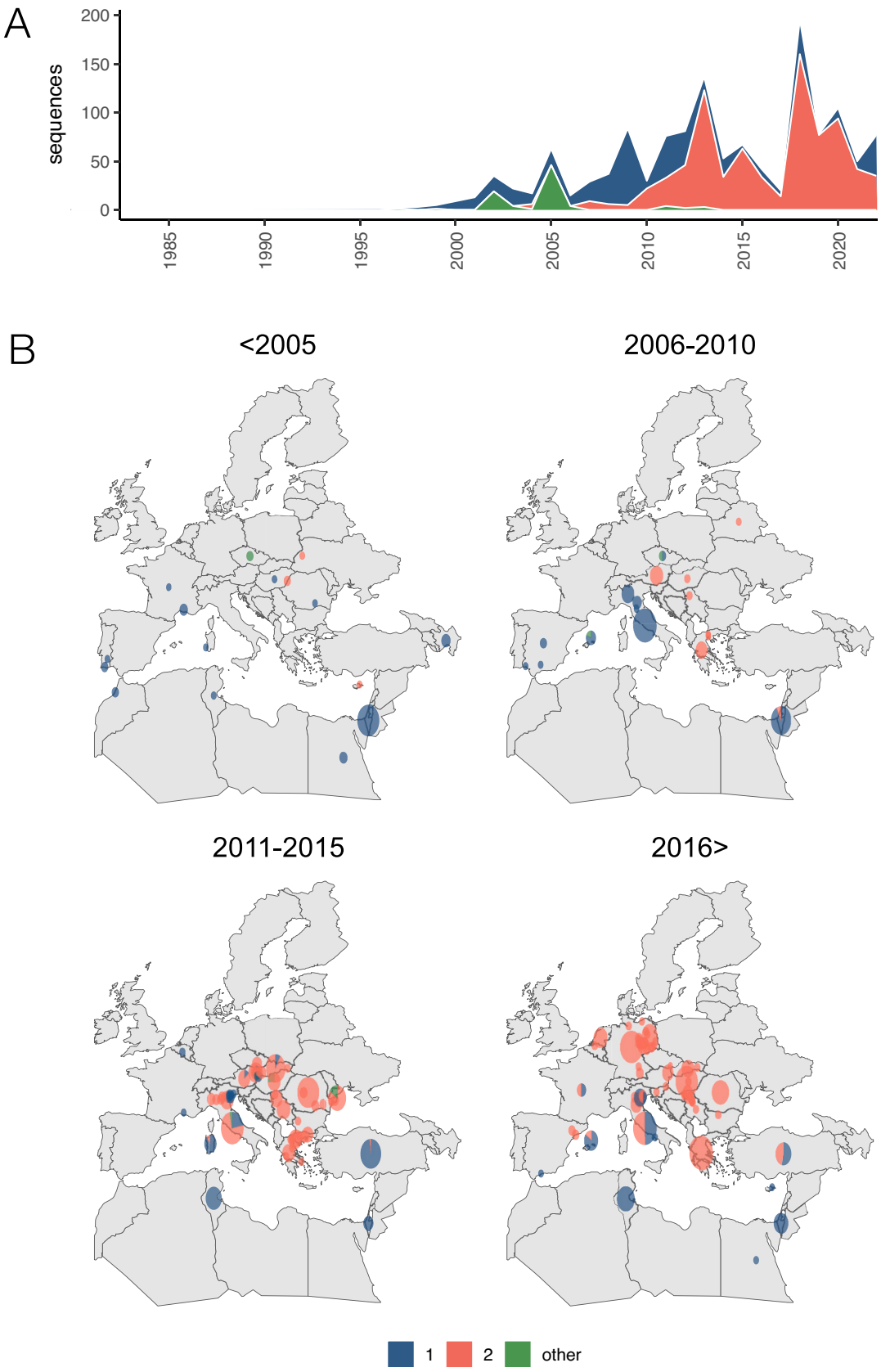

Fig. 5. Intracontinental West Nile virus lineage dynamics. A) Time series of European partial and whole genomes available on NCBI GenBank that included collection date and location. B) Map of European partial and whole genomes available on NCBI GenBank that included collection date and location. Lineages were assigned using the Genome Detective West Nile virus typing tool [17].

6. Need for expanded genomic surveillance

Genomic surveillance is a powerful tool to track the emergence and spread of newly emerging virus variants [91]. For West Nile virus, genomic surveillance provided important insights in the single introduction of lineage 1a into North America, and the subsequent evolution and spread. In contrast, genomic surveillance in other parts of the world is much more sparse, leaving critical gaps in our understanding of West Nile virus transmission dynamics. Particularly in Europe, with frequent introductions and a higher diversity of lineages, genomic surveillance can help to better understand patterns of emergence and spread, determine which strains are responsible for causing outbreaks, and to identify broader networks of transmission. With the recent shift from lineage 1a to 2 and emergence into more northern regions, there is a critical need to expand on genomic surveillance in Europe at a continental scale. This is also the case for Africa where the virus is believed to have originated and which appears to exchange virus lineages with regularity [19].

During the COVID-19 pandemic, laboratories around the world have invested in establishing whole genome sequencing workflows [11]. Utilizing this genomic infrastructure to sequence other viruses such as West Nile virus, along with a rapid decrease in cost associated with sequencing can help to transition from partial to whole genome sequencing. Expanding genomic surveillance in endemic regions as well as regions at risk for future expansion, would benefit from routine genomic surveillance. Additionally, building global genomic surveillance initiatives would be powerful to better track the intercontinental spread of West Nile virus lineages, by not only focusing on introductions into Europe, but also to better characterize the frequency and patterns of intercontinental emergence and spread between continents that are connected through major bird migration routes.

Understanding the transmission dynamics of West Nile virus lineages holistically is key for animal and public health agencies to respond to evidence of West Nile virus in their region. More whole genome sequencing could illuminate key lineage specific mutations that impact transmission potential and virulence [35,51]. Temporal information is also critical, as a novel introduction indicates swift action is needed to ramp up surveillance and mosquito control to prevent the virus from becoming established and leading to an outbreak of animal and human cases. Repeated introductions year-over-year could stymie such control efforts, and evidence of sustained transmission year-over-year indicates the need to prepare for cyclical outbreaks in the future. Integrating genomic data with climatic modeling and surveillance could help public health identify better indicators of high-risk years and the need to ensure hospital capacity and planning.

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CRediT authorship contribution statement

R. Tobias Koch: Conceptualization, Data curation, Formal analysis, Methodology, Visualization, Writing – original draft, Writing – review & editing. **Diana Erazo:** Validation, Writing – review & editing. **Arran J. Folly:** Validation, Writing – review & editing. **Nicholas Johnson:** Validation, Writing – review & editing. **Simon Dellicour:** Validation, Visualization, Writing – review & editing. **Nathan D. Grubaugh:** Conceptualization, Validation, Supervision, Writing – review & editing. **Chantal B.F. Vogels:** Conceptualization, Validation, Supervision, Writing – original draft, Writing – review & editing.

Declaration of Competing Interest

None.

Data availability

All data are available in the manuscript.

References

[1] G. Fall, N. Di Paola, M. Faye, M. Dia, C.C.M. de Freire, C. Loucoubar, P.M.A. de Zanotto, O. Faye, A.A. Sall, Biological and phylogenetic characteristics of West African lineages of West Nile virus, PLoS Negl. Trop. Dis. 11 (2017), e0006078.
[2] G. Mencattelli, M.H.D. Ndione, R. Rosà, G. Marini, C.T. Diagne, M.M. Diagne, G. Fall, O. Faye, M. Diallo, O. Faye, Epidemiology of West Nile virus in Africa: an underestimated threat, PLoS Negl. Trop. Dis. 16 (2022), e0010075.
[3] K. Pachler, K. Lebl, D. Berer, I. Rudolf, Z. Hubalek, N. Nowotny, Putative new West Nile virus lineage in Uranotaenia unguiculata mosquitoes, Austria, 2013, Emerg. Infect. Dis. 20 (2014) 2119.
[4] A. Rizzoli, M.A. Jiménez-Clavero, L. Barzon, P. Cordioli, J. Figuerola, P. Koraka, B. Martina, A. Moreno, N. Nowotny, N. Pardigon, N. Sanders, S. Ulbert, A. Tenorio, The challenge of West Nile virus in Europe: knowledge gaps and research priorities, Eurosurveillance. 20 (2015) 21135, https://doi.org/10.2807/1560-7917.ES2015.20.20.21135.
[5] L.E. Davis, R. DeBiasi, D.E. Goade, K.Y. Haaland, J.A. Harrington, J.B. Harnar, S. A. Pergam, M.K. King, B. DeMasters, K.L. Tyler, West Nile virus neuroinvasive disease, Ann. Neurol. Off. J. Am. Neurol. Assoc. Child Neurol. Soc. 60 (2006) 286–300.
[6] L.R. Petersen, A.C. Brault, R.S. Nasci, West Nile virus: review of the literature, JAMA. 310 (2013) 308–315, https://doi.org/10.1001/jama.2013.8042.
[7] K.M. van der Meulen, M.B. Pensaert, H.J. Nauwynck, West Nile virus in the vertebrate world, Arch. Virol. 150 (2005) 637–657, https://doi.org/10.1007/s00705-004-0463-z.
[8] T.L. George, R.J. Harrigan, J.A. LaManna, D.F. DeSante, J.F. Saracco, T.B. Smith, Persistent impacts of West Nile virus on north American bird populations, Proc. Natl. Acad. Sci. 112 (2015) 14290–14294.
[9] A.D.T. Barrett, West Nile in Europe: an increasing public health problem, J. Travel Med. 25 (2018) tay096, https://doi.org/10.1093/jtm/tay096.
[10] T. Bakonyi, J.M. Haussig, West Nile virus keeps on moving up in Europe, Eurosurveillance. 25 (2020) 2001938, https://doi.org/10.2807/1560-7917.ES.2020.25.46.2001938.
[11] V. Hill, G. Githinji, C.B.F. Vogels, A.I. Bento, C. Chaguza, C.V.F. Carrington, N. D. Grubaugh, Toward a global virus genomic surveillance network, Cell Host Microbe (2023), https://doi.org/10.1016/j.chom.2023.03.003.
[12] A.K. Keita, F.R. Koundouno, M. Faye, A. Düx, J. Hinzmann, H. Diallo, A. Ayouba, F. Le Marcis, B. Soropogui, K. Ifono, M.M. Diagne, M.S. Sow, J.A. Bore, S. Calvignac-Spencer, N. Vidal, J. Camara, M.B. Keita, A. Renevey, A. Diallo, A. K. Soumah, S.L. Millimono, A. Mari-Saez, M. Diop, A. Doré, F.Y. Soumah, K. Kourouma, N.J. Vielle, C. Loucoubar, I. Camara, K. Kourouma, G. Annibaldis, A. Bah, A. Thielebein, M. Pahlmann, S.T. Pullan, M.W. Carroll, J. Quick, P. Formenty, A. Legand, K. Pietro, M.R. Wiley, N. Tordo, C. Peyrefitte, J. T. McCrone, A. Rambaut, Y. Sidibé, M.D. Barry, M. Kourouma, C.D. Saouromou, M. Condé, M. Baldé, M. Povogui, S. Keita, M. Diakite, M.S. Bah, A. Sidibe, D. Diakite, F.B. Sako, F.A. Traore, G.A. Ki-Zerbo, P. Lemey, S. Günther, L. E. Kafetzopoulou, A.A. Sall, E. Delaporte, S. Duraffour, O. Faye, F.H. Leendertz, M. Peeters, A. Toure, N.F. Magassouba, Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks, Nature. 597 (2021) 539–543, https://doi.org/10.1038/s41586-021-03901-9.
[13] J.D. Robishaw, S.M. Alter, J.J. Solano, R.D. Shih, D.L. DeMets, D.G. Maki, C. H. Hennekens, Genomic surveillance to combat COVID-19: challenges and opportunities, Lancet Microbe. 2 (2021) e481–e484, https://doi.org/10.1016/S2666-5247(21)00121-X.
[14] S.K. Gire, A. Goba, K.G. Andersen, R.S.G. Sealfon, D.J. Park, L. Kanneh, S. Jalloh, M. Momoh, M. Fullah, G. Dudas, S. Wohl, L.M. Moses, N.L. Yozwiak, S. Winnicki, C.B. Matranga, C.M. Malboeuf, J. Qu, A.D. Gladden, S.F. Schaffner, X. Yang, P.-P. Jiang, M. Nekoui, A. Colubri, M.R. Coomber, M. Fonnie, A. Moigboi, M. Gbakie, F.K. Kamara, V. Tucker, E. Konuwa, S. Saffa, J. Sellu, A.A. Jalloh, A. Kovoma, J. Koninga, I. Mustapha, K. Kargbo, M. Foday, M. Yillah, F. Kanneh, W. Robert, J.L. B. Massally, S.B. Chapman, J. Bochicchio, C. Murphy, C. Nusbaum, S. Young, B. W. Birren, D.S. Grant, J.S. Scheiffelin, E.S. Lander, C. Happi, S.M. Gevao, A. Gnirke, A. Rambaut, R.F. Garry, S.H. Khan, P.C. Sabeti, Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 Outbreak, Science. 345 (2014) 1369–1372, https://doi.org/10.1126/science.1259657.
[15] J. Hadfield, A.F. Brito, D.M. Swetnam, C.B. Vogels, R.E. Tokarz, K.G. Andersen, R. C. Smith, T. Bedford, N.D. Grubaugh, Twenty years of West Nile virus spread and evolution in the Americas visualized by Nextstrain, PLoS Pathog. 15 (2019), e1008042.
[16] Nextstrain / community / grubaughlab / WNV-Global. https://nextstrain.org/community/grubaughlab/WNV-Global, 2023 accessed August 16.

[17] West Nile Virus Typing Tool. https://www.genomedetective.com/app/typingtool/wnv/, 2023 accessed April 19.

[18] K.C. Smithburn, T.P. Hughes, A.W. Burke, J.H. Paul, A neurotropic virus isolated from the blood of a native of Uganda, Am. J. Trop. Med. 20 (1940) 471–472.

[19] F.J. May, C.T. Davis, R.B. Tesh, A.D. Barrett, Phylogeography of West Nile virus: from the cradle of evolution in Africa to Eurasia, Australia, and the Americas, J. Virol. 85 (2011) 2964–2974.

[20] Z. Hubalek, European experience with the West Nile virus ecology and epidemiology: could it be relevant for the New World? Viral Immunol. 13 (2000) 415–426.

[21] W.F. Sule, D.O. Oluwayelu, L.M. Hernández-Triana, A.R. Fooks, M. Venter, N. Johnson, Epidemiology and ecology of West Nile virus in sub-Saharan Africa, Parasit. Vectors 11 (2018) 414, https://doi.org/10.1186/s13071-018-2998-y.

[22] G. Mencattelli, M.H.D. Ndione, A. Silverj, M.M. Diagne, V. Curini, L. Teodori, M. Di Domenico, R. Mbaye, A. Leone, M. Marcacci, A. Gaye, E. Ndiaye, D. Diallo, M. Ancora, B. Secondini, V. Di Lollo, I. Mangone, A. Bucciacchio, A. Polci, G. Marini, R. Rosà, N. Segata, G. Fall, C. Cammà, F. Monaco, M. Diallo, O. Rota-Stabelli, O. Faye, A. Rizzoli, G. Savini, Spatial and temporal dynamics of West Nile virus between Africa and Europe, Nat. Commun. 14 (2023) 6440, https://doi.org/10.1038/s41467-023-42185-7.

[23] K. Marberg, N. Goldbltjm, V.V. Sterk, W. Jasinska-klingbehg, M.A. Klingberg, The natural history of West Nile fever. I. Clinical observations during an epidemic in Israel, Am. J. Hyg. 64 (1956) 259–269.

[24] R. Taylor, T. Work, H. Hurlbut, F. Rizk, A study of the ecology of West Nile virus in Egypt1, Am. J. Trop. Med. Hyg. 5 (1956) 579–620.

[25] V. Bárdos, J. Adamcová, S. Dedei, N. Gjini, B. Rosický, A. Simková, Neutralizing antibodies against some neurotropic viruses determined in human sera in Albania, J. Hyg. Epidemiol. Microbiol. Immunol. 3 (1959) 277–282.

[26] B. Murgue, S. Murri, H. Triki, V. Deubel, H.G. Zeller, West Nile in the Mediterranean Basin: 1950-2000, Ann. N. Y. Acad. Sci. 951 (2001) 117–126, https://doi.org/10.1111/j.1749-6632.2001.tb02690.x.

[27] G.L. Campbell, C.S. Ceianu, H.M. Savage, Epidemic West Nile encephalitis in Romania, Ann. N. Y. Acad. Sci. 951 (2001) 94–101, https://doi.org/10.1111/j.1749-6632.2001.tb02688.x.

[28] T. Tsai, F. Popovici, C. Cernescu, G. Campbell, N. Nedelcu, West Nile encephalitis epidemic in southeastern Romania, Lancet 352 (1998) 767–771, https://doi.org/10.1016/S0140-6736(98)03538-7.

[29] A.E. Platonov, G.A. Shipulin, O.Y. Shipulina, E.N. Tyutyunnik, T.I. Frolochkina, R. S. Lanciotti, S. Yazyshina, O.V. Platonova, I.L. Obukhov, A.N. Zhukov, Outbreak of West Nile virus infection, Volgograd region, Russia, 1999, Emerg. Infect. Dis. 7 (2001) 128.

[30] D. Nash, F. Mostashari, A. Fine, J. Miller, D. O'Leary, K. Murray, A. Huang, A. Rosenberg, A. Greenberg, M. Sherman, S. Wong, G.L. Campbell, J.T. Roehrig, D. J. Gubler, W.-J. Shieh, S. Zaki, P. Smith, M. Layton, The outbreak of West Nile virus infection in the new York City area in 1999, N. Engl. J. Med. 344 (2001) 1807–1814, https://doi.org/10.1056/NEJM200106143442401.

[31] M. Giladi, E. Metzkor-Cotter, D.A. Martin, Y. Siegman-Igra, A.D. Korczyn, R. Rosso, S.A. Berger, G.L. Campbell, R.S. Lanciotti, West Nile encephalitis in Israel, 1999: the New York connection, Emerg. Infect. Dis. 7 (2001) 659–661.

[32] W. Reisen, H. Lothrop, R. Chiles, M. Madon, C. Cossen, L. Woods, S. Husted, V. Kramer, J. Edman, West Nile virus in California, Emerg. Infect. Dis. 10 (2004) 1369–1378, https://doi.org/10.3201/eid1008.040077.

[33] Final Cumulative Maps and Data | West Nile Virus | CDC. https://www.cdc.gov/westnile/statsmaps/cumMapsData.html, 2022 (accessed April 6, 2022).

[34] T. Bakonyi, É. Ivanics, K. Erdélyi, K. Ursu, E. Ferenczi, H. Weissenböck, N. Nowotny, Lineage 1 and 2 strains of encephalitic West Nile virus, Central Europe, Emerg. Infect. Dis. 12 (2006) 618–623, https://doi.org/10.3201/eid1204.051379.

[35] A. Papa, T. Bakonyi, K. Xanthopoulou, A. Vázquez, A. Tenorio, N. Nowotny, Genetic characterization of West Nile virus lineage 2, Greece, Emerg. Infect. Dis. 17 (2011) (2010) 920–922, https://doi.org/10.3201/eid1705.101759.

[36] Surveillance and Disease data for West Nile Virus Infections. https://www.ecdc.europa.eu/en/west-nile-fever/surveillance-and-disease-data, 2010 (accessed May 1, 2023).

[37] O. Engler, G. Savini, A. Papa, J. Figuerola, M.H. Groschup, H. Kampen, J. Medlock, A. Vaux, A.J. Wilson, D. Werner, H. Jöst, M. Goffredo, G. Capelli, V. Federici, M. Tonolla, N. Patocchi, E. Flacio, J. Portmann, A. Rossi-Pedruzzi, S. Mourelatos, S. Ruiz, A. Vázquez, M. Calzolari, P. Bonilauri, M. Dottori, F. Schaffner, A. Mathis, N. Johnson, European surveillance for West Nile virus in mosquito populations, Int. J. Environ. Res. Public Health 10 (2013) 4869–4895, https://doi.org/10.3390/ijerph10104869.

[38] D.R. Vlaskamp, S.F. Thijsen, J. Reimerink, P. Hilkens, W.H. Bouvy, S.E. Bantjes, B. J. Vlaminckx, H. Zaaijer, H.H. van den Kerkhof, S.F. Raven, C.B. Reusken, First autochthonous human West Nile virus infections in the Netherlands, July to august 2020, Eurosurveillance. 25 (2020) 2001904, https://doi.org/10.2807/1560-7917.ES.2020.25.46.2001904.

[39] U. Ziegler, P.D. Santos, M.H. Groschup, C. Hattendorf, M. Eiden, D. Höper, P. Eisermann, M. Keller, F. Michel, R. Klopfleisch, K. Müller, D. Werner, H. Kampen, M. Beer, C. Frank, R. Lachmann, B.A. Tews, C. Wylezich, M. Rinder, L. Lachmann, T. Grünewald, C.A. Szentiks, M. Sieg, J. Schmidt-Chanasit, D. Cadar, R. Lühken, West Nile virus epidemic in Germany triggered by epizootic emergence, 2019, Viruses. 12 (2020) 448, https://doi.org/10.3390/v12040448.

[40] Historical data by year - West Nile virus seasonal surveillance, Eur. Cent. Dis. Prev. Control. https://www.ecdc.europa.eu/en/west-nile-fever/surveillance-and-disease-data/historical, 2022 accessed April 8.

[41] Diagnostic Testing | West Nile Virus | CDC. https://www.cdc.gov/westnile/healthcareproviders/healthCareProviders-Diagnostic.html, 2023 (accessed May 16, 2023).

[42] L. Barzon, M. Pacenti, S. Ulbert, G. Palù, Latest developments and challenges in the diagnosis of human West Nile virus infection, Expert Rev. Anti-Infect. Ther. 13 (2015) 327–342, https://doi.org/10.1586/14787210.2015.1007044.

[43] J.T. Ladner, N.D. Grubaugh, O.G. Pybus, K.G. Andersen, Precision epidemiology for infectious disease control, Nat. Med. 25 (2019) 206–211, https://doi.org/10.1038/s41591-019-0345-2.

[44] C. Cantile, G. Di Guardo, C. Eleni, M. Arispici, Clinical and neuropathological features of West Nile virus equine encephalomyelitis in Italy, Equine Vet. J. 32 (2000) 31–35, https://doi.org/10.2746/042516400777612080.

[45] F. Monaco, G. Savini, P. Calistri, A. Polci, C. Pinoni, R. Bruno, R. Lelli, West Nile disease epidemic in Italy: first evidence of overwintering in Western Europe? Res. Vet. Sci. 91 (2011) (2009) 321–326, https://doi.org/10.1016/j.rvsc.2011.01.008.

[46] S. Linke, M. Niedrig, A. Kaiser, H. Ellerbrok, K. Müller, T. Müller, F.J. Conraths, R.-U. Mühle, D. Schmidt, U. Köppen, F. Bairlein, P. Berthold, G. Pauli, Serologic evidence of West Nile virus infections in wild birds captured in Germany, Am. J. Trop. Med. Hyg. 77 (2007) 358–364.

[47] P.D. Santos, A. Günther, M. Keller, T. Homeier-Bachmann, M.H. Groschup, M. Beer, D. Höper, U. Ziegler, An advanced sequence clustering and designation workflow reveals the enzootic maintenance of a dominant West Nile virus subclade in Germany, Virus Evol. 9 (2023), https://doi.org/10.1093/ve/vead013 vead013.

[48] C. Holicki, U. Ziegler, C. Raileanu, H. Kampen, D. Werner, J. Schulz, C. Silaghi, M. Groschup, A. Vasic, West Nile virus lineage 2 vector competence of indigenous Culex and Aedes mosquitoes from Germany at temperate climate conditions, Viruses. 12 (2020) 561, https://doi.org/10.3390/v12050561.

[49] U. Ziegler, D. Seidowski, J. Angenvoort, M. Eiden, K. Müller, N. Nowotny, M. Groschup, Monitoring of West Nile virus infections in Germany, Zoonoses Public Health 59 (2012) 95–101.

[50] G. Dudas, T. Bedford, The ability of single genes vs full genomes to resolve time and space in outbreak analysis, BMC Evol. Biol. 19 (2019) 1–17.

[51] E.M. Botha, W. Markotter, M. Wolfaardt, J.T. Paweska, R. Swanepoel, G. Palacios, L.H. Nel, M. Venter, Genetic determinants of virulence in pathogenic lineage 2 West Nile virus strains, Emerg. Infect. Dis. 14 (2008) 222–230, https://doi.org/10.3201/eid1402.070457.

[52] N.D. Grubaugh, J.T. Ladner, M.U.G. Kraemer, G. Dudas, A.L. Tan, K. Gangavarapu, M.R. Wiley, S. White, J. Thézé, D.M. Magnani, K. Prieto, D. Reyes, A.M. Bingham, L.M. Paul, R. Robles-Sikisaka, G. Oliveira, D. Pronty, C.M. Barcellona, H.C. Metsky, M.L. Baniecki, K.G. Barnes, B. Chak, C.A. Freije, A. Gladden-Young, A. Gnirke, C. Luo, B. MacInnis, C.B. Matranga, D.J. Park, J. Qu, S.F. Schaffner, C. Tomkins-Tinch, K.L. West, S.M. Winnicki, S. Wohl, N.L. Yozwiak, J. Quick, J.R. Fauver, K. Khan, S.E. Brent, R.C. Reiner, P.N. Lichtenberger, M.J. Ricciardi, V.K. Bailey, D. I. Watkins, M.R. Cone, E.W. Kopp, K.N. Hogan, A.C. Cannons, R. Jean, A. J. Monaghan, R.F. Garry, N.J. Loman, N.R. Faria, M.C. Porcelli, C. Vasquez, E. R. Nagle, D.A.T. Cummings, D. Stanek, A. Rambaut, M. Sanchez-Lockhart, P. C. Sabeti, L.D. Gillis, S.F. Michael, T. Bedford, O.G. Pybus, S. Isern, G. Palacios, K. G. Andersen, Genomic epidemiology reveals multiple introductions of Zika virus into the United States, Nature. 546 (2017) 401–405, https://doi.org/10.1038/nature22400.

[53] H. Tian, Z. Sun, N.R. Faria, J. Yang, B. Cazelles, S. Huang, B. Xu, Q. Yang, O. G. Pybus, B. Xu, Increasing airline travel may facilitate co-circulation of multiple dengue virus serotypes in Asia, PLoS Negl. Trop. Dis. 11 (2017), e0005694, https://doi.org/10.1371/journal.pntd.0005694.

[54] L.D. Kramer, L.M. Styer, G.D. Ebel, A global perspective on the epidemiology of West Nile virus, Annu. Rev. Entomol. 53 (2008) 61–81.

[55] J.H. Rappole, S.R. Derrickson, Z. Hubálek, Migratory birds and spread of West Nile virus in the Western hemisphere, Emerg. Infect. Dis. 6 (2000) 319–328, https://doi.org/10.3201/eid0604.000401.

[56] Globalization, Land Use, and the Invasion of West Nile Virus | Science, 2023, https://doi.org/10.1126/science.1201010 accessed July 25.

[57] X.-Y. Jia, T. Briese, I. Jordan, A. Rambaut, H.C. Chi, J.S. Mackenzie, R.A. Hall, J. Scherret, W.I. Lipkin, Genetic analysis of West Nile New York 1999 encephalitis virus, Lancet 354 (1999) 1971–1972, https://doi.org/10.1016/S0140-6736(99)05384-2.

[58] R. Lanciotti, J. Roehrig, V. Deubel, J. Smith, M. Parker, K. Steele, B. Crise, K. Volpe, M. Crabtree, J. Scherret, Origin of the West Nile virus responsible for an outbreak of encephalitis in the northeastern United States, Science. 286 (1999) 2333–2337.

[59] G. Zehender, E. Ebranati, F. Bernini, A.L. Presti, G. Rezza, M. Delogu, M. Galli, M. Ciccozzi, Phylogeography and epidemiological history of West Nile virus genotype 1a in Europe and the Mediterranean basin, Infect. Genet. Evol. 11 (2011) 646–653, https://doi.org/10.1016/j.meegid.2011.02.003.

[60] F. Di Giallonardo, J.L. Geoghegan, D.E. Docherty, R.G. McLean, M.C. Zody, J. Qu, X. Yang, B.W. Birren, C.M. Malboeuf, R.M. Newman, H.S. Ip, E.C. Holmes, Fluid spatial dynamics of West Nile virus in the United States: rapid spread in a permissive host environment, J. Virol. 90 (2015) 862–872, https://doi.org/10.1128/jvi.02305-15.

[61] West Nile Virus spread in Europe - phylogeographic pattern analysis and key drivers | bioRxiv. https://www.biorxiv.org/content/10.1101/2022.11.10.515886v1.full, 2023 accessed March 9.

[62] E. Jourdain, M. Gauthier-Clerc, D. Bicout, P. Sabatier, Bird migration routes and risk for pathogen dispersion into Western Mediterranean wetlands, Emerg. Infect. Dis. 13 (2007) 365–372, https://doi.org/10.3201/eid1303.060301.

[63] P. Aguilera-Sepúlveda, B. Gómez-Martín, M. Agüero, M. Jiménez-Clavero, J. Fernández-Pinero, A new cluster of West Nile virus lineage 1 isolated from a northern goshawk in Spain, Transbound. Emerg. Dis. 69 (2021), https://doi.org/10.1111/tbed.14399.

[64] M.M. Akıner, M. Öztürk, A.B. Başer, F. Günay, S. Hacıoğlu, A. Brinkmann, N. Emanet, B. Alten, A. Özkul, A. Nitsche, Y.-M. Linton, K. Ergünay, Arboviral screening of invasive Aedes species in northeastern Turkey: West Nile virus circulation and detection of insect-only viruses, PLoS Negl. Trop. Dis. 13 (2019), e0007334, https://doi.org/10.1371/journal.pntd.0007334.
[65] A.R. McMullen, H. Albayrak, F.J. May, C.T. Davis, D.W.C. Beasley, A.D.T. Barrett, Molecular evolution of lineage 2 West Nile virus, J. Gen. Virol. 94 (2013) 318–325, https://doi.org/10.1099/vir.0.046888-0.
[66] H. Srihi, N. Chatti, M. Ben Mhadheb, J. Gharbi, N. Abid, Phylodynamic and phylogeographic analysis of the complete genome of the West Nile virus lineage 2 (WNV-2) in the Mediterranean basin, BMC Ecol. Evol. 21 (2021) 1–13.
[67] A. Tomazatos, S. Jansen, S. Pfister, E. Török, I. Maranda, C. Horváth, L. Keresztes, M. Spînu, E. Tannich, H. Jöst, J. Schmidt-Chanasit, D. Cadar, R. Lühken, Ecology of West Nile virus in the Danube Delta, Romania: Phylogeography, Xenosurveillance and Mosquito Host-Feeding Patterns, Viruses. 11 (2019) 1159, https://doi.org/10.3390/v11121159.
[68] P. Del Giudice, I. Schuffenecker, F. Vandenbos, E. Counillon, H. Zeller, Human West Nile Virus, France, Emerg. Infect. Dis. 10 (2004) 1885–1886, https://doi.org/10.3201/eid1010.031021.
[69] R. Parreira, P. Severino, F. Freitas, J. Piedade, A. Almeida, A. Esteves, Two distinct introductions of the West Nile virus in Portugal disclosed by phylogenetic analysis of genomic sequences, Vector Borne Zoonotic Dis. Larchmt. N. 7 (2007) 344–352, https://doi.org/10.1089/vbz.2006.0632.
[70] I. Schuffenecker, C.N. Peyrefitte, M. el Harrak, S. Murri, A. Leblond, H.G. Zeller, West Nile virus in Morocco, Emerg. Infect. Dis. 11 (2005) (2003) 306–309, https://doi.org/10.3201/eid1102.040817.
[71] L. Barzon, M. Pacenti, F. Montarsi, D. Fornasiero, F. Gobbo, E. Quaranta, I. Monne, A. Fusaro, A. Volpe, A. Sinigaglia, S. Riccetti, E. Dal Molin, S. Satto, V. Lisi, F. Gobbi, S. Galante, G. Feltrin, V. Valeriano, L. Favero, F. Russo, M. Mazzucato, A. Bortolami, P. Mulatti, C. Terregino, G. Capelli, Rapid spread of a new West Nile virus lineage 1 associated with increased risk of neuroinvasive disease during a large outbreak in Italy in 2022, J. Travel Med. (2022) taac125, https://doi.org/10.1093/jtm/taac125.
[72] M.H.D. Ndione, E.H. Ndiaye, M. Faye, M.M. Diagne, D. Diallo, A. Diallo, A.A. Sall, C. Loucoubar, O. Faye, M. Diallo, O. Faye, M.A. Barry, G. Fall, Re-introduction of West Nile virus lineage 1 in Senegal from Europe and subsequent circulation in human and mosquito populations between 2012 and 2021, Viruses. 14 (2022) 2720, https://doi.org/10.3390/v14122720.
[73] M.J. Ruiz-López, M. Muñoz-Chimeno, J. Figuerola, A.M. Gavilán, S. Varona, I. Cuesta, J. Martínez-de la Puente, Á. Zaballos, F. Molero, R.C. Soriguer, M. P. Sánchez-Seco, S. Ruiz, A. Vázquez, Genomic analysis of West Nile virus lineage 1 detected in mosquitoes during the 2020–2021 outbreaks in Andalusia, Spain, Viruses. 15 (2023) 266, https://doi.org/10.3390/v15020266.
[74] A.E. Platonov, L.S. Karan, T.A. Shopenskaia, M.V. Fedorova, N.M. Koliasnikova, N. M. Rusakova, L.V. Shishkina, T.E. Arshba, V.I. Zhuravlev, M.V. Govorukhina, A. A. Valentseva, G.A. Shipulin, Genotyping of West Nile fever virus strains circulating in southern Russia as an epidemiological investigation method: principles and results, Zh. Mikrobiol. Epidemiol. Immunobiol. (2011) 29–37.
[75] M. Ciccozzi, S. Peletto, E. Cella, M. Giovanetti, A. Lai, E. Gabanelli, P.L. Acutis, P. Modesto, G. Rezza, A.E. Platonov, A. Lo Presti, G. Zehender, Epidemiological history and phylogeography of West Nile virus lineage 2, Infect. Genet. Evol. 17 (2013) 46–50, https://doi.org/10.1016/j.meegid.2013.03.034.
[76] Е.В. Путинцева, С.К. Удовиченко, Д.Н. Никитин, Н.В. Бородай, И.М. Шпак, В.К. ФоМина, А.В. Несговорова, А.А. Батурин, Е.В. Молчанова, Д.Р. Прилепская, Е.В. ПиМенова, Д.В. Викторов, А.В. Топорков, Лихорадка Западного Нила: результаты Мониторинга за возбудителеМ в 2021 г. в Российской Федерации, прогноз заболеваеМости на 2022 г, ПроблеМы Особо Опасных Инфекций. 0 (2022) 43–53.
[77] N. Shartova, V. Mironova, S. Zelikhina, F. Korennoy, M. Grishchenko, Spatial patterns of West Nile virus distribution in the Volgograd region of Russia, a territory with long-existing foci, PLoS Negl. Trop. Dis. 16 (2022), e0010145, https://doi.org/10.1371/journal.pntd.0010145.
[78] Commission Implementing Decision of 27 November 2012 amending Annexes I and II to Council Directive 82/894/EEC on the notification of animal diseases within the Community (notified under document C(2012) 8518)Text with EEA relevance, 2012.
[79] L. Barzon, A. Papa, E. Lavezzo, E. Franchin, M. Pacenti, A. Sinigaglia, G. Masi, M. Trevisan, L. Squarzon, S. Toppo, E. Papadopoulou, N. Nowotny, S. Ulbert, A. Piralla, F. Rovida, F. Baldanti, E. Percivalle, G. Palù, Phylogenetic characterization of central/southern European lineage 2 West Nile virus: analysis of human outbreaks in Italy and Greece, 2013–2014, Clin. Microbiol. Infect. 21 (1122) (2015) e1–1122.e10, https://doi.org/10.1016/j.cmi.2015.07.018.
[80] L. Barzon, F. Montarsi, E. Quaranta, I. Monne, M. Pacenti, A. Michelutti, F. Toniolo, P. Danesi, G. Marchetti, F. Gobbo, A. Sinigaglia, S. Riccetti, E.D. Molin, L. Favero, F. Russo, G. Capelli, Early start of seasonal transmission and co-circulation of West Nile virus lineage 2 and a newly introduced lineage 1 strain, northern Italy, June 2022, Eurosurveillance. 27 (2022) 2200548, https://doi.org/10.2807/1560-7917.ES.2022.27.29.2200548.
[81] J. Schneider, F. Bachmann, M. Choi, L. Kurvits, M.L. Schmidt, L. Bergfeld, I. Meier, M. Zuchowski, D. Werber, J. Hofmann, K. Ruprecht, K.-U. Eckardt, T.C. Jones, C. Drosten, V.M. Corman, Autochthonous West Nile virus infection in Germany: increasing numbers and a rare encephalitis case in a kidney transplant recipient, Transbound. Emerg. Dis. 69 (2022) 221–226, https://doi.org/10.1111/tbed.14406.
[82] U. Ziegler, R. Lühken, M. Keller, D. Cadar, E. van der Grinten, F. Michel, K. Albrecht, M. Eiden, M. Rinder, L. Lachmann, D. Höper, A. Vina-Rodriguez, W. Gaede, A. Pohl, J. Schmidt-Chanasit, M.H. Groschup, West Nile virus epizootic in Germany, 2018, Antivir. Res. 162 (2019) 39–43, https://doi.org/10.1016/j.antiviral.2018.12.005.
[83] R.S. Sikkema, M. Schrama, T. van den Berg, J. Morren, E. Munger, L. Krol, J.G. van der Beek, R. Blom, I. Chestakova, A. van der Linden, M. Boter, T. van Mastrigt, R. Molenkamp, C.J. Koenraadt, J.M. van der Brand, B.B. Oude Munnink, M. P. Koopmans, H. van der Jeugd, Detection of West Nile virus in a common whitethroat (Curruca communis) and Culex mosquitoes in the Netherlands, 2020, Eurosurveillance. 25 (2020) 2001704, https://doi.org/10.2807/1560-7917.ES.2020.25.40.2001704.
[84] Grey heron infected with West Nile virus | RIVM. https://www.rivm.nl/en/news/grey-heron-infected-with-west-nile-virus, 2023 accessed August 24.
[85] S. Paz, J.C. Semenza, Environmental drivers of West Nile fever epidemiology in Europe and Western Asia—a review, Int. J. Environ. Res. Public Health 10 (2013) 3543–3562, https://doi.org/10.3390/ijerph10083543.
[86] J.-P. Martinet, H. Ferté, A.-B. Failloux, F. Schaffner, J. Depaquit, Mosquitoes of North-Western Europe as potential vectors of arboviruses: a review, Viruses. 11 (2019) 1059, https://doi.org/10.3390/v11111059.
[87] J. Heidecke, A.L. Schettini, J. Rocklöv, West Nile virus eco-epidemiology and climate change, PLoS Clim. 2 (2023), e0000129, https://doi.org/10.1371/journal.pclm.0000129.
[88] M.J. Watts, V. Sarto i Monteys, P.G. Mortyn, P. Kotsila, The rise of West Nile virus in southern and southeastern Europe: a spatial–temporal analysis investigating the combined effects of climate, land use and economic changes, One Health. 13 (2021), 100315, https://doi.org/10.1016/j.onehlt.2021.100315.
[89] M. Marcantonio, A. Rizzoli, M. Metz, R. Rosà, G. Marini, E. Chadwick, M. Neteler, Identifying the environmental conditions Favouring West Nile virus outbreaks in Europe, PLoS One 10 (2015), e0121158, https://doi.org/10.1371/journal.pone.0121158.
[90] G. Marini, M. Manica, L. Delucchi, A. Pugliese, R. Rosà, Spring temperature shapes West Nile virus transmission in Europe, Acta Trop. 215 (2021), 105796, https://doi.org/10.1016/j.actatropica.2020.105796.
[91] N.D. Grubaugh, J.T. Ladner, P. Lemey, O.G. Pybus, A. Rambaut, E.C. Holmes, K. G. Andersen, Tracking virus outbreaks in the twenty-first century, Nat. Microbiol. 4 (2019) 10–19, https://doi.org/10.1038/s41564-018-0296-2.