Originally published as:

**Mankertz A, Mulders MN, Shulga S, Kremer JR, Brown KE, Santibanez S, et al. Molecular genotyping and epidemiology of measles virus transmission in the World Health Organization European Region, 2007-2009.**
**(2011) Journal of Infectious Diseases, 204 (Suppl. 1), pp. 335-342.**

**DOI: 10.1093/infdis/jir101**

# Molecular Genotyping and Epidemiology of Measles Virus Transmission in the World Health Organization European Region, 2007–2009

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## *Abstract*

***Background.*** *In 2002, the World Health Organization (WHO) adopted a goal to eliminate measles in the European Region by 2010. Measles elimination is defined as the interruption of indigenous measles virus (MV) transmission. The molecular epidemiology of MV transmission in the WHO European Region was studied through the investigation of reported cases and outbreaks to monitor the region's progress toward its measles elimination goal.*

***Methods.*** *National and regional laboratories performed molecular characterization of MV detected between 2007 and 2009 in the WHO European Region. To document indigenous transmission and importations into the region, we analyzed genotyping results and epidemiological data on measles outbreaks reported by the member states.*

***Results.*** *Since 2007, MV genotype D6 has not been reported in the WHO European Region, suggesting that its chains of transmission have been interrupted, whereas several other MV genotypes are still circulating. Although several European countries have already interrupted indigenous MV transmission, genotyping showed that 3 endemic MV transmission chains have been reestablished in other countries.*

***Conclusions.*** *The WHO European Region 2010 goal will not be met, as indigenous transmission of MV has not been interrupted. As the region begins to document its process of elimination verification to monitor progress toward the goal, countries will need to ensure that genotyping is performed in all measles outbreaks.*

*Following the elimination of measles in the Americas and based on the achievements in measles control in Europe, the World Health Organization (WHO) adopted a goal to eliminate measles from the European Region by 2010 [1]. The target date has recently been changed to 2015 [2]. The national immunization programs of all 53 European Region member states include a routine 2-dose immunization schedule with measles- and rubella-containing vaccines, and each member state, excepting only Switzerland, has nominated a national measles laboratory as part of the WHO laboratory network. Measles elimination is defined as the interruption of indigenous transmission of measles virus (MV) for a 12-month period. In this setting, secondary spread from an imported measles case is limited [3, 4]. To verify that elimination has been achieved, the interruption of indigenous*

*transmission has to be documented by each member state. The indicators used to monitor progress toward the elimination goals are low incidence of measles (<1 measles case per million population), 0 cases of measles caused by an endemic virus for at least 12 consecutive months, and very high (>95%) vaccination rates for both first and second routine doses of measles-containing vaccine [4].*

*Strong national surveillance systems are the cornerstones for member states to detect clinical cases of measles and conduct in-depth case investigations, including laboratory confirmation of suspected measles cases and analysis of MV isolates. Laboratory diagnosis is required to confirm measles cases, particularly when measles incidence is low and more cases of rash and fever illness are actually caused by other infections or syndromes. Once case investigators collect adequate information on the epidemiology and identify the virus genotype for laboratory-confirmed measles, a case is classified as either endemic or an importation. Molecular genotyping of MV is the only tool that demonstrates the interruption of circulating endemic virus, which becomes increasingly important during elimination, when incidence is approaching 0 [3]. This is one of the key components of the verification of measles elimination.*

*Since the resolution to eliminate measles, member states have worked to strengthen both the epidemiological and laboratory components of their surveillance systems to implement case-based surveillance, thus allowing progress toward the European Region's goal to be monitored. This report investigates the transmission of MV in the European Region from 2007 to 2009 and provides an update on the molecular epidemiological characterization of viruses circulating.*

## *Methods*

### Epidemiologic Data

A variety of sources supplied information on measles outbreaks in the European Region during 2007–2009 as part of the routine monitoring system. Member states reported outbreaks to either the WHO Regional Office for Europe or through EUVAC.NET using a standardized outbreak-reporting form, and through the annual WHO/United Nations Children's Fund (UNICEF) Joint Reporting Form. Member states also reported their official measles–case–based surveillance data monthly to the WHO Centralized Information System for Infectious Diseases (http://cisid.euro.who.int/). Additional sources for outbreak reports included direct official communication to the WHO country offices, reports through the WHO Event Information Site for International Health Regulations National Focal Points, and reports through the Early Warning and Response System for the European Union. We used publicly available information on measles outbreaks from other sources, such as Web pages of the ministries of health, public health institutes, national surveillance bulletins, published scientific articles, and other periodicals as resources. As part of routine surveillance activities of the WHO Regional Office for Europe, officials in the respective member states verified unofficial reports from public sources. The WHO Regional Office receives case-based data from 39 member states.

### Molecular Data

Genotyping of MV was performed as recommended by WHO [5] either by the national measles laboratory (NML) or samples were sent to the three regional reference laboratories (RRL) in Berlin, Luxemburg and Moscow or the global specialized laboratory (GSL) in London. A 450-nucleotide fragment encoding the C-terminal end of the nucleoprotein N was used for sequence analysis. The NMLs performed sequencing using various protocols that were developed either in-house or by the designated RRL. If the sequence information was not generated in the NML, clinical samples, virus isolates, or polymerase chain reaction (PCR) products were sent to the regional reference laboratory. We performed sequencing and genotyping. We aligned sequences using ClustalW [6] and further analyzed using SeqScape 2.5, and MEGA 5.0 DNA-analysis software [7]. We constructed phylogenetic trees using the neighbor-joining method. Genotype assignment was performed by phylogenetic comparison with the MV reference strains as designated by WHO [5]. The GSL and the RRLs submitted the sequence data, the genotype, the official WHO MV sequence name, and relevant epidemiologic data to the WHO database, MeaNS (http://www.hpa-bioinformatics.org.uk/Measles/Public/Web_Front/main.php), or GenBank. MV sequences used in this

study are characterized by their prefix, MVi stands for a measles virus sequence from isolates while MVs indicates a measles virus sequence from clinical specimens.

## *Results*

During 2007–2009, the European Region reported a total of 23,229 measles cases (6969–8983 cases annually), with the most cases in 2008 (Table 1). The annual measles incidence in the region during this period was at an all-time low [8], ranging between 7.8 and 10.1 cases per million population. During 2007–2009, the number of countries with low incidence of measles (<1 case per million population) increased from 29 to 38, and number of countries with high incidence (>10 cases per million population) decreased from 11 to 5 (Table 2). Georgia, Ireland, Israel, Switzerland, and the United Kingdom reported a high incidence for 2 or even 3 consecutive years (Table 3). Whereas the number of countries reporting measles outbreaks declined from 19 in 2007 to 9 in 2009 (Table 1), the number of outbreak-related cases increased from 2750 in 2007 to 4354 in 2009. This increase was mainly due to a large outbreak in Bulgaria affecting primarily persons of Roma ethnicity [9]. The percentage of outbreaks with molecular genotyping increased from 41% in 2007 to 75% in 2009. The distribution of genotypes varied by year (Table 2). In 2007, most detected MV belonged to genotypes D4, D5, and D6, whereas genotypes B3, D8, D9, and H1 were detected only rarely. In 2008 and 2009, D6 was no longer detected, and D4 and D5 became the predominant genotypes. The genotypes B3, D8, D9, and H1 were detected sporadically in a few countries. Overall, D4 and D5 were the predominant genotypes in 2007–2009.

### Termination of Endemic Measles Transmission Chains Between 2007 and 2009

From late 2004 until early 2007, a nationwide outbreak associated with MV genotype D4 occurred in Romania [10]. Several closely related subvariants of D4 were identified during this epidemic as measles virus sequences from isolates (MVi) or from clinical specimens (MVs). In early 2005, a Roma group traveling from Romania to Germany transmitted the predominant virus variant (MVs/Bucharest.ROU/48.04/2, “D4-Bucharest”). Variant MVs/Frankfurt.DEU/03.05 started an outbreak in the Federal State of Hesse [11]. Additional cases associated with the same virus variant (Figure 1) were detected in other parts of Germany (MVs/Berlin.DEU/16.05) and in Switzerland (MVs/Aarau.CHE/15.05). Related virus variants were observed in Portugal (MVs/Guimaraes.PRT/29.05) and Spain (MVs/Tarragona.ESP/27.05) in 2005, and later on in France (MVi/Lyon.FRA/21.06), Italy (MVs/Merano.ITA/33.06), Bosnia and Herzegovina (MVs/Sarajevo.BIH/11.07), and Serbia (MVs/Sombor.SER/20.07). The last virus belonging to the Romanian lineage was detected in Romania in September of 2007 (MVs/Arad.ROU/38.07/2). Viruses of this D4-subvariant transmission chain circulated over a period of nearly 3 years in parts of southern, central, and western Europe, and >9,000 cases were reported.

In 2007, genotype D6 circulated in Poland (MVi/Warsaw.POL/12.07), the Republic of Moldova (MVs/StefanVoda.MDA/6.07/1), and the Ukraine (MVs/Ivano-Frankivs'k.UKR/13.7/1). The viruses were identical to the D6 strain MVs/Kyiv.UKR/03.06/1 associated with the large outbreak in the Ukraine that caused >50,000 cases during 2005–2006 [12]. This “Ukrainian lineage” was more closely related to contemporary D6 viruses seen in Kazakhstan (MVs/Mangistau.KAZ/36.07) and viruses of the previously detected “German/Turkish line,” MVi/Berlin.DEU/47.00 and MVi/Ankara.TUR/29.04. Another lineage of closely related D6 variants was found predominantly in the newly independent states of the former USSR in 2007 [13]. It caused an outbreak in Uzbekistan (MVs/Andijon.UZB/5.07/1) and was exported to neighboring countries of Kyrgyzstan (MVs/Osh.KGZ/20.07/1) and the Russian Federation (MVs/Moscow.RUS/15.07/1). These lineages found in 2006 and 2007, however, were distinct from the D6 variants indigenous to the European Region in previous years (MVs/Berlin.DEU/08.96, MVi/DNK/96) [10, 14] (Figure 2). Although D6 was 1 of the predominant genotypes in 2007, it was no longer found in the following years.

### Results of MV Introduction in 2007–2009

The effect of MV introduction into a member state was found to be dependent on the susceptibility profiles of the general population. Between 2007 and 2009, importation of MV led to different results,

ranging from (i) no or short chains of subsequent virus transmission, to (ii) timely and district-limited outbreaks and to (iii) epidemics or even reestablishment of endemic circulation.

### Measles Introduction Without Secondary Spread

The importation of a D4 genotype virus from the United Kingdom into Norway by a group from the traveling community did not lead to any secondary cases among the highly immunized Norwegian population [15]. Similar findings were seen in countries already demonstrating interruption of endemic MV and reporting high immunization coverage with 2 doses of measles vaccine.

### Measles Introduction With Limited Spread

In 2008, a passenger from Djibouti introduced a genotype B3 variant to Denmark, which was transmitted nosocomially to 6 patients [16]. In Austria, introduction of a genotype H1 strain to an anthroposophic school led to 37 cases in 2009 [17]. In Germany, the importation of a genotype D8 virus from India to an anthroposophic school and kindergarten in late 2009 led to 62 cases [18]. Similar limited outbreaks following MV introductions were detected in Kyrgyzstan, Russian Federation, Italy, France, Israel, the former Yugoslav Republic of Macedonia, Serbia, and Poland [19]. In these outbreaks, MV was introduced into susceptible populations that were encircled by a general population protected by high immunization coverage rates, therefore further transmission did not occur. Between 2007 and 2009, a number of introductions of various MV genotypes started limited chains of transmission that did not reestablish endemic transmission. In 2007, a D8 virus was introduced to the federal state of North Rhine-Westphalia, Germany, where coverage did not exceed 95% for both doses of measles-containing vaccines. North Rhine-Westphalia reported >200 cases, but the virus did not spread to other German states [20].

### Measles Introduction With Reestablishment of Endemicity

In Switzerland, the introduction of genotype D5 MVs/Lucerne.SWI/46.06 resulted in a large-scale nationwide epidemic with >4000 cases between 2006 and 2009 [21]. In addition to sustained nationwide circulation of D5 virus in Switzerland, export of this outbreak virus led to large secondary outbreaks, often associated with anthroposophic communities, in Germany, Austria, Belgium, and France [22, 23, 24]. Most of the viruses identified from these subsequent outbreaks were identical in sequence to the MVs/Lucerne.SWI/46.06 outbreak strain, indicating prolonged transmission of D5 genotype in Switzerland and neighboring countries (Santibanez, personal communication). In the United Kingdom, measles endemicity was reestablished with genotype D4 (MVs/Enfield.UNK/14.07) as the predominant genotype in 2007. It was first identified during an outbreak among members of the Irish Travelers community [25, 26]. Since then, multiple closely related variants of the dominant genotype D4 have been circulating in the general population [27] and were exported to several other countries, including Belgium [28], Israel, Germany, and Italy. In spring 2009, Bulgaria reported an outbreak that continued to spread through the country. It was associated with a genotype D4 strain (MVs/Shumen.BUL/15.09/1), which was introduced into northeastern Bulgaria in March 2009 from Germany. Subsequently, the virus spread across the entire country, primarily among the Roma population [9]. All 3 chains of transmission have been active for >12 months, and endemicity was thus reestablished.

## *Discussion*

Implementation of the components of the WHO Regional Office for Europe's strategic plan for measles and rubella elimination 2005–2010 [3] has resulted in a dramatic decrease in measles incidence in the European Region. Several member states have achieved interruption of indigenous MV for a 12-month consecutive period. Furthermore, Andorra, Armenia, Belarus, Czech Republic, Estonia, Finland, Greece, Hungary, Iceland, Lithuania, Montenegro, Portugal, San Marino, Slovakia, Slovenia, Tajikistan, and Turkey reported 0 or very low incidence each year from 2007 to 2009. Molecular genotyping of MV in earlier years indicated that from the late 1990s until 2003, several distinct genotype C2 and D6 variants were indigenous to central and western Europe [29, 30, 31, 32]. In parts of the region, they were displaced by the new genotype D7 [14]. In the newly independent states of the former USSR, genotypes D4 and D6 were found to be the predominant genotypes since 2003. From 2004 onward, however, genotypes C2 and D7 have not been detected again. Several lineages of MV genotype D6 were prevalent in the region; the MV genotype D6 was last detected in 2007 [13]. In addition, a subvariant of D4 (Bucharest.ROU/48.04) was no longer detected after 2007, suggesting that several long-lasting transmission chains have been interrupted. We observed that importation of genotypes B3, D6, D8, D9, and H1 did not lead to endemic circulation. Recently, the whole European Region has made substantial progress toward measles elimination.

The molecular-genotyping results indicated, however, that endemic measles circulation has been reestablished by 3 separate chains of transmission in Switzerland (D5), the United Kingdom (D4), and Bulgaria (D4), with subsequent spread to other member states. The nationwide outbreak in Bulgaria, which began in 2009, occurred after the absence of indigenous MV transmission for 7 years. In addition to these 3 countries, a high measles incidence of >10 per million population was reported in Albania, Austria, Bosnia and Herzegovina, Croatia, France, Georgia, Germany, Ireland, Israel, Italy, Romania, Serbia, the former Yugoslav Republic of Macedonia, Turkmenistan, Ukraine, and Uzbekistan at least for 1 year between 2007 and 2009. This clearly demonstrates that there is indigenous measles transmission in many member states of the European Region, and importation remains a high risk in geographic areas with low herd immunity.

During the verification of elimination in the WHO European Region, molecular genotyping provides information critical to understanding MV importations and transmission pathways. As a consequence of improved molecular epidemiological surveillance, the number of outbreaks in the region for which genotype information is available has increased. Whereas these data are highly useful, the actual incidence of a single genotype in the WHO European Region cannot be determined, both because the proportion of samples tested varied widely across the region and because genotype information is currently available for only 15% of all cases reported.

The level of population susceptibility in a given geographic area affects the impact of MV importation [33]. Where immunization coverage is high, an importation can lead to no or minimal spread of virusIn countries with pockets of unimmunized populations at the subnational levels, importations can lead to time-limited spread with few chains of transmission due to high population immunity overall. In countries with larger cohorts of unimmunized populations or low national coverage, importations have led to reestablishment of endemic measles and prolonged outbreaks. The reasons for the differing levels of population susceptibility in countries vary. For example, the impact of herd immunity as a public good and views on social responsibility to protect vulnerable groups in society is not sufficiently appreciated and should be emphasized [34]. There are also groups that refuse vaccination due to cultural, philosophical, or religious beliefs, or based on concerns about measles, mumps, and rubella (MMR) vaccine safety [35]. Moreover, the antivaccination movement is highly active in Europe, and modern networking facilitates the dissemination of antivaccination ideas. The misinformation about vaccines and adverse events delay efforts by the public health community to achieve measles and rubella elimination [36]. However, the consequences are the same: Populations susceptible to MV are at risk of potential outbreaks if the virus is imported. To follow importations and distinguish these from endemic circulation, molecular genotyping of MV is the method of choice.

As the WHO European Region begins to document the verification of measles elimination, it will face with challenges that need to be addressed. Currently, genotyping is not conducted in all countries, thus not all MV genotypes are monitored. The absence of D6 and D4-Bucharest from reports in 2008 and 2009 does not necessarily mean that circulation has been completely interrupted, as data from

some countries are missing. In addition, national surveillance systems are adapted to specific needs and available resources, and member states use slightly different definitions for a measles outbreak. However, to avoid misinterpretation, we followed every chain of transmission of measles using the appropriate nationally employed definition. In 2009, the WHO Regional Office for Europe received case-based data, which are required for linking the clinical and epidemiological information to the molecular data, from only 39 of 53 member states. Reporting by member states must be strengthened, to track the number of outbreaks and the total number of cases in each outbreak. An indication of a high-quality surveillance system is that genotype information is available for all outbreaks when verifying elimination. The verification process of measles elimination will require the formation of a regional verification commission and national committees. These committees will require documentation and evidence, especially on the molecular genotyping of circulating MV, to verify that there is no indigenous transmission of MV for a defined period of time. Therefore, genotyping results are indispensible, and accelerated efforts are needed to ensure this information is collected and interpreted so that the process for verifying elimination can be implemented.

## *Acknowledgments*

The national measles laboratories are acknowledged for their contribution to the measles genotype surveillance in the WHO European Region. We are grateful to Ajay Goel, WHO, for his data analysis.

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## *Tables and Figures*

**Table 1.** Reported Measles Cases, Recognized Outbreaks, and Measles Virus Genotypes, World Health Organization European Region, 2007–2009

| Parameters | 2007 | 2008 | 2009 |
|---|---|---|---|
| Number of reported measles cases (measles cases per million population) | 6969 (7.8) | 8983 (10.1) | 7277 (8.2) |
| Number of member states with reported aboratory-confirmed measles cases | 38 | 38 | 32 |
| Number of member states with recognized outbreaks (% of all member states) | 19 (35.8) | 15 (28.3) | 9 (17.0) |
| Total number of recognized outbreaks through any source | 34 | 29 | 16 |
| Number of recognized outbreaks with genotype information (% of all recognized outbreaks) | 14 (41.2) | 16 (55.2) | 12 (75.0) |
| Predominant genotypes of measles virus circulating | D4, D5, D6 | D4, D5 | D4 |

**Table 2.** Measles Genotypes Isolated in the World Health Organization European Region by Number of Member States, 2007–2009.

| Measles genotype | 2007 | 2008 | 2009 |
|---|---|---|---|
| B3 | 3 | 2 | 5 |
| D4 | 7 | 16 | 12 |
| D5 | 8 | 11 | 5 |
| D6 | 8 | - | - |
| D8 | 3 | 6 | 5 |
| D9 | 1 | 7 | 5 |
| H1 | 3 | 3 | 4 |

**Table 3.** Reported Incidence of Measles, Cases per Million Population, World Health Organization European Region, 2007–2009

| Countries | 2007 | 2008 | 2009 |
|---|---|---|---|
| Incidence per million population | | | |
| Albania | 11.0 | 0 | 0 |
| Andorra | 0 | 0 | 0 |
| Armenia | .3 | 0 | 0 |
| Austria | 2.4 | 53.4 | 5.0 |
| Azerbaijan | 0 | .6 | .1 |
| Belarus | .1 | 0 | 0 |
| Belgium | 6.1 | 9.4 | 3.1 |
| Bosnia and Herzegovina | 42.2 | 2.0 | 2.0 |
| Bulgaria | .1 | .1 | 296.6 |
| Croatia | 0 | 11.2 | .4 |
| Cyprus | 0 | 1.2 | 0 |
| Czech Republic | .2 | .2 | .5 |
| Denmark | .4 | 2.6 | 1.5 |
| Estonia | .7 | 0 | 0 |
| Finland | 0 | .9 | .6 |
| France | .6 | 9.8 | 23.9 |
| Georgia | 10.0 | 12.8 | 5.3 |
| Germany | 6.9 | 11.1 | 6.9 |
| Greece | .2 | .1 | .2 |
| Hungary | 0 | 0 | .1 |
| Iceland | 0 | 0 | 0 |
| Ireland | 14.9 | 13.0 | 37.3 |
| Israel | 77.8 | 132.2 | .7 |
| Italy | 5.5 | 27.4 | 2.4 |
| Kazakhstan | .8 | 1.3 | 0 |
| Kyrgyzstan | 7.5 | 3.0 | 0 |
| Latvia | 0 | 1.3 | 0 |
| Lithuania | 0 | .3 | 0 |
| Luxembourg | 0 | 2.1 | 0 |
| Malta | 4.9 | 2.4 | 2.4 |
| Monaco | | | 0 |
| Montenegro | 0 | 0 | 0 |
| Netherlands | .6 | 6.6 | .5 |
| Norway | 4.3 | .8 | .4 |
| Poland | 1.1 | 2.6 | 4.2 |
| Portugal | 0 | .1 | .3 |
| Republic of Moldova | 2.6 | 0 | 0 |
| Romania | 16.5 | .6 | .3 |
| Russian Federation | 1.2 | .2 | .7 |
| San Marino | 0 | 0 | 0 |
| Serbia | 20.4 | .2 | .1 |
| Slovakia | 0 | 0 | 0 |
| Slovenia | 0 | 0 | 0 |
| Spain | 6.0 | 6.7 | .9 |
| Sweden | .1 | 2.7 | .3 |
| Switzerland | 135.6 | 269.2 | 133.3 |
| Tajikistan | .3 | 0 | 0 |
| The former Yugoslav Republic of Macedonia | .5 | 13.2 | 1.5 |
| Turkey | .0 | .1 | .1 |

**Table 3.** (Continued)

| Countries | 2007 | 2008 | 2009 |
|---|---|---|---|
| Turkmenistan | 11.9 | 0 | 0 |
| Ukraine | 21.8 | 1.0 | .5 |
| United Kingdom | 16.8 | 23.7 | 19.3 |
| Uzbekistan | 31.5 | .1 | 0 |
| World Health Organization European Region | 7.8 | 10.1 | 8.2 |
| Countries by incidence level, *n* | | | |
| Low (<1 per million population) | 29 | 27 | 38 |
| Medium (1–10 per million population) | 12 | 15 | 10 |
| High(>10 per million population) | 11 | 10 | 5 |

**Figure 1.** Phylogenetic analysis of measles virus genotype D4 detected in the World Health Organization European Region. This phylogenetic tree comprises representative measles virus strains of genotype D4 detected in the European Region between 2007 and 2009 aligned to the World Health Organization's D4 genotype reference strain, MVi/Montreal.CAN/89. The ”D4-Bucharest”–related viruses are indicated. This Romanian lineage was widespread from 2004 onward and was no longer detected after 2007, whereas circulation of other D4 variants is ongoing. GenBank accession numbers are as follows: MVs/Gorj.ROU/07.07/1, HQ704308; MVs/Arad.ROU/38.07/2, HQ704309; MVi/Lyon.FRA/21.06, EF428176; MVs/Sombor.SRB/20.07, n.a.; MVs/Bucharest.ROU/04.06/6, n.a.; MVs/Meran.ITA/33.06, AM849094; MVs/Barcelona.ESP/41.06, EU086731; MVs/Roma.ITA/41.06, EF533887; MVi/Bucharest.ROU/47.05/1, AM849059; MVs/Bucharest.ROU/04.06/1, n.a.; MVs/Barcelona.ESP/07.06/2, EU086732; MVs/Valencia.ESP/22.06/2, EU086729; MVs/Novi Sad.SRB/05.07, AM849060; MVs/Sarajevo.BIH/11.07/1, AM849061; MVs/Frankfurt.DEU/03.05, DQ903068; MVs/Aarau.CHE/15.05, AM849090; MVs/Berlin.DEU/16.05, AM849083; MVs/Guimaraes.PRT/29.05, AM849058; MVs/Bucharest.ROU/48.04/1, AM849091; MVs/Tarragona.ESP/27.05, EU086723; MVs/Bucharest.ROU/48.04/2, AM849093; MVs/Carlisle.GBR/4.05/2, n.a.; MVs/Dublin.IRL/19.04, n.a.; MVi/Wisconsin.USA/15.05, DQ888747; MVs/Manchester.GBR/1.06, EF079147; MVs/Uvbridge.GBR/37.09, GU120181; MVs/London.GBR/37.05, EF079130; MVi/Montreal.CAN/89, U01976; MVs/Moscow.RUS/4.09, GQ260663; MVs/Grosseto.ITA/38.06, EF017348; MVs/Aberdeen.GBR/11.09, GQ370462; MVs/Enfield.GBR/14.07, EF600554; MVs/Hamburg.DEU/03.09, HQ436108; MVs/Poitiers.FRA/07.09, FN663615; MVs/Manchester.GBR/10.09, GQ370461.

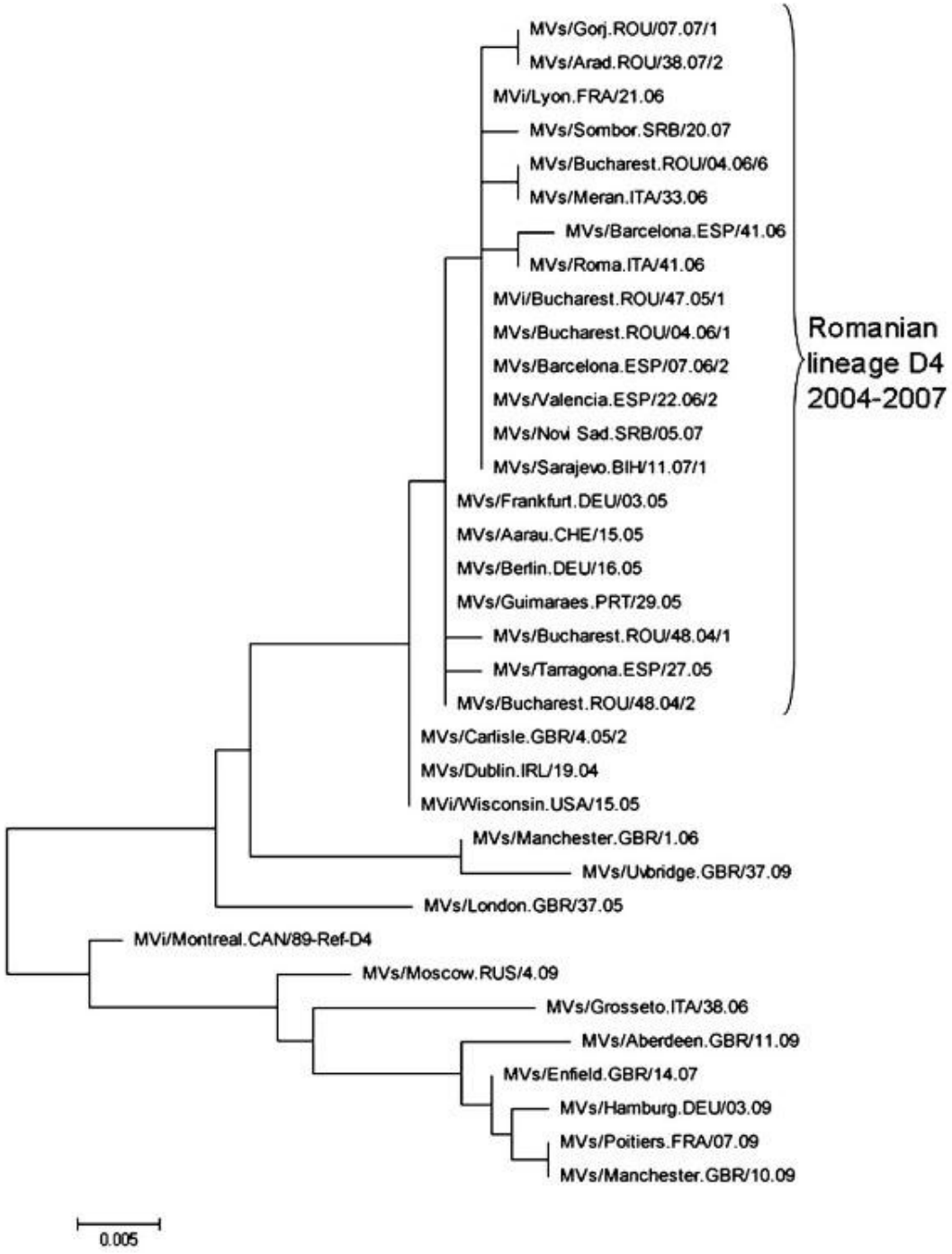

**Figure 2.** Phylogenetic tree of measles virus genotype D6 detected in the World Health Organization European Region. This phylogenetic tree comprises representative measles virus strains detected in the European Region between 2000 and 2007 aligned to the World Health Organization's reference strain for the D6 genotype, New Jersey.USA/94/1. To the best of our knowledge, genotype D6 measles virus was not detected after 2007, suggesting that its transmission chains were interrupted. GenBank accession numbers are as follows: MVs/Ivano-Frankivsk.UKR/13.7/1, GU371650; MVs/Siegen.DEU/07.06, DQ903070; MVs/Warsaw.POL/12.07, HQ721188; MVs/Odesa.UKR/13.7/2, GU371652; MVs/Moscow.RUS/4.07, EU597253; MVs/StefanVoda.MDA/6.07/1, GU371646; MVs/Chernivtsi.UKR/13.7, GU371649; MVs/Kyiv.UKR/03.06/1, EU105462; MVi/Berlin.DEU/47.00, AF474936; MVi/Ankara.TUR/29.04, DQ263696; MVs/NizhnyNovgorod.RUS/8.07, EU597254; MVs/Chuy.KGZ/17.07, GU371647; MVs/Mangistau.KAZ/36.07, GU371653; MVs/Munich.DEU/17.05, DQ903069; MVs/Andijon.UZB/5.07/1, EU597265; MVs/Moscow.RUS/15.07/1, EU597255; MVs/Osh.KGZ/20.07/1, GU371648; MVs/Fargona.UZB/13.07/2, GU371651; MVi/DNK/96, AF276683; MVi/New Jersey.USA/94/1, L46750; Edmonston-wt.USA/54, U01987.