
# Annual OIE/FAO FMD Reference Laboratory Network Report

## January – December 2008

*FAO World Reference Laboratory and OIE Reference Laboratory for FMD (WRLFMD or WRL), Institute for Animal Health, Pirbright, UK: David Paton, Nigel Ferris, Don King, Nick Knowles, Yanmin Li, Bob Statham, John Bashiruddin, Jef Hammond.*

*Centro Panamericano de Fiebre Aftosa (PANAFTOSA) and OIE Reference Laboratory for FMD, Rio de Janeiro, Brazil: Ingrid Bergmann, Viviana Malirat.*

*Federal Governmental Institute, Centre for Animal Health (FGI ARRIAH) and OIE Reference Laboratory for FMD, Vladimir, Russia: Valery Zakharov, Vladimir Borisov, Aleksey Scherbakov, Svetlana Kremenchugskaya.*

*OIE Regional Reference Laboratory for Sub-Saharan Africa (RRLSSA), Gabarone, Botswana: Gaolathe Thobokwe, Lindani Mozola, George Matlho.*

*OIE Reference Laboratory for Foot and Mouth Disease, Laboratorio de Fiebre Aftosa de la Dirección de Laboratorios y Control Técnico (LFADLCT), Argentina: Eduardo Maradei.*

*FAO/OIE FMD Reference Laboratory, Transboundary Animal Diseases Programme, ARC-Onderstepoort Veterinary Institute (ARC-OVI), South Africa: Francois Maree, Belinda Blignaut.*

*FAO FMD Reference Laboratory, Foreign Animal Disease Diagnostic Lab, Plum Island Animal Disease Center (PIADC), Greenport, USA: Samia Metwally*

*OIE collaborating centre for validation, quality assessment and quality control of diagnostic assays and vaccine testing for vesicular diseases in Europe, CODA-CERVA-VAR, Ukkel, Belgium: Kris De Clercq*

*National FMD Laboratory, Lanzhou Veterinary Research Institute (LVRI), CAAS, Gansu, P. R. China: Xuepeng Cai, Xiangtao Liu.*

*Project Directorate on FMD (PDFMD), Indian Council for Agricultural Research, Mukteswar, Nainital (Uttarakhand), India: D. Hemadri, A. Sanyal, R. Venkataramanan[*], Lal Krishna[**], K.M.Bujarbaruah[**], B. Pattnaik.*

*Regional Reference Laboratory for Foot and Mouth Disease in the South East (RRLSEA), Department of Livestock Development, Pakchong, Thailand: Wilai Linchongsubongkoch.*

[*]*IVRI, Bangalore, India* [**]*ICAR, New Delhi, India*

# Introduction to the OIE/FAO FMD Reference Laboratory Network Report

The Network of OIE/FAO FMD Reference Laboratories has been established with two principal goals, namely:

(1) understanding global virus distribution and patterns and making vaccine recommendations,

and

(2) improving the quality of laboratory tests from international and national reference laboratories.

This requires sharing and joint evaluation of surveillance information on laboratory diagnoses, serotyping, genetic characterisations and vaccine matching tests and harmonising standards for diagnostic procedures.

This report is divided into two parts providing an update on progress towards each of these goals.

Additional information about the Network can be found at: http://www.foot-and-mouth.org/

# PART 1

# *Genetic and antigenic diversity and global distribution of foot-and-mouth disease viruses. Information gaps, threats and vaccine recommendations*

## 1.1. Summary of FMD outbreaks and surmised global situation

**Figure 1.** FMD outbreaks reported to FAO/OIE[1] during 2008 and identified at country level (although some may be highly localised)

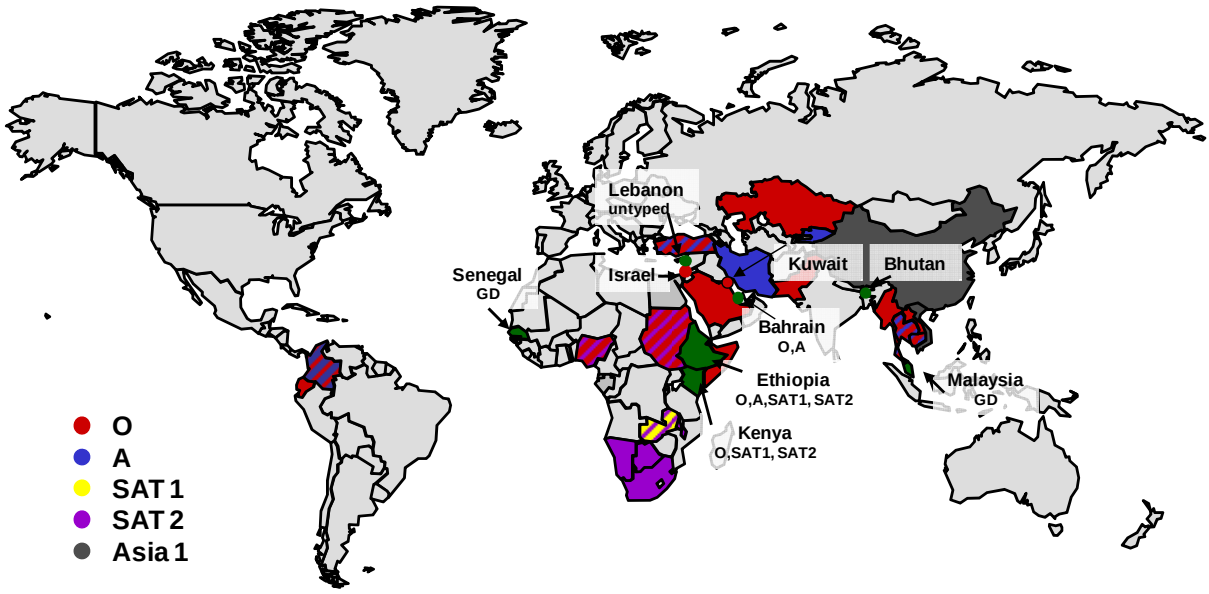
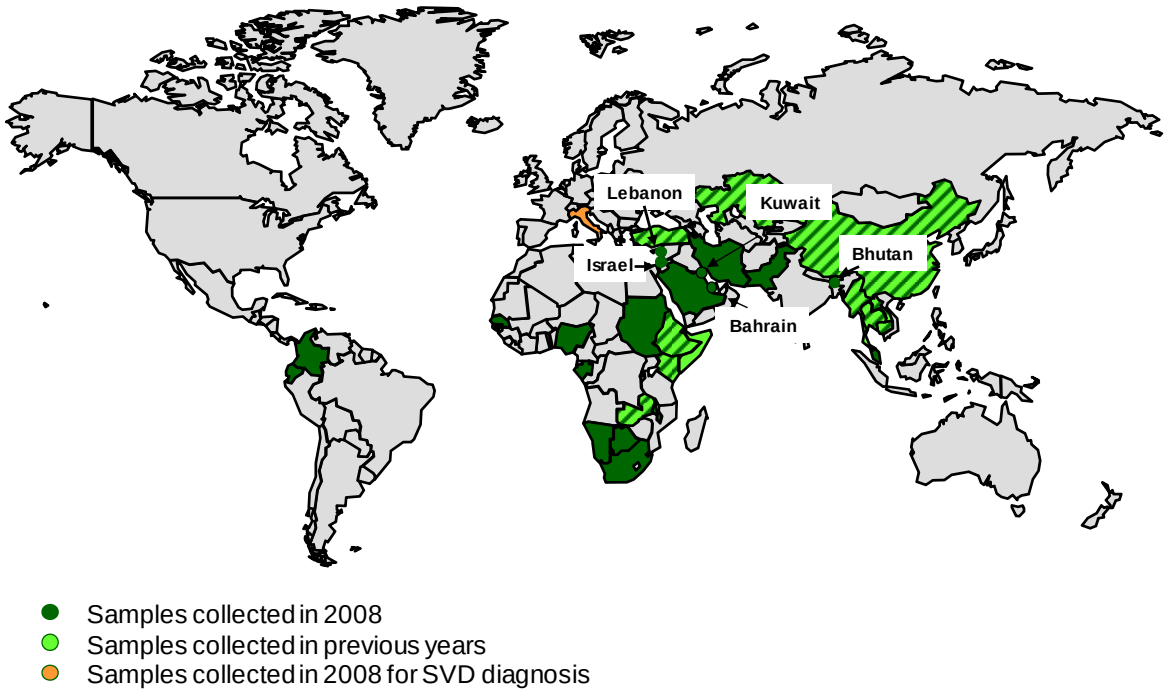



**Figure 2.** Countries submitting samples to the Network Laboratories for FMD diagnosis in 2008




[1] The WAHID Interface provides access to all data held within OIE's new World Animal Health Information System (WAHIS): http://www.oie.int/wahid-prod/public.php?page=home

**Figure 3.** The conjectured status of FMD[2] showing epidemiologically significant events in 2008

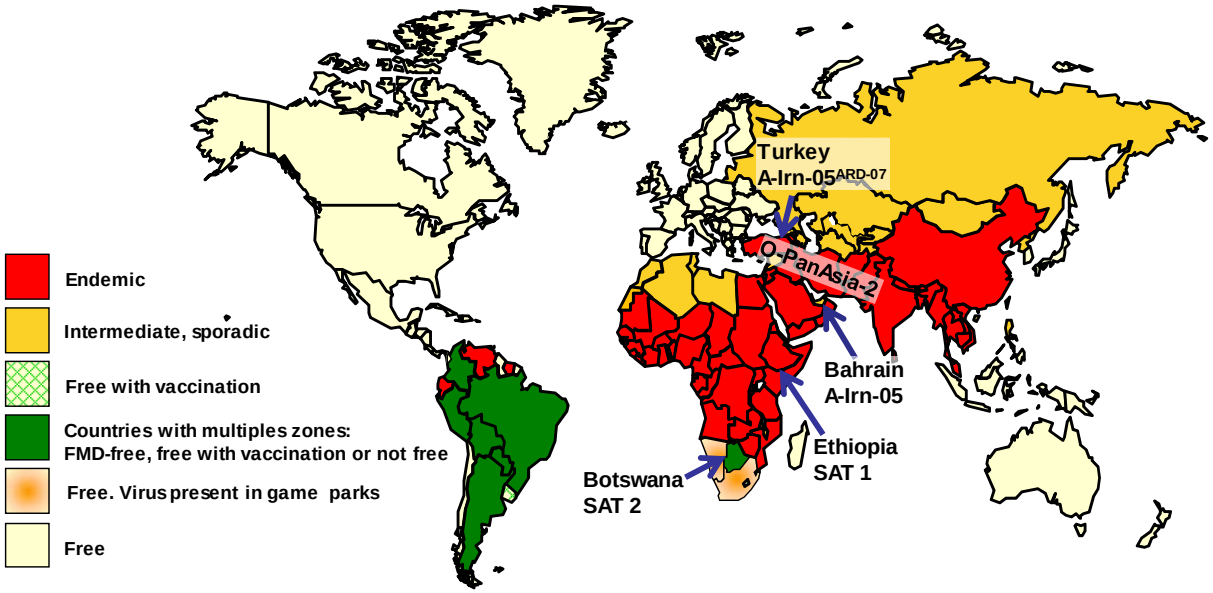
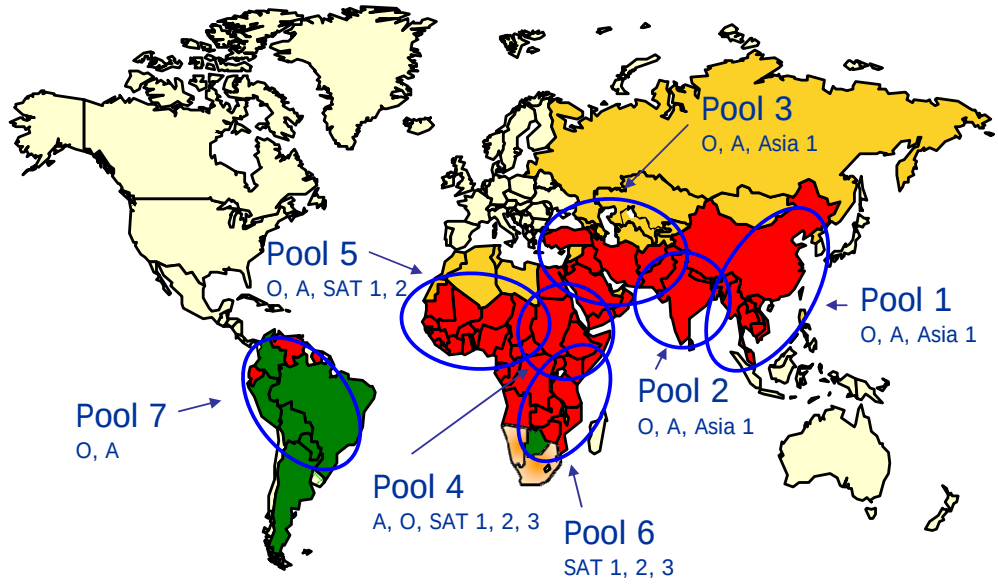



**Figure 4.** Regional virus pools




[2] See detailed regional map of America-South on page 14

## 1.2. Introduction

Global surveillance for foot-and-mouth disease (FMD) aims to identify the current hazards and to predict heightened risk so that appropriate diagnostics and vaccines are available for their detection and control. This requires sustained effort directed towards the monitoring of FMD outbreaks and ideally also of FMD virus (FMDV) circulation and persistence, along with collection and characterisation of FMD viruses and integration of findings with associated epidemiological intelligence. Such an extensive effort requires a team approach encompassing national and international disease control services and their laboratories along with commercial vaccine and diagnostic providers.

The work of international FMD reference laboratories in collecting and characterising FMDV isolates has been reviewed (Ferris and Donaldson, 1992; Kitching 2000) and more recently with emphasis on the requirements and methodologies for vaccine selection (Paton et al., 2005). FMDV is unevenly distributed throughout the world reflecting factors such as livestock density and species mix, patterns of husbandry, animal movement and trade, wildlife reservoirs and incentives and capacities for disease control. The virus exists as multiple serotypes and subtypes with absent or incomplete cross-immunity, likely differences in species predilections and modes of persistence and transmission, and with distributions that are partly based on historical and chance events. The situation is dynamic and affected by viral evolution, waxing and waning host immunity and changing ecosystems and trading patterns. Despite the propensity and opportunities for spread of FMDV into new regions, comparisons of VP1 gene sequences of viruses submitted over many years do show a tendency for similar viruses to recur in the same parts of the world (Knowles and Samuel, 2003; Rweyemamu et al., 2008) and this presumably reflects some degree of either ecological isolation or adaptation. On this basis, the global pool of FMD viruses can be subdivided into seven 'regional pools' in which genetically and antigenically distinctive virus strains tend to occur within a defined region.

The seven 'Regional Pools' referred to throughout this report are shown in Figure 4 and represent:

| | | |
|---|---|---|
| Pool 1 – Asia east | Pool 4 – Africa east | Pool 7 – America south |
| Pool 2 – Asia south | Pool 5 – Africa west | |
| Pool 3 – Eur-Asia | Pool 6 – Africa south | |

Virus circulation and evolution within regional virus pools results in changing priorities for appropriately adapted vaccines. Periodically, viruses spread between pools and to free regions.

Ferris NP, Donaldson AI. (1992) Rev Sci Tech.11(3):657-84.
Kitching RP. (2000) Ann N Y Acad Sci. 916:139-46.
Paton DJ, Valarcher JF, Bergmann I, Matlho OG, Zakharov VM, Palma EL, Thomson GR. (2005) Rev Sci Tech. 24(3):981-93.
Knowles NJ, Samuel AR. (2003) Virus Res.91(1):65-80.
Rweyemamu M, Roeder P, Mackay D, Sumption K, Brownlie J, Leforban Y, Valarcher JF, Knowles NJ, Saraiva V. (2008) Transbound Emerg Dis. 55(1):57-72.

## 1.3. Overview

FMD remained largely confined to traditionally infected areas between January and December 2008.

No outbreaks were reported in countries listed by OIE as FMD-free without vaccination.

There were two changes in OIE FMD status[3]:

(i) Following a report from the OIE Delegate of Botswana of an outbreak of FMD in the Northern part of the veterinary control zone 12, in the Kuke extension area of the Ghanzi district, the status of the 'FMD free zone without vaccination' for Botswana as recognised by the International Committee of the OIE in terms of Resolution XXI of 22 May 2007, was suspended with effect from 27 October 2008.

(ii) As from 29 July 2008 the State of Mato Grosso do Sul, Brazil has regained its status as a zone free from FMD with vaccination.

Within endemically and sporadically infected parts of the world there have been upsurges of cases, sometimes leading to the submission of samples to reference laboratories and indicating an enhanced risk of collateral spread.

The majority of viruses have been isolated from samples submitted from Africa and Asia which remain the major reservoirs for the FMD virus.

### Information gaps

Submission of samples from endemic regions has continued to be mainly in response to perceptions of increased number or severity of outbreaks, although in some cases there are proactive projects promoting sample submission. Reactive sampling provides an incomplete survey of the global virus pool and often lacks context in the form of information on the history accompanying the samples. Nevertheless, the bias towards things that are out of the ordinary may be helpful in providing early warning for new epidemics.

The main gaps in knowledge about the global distribution of FMDV come from countries without control schemes, especially in sub-Saharan Africa and in southern and central Asia.

### Threats

The greatest diversity of FMD viruses are in Africa and there are relatively few vaccines available that have been developed to protect against current African strains. Vaccines used in Africa may also lack stability and potency contributing to poor protection and increasing the threat of spread of outbreaks in the region and beyond.

[3] http://www.oie.int/eng/Status/FMD/en_fmd_change.htm

Southern Asia remains an important reservoir for serotypes O, A and Asia 1. FMD viruses have traditionally spread from here into western Asia threatening FMD-free regions to the north and west in Central Asia and Europe. The latest incursions have been of the O PanAsia 2 and A Iran 05 strains and these still present a significant threat for further spread.

**Vaccine recommendations**

Matching tests to check the antigenic suitability of vaccines to protect against circulating strains continue to reveal gaps in cover, especially against serotype A and SAT 2. Some recent A Iran 05 viruses from Turkey have shown consistently weak matches to the $A_{22}$ Iraq vaccine virus that is used in some Middle Eastern countries and is an important component in European vaccine banks. Viruses isolated from recent outbreaks due to SAT 2 in Botswana, as well as in other parts of Africa, have also shown poor matches to available vaccine strains. Continuous molecular and antigenic characterisation of field viruses is of utmost importance to facilitate rapid development of new vaccines that will provide coverage for specific regions. In addition, there is an urgent need for new SAT vaccine strains with good immunogenicity, adaptation to suspension cultures of BHK-21 cells and post-inactivation stability.

## 1.4. Regional situation

**Pool 1: ASIA-EAST**

Network labs receiving samples in 2008:

| Laboratory | Sample Nos. | Countries of origin |
|---|---|---|
| WRLFMD | 9 | Laos, Malaysia, Thailand |
| RRLSEA | 286 | Cambodia, Laos, Myanmar, Thailand |
| LVRI | 3 | China |

Japan, S Korea, Indonesia and the island states of Malaysia remained FMD-free without vaccination. Brunei has attained OIE recognition as FMD-free without vaccination. Taiwan was FMD-free with vaccination.

In China, small numbers of outbreaks have been reported due to type Asia1 and 8 outbreaks were confirmed as caused by this serotype at LVRI. An Asia 1 virus isolated at WRLFMD from an outbreak in North Korea in 2007 was shown by partial sequencing to be related to recent outbreaks in China; serology showed a match to the Asia 1 Shamir vaccine strain.

The SEAFMD website (http://www.seafmd-rcu.oie.int/index.php) provides summary information, details and maps showing countries in southeast Asia that have experienced outbreaks in each month of 2008. The Philippines continues along the pathway to freedom with no outbreaks. On the mainland in SE Asia, outbreaks of FMD have been reported in 2008 from Peninsular Malaysia, Vietnam, Thailand, Myanmar, Cambodia and Laos.

Samples were sent to RRLSEA in Pakchong from Thailand, Myanmar, Cambodia and Laos and type O FMD viruses were recovered from all of these countries. Type A

viruses were also detected in samples from Thailand and Cambodia. Samples were sent to WRLFMD in Pirbright from Malaysia, Thailand and Laos resulting in recovery of FMD virus of type O from Thailand and Laos, whilst FMDV genome was detected in samples from Malaysia. Genetic analysis of the type O viruses from Thailand and Laos showed that both were indigenous types, being of the Myanmar-98 strain of the SE Asia topotype.

Vaccine strains that may be suitable for use in the region include:

| Serotype | Internationally available | Locally produced |
|---|---|---|
| O | $O_1$ Manisa | China 1999, Thailand 189/87 |
| A | Malaysia 97 | China 1972, Thailand 118/87 |
| Asia 1 | Shamir | China 2005, Thailand 85 |

Serotype O Cathay-like virus vaccines (e.g. O Taiwan 97, O Philippine 97, or O 1685 Russia 95) could also be useful where viruses of this topotype affect pigs.

**Pool 2: ASIA-SOUTH**.

Network labs receiving samples in 2008:

| Laboratory | Sample Nos. | Countries of origin |
|---|---|---|
| WRLFMD | 9 | Bhutan, Pakistan |
| INDIA | 2258 | India |

*collected from 1211 outbreaks during 2007-2008.

India, Pakistan, Sri Lanka, Bangladesh, Bhutan and Nepal remain endemically infected with FMDV.

The overall incidence of FMD in India has come down since the year 2006, particularly in Northern India, due to the mass vaccination campaign conducted under the FMD Control Programme launched by Govt. of India since 2004. Nevertheless, FMD still remains endemic in most parts of the country with involvement of Serotypes O, A and Asia1. Serotype O caused most of the outbreaks and was recovered from almost all parts of the country, while Asia 1 was recovered mainly from Eastern India and type A from a few southern and northern states of India. Serotype A and Asia1 is almost absent in the Northern States of Punjab, Haryana and Delhi. Most serotype O virus isolates belonged to ME-SA topotype and PanAsia-1 and 2 lineages (Fig. 20) while type Asia 1 viruses were of lineage C-II (Fig. 21). Serotype A isolates have been exclusively of Genotype VII that is unique to India. In recent times, viruses with $VP3^{59}$-deletion within the lineage VII caused some outbreaks (Fig. 22). This deletion mutant group is antigenically heterogeneous, and being monitored at the country level.

Few samples were submitted to WRLFMD from the region and only 6 isolates, all serotype O, were made from samples collected in 2008; 4 from Pakistan and 2 from Bhutan. The O serotype viruses were of ME-SA topotype and PanAsia-2 lineage. A single A serotype virus, collected in Pakistan in 2007, was unrelated to A-Iran-05-like viruses previously found in Pakistan and fell on a distinct lineage most closely related to viruses from Iran and Pakistan in 2000-2003.

Vaccine strains that may be suitable for use in the region include:

| Serotype | Internationally available | Locally produced |
|---|---|---|
| O | $O_1$ Manisa | IND R2/75* |
| A | $A_{22}$ Iraq | IND 40/2000* |
| Asia 1 | Shamir | IND 63/72* |

* Trivalent vaccine comprising these three strains is nationally mandated in India

**Pool 3: EUR-ASIA**

Network labs receiving samples in 2008:

| Laboratory | Sample Nos. | Countries of origin |
|---|---|---|
| WRLFMD | 67 | Bahrain, Iran, Kuwait, Saudi Arabia, Turkey |
| FGI-ARRIAH | 1 | Kyrgyzstan |
| PAIDC | 1 | Israel |

FMD viruses continue to circulate in many Middle-Eastern countries, the prevailing serotypes in 2008, being as in 2007, O (PanAsia-2 lineage) and A (Iran 05 lineage).

Serotype O, strain PanAsia-2 viruses were recovered from samples sent to WRLFMD from Turkey, Iran, Bahrain, Kuwait and Saudi Arabia. Some viruses from Saudi Arabia, Kuwait and Iran shared a recent common origin. A Iran 05 viruses were recovered from samples from Bahrain, Iran and Turkey. In the case of Bahrain, this is the first report of serotype A infection since 1965. In Turkey, all of the serotype A isolates examined at WRLFMD were of the Iran-$05^{ARD-07}$ sub-lineage which is unique to Turkey and gives rise to concern on account of the poor serological match to the $A_{22}$ Iraq vaccine strain that is widely used in the Middle East.

No samples collected in 2008 were received from Afghanistan or from the countries of the former Soviet Union. A virus from Kyrgyzstan in 2007 was characterised at FGI ARRIAH and shown to be serotype A of the Iran 05 lineage. In 2007, Israel was affected by serotype O epidemics despite the presence of a national compulsory vaccination program using a trivalent vaccine in cattle (containing types O, A22 and Asia1) and a monovalent vaccine in small ruminants (containing type O). Three strains of serotype O are included in the vaccine: O1 Manisa, Geshure Isr/2/85 and 3039. Virus was characterized at PIADC and shown to belong to sublineage of serotype O which is distinct from the vaccine used in the region. In addition, the virus showed close identity to the 2003 and 2004 isolates in South Asia and could be of a recombination between different serotypes. Pathogenicty study done at PIADC showed that the virus was highly virulent; causing myocarditis and mortalities in the U.S. Holstein cattle while mortality was only observed in goats during the disease outbreak.

Vaccine strains that may be suitable for use in the region include:

| Serotype | Internationally available | Locally produced* |
|---|---|---|
| O | $O_1$ Manisa | Russian $O_1$ PanAsia |
| A | $A_{22}$ Iraq | Turkey 1/2006 (A Iran 05 lineage) |
| Asia 1 | Shamir | Georgia 2000 |

* Vaccines are also produced locally in Iran, Turkey, Egypt and Jordan

The main differences between vaccine requirements of pools 1-3 relate to serotype A. The serological match between $A_{22}$ Iraq and some A Iran 05 lineage field isolates is poor.

**Pool 4: AFRICA-EAST**

Network labs receiving samples in 2008:

| Laboratory | Sample Nos. | Countries of origin |
|---|---|---|
| WRLFMD | 103 | Ethiopia, Kenya, Somalia |

Serotypes O, A, SAT 1 and SAT 2 have all been reported from this area in recent years and all countries are thought to be endemically infected with FMD virus. Some countries where disease has been reported in the press (e.g. Uganda) have not submitted samples to a Network laboratory.

In 2008, samples were sent to WRLFMD from Ethiopia, Kenya and Somalia. Material received from Ethiopia has been characterized as belonging to 4 different FMDV serotypes. This is the first description of SAT 1 in Ethiopia and the genetic separation of many of these viruses of differing serotypes, from previously analyzed strains, indicates that there is a considerable amount of uncharacterized FMDV circulating in the region. Kenyan isolates were serotyped as O, A, SAT 1 and SAT 2, all being relatively similar to previously characterised isolates from the region. Three type O viruses, collected in Somalia in 2007, belonged to the EA-3 topotype and were most closely related to viruses from the Yemen Arab Republic collected between 2003 and 2006.

Vaccine strains that may be suitable for use in the region include:

| Serotype | Internationally available | Locally produced |
|---|---|---|
| O | $O_1$ Manisa | Kenya 77/78, Egypt 2/72 |
| A | Eritrea 98 | Kenya 5/80, Egypt 06 |
| SAT 1 | See pool 6 | Kenya T155/71 |
| SAT 2 | Saudi 2000, Eritrea 98, see pool 6 | Kenya 52/84, Kenya 65/82 |

**Pool 5: AFRICA-WEST**

Network labs receiving samples in 2008:

| Laboratory | Sample Nos. | Countries of origin |
|---|---|---|
| WRLFMD | 32 | Gabon, Nigeria, Senegal |

This is one of the least well sampled areas of endemic FMD. Samples collected in 2007 and 2008 were submitted to WRLFMD from Nigeria for the first time in many years, resulting in the identification of serotypes O and SAT 2. Interestingly, isolates of both serotypes were genetically closest to previously characterised isolates from Sudan (Pool 4) obtained between 2005 and 2007. More studies are required to define the relationships between viruses in pools 4 and 5. No FMDV were recovered from

samples received from Senegal and Gabon, possibly due to degradation in storage or shipment.

Vaccine strains that may be suitable for use in the region include:

| Serotype | Internationally available | Locally produced |
|---|---|---|
| O | $O_1$ Manisa | |
| A | Eritrea 98, $A_{22}$ Iraq | |
| SAT 1 | See pool 6 | |
| SAT 2 | Saudi 2000, Eritrea 98, see pool 6 | Nigeria 6/81* |

* Current availability of this vaccine is not known

**Pool 6: AFRICA-SOUTH**

Network labs receiving samples in 2008:

| Laboratory | Sample Nos. | Countries of origin |
|---|---|---|
| WRLFMD | 35 | Botswana, Namibia, Zambia |
| ARC-OVI | 13 | Namibia, Malawi |
| RRLSSA | 246 | Botswana, Namibia, Zambia |

Outbreaks of FMD serotype SAT 2 have occurred in FMD-free regions of Botswana and in the neighbouring Caprivi strip region of Namibia. Zambia, a country without FMD-free status has also recorded outbreaks. The situation in Zimbabwe is unknown but FMD control is unlikely to have received a high priority. Samples were also submitted to ARC-OVI from Malawi.

Genetic analysis based on VP1 gene sequencing and phylogenetic analyses at both WRLFMD and ARC-OVI has helped to understand the epidemiology of outbreaks in Botswana and their links to those in surrounding regions (Namibia and Zambia). There have been three separate introductions of SAT 2 viruses into cattle in Botswana. The virus that affected the FMD-free zone of Ghanzi was closely related to viruses made in the adjacent region to the north (Maun) in 2007 and 2008. These belonged to SAT 2 topotype III. Meanwhile, two separate incursions occurred near the border with Namibia, one to the east closely related to isolates from the Eastern Caprivi Strip and from Zambia (Kazungula), the other, most closely related to a virus from the Kavango outbreak in Namibia. The virus isolates from the Caprivi Strip (Namibia), Kazungula (Zambia) and Khundu (Botswana) clustered as part of SAT 2 topotype III and grouped with previously characterised SAT 2 isolates from Namibia, Zimbabwe and Botswana with a 13%, 15% and 16% nucleotide level difference, respectively; they were however, distinct from the topotype III viruses from the Maun area of Botswana. The viruses from Kavango (Namibia) and Tshethana (Botswana) clustered with previously characterised SAT 2 strains from Namibia (NAM/304/98 and NAM/01/92) as part of SAT 2 topotype II. These isolates differed by approximately 8% from the 1998 and 1992 Namibian isolates, while the difference at nucleotide level between these isolates and the isolates from the Eastern Caprivi cluster was 28%. Thus the SAT 2 outbreak strains from Namibia/Zambia/Botswana clustered in two different topotypes, indicating a diversity of SAT 2 strains circulating in the region.

Additional isolates from southern Zambia were of SAT 1 serotype and related to viruses previously found in Zambia in 2004-05.

Sequencing and subsequent phylogenetic analysis showed that the Malawi 2008 outbreak strain differed by 10% at nucleotide level from a SAT 2 outbreak strain characterised from Malawi during 2003.

Antigenic matching is hampered by difficulty in growing virus isolates to sufficient titre in vitro as well as unavailability of some vaccine antisera. Such testing as can be done often reveals an inadequate match.

Vaccine strains that may be suitable for use in the region include:

| Serotype | Internationally available | Locally produced |
|---|---|---|
| O | $O_1$ Manisa | Kenya 77/78, Egypt 2/72 |
| A | Eritrea 98 | Kenya 5/80, Egypt 06 |
| SAT 1 | Rhodesia 12/78, Botswana 1/68, | Botswana 1/77, KNP 196/91, Kenya T155/71, SAR 9/81 |
| SAT 2 | Zimbabwe 7/83, Eritrea 98, Saudi 2000 | Zimbabwe 11/89, Zimbabwe 5/81, Zambia 3/81, KNP 19/81, Kenya 52/84, Kenya 65/82 |
| SAT 3 | Zimbabwe 9/81, Zimbabwe 2/83 | KNP 10/90 |

Not all of the above-mentioned vaccine strains are in production and there are major problems in finding new strains suitable for vaccine production. This is not only due to the lack of availability of field isolates and sera for use in vaccine matching tests, but also the fact that prospective vaccine strain adaptation for production purposes is a cumbersome process and that commercial returns are uncertain on investment to generate new vaccine strains.

**Pool 7: AMERICA-SOUTH**

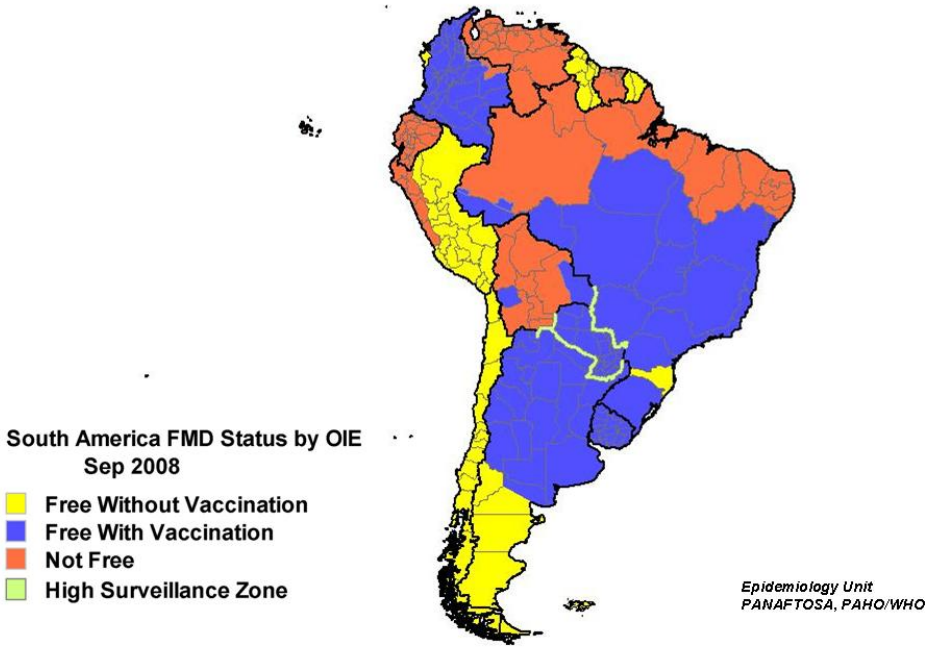
Network labs receiving samples in 2008:

| Laboratory | Sample Nos. | Countries of origin |
|---|---|---|
| PANAFTOSA | 37 | Colombia, Ecuador |

In South America, FMD outbreaks (4 of serotype O and 3 of serotype A) reported to have caused the emergency situation in Colombia, during the months of June-July, near the border with Venezuela, have been brought under control using a “stamping out” and vaccination (bivalent O and A vaccine) campaign, followed by a thorough sentinel program and serosampling with negative results. Elsewhere, outbreaks of serotype O were reported in Ecuador (14), and, in addition, FMDV serotypes O (20) and A (27) continue to cause outbreaks in Venezuela. Genetic and antigenic typing results obtained for isolates studied in South America in 2008 (causing the emergency in Colombia and from endemic regions in Ecuador) showed that they all belong to the endogenous topotypes (Euro-SA) and were related to viruses circulating in endemic areas of the Andean region .Vaccine matching studies suggest that vaccines that are currently in use should protect against infection when applied under systematic vaccination schemes

Areas of Mato Grosso do Sul (MS) in the western-centre of Brazil had their status reinstated by OIE after the emergency in 2005. Serosurveillance carried out indicated that FMDV is not circulating.

The 15 km wide high surveillance zone (HSZ), created in the common borders of Argentina, Bolivia, Brazil and Paraguay was subjected to a longitudinal surveillance scheme based on geographic risk characterization (farm level) and is at present being closely monitored through a NSP serosurveillance study being implemented to assess absence of viral circulation (~8000 sera) .




Vaccine strains recommended for use in the region*:

| Serotype | Internationally available | Locally produced |
|---|---|---|
| O | $O_1$ Campos, | $O_1$ Campos |
| A | $A_{24}$ Cruzeiro, Argentina 2001 | $A_{24}$ Cruzeiro, Argentina 2001 |
| C | $C_3$ Indaial | $C_3$ Indaial |

* PANAFTOSA recommendation is as High Priority: $O_1$ Campos, $A_{24}$ Cruzeiro, $C_3$ Indaial, and as medium priority: A Argentina 2001

## 1.5. Clinical samples and FMDV isolates submitted to reference laboratories of the FMD network during the year in question.

### 1.5.1. Overview of samples received and serotyping results

Samples received for FMDV detection and characterised in 2008 by network lab and year of collection

| Laboratory | Collected in 2008 | | Collected earlier | |
|---|---|---|---|---|
| | Samples | Countries | Samples | Countries |
| WRLFMD | 187 | 18 | 68 | 7 |
| PANAFTOSA | 37 | 2 | - | - |
| FGI-ARRIAH | - | - | 3 | 1 |
| RRLSSA | 246 | 3 | - | - |
| ARC-OVI | 13 | 2 | - | - |
| PIADC | - | - | 7 | 1 |
| LVRI | 3 | 1 | 8 | 1 |
| PDFMD | 2258* | 1 | * | 1 |
| RRLSEA | 226 | 4 | 60 | 3 |

* collected from 1211 outbreaks during 2007-2008

A searchable on-line database of samples is available via the Reference Laboratories Information System (ReLaIS) for the OIE/FAO FMD Reference Laboratories Network http://www.foot-and-mouth.org/.

Characterisation results obtained on samples received by WRLFMD and PANAFTOSA can be found respectively at: http://www.wrlfmd.org/ and at: http://www.panaftosa.org.br.

### 1.5.2. Serotyping and molecular detection results of samples received in 2008, corresponding to outbreaks that occurred in 2008

| Pool | Country | No. of samples | Virus isolation in cell culture/ELISA FMD virus serotypes | | | | | | | SVD virus | NVD | RT-PCR for FMD (or SVD Laboratory virus (where appropriate) | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | O | A | C | SAT 1 | SAT 2 | SAT 3 | Asia 1 | | | Positive | Negative | |
| **ASIA-EAST** | CAMBODIA | 17 | 10 | 1 | - | - | - | - | - | - | 6 | - | - | RRLSEA |
| | MALAYSIA | 3 | - | - | - | - | - | - | - | - | 3 | 3 | - | WRLFMD |
| | MYANMAR | 4 | 3 | - | - | - | - | - | - | - | 1 | - | - | RRLSEA |
| | LAOS | 1 | 1 | - | - | - | - | - | - | - | - | 1 | - | WRLFMD |
| | | 11 | 11 | - | - | - | - | - | - | - | - | - | - | RRLSEA |
| | THAILAND | 79 | 31 | 25 | - | - | - | - | - | - | 23 | - | - | RRLSEA |
| | | 1 | - | - | - | - | - | - | - | - | 1 | 1 | - | WRLFMD |
| | | 115 | 56 | 26 | - | - | - | - | - | - | 33 | - | - | RRLSEA |
| **ASIA-SOUTH** | BHUTAN | 3 | 2 | - | - | - | - | - | - | - | 1 | 3 | - | WRLFMD |
| | INDIA | 2258[a] | 1049 | 130 | - | - | - | - | 97 | - | 982[b] | 40[c] | 102 | PDFMD |
| | PAKISTAN | 6 | 4 | - | - | - | - | - | - | - | 2 | 4 | 2 | WRLFMD |
| **EUR-ASIA** | BAHRAIN | 7 | 3 | 2 | - | - | - | - | - | - | 2 | 6 | 1 | WRLFMD |
| | IRAN | 6 | - | 3 | - | - | - | - | - | - | 3 | 4 | 2 | WRLFMD |
| | KUWAIT | 10 | 10 | - | - | - | - | - | - | - | - | 10 | - | WRLFMD |
| | SAUDI ARABIA | 10 | 7 | - | - | - | - | - | - | - | 3 | 10 | - | WRLFMD |
| | TURKEY | 33 | 8 | 23 | - | - | - | - | - | - | 2 | 32 | 1 | WRLFMD |
| **AFRICA-EAST** | ETHIOPIA | 26 | 8 | 3 | - | - | - | - | - | - | 15 | 16 | 10 | WRLFMD |
| | KENYA | 16 | 7 | 2 | - | - | 1 | - | - | - | 6 | 13 | 3 | WRLFMD |
| **AFRICA-WEST** | NIGERIA | 10 | - | - | - | - | 8 | - | - | - | 2 | 8 | 2 | WRLFMD |
| | SENEGAL | 8 | - | - | - | - | - | - | - | - | 8 | 2 | 6 | WRLFMD |
| | GABON | 12 | - | - | - | - | - | - | - | - | 12 | - | 12 | WRLFMD |
| **AFRICA-SOUTH** | BOTSWANA | 18 | - | - | - | - | 12 | - | - | - | 6 | 13 | 5 | WRLFMD |
| | | 227 | - | - | - | - | 19 | - | - | - | 208 | - | - | RRLSSA |
| | NAMIBIA | 4 | - | - | - | - | 4 | - | - | - | - | 4 | - | WRLFMD |
| | | 4 | - | - | - | - | 4 | - | - | - | - | - | - | RRLSSA |
| | | 4 | - | - | - | - | 3 | - | - | - | 1 | 3 | 1 | ARC-OVI |
| | ZAMBIA | 13 | - | - | - | 8 | 1 | - | - | - | 4 | 10 | 3 | WRLFMD |
| | | 15 | - | - | - | 15 | - | - | - | - | - | - | - | RRLSSA |
| | MALAWI | 9 | - | - | - | - | 1 | - | - | - | 8 | 1 | 8 | ARC-OVI |
| **AMERICA-SOUTH** | COLOMBIA | 35 | 11 | 6 | - | - | - | - | - | - | 18 | 7 | - | PANAFTOSA |
| | ECUADOR | 2 | 1 | - | - | - | - | - | - | - | 1 | 2 | - | PANAFTOSA |
| **TOTAL** | **24 countries** | **2967** | **1222** | **221** | **0** | **23** | **53** | **0** | **97** | **0** | **1351** | **193** | **158** | |

[a] collected from 1211 outbreaks during 2007-8, [b] from 368 outbreaks, [c] number of outbreaks diagnosed

### 1.5.3. Serotyping and molecular detection results of samples collected earlier but received in 2008

| Pool | Country | Sample year | No. of samples | Virus isolation in cell culture/ELISA FMD virus serotypes | | | | | | | SVD virus | NVD | RT-PCR for FMD (or SVD) virus | | Laboratory |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | O | A | C | SAT 1 | SAT 2 | SAT 3 | Asia 1 | | | Positive | Negative | |
| **ASIA-EAST** | CHINA | 2007 | 3 | - | - | - | - | - | - | 3 | - | - | | | LVRI |
| | LAOS | 2007 | 4 | 4 | - | - | - | - | - | - | - | - | 4 | - | WRLFMD |
| | LAOS | 2007 | 20 | 3 | 16 | | | | | | | 1 | | | RRLSEA |
| | MYANMAR | 2007 | 5 | 4 | | | | | | | | 1 | | | RRLSEA |
| | THAILAND | 2007 | 35 | 15 | 11 | | | | | | | 9 | - | | RRLSEA |
| **EUR-ASIA** | KYRGYZSTAN | 2007 | 1 | | 1 | | | | | | | | | | FGI-ARRIAH |
| | TURKEY | 2007 | 1 | 1 | - | - | - | - | - | - | - | - | 1 | - | WRLFMD |
| | ISRAEL | 2007 | 7 | 6 | - | - | - | - | - | - | - | - | 6 | 1 | PIADC |
| **AFRICA-EAST** | ETHIOPIA | 2007 | 28 | 4 | 1 | - | 4 | 1 | - | - | - | 18 | 8 | 20 | WRLFMD |
| | KENYA | 2006 | 4 | - | - | - | 2 | - | - | - | - | 2 | 3 | 1 | WRLFMD |
| | KENYA | 2007 | 25 | 4 | - | - | - | 14 | - | - | - | 7 | 24 | 1 | WRLFMD |
| | SOMALIA | 2007 | 4 | 3 | - | - | - | - | - | - | - | 1 | 4 | - | WRLFMD |
| **AFRICA-WEST** | NIGERIA | 2007 | 2 | 1 | - | - | - | 1 | - | - | - | - | 2 | - | WRLFMD |
| **TOTAL** | **11 countries** | | **139** | **45** | **29** | **0** | **6** | **16** | **0** | **3** | **0** | **39** | **52** | **23** | |

| | |
|---|---|
| VI/ELISA | FMD (or SVD) virus serotype identified following virus isolation in cell culture and antigen detection ELISA |
| FMD | foot-and-mouth disease |
| SVD | swine vesicular disease |
| NVD | no foot-and-mouth disease, swine vesicular disease or vesicular stomatitis virus detected |
| RT-PCR | reverse transcription polymerase chain reaction for FMD (or SVD) viral genome |

## 1.6. Genetic and antigenic typing of FMD virus isolates submitted to the Reference Laboratories

### 1.6.1. Summary of genetic typing

The table below lists VP1 gene sequences obtained from FMD viruses by some of the Network Laboratories during 2008. The viruses are cross-referenced to phylogenetic trees showing the deduced relationship between representatives of these viruses and those for which sequences were already available.

Additional phylogenetic trees and observations on them can be found at http://www.wrlfmd.org/ for all of the viruses that were analysed at WRLFMD. The VP1 gene sequences of a selection of virus isolates representative of all of the topotypes of FMDV can also be found at this website.

| FMDV isolate | Region sequenced | No. of bases | Topotype | Strain | Reference for dendrogram[4] | Laboratory |
|---|---|---|---|---|---|---|
| **Serotype O** | | | | | | |
| BAR/1/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| BAR/2/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| BAR/3/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| BHU/2/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| BHU/3/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| ETH/1/2007 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |
| ETH/26/2007 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |
| ETH/27/2007 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |
| ETH/28/2007 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |
| ETH/13/2008 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |
| ETH/15/2008 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |
| ETH/19/2008 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |
| ETH/20/2008 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |
| ETH/21/2008 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |
| ETH/23/2008 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |
| ETH/24/2008 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |

[4] Additional figures show phylogenies from unlisted viruses analysed at PDFMD and PIADC

| | | | | | | |
|---|---|---|---|---|---|---|
| ETH/25/2008 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |
| KEN/3/2007 | VP1 | 639 | EA-2 | - | Figure 7 | WRLFMD |
| KEN/12/2007 | VP1 | 639 | EA-2 | - | Figure 7 | WRLFMD |
| KEN/17/2007 | VP1 | 639 | EA-2 | - | Figure 7 | WRLFMD |
| KEN/20/2007 | VP1 | 639 | EA-2 | - | Figure 7 | WRLFMD |
| KEN/1/2008 | VP1 | 639 | EA-2 | - | Figure 7 | WRLFMD |
| KEN/3/2008 | VP1 | 639 | EA-2 | - | Figure 7 | WRLFMD |
| KEN/4/2008 | VP1 | 639 | EA-2 | - | Figure 7 | WRLFMD |
| KEN/9/2008 | VP1 | 639 | EA-2 | - | Figure 7 | WRLFMD |
| KEN/10/2008 | VP1 | 639 | EA-2 | - | Figure 7 | WRLFMD |
| KEN/14/2008 | VP1 | 639 | EA-2 | - | Figure 7 | WRLFMD |
| KEN/15/2008 | VP1 | 639 | EA-2 | - | Figure 7 | WRLFMD |
| KUW/1/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| KUW/2/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| KUW/3/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| KUW/4/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| KUW/5/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| KUW/6/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| KUW/7/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| KUW/8/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| KUW/9/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| KUW/10/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| IND/44/07 | VP1 | 410/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/45/07 | VP1 | 468/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/46/07 | VP1 | 438/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/170/07 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/182/07 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/222/07 | VP1 | 477/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/223/07 | VP1 | 285/633 | ME-SA | - | Figure 20 | PDFMD |
| IND/246/07 | VP1 | 354/633 | ME-SA | PanAsia-1 | Figure 20 | PDFMD |
| IND/250/07 | VP1 | 414/633 | ME-SA | PanAsia-1 | Figure 20 | PDFMD |
| IND/253/07 | VP1 | 555/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/263/07 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/265/07 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |

| | | | | | | |
|---|---|---|---|---|---|---|
| IND/269/07 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/272/07 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/271/07 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/275/07 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/305/07 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/324/07 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/344/07 | VP1 | 393/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/345/07 | VP1 | 462/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/347/07 | VP1 | 465/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/348/07 | VP1 | 429/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/351/07 | VP1 | 240/633 | ME-SA | PanAsia-1 | Figure 20 | PDFMD |
| IND/357/07 | VP1 | 633/633 | ME-SA | - | Figure 20 | PDFMD |
| IND/359/07 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/388/07 | VP1 | 405/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/404/07 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/411/07 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/420/07 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/428/07 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/432/07 | VP1 | 462/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/433/07 | VP1 | 546/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/2/08 | VP1 | 474/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/12/08 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/22/08 | VP1 | 477/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/36/08 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/42/08 | VP1 | 624/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/49/08 | VP1 | 465/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/55/08 | VP1 | 633/633 | ME-SA | - | Figure 20 | PDFMD |
| IND/56/08 | VP1 | 493/633 | ME-SA | - | Figure 20 | PDFMD |
| IND/57/08 | VP1 | 426/633 | ME-SA | - | Figure 20 | PDFMD |
| IND/67/08 | VP1 | 477/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/70/08 | VP1 | 480/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/87/08 | VP1 | 452/633 | ME-SA | IND 2001 | Figure 20 | PDFMD |
| IND/88/08 | VP1 | 633/633 | ME-SA | IND 2001 | Figure 20 | PDFMD |
| IND/89/08 | VP1 | 633/633 | ME-SA | IND 2001 | Figure 20 | PDFMD |

| | | | | | | |
|---|---|---|---|---|---|---|
| IND/111/08 | VP1 | 477/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/117/08 | VP1 | 462/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| IND/160/08 | VP1 | 633/633 | ME-SA | PanAsia-2 | Figure 20 | PDFMD |
| LAO/1/2007 | VP1 | 639 | SEA | Mya-98 | Figure 6 | WRLFMD |
| LAO/2/2007 | VP1 | 639 | SEA | Mya-98 | Figure 6 | WRLFMD |
| LAO/3/2007 | VP1 | 639 | SEA | Mya-98 | Figure 6 | WRLFMD |
| LAO/4/2007 | VP1 | 639 | SEA | Mya-98 | Figure 6 | WRLFMD |
| LAO/1/2008 | VP1 | 639 | SEA | Mya-98 | Figure 6 | WRLFMD |
| NIG/1/2007 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |
| PAK/31/2005 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/32/2005 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/33/2005 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/34/2005 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/35/2005 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/38/2005 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/60/2006 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/61/2006 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/63/2006 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/66/2006 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/67/2006 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/68/2006 | VP1 | 639 | ME-SA | PanAsia | Figure 5 | WRLFMD |
| PAK/70/2006 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/71/2006 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/72/2006 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/73/2006 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/74/2006 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/53/2007 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/56/2007 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/60/2007 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/61/2007 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/63/2007 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/66/2007 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/68/2007 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/69/2007 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |

| | | | | | | |
|---|---|---|---|---|---|---|
| PAK/70/2007 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/71/2007 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/1/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/2/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/3/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| PAK/6/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| SAU/1/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| SAU/2/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| SAU/3/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| SAU/4/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| SAU/5/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| SAU/6/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| SAU/7/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| SAU/11/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| SOM/1/2007 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |
| SOM/2/2007 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |
| SOM/4/2007 | VP1 | 639 | EA-3 | - | Figure 7 | WRLFMD |
| TAI/4/2007 | VP1 | 639 | SEA | Mya-98 | Figure 6 | WRLFMD |
| TAI/5/2007 | VP1 | 639 | SEA | Mya-98 | Figure 6 | WRLFMD |
| TAI/6/2007 | VP1 | 639 | SEA | Mya-98 | Figure 6 | WRLFMD |
| TAI/7/2007 | VP1 | 639 | SEA | Mya-98 | Figure 6 | WRLFMD |
| TAI/8/2007 | VP1 | 639 | SEA | Mya-98 | Figure 6 | WRLFMD |
| TAI/9/2007 | VP1 | 639 | SEA | Mya-98 | Figure 6 | WRLFMD |
| TAI/10/2007 | VP1 | 639 | SEA | Mya-98 | Figure 6 | WRLFMD |
| TAI/12/2007 | VP1 | 639 | SEA | Mya-98 | Figure 6 | WRLFMD |
| TAI/13/2007 | VP1 | 639 | SEA | Mya-98 | Figure 6 | WRLFMD |
| TAI/14/2007 | VP1 | 639 | SEA | Mya-98 | Figure 6 | WRLFMD |
| TUR/31/2007 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| TUR/4/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| TUR/5/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| TUR/9/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| TUR/10/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| TUR/16/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| TUR/25/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |

| | | | | | | |
|---|---|---|---|---|---|---|
| TUR/26/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| TUR/30/2008 | VP1 | 639 | ME-SA | PanAsia-2 | Figure 5 | WRLFMD |
| O/Cúcuta/N. Santander/Col/08 (1) | VP1 | 639 | EURO-SA | - | Figure 18 | PANAFTOSA |
| O/Cúcuta/N. Santander/Col/08 (2) | VP1 | 639 | EURO-SA | - | Figure 18 | PANAFTOSA |
| O/Eloy Alfaro/Esmeraldas/Ecu/08 | VP1 | 639 | EURO-SA | - | Figure 18 | PANAFTOSA |
| O/Valencia/Los Rios/Ecu/08 | VP1 | 639 | EURI-SA | - | Figure 18 | PANAFTOSA |
| **Serotype A** | | | | | | |
| BAR/6/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| BAR/7/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| ETH/4/2007 | VP1 | 639 | AFRICA | G-VII | Figure 10 | WRLFMD |
| ETH/7/2008 | VP1 | 639 | AFRICA | G-VII | Figure 10 | WRLFMD |
| ETH/8/2008 | VP1 | 639 | AFRICA | G-VII | Figure 10 | WRLFMD |
| ETH/9/2008 | VP1 | 639 | AFRICA | G-VII | Figure 10 | WRLFMD |
| IND/49/07 | VP1 | 639 | VII | - | 22 | PDFMD |
| IND/53/07 | VP1 | 639 | VII | - | 22 | PDFMD |
| IND/195/07 | VP1 | 639 | VII | - | 22 | PDFMD |
| IND/196/07 | VP1 | 639 | VII | - | 22 | PDFMD |
| IND/245/07 | VP1 | 639 | VII | g | 22 | PDFMD |
| IND/360/07 | VP1 | 639 | VII | g | 22 | PDFMD |
| IND/407/07 | VP1 | 639 | VII | g | 22 | PDFMD |
| IND/413/07 | VP1 | 639 | VII | g | 22 | PDFMD |
| IND/417/07 | VP1 | 639 | VII | g | 22 | PDFMD |
| IND/122/08 | VP1 | 639 | VII | g | 22 | PDFMD |
| IND/123/08 | VP1 | 639 | VII | g | 22 | PDFMD |
| IND/124/08 | VP1 | 639 | VII | g | 22 | PDFMD |
| IND/126/08 | VP1 | 639 | VII | g | 22 | PDFMD |
| IND/127/08 | VP1 | 639 | VII | g | 22 | PDFMD |
| IND/128/08 | VP1 | 639 | VII | g | 22 | PDFMD |
| IND/163/08 | VP1 | 639 | VII | f | 22 | PDFMD |
| IND/165/08 | VP1 | 639 | VII | f | 22 | PDFMD |
| IRN/1/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |

| | | | | | | |
|---|---|---|---|---|---|---|
| IRN/4/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| IRN/5/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| KEN/7/2008 | VP1 | 639 | AFRICA | G-I | Figure 10 | WRLFMD |
| KEN/8/2008 | VP1 | 639 | AFRICA | G-I | Figure 10 | WRLFMD |
| KRG/2007 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | FGI-ARRIAH |
| PAK/73/2007 | VP1 | 639 | ASIA | - | Figure 8 | WRLFMD |
| TAI/3/2007 | VP1 | 636 | ASIA | - | Figure 9 | WRLFMD |
| TAI/11/2007 | VP1 | 636 | ASIA | - | Figure 9 | WRLFMD |
| TUR/1/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/2/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/3/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/6/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/7/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/8/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/11/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/12/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/13/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/14/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/17/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/18/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/19/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/20/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/21/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/22/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/23/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/24/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/27/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/28/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/29/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/32/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| TUR/33/2008 | VP1 | 639 | ASIA | Iran-05 | Figure 8 | WRLFMD |
| A/Sardinata/N. Santander/Col/08 (541101) | VP1 | 639 | EURO-SA | - | Figure 17 | PANAFTOSA |
| A/Sardinata/N. | VP1 | 639 | EURO-SA | - | Figure 17 | PANAFTOSA |

| | | | | | | |
|---|---|---|---|---|---|---|
| Santander/Col/08 (541171) | | | | | | |
| A/Sardinata/N. Santander/Col/08 (541172) | VP1 | 639 | EURO-SA | - | Figure 17 | PANAFTOSA |
| A/Sardinata/N. Santander/Col/08 (541180) | VP1 | 639 | EURO-SA | - | Figure 17 | PANAFTOSA |
| A/Sardinata/N. Santander/Col/08 (542106) | VP1 | 639 | EURO-SA | - | Figure 17 | PANAFTOSA |
| A/Sardinata/N. Santander/Col/08 (542114) | VP1 | 639 | EURO-SA | - | Figure 17 | PANAFTOSA |
| **Serotype Asia 1** | | | | | | |
| IND/12/07 | VP1 | 633/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/227/07 | VP1 | 633/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/356/07 | VP1 | 633/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/29/08 | VP1 | 555/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/30/08 | VP1 | 321/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/31/08 | VP1 | 393/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/32/08 | VP1 | 633/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/35/08 | VP1 | 483/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/37/08 | VP1 | 381/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/90/08 | VP1 | 430/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/93/08 | VP1 | 633/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/94/08 | VP1 | 633/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/95/08 | VP1 | 633/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/96/08 | VP1 | 633/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/97/08 | VP1 | 633/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/98/08 | VP1 | 555/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/100/08 | VP1 | 430/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/112/08 | VP1 | 633/633 | - | Lineage CI | Figure 21 | PDFMD |
| IND/137/08 | VP1 | 633/633 | - | Lineage CI | Figure 21 | PDFMD |
| KRG/1/2004* | VP1 | 633 | - | - | Figure 11 | FGI-ARRIAH |
| KRG/2/2004* | VP1 | 633 | - | - | Figure 11 | FGI-ARRIAH |
| TAJ/1/2003* | VP1 | 633 | - | - | Figure 11 | FGI-ARRIAH |
| TAJ/2/2003* | VP1 | 633 | - | - | Figure 11 | FGI-ARRIAH |
| TAJ/3/2003* | VP1 | 633 | - | - | Figure 11 | FGI-ARRIAH |

| | | | | | | |
|---|---|---|---|---|---|---|
| UZB/2003* | VP1 | 625 | - | - | Figure 11 | FGI-ARRIAH |
| **Serotype SAT 1** | | | | | | |
| ETH/3/2007 | VP1 | 663 | V | - | Figure 13 | WRLFMD |
| ETH/18/2007 | VP1 | 663 | V | - | Figure 13 | WRLFMD |
| ETH/19/2007 | VP1 | 663 | V | - | Figure 13 | WRLFMD |
| ETH/21/2007 | VP1 | 663 | V | - | Figure 13 | WRLFMD |
| KEN/11/2006 | VP1 | 663 | I (NWZ) | - | Figure 12 | WRLFMD |
| KEN/14/2006 | VP1 | 663 | I (NWZ) | - | Figure 12 | WRLFMD |
| ZAM/5/2008 | VP1 | 663 | I (NWZ) | - | Figure 12 | WRLFMD |
| ZAM/6/2008 | VP1 | 663 | I (NWZ) | - | Figure 12 | WRLFMD |
| ZAM/7/2008 | VP1 | 663 | I (NWZ) | - | Figure 12 | WRLFMD |
| ZAM/9/2008 | VP1 | 663 | I (NWZ) | - | Figure 12 | WRLFMD |
| ZAM/10/2008 | VP1 | 663 | I (NWZ) | - | Figure 12 | WRLFMD |
| ZAM/11/2008 | VP1 | 663 | I (NWZ) | - | Figure 12 | WRLFMD |
| ZAM/12/2008 | VP1 | 663 | I (NWZ) | - | Figure 12 | WRLFMD |
| ZAM/13/2008 | VP1 | 663 | I (NWZ) | - | Figure 12 | WRLFMD |
| **Serotype SAT 2** | | | | | | |
| BOT/6/2008 | VP1 | 648 | III | - | Figure 16 | WRLFMD |
| BOT/7/2008 | VP1 | 648 | III | - | Figure 16 | WRLFMD |
| BOT/8/2008 | VP1 | 648 | III | - | Figure 16 | WRLFMD |
| BOT/9/2008 | VP1 | 648 | III | - | Figure 16 | WRLFMD |
| BOT/10/2008 | VP1 | 648 | III | - | Figure 16 | WRLFMD |
| BOT/11/2008 | VP1 | 648 | III | - | Figure 16 | WRLFMD |
| BOT/12/2008 | VP1 | 648 | II | - | Figure 15 | WRLFMD |
| BOT/13/2008 | VP1 | 648 | II | - | Figure 15 | WRLFMD |
| BOT/14/2008 | VP1 | 648 | III | - | Figure 16 | WRLFMD |
| BOT/15/2008 | VP1 | 648 | III | - | Figure 16 | WRLFMD |
| BOT/16/2008 | VP1 | 648 | III | - | Figure 16 | WRLFMD |
| BOT/18/2008 | VP1 | 648 | III | - | Figure 16 | WRLFMD |
| ETH/2/2007 | VP1 | 648 | XIII | - | Figure 14 | WRLFMD |
| KEN/2/2007 | VP1 | 648 | IV | - | Figure 16 | WRLFMD |
| KEN/4/2007 | VP1 | 648 | IV | - | Figure 16 | WRLFMD |
| KEN/5/2007 | VP1 | 648 | IV | - | Figure 16 | WRLFMD |

| | | | | | | |
|---|---|---|---|---|---|---|
| KEN/7/2007 | VP1 | 648 | IV | - | Figure 16 | WRLFMD |
| KEN/8/2007 | VP1 | 648 | IV | - | Figure 16 | WRLFMD |
| KEN/9/2007 | VP1 | 648 | IV | - | Figure 16 | WRLFMD |
| KEN/10/2007 | VP1 | 648 | IV | - | Figure 16 | WRLFMD |
| KEN/11/2007 | VP1 | 648 | IV | - | Figure 16 | WRLFMD |
| KEN/13/2007 | VP1 | 648 | IV | - | Figure 16 | WRLFMD |
| KEN/14/2007 | VP1 | 648 | IV | - | Figure 16 | WRLFMD |
| KEN/16/2007 | VP1 | 648 | IV | - | Figure 16 | WRLFMD |
| KEN/19/2007 | VP1 | 648 | IV | - | Figure 16 | WRLFMD |
| KEN/22/2007 | VP1 | 648 | IV | - | Figure 16 | WRLFMD |
| KEN/23/2007 | VP1 | 648 | IV | - | Figure 16 | WRLFMD |
| KEN/2/2008 | VP1 | 648 | IV | - | Figure 16 | WRLFMD |
| NIG/2/2007 | VP1 | 648 | VII | - | Figure 14 | WRLFMD |
| NIG/1/2008 | VP1 | 648 | VII | - | Figure 14 | WRLFMD |
| NIG/2/2008 | VP1 | 648 | VII | - | Figure 14 | WRLFMD |
| NIG/3/2008 | VP1 | 648 | VII | - | Figure 14 | WRLFMD |
| NIG/4/2008 | VP1 | 648 | VII | - | Figure 14 | WRLFMD |
| NIG/5/2008 | VP1 | 648 | VII | - | Figure 14 | WRLFMD |
| NIG/6/2008 | VP1 | 648 | VII | - | Figure 14 | WRLFMD |
| NIG/7/2008 | VP1 | 648 | VII | - | Figure 14 | WRLFMD |
| NIG/8/2008 | VP1 | 648 | VII | - | Figure 14 | WRLFMD |
| NMB/1/2008 | VP1 | 648 | III | - | Figure 16 | WRLFMD |
| NMB/2/2008 | VP1 | 648 | III | - | Figure 16 | WRLFMD |
| NMB/3/2008 | VP1 | 648 | III | - | Figure 16 | WRLFMD |
| NMB/4/2008 | VP1 | 648 | III | - | Figure 16 | WRLFMD |
| ZAM/8/2008 | VP1 | 648 | III | - | Figure 16 | WRLFMD |
| NAM/1/2008 | VP1 | 418 | Northern | - | Figure 23 | ARC-OVI |
| NAM/467/2008 | VP1 | 418 | Western | - | Figure 25 | ARC-OVI |
| MAL/716/08 | VP1 | 418 | - | - | Figure 24 | ARC-OVI |

n.d., none defined
*, not WRLFMD Ref. No.

### 1.6.2. Summary of antigenic typing

Vaccine efficacy is influenced by both vaccine potency and vaccine match and poor match may to some extent be compensated by high potency. Thus, a vaccine with a weak antigenic match to a field isolate, as determined by serology, may nevertheless afford some protection if it is of sufficiently high potency. Therefore, in the absence of a good match, or where the match is unknown, vaccines of high potency should preferably be used. Potency can be augmented by booster vaccination. The $r_1$ values shown below, represent the one way serological match between vaccine strain and field isolate, calculated from the comparative reactivity of an antiserum, raised against the vaccine in question, to the vaccine virus and the field isolate.

### 1.6.3. Antigenic characterisation of field isolates by matching with vaccine strains at FGI-ARRIAH

The properties of FMDV strain of A/Kyrgyzstan/07 type were studied. Antigenic characteristics of field isolate A/Kyrgyzstan/07 were determined by micro-neutralization and compared with those of FMDV type A strains with sera from vaccinated cattle ($r_1$). The given virus was antigenically related to A Turkey/06 and $A_{22}$ Iraq 24/64 strains ($r_1$=0,5 and 0,7, respectively) and antigenically different from strains $A_{22}$ №550 and A Iran/97 ($r_1$=0,21 and 0,125, respectively).

### 1.6.4. Antigenic characterisation of field isolates by matching with vaccine strains at PANAFTOSA

Antigenic match of O Colombia/08 to vaccine strain $O_1$ Campos studied by Expectancy of Protection (EPP), using sera from 30 cattle at 30-days after vaccination and 60 days after re-vaccination.

| Strain | $O_1$ Campos |
|---|---|
| | elisa |
| O Colombia/08, 30 days post-vaccination * | 87.39% |
| O Colombia/08, 60 days post-vaccination * | 98.25% |

The $r_1$ value for this sample obtained by CF against $O_1$ Campos was 0.5

In the case of Expectancy of Protection (EPP) + $r_1$ value:
The two values are used in conjunction: r1 values greater than 0.25 indicate that the field isolate is sufficiently similar to the vaccine strain and that use of the vaccine is likely to confer protection against challenge with the field strain.
An EPP <75% (when sera from a group of 16 re-vaccinated animals are used) and <70% (when sera from a group of 30 re-vaccinated animals are used) is an indication that the vaccines will give a low protection against the field strain.

### 1.6.5. Antigenic characterisation of field isolates by matching with vaccine strains

**$r_1$ values were obtained by VNT or ELISA at WRLFMD**

**Serotype O**

| Field isolate | Vaccine strain | | | |
|---|---|---|---|---|
| | **O Manisa** | **O IND R2/75** | **$O_1$ BFS 1860** | **$O_1$ Kaufbeuren** |
| | VNT | VNT | VNT | VNT |
| O/BAR/2/2008 | 0.32 | 0.6 | 0.37 | |
| O/BHU/2/2008 | 0.38 | >1.0 | 0.75 | >1.0 |
| O/BHU/3/2008 | 0.39 | >1.0 | 0.84 | 0.81 |
| O/ETH/26/2007 | 0.54 | | | |
| O/IRN/26/2007 | >1.00 | | | |
| O/IRN/30/2007 | >0.54 | | | |
| O/KEN/20/2007 | <0.14 | <0.15 | | |
| O/KEN/3/2008 | 0.31 | | | |
| O/KEN/14/2008 | 0.42 | | | |
| O/KUW/4/2008 | 0.72 | >1.0 | 0.31 | |
| O/NIG/1/2007 | 0.40 | | | |
| O/PAK/68/2007 | 0.55 | 0.66 | 0.40 | |
| O/PAK/71/2007 | 0.39 | 0.49 | 0.18 | |
| O/PAK/1/2008 | 0.67 | >1.0 | 0.73 | |
| O/PAK/2/2008 | 0.8 | >1.0 | 0.41 | |
| O/SAU/2/2008 | 0.3/0.71 | 0.4/>1.0 | >0.8 | |
| O/SAU/11/2008 | 0.46 | | | |
| O/SOM/1/2007 | 0.64 | >1.0 | | |
| O/TUR/4/2008 | 0.35 | | | |
| O/TUR/10/2008 | 0.50 | | | |
| O/TUR/26/2008 | 0.41 | | | |
| O/TUR/30/2008 | 0.46 | | | |
| O/YEM/4/2006 | 0.35 | 0.22 | 0.17/0.23 | |
| O/YEM/29/2006 | 0.17 | 0.25 | 0.41/0.17 | |

## Serotype A

| Field Isolate | Vaccine strain | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | **$A_{22}$ Iraq** VNT | **A IND 17/82** VNT | **A TUR 06** VNT | **A IRN 87** VNT | **A IRN 96** VNT | **A MAY 97** VNT | **A ERI 98** VNT | **A IRN 99** VNT | **A 5925** VNT | **A SAU 95** VNT | **A SAU 91** VNT | **A IRN 01** VNT |
| A/ETH/4/2007 | 0.16 | | | | | | 0.10 | | | | | |
| A/IRN/36/2007 | 0.21 | 0.21 | 0.39 | | 0.14 | 0.17 | | 0.23 | | | | |
| A/IRN/39/2007 | 0.13 | 0.28 | 0.69 | | 0.14 | 0.29 | | 0.30 | | | | |
| A/IRN/1/2008 | 0.15 | 0.14 | 0.74 | | | | | | | | | |
| A/KEN/7/2008 | 0.67 | 0.09 | >0.97 | | | | 0.12 | | | | | |
| A/KEN/8/2008 | 0.13 | 0.05 | 0.33 | | | | | | | | | |
| A/MAY/1/2007 | 0.34 | 0.07 | 0.36 | | | 0.28 | | | | | | |
| A/MAY/3/2007 | <0.06 | 0.11 | 0.13 | | | 0.32 | | | | | | |
| A/PAK/73/2007 | >0.75 | >1.0 | 0.26 | | | | | | | | | |
| A/TUR/1/2008 | 0.19 | | | | | | | | | | | |
| A/TUR/6/2008 | | 0.28 | >0.83 | | | | 0.12 | | | | | |
| A/TUR/7/2008 | 0.12 | 0.23 | >0.97 | 0.20 | 0.07 | 0.18 | 0.12 | 0.14 | 0.28 | 0.10 | 0.02 | 0.10 |
| A/TUR/8/2008 | | 0.36 | >1.0 | | | | 0.19 | | | | | |
| A/TUR/11/2008 | 0.12 | 0.25 | 0.91 | 0.30 | 0.12 | 0.21 | 0.19 | 0.16 | 0.34 | 0.14 | 0.02 | 0.08 |
| A/TUR/28/2008 | 0.15 | | | | | | | | | | | |
| A/TUR/32/2008 | <0.17 | | | | | | | | | | | |
| A/TUR/33/2008 | 0.13 | | | | | | | | | | | |

## Serotype Asia 1

| Field Isolate | Vaccine strain | |
|---|---|---|
| | **Asia 1 IND 8/79** VNT | **Asia 1 Shamir** VNT |
| Asia1/KRG/1/2004 | 0.31 | 0.51 |
| Asia1/NKR/2/2007 | 0.28 | 0.45 |

## Serotype SAT 1

| Field Isolate | Vaccine strain |
|---|---|
| | **SAT1 RHO 12/78** VNT |
| SAT1/BOT/20/2006 | 0.37 |
| SAT1/BOT/22/2006 | 0.43 |
| SAT1/ETH/18/2007 | 0.13 |
| SAT1/ETH/21/2007 | 0.25 |
| SAT1/ETH/3/2007 | 0.15 |
| SAT1/KEN/11/2006 | 0.87 |
| SAT1/KEN/14/2006 | 0.59 |
| SAT1/ZAM/7/2008 | 0.11 |
| SAT1/ZAM/9/2008 | 0.17 |
| SAT1/ZAM/13/2008 | 0.22 |

## Serotype SAT 2

| Field isolate | Vaccine strain | | | | | |
|---|---|---|---|---|---|---|
| | **SAT 2 ERI 98** | **SAT 2 ZIM 7/83** | **SAT 2 KEN 52/84** | **SAT 2 KEN 65/82** | **SAT 2 NIG 6/81** | **SAT 2 ZIM 11/89** |
| | VNT | VNT | ELISA | ELISA | ELISA | ELISA |
| SAT2/BOT/11/2008 | 0.16 | 0.21 | | 0.26 | 0.17 | |
| SAT2/BOT/12/2008 | 0.33 | 0.27 | | 0.29 | 0.17 | |
| SAT2/ETH/2/2007 | 0.15 | 0.14 | | | | |
| SAT2/KEN/7/2007 | 0.18 | 0.26 | | | | |
| SAT2/KEN/9/2007 | | 0.08 | | | | |
| SAT2/KEN/16/2007 | | 0.04 | | | | |
| SAT2/KEN/2/2008 | 0.19 | 0.11 | | | | |
| SAT2/NIG/2/2007 | 0.49 | 0.32 | | | | |
| SAT2/NIG/7/2007 | | 0.13 | | | | |
| SAT2/NMB/1/2008 | 0.16 | 0.10 | | | | |
| SAT2/NMB/2/2008 | 0.10 | 0.08 | 0.22 | 0.43 | 0.19 | 0.61 |
| SAT2/NMB/4/2008 | 0.14 | 0.09 | 0.38 | 0.22 | 0.11 | 0.75 |

**Acknowledgement**
For the work carried out at Pirbright, the majority of the vaccine strains and vaccine antisera used for these tests have been supplied to the WRLFMD by Merial. Some strains and/or antisera were supplied to WRLFMD by Intervet, ARRIAH and the Thai Regional Reference Laboratory at Pakchong

**Interpretation of $r_1$ values**

In the case of VNT:

$r_1$ = ≥ 0.3 suggests that there is a close relationship between field isolate and vaccine strain. A potent vaccine containing the vaccine strain is likely to confer protection.

$r_1$ = < 0.3 suggests that the field isolate is so different from the vaccine strain that the vaccine is unlikely to protect unless a vaccine of very high potency is used or animals are vaccinated more than once.

In the case of ELISA:

$r_1$ = 0.4-1.0 suggests that there is a close relationship between field isolate and vaccine strain. A potent vaccine containing the vaccine strain is likely to confer protection.

$r_1$ = 0.2-0.39 suggests that the field isolate is antigenically related to the vaccine strain. The vaccine strain might be suitable for use if no closer match can be found provided that a potent vaccine is used and animals are preferably immunised more than once.

$r_1$ = <0.2 suggests that the field isolate is so different from the vaccine strain that the vaccine is unlikely to protect

**WRLFMD Vaccine Recommendations**

## High Priority

O Manisa (*covers panasian topotype)*
O BFS or Campos
A24 Cruzeiro
Asia 1 Shamir
A22 Iraq
SAT 2 Saudi Arabia *(or equivalent)*
(not in order of importance)

## Medium Priority

A Eritrea
A Iran '96
SAT 2 Zimbabwe
A Iran 87 or A Saudi Arabia 23/86 *(or equivalent)*
SAT 1 South Africa
A Malaysia 97 *(or Thai equivalent such as A/NPT/TAI/86)*
A Argentina 2001
O Taiwan 97 *(pig-adapted strain or Philippine equivalent)*
A Iran '99 (not in order of importance)

## Low Priority

A15 Bangkok related strain
A87 Argentina related strain
C Noville
SAT 2 Kenya
SAT 1 Kenya
SAT 3 Zimbabwe
A Kenya (not in order of importance)

# PART 2

# *Improving the quality of laboratory tests from international and national reference laboratories*

## 2.1. Inter-laboratory comparative testing exercises

### 2.1.1. Vaccine Matching by serology

At their meeting in Botswana in June 2007, the Network of FMD Reference Laboratories agreed to carry out an inter-laboratory trial to compare vaccine matching tests in 2008. The results of the trial were discussed at the next Annual Network meeting in China in September 2008.

The aim of the exercise was to evaluate whether similar vaccine matching results are obtained by laboratories using their own methods but with the same FMD vaccine virus, bovine vaccine sera (BVS) and field isolates. This is the first step by the OIE/FAO Network in working towards establishing equivalence in the vaccine matching that is done in different laboratories. The benefits of this work should be that the vaccine matching data produced in different labs is comparable and can therefore be integrated to produce a more reliable and complete set of recommendations on vaccine selection for different settings. An added benefit should be a reduced requirement for international exchange of viruses in the future; something that is constrained by cost, bureaucracy and risk.

A historical Eurasian FMD virus $A_{22}$ Iraq 24/64 was chosen to be used as the vaccine strain. Five cattle were vaccinated with this virus in ARC-OVI to generate the BVS, and five FMD serotype A field isolates were selected and grown up in vitro at WRLFMD to be matched against the $A_{22}$ Iraq 24/64 vaccine for this study. Guinea pig and rabbit antisera were also prepared at ARC-OVI for use in matching tests based on the liquid phase blocking ELISA (LPBE).

The necessary permits were obtained for the reagents to be dispersed and then WRLFMD sent out 15 ml of each of five BVS, 8 ml of the vaccine virus $A_{22}$ Iraq 24/64 and 5 ml of each of 5 coded FMD serotype A field isolates. Participants were then asked to calculate and provide "$r_1$" values for individual BVS and pooled BVS comparing each field isolate against $A_{22}$ Iraq 24/64. In this first phase of testing, emphasis was placed on use of VNT as the serological method with which to estimate generate $r_1$ values. All Network partners participated in the trial except for PANAFTOSA who were unable to import the live viruses. They will participate in the next phase using LPBE and inactivated viruses.

The VNT results obtained showed discrepancies between the findings of some labs despite using the same vaccine virus, BVS and field isolates and that the results of two labs were particularly discordant. Some differences in r values were obtained for BVS from different cattle. Differences in methodology might explain the variation between labs. There did appear to be good repeatability within labs and pooling of BVS gave similar results to averaging results from individual sera.

Preliminary analysis suggested that at least 5 sera may be necessary for a pooled sample, which could then be used as representative of one vaccine in the VNT to generate $r_1$ values. The use of more animals to generate sera was suggested, but this would be a costly exercise. The cut-off values used differed between laboratories; where most laboratories used values of $< 0.3$ and $\geq 0.3$, BVI and OVI used values of 0-0.19, 0.2-0.39 and $\geq 0.4$ for the SAT types in Southern Africa. The interpretation of $r_1$-values was discussed and it was emphasized that these values should be interpreted with caution. Multiple field isolates should be used to accurately determine $r_1$ values, as there may be variations within an outbreak. The methodology/rationale used concerning repeats of tests was questioned. Some laboratories

repeat the test if dissimilar results are obtained for two repeats of the same sample. Some labs routinely use pooled sera.

Several options for further actions were proposed: it was agreed that partners should provide details of the methodologies they had used and should use the already circulated reagents to carry out LPBE testing if this is a method that they use routinely. If sufficient reagents remained with participants, then testing should be repeated perhaps using a unified methodology. Finally, more isolates of type A could be circulated for testing. PANAFTOSA reiterated its interest in participating in this extended exercise, particularly with LPBE with inactivated samples. It was recognized that regular meetings on vaccine matching should be organized and laboratories should participate in a continuous manner in the collection of information regarding new strains emerging in the field.

In the meantime, plans would be developed to do similar work with other serotypes, both through multilateral trials such as the one just described, but also by bilateral studies involving laboratories with shared priority vaccines. The need for further research work on vaccine matching was highlighted and members were encouraged to work together on types and strains that were important in their region. Ultimately, the aim should be to further standardize methods for inclusion into the OIE Diagnostic Manual.

An inventory of vaccine strains and antisera available in the different Network laboratories should also be established.

### 2.1.2. Virus isolation and serology

#### 2.1.2.1. Proficiency testing study (PTS) organised by WRLFMD/CRLFMD

During 2008, the European Community Reference Laboratories for FMD and SVD, in association with WRLFMD, organised a round of inter-laboratory proficiency testing to help quality assure FMD and SVD diagnosis. The first priority was to supply proficiency panels to member states of the EU and of the EUFMD, but the panels were also made available more widely, including targeting of the OIE/FAO FMD Network Laboratories.

This study involved panels of materials for testing by serology and virus detection methods. All samples were analysed sufficiently prior to selection to ensure that they would give consistent positive or negative results in tests by index methods. One panel included live virus so that virus isolation testing could be evaluated. Virus in other panels was inactivated so that they can be evaluated in laboratories that do not work at the highest containment levels.

The test purposes evaluated in this PTS were primary outbreak detection and post-outbreak serosurveillance conducted after both vaccination and non-vaccination.

Participants were asked to give results for individual tests on each sample and where multiple tests were used, an overall result was required for each sample. Laboratories were instructed to take account of the test purpose when selecting and interpreting tests.

Preliminary findings were discussed at the Open Session of the Research Group of the European Commission for the Control of FMD in Erice in October 2008. Further discussions took place at the annual meeting of the EU's National Reference Laboratories for FMD and

SVD in January 2009. Laboratories were given individual feedback on their results including observations and non-conformities according to predefined criteria. Laboratories with non-conformities will be followed up to determine a course of action to rectify any test deficiencies.

Four panels of materials were distributed:

Panel 1: Infectious materials from cattle or pigs with a vesicular condition for virus detection.

Panel 2: Non-infectious materials originating from cattle or pigs for virus detection.

Panel 3: Non-infectious materials from vaccinate or non-vaccinated cattle for FMD serotype O or A post-outbreak serosurveillance.

Panel 4: Non-infectious materials from pigs for SVD post-outbreak serosurveillance.

Principal conclusions of the exercise

1. Laboratories from 66 countries were invited to participate and 35 did so.
2. Information was collected on tests in use, strains of virus used in tests, extent of ongoing testing, and quality accreditation status of tests.
3. In general, although some discrepancies were identified in results for individual samples, most labs gave the correct overall interpretation for each case.
4. The following types of non-conformities were identified:
    a. Failure to detect viruses and false positive results.
    b. Failure to correctly type FMD viruses.
    c. Failure to detect antibodies and false positive detections

### 2.1.2.2. Initiatives of PANAFTOSA on laboratory testing harmonization

During 2008 PANAFTOSA organised its annual rounds of inter-laboratory proficiency testing for FMD diagnosis and serosurveillance. These rounds involved panels of materials for testing by: NSP-serology (I-ELISA 3ABC/EITB System), antigen detection and typing (IS-ELISA and Complement fixation), molecular detection and typing (PCR). All samples were analysed sufficiently prior to selection to ensure that they would give consistent positive or negative results in tests by index methods. Viruses were sent inactivated so that they can be evaluated in laboratories that do not work at the highest containment levels. Thirteen (13) laboratories of 10 South American countries participated in the NSP serology testing, eleven (11) laboratories of 10 South American countries participated in the antigen detection and typing methods and four (4) of the ten invited laboratories participated in the molecular detection/typing techniques. Laboratories were given individual feedback on their results including observations and non-conformities according to predefined criteria. Laboratories with non-conformities will be followed up to determine a course of action to rectify any test deficiencies.

Within the framework of PAMA/CMA/CVP project FOCEM, and during the Laboratory Expert Meeting on Biosecurity and Vaccine Quality Control (19-22 February, 2008), the Southern Cone harmonized the methodology for auditing biosafety and biosecurity in Official and Private Laboratories that manipulate FMDV. The following guidelines were elaborated:

"Guideline for Evaluation of Biosecurity during FMD vaccine production"; "Guideline for evaluation of Biosecurity in Units where FMD is Manipulated"; Check List for Evaluating Laboratories that control FMD Vaccine Quality.

### 2.1.2.3. North American initiatives on diagnostic harmonization

The North American Animal Health Laboratory Network between the US, Canada and Mexico was established in 2007 to harmonize test used for the diagnosis of animal diseases. This initiative addresses a key objective of the security and prosperity partnership of North America towards creating a safer and more reliable food supply while facilitating agriculture trade. Initial harmonization effort is to focus on vesicular diseases, tuberculosis and avian influenza. The main objective is to ensuring an equivalency of diagnostic test results between the laboratories regardless of protocol practiced by each country.

For each disease category, a working group was assembled to include subject matter experts, a coordinator and a statistician. The basic approach is to develop harmonization panels to address performance of each method utilized for specific analyte. A number of assays for Food-and-mouth disease are being harmonized with expected completion by end of CY2009. Further, cross training is supported to expand and enhance diagnostic capability.

PIADC-FADDL provides annual proficiency panels for FMD rRT-PCR to the 37 NAHLN (National Animal Health Laboratory Network) laboratories that are established across the 50 States.

## 2.2. Training

2.2.1. WRLFMD. During April 2008, a two week training course on FMD Diagnostic Techniques was provided at Pirbright for scientists from other diagnostic laboratories. There were 7 participants from Austria, Ethiopia, Macedonia, Mongolia, Romania, Russia and Sudan. The IAH has also hosted scientists from other countries for longer term training exercises (USA). In addition, IAH has provided a course instructor for diagnostic training missions organised in Kazakhstan and Uzbekistan.

2.2.2. PANAFTOSA provides on a yearly basis, 8 training courses covering areas of diagnosis serosurveillance and vaccine control. This year, 25 participants from Brazil, Chile, Paraguay and Uruguay have participated in these two-week courses. Additionally, individual training was provided for 2 specialists from Brazil, in the molecular diagnosis topics. PANAFTOSA co-organized the international training course on real-time PCR for the diagnosis of FMD and vesicular stomatitis at the National Center for Foreign Animal Diseases, Winnipeg, Canada in which one participant of Venezuela, Colombia, Bolivia and Peru were present. This course was supported by the Department of Foreign Affairs and International Trade, Canada and PANAFTOSA(PAHO/WHO) and was directed to Venezuela, Colombia, Ecuador, Bolivia and Peru

2.2.3. FGI-ARRIAH provided training for 3 specialists from the Kyrgyzstan Research Institute for Animal Husbandry, Veterinary Medicine and Pastures named after A. Duisheyev (Bishkek) in up-to-date methods for FMD diagnosis in case of suspicion for vesicular syndrome (15 September – 3 October 2008).

2.2.4. RRLSSA. During April 2008, two Zambian veterinarians were at RRLSSA for 2 weeks training in FMD diagnostics techniques. From sample treatment, and inoculation, ELISA typing, and molecular diagnostics techniques. Scientific discussions on FMD epidemiology, vaccine production and diagnostics were held in Zimbabwe and Namibia with technicians and veterinarians.

2.2.5. PIADC-FADDL provides, on a regular basis, training courses (5 courses per year) on foreign animal diseases to veterinary students, university professors and veterinarians from all over the United States and other countries. These two week courses include lectures, clinical rounds and necropsy of animals that are experimentally infected with various foreign animal diseases. This year, there were 8 participants from Russia, Israel, Jordon, Yemen and Egypt.
PIADC-FADDL participated in the international training course on realtime PCR for the diagnosis of FMD and vesicular stomatitis at the National Center for Foreign Animal Diseases, Winnipeg, Canada. This course was supported by the Department of Foreign Affairs and International Trade, Canada and PAHO/WHO (Panaftosa) and was directed to Venezuela, Colombia, Ecuador, Bolivia and Peru.

### 2.3. Reagent and test kit supply

2.3.1. In 2008, WRLFMD supplied to third countries: 140 ml rabbit/guinea-pig FMDV antisera, 230 ml FMDV reference sera, 230 ml inactivated FMDV, 115 ml live FMDV, 34 Antigen detection ELISA test kits, 58 antibody detection ELISA test kits.

2.3.2 ARC-OVI supplied BVS, rabbit and guinea pig antisera for type A, $A_{22}$ FMD virus to be used in the vaccine matching trial as discussed in 2.1.1.

2.3.3. FGI-ARRIAH supplied:

- Kits for detection of FMDV antibody in sera from farm animals using ELISA – 235 (Armenia, Republic of Kazakhstan, Taiwan, regions of the RF, including the number of kits used in the laboratory);
- Kits for detection of FMDV antigen in samples using ELISA – 271;
- Diagnostic reagents for FMDV typing using CFT:
    - antigens – 47 мл;
    - sera – 40 мл (regions of the RF, including the number of samples tested in the laboratory).

2.3.4. PANAFTOSA's laboratory collaborates with the National Laboratories of the South American countries by producing, controlling and distributing reference reagents for their diagnosis, serosurveillance and vaccine control activities. The following tables summarize the reagents (A) or complete kits (B) supplied to the different countries during 2008.

Additionally, cell lines have been distributed for diagnosis and vaccine production:
BHK-21 C13, IBRS II, MDBK, and Vero for Brazil, Colombia and Paraguay, and control reagents for molecular detection methods to Colombia.

With the objective to make available a rapid and efficient tool capable of discriminating the performance of NSP tests, an international evaluation bovine serum panel was constituted and fully characterized, which has been accepted by the BSC.

A. Set of reagents from PANAFTOSA for the number of indicated tests

| País / Tests | Argentina | Bolivia | Brasil | Chile | Colombia | Paraguay | Perú | Rep. Dominicana | Venezuela | Total |
|---|---|---|---|---|---|---|---|---|---|---|
| IS-ELISA-SI (Typing FMDV/VSV) | 4,550 | 700 | 1.400 | | 2.450 | | 700 | | 2.450 | **12.250** |
| CF 50% (Typing FMDV/VSV ) HIS (ml) | | | 20.000 | | 16.500 | | | | 9.000 | **29.500** |
| LPBE ELISA FMD Surveillance/Vaccination efficacy | 10.000 | 20.000 | 26.000 | 3.000 | 12.000 | 90.000 | | | 2.000 | **163.000** |
| LPBE ELISA FMD Vaccine Control | 5.000 | | 268.000 | | 55.000 | 30.000 | | | 24.000 | **382.000** |
| AGID-3D (FMD) Surveillance | | 6.000 | 22.000 | | 4.000 | | 4.000 | | 1.000 | **37.000** |
| LPBE ELISA VSV Surveillance | 30.000 | 1.000 | 9.000 | 6.000 | 2.000 | | | 3.000 | | **51.000** |
| ELISA CFL Control Vacuna (EV) | | | | | 2.000 | | | | | **2.000** |
| IDGA-LA | | 1.000 | 9.000 | 1.000 | 1.000 | | | | | **12.000** |
| ELISA CFS-LA | | 1.000 | 1.000 | | 3.000 | | | | | **5.000** |
| ELISA CFS-IBR | | 1.000 | 1.000 | 1.000 | | | | | | **3.000** |

B. Complete kits from PANAFTOSA for the number of indicated tests

| País / Tests | Argentina | Bolivia | Brasil | Chile | Colombia | Ecuador | Paraguay | Peru | Venezuela | Total |
|---|---|---|---|---|---|---|---|---|---|---|
| **I-ELISA 3ABC NSP Serology** | **72.160** | **29.040** | **139.040** | **880** | **40.480** | **880** | **74.800** | **6.160** | **2.640** | **366.080** |
| **EITB NSP Confirmatory Serology** | **5.400** | **1.800** | **20.800** | **200** | **2.800** | **200** | **6.400** | **800** | **400** | **38.800** |

## Annex 1 Phylogenetic trees

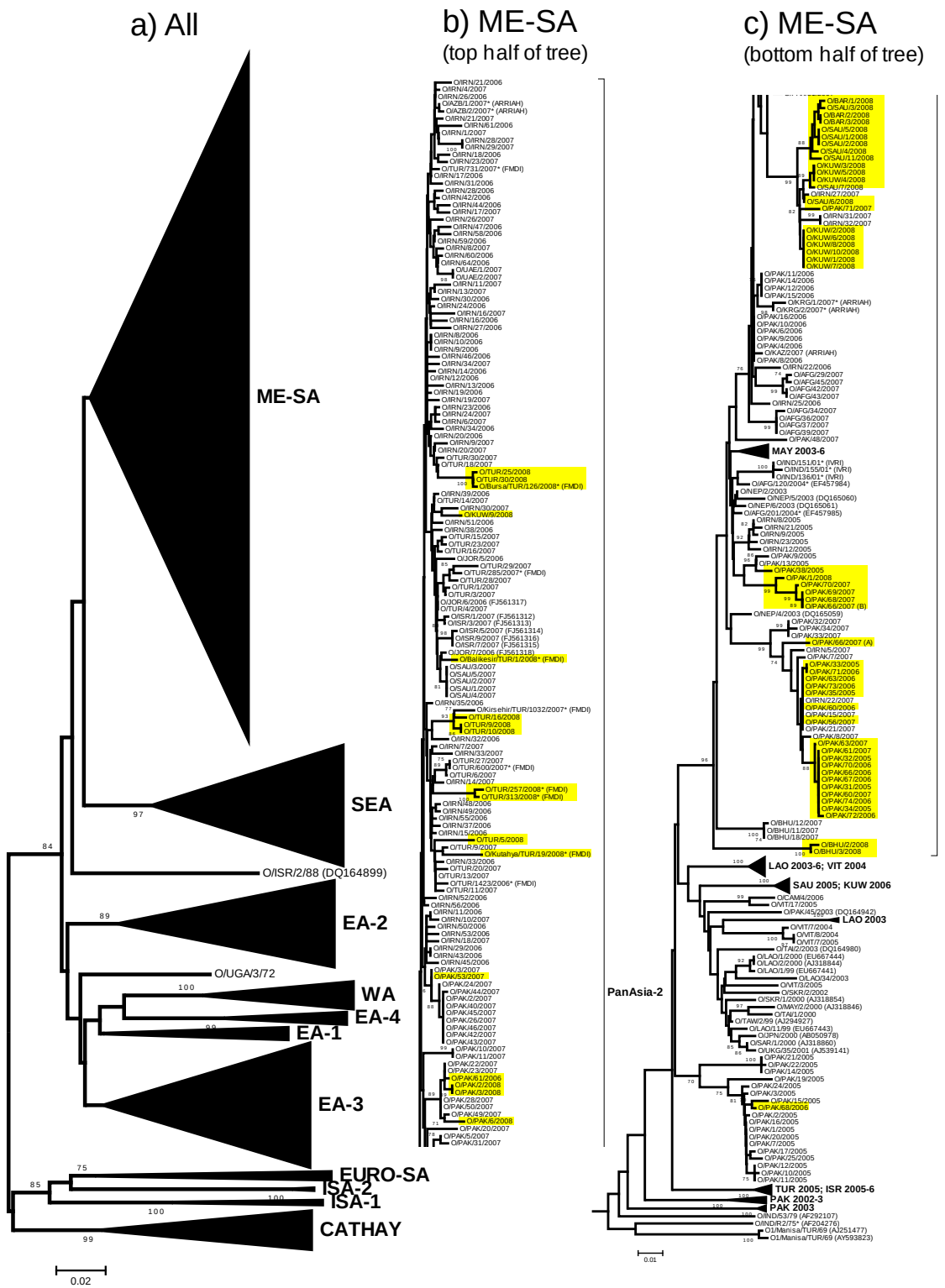



Fig. 5. FMDV type O in the Middle East.

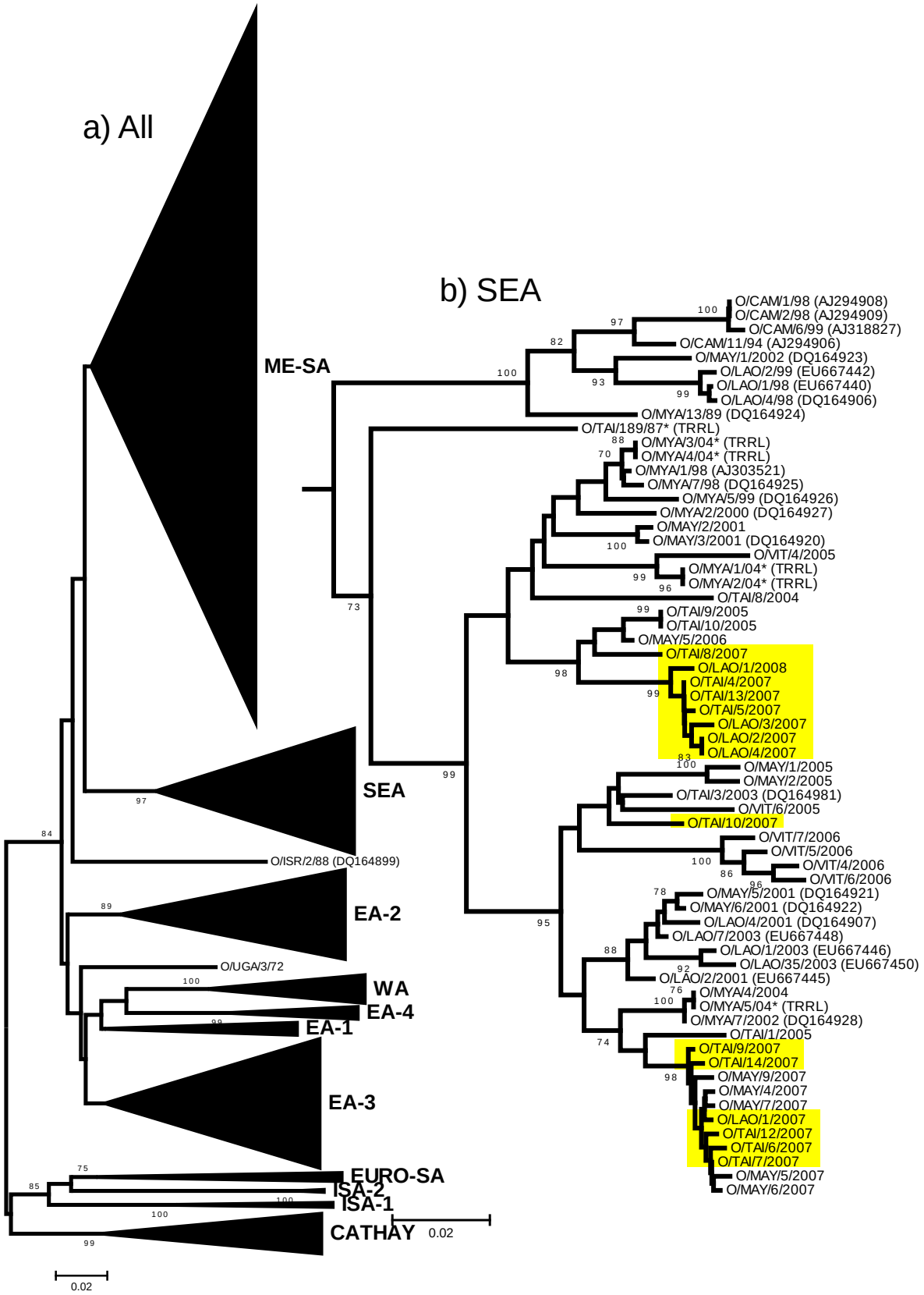



Fig. 6. FMDV type O in Southeast Asia.

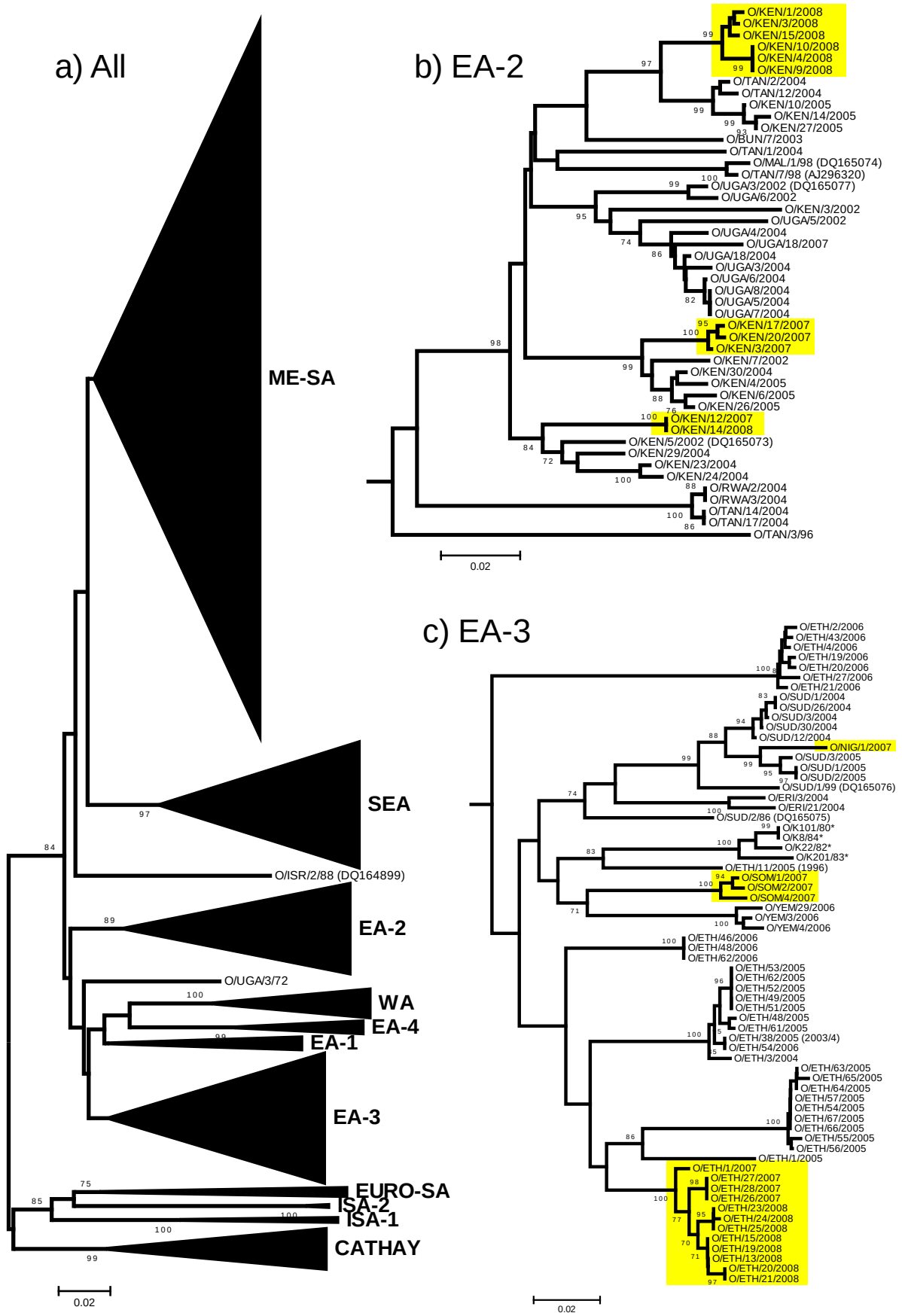



Fig 7. FMDV type O in Africa.

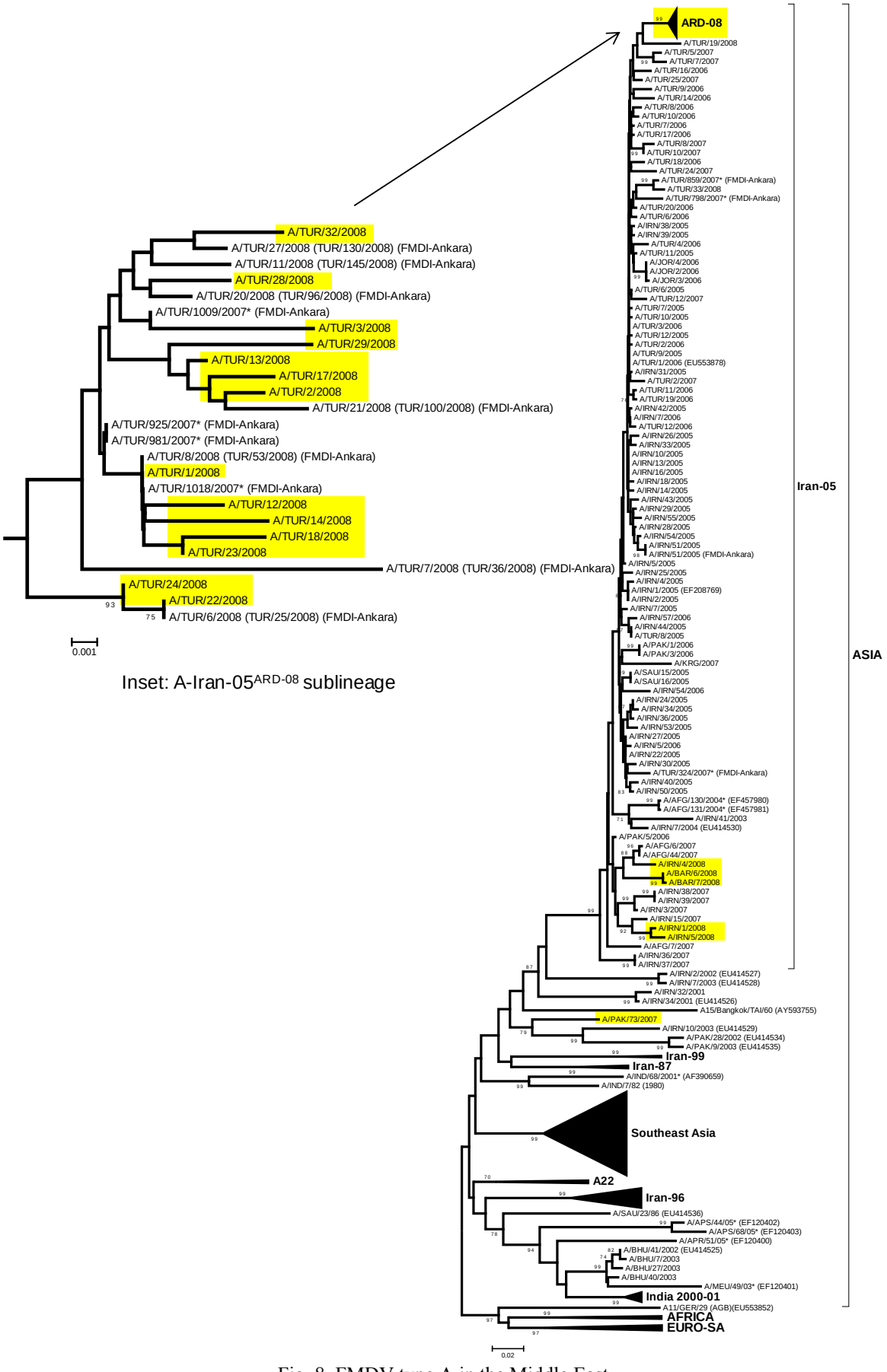



Fig. 8. FMDV type A in the Middle East.

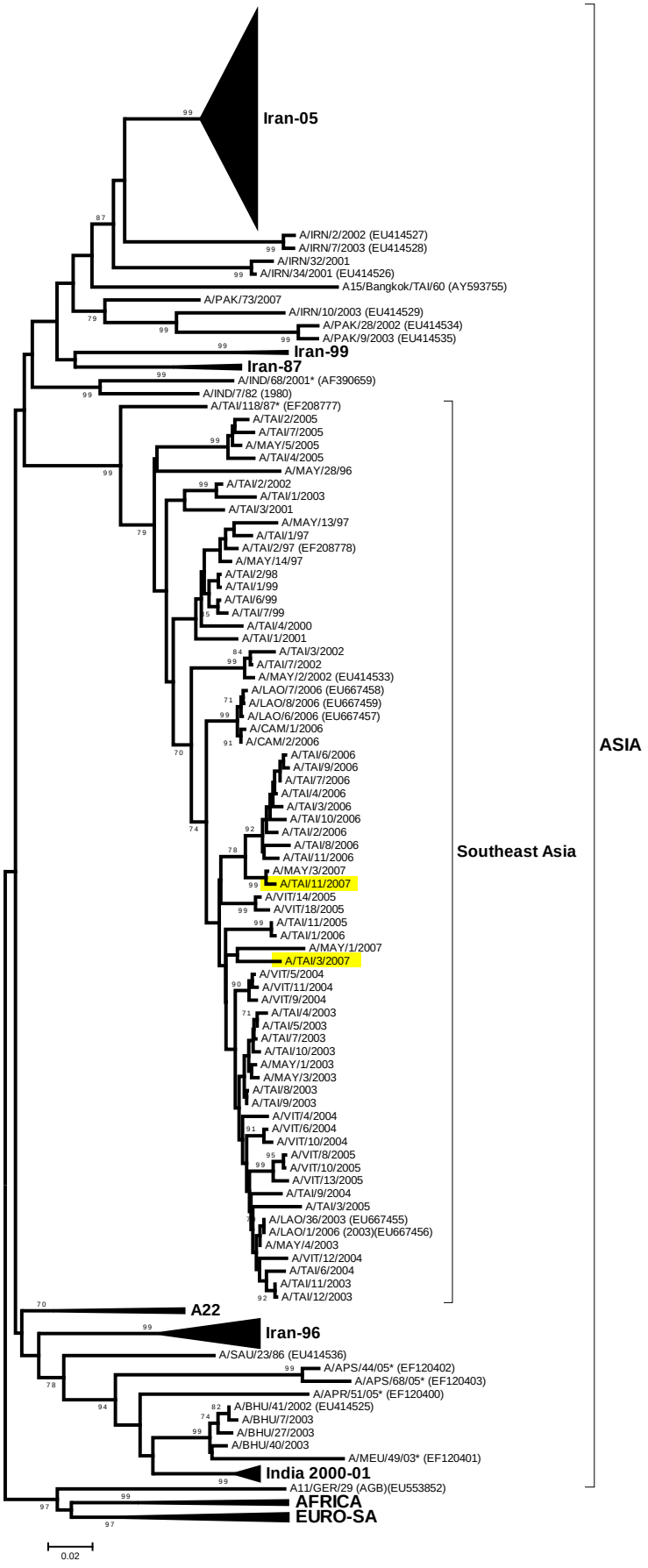



Fig. 9. FMDV type A in Southeast Asia.

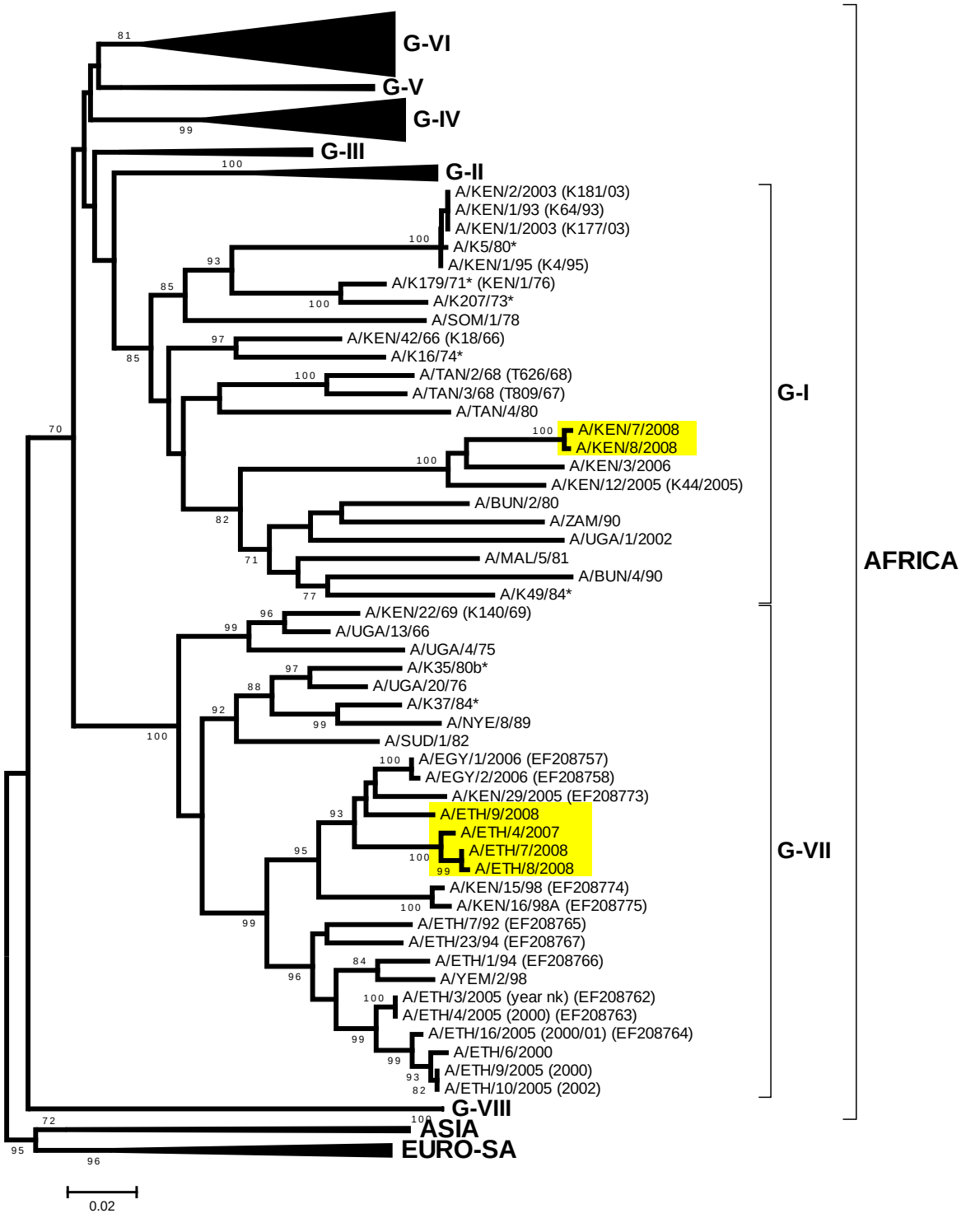



Fig. 10. FMDV type A in Africa.

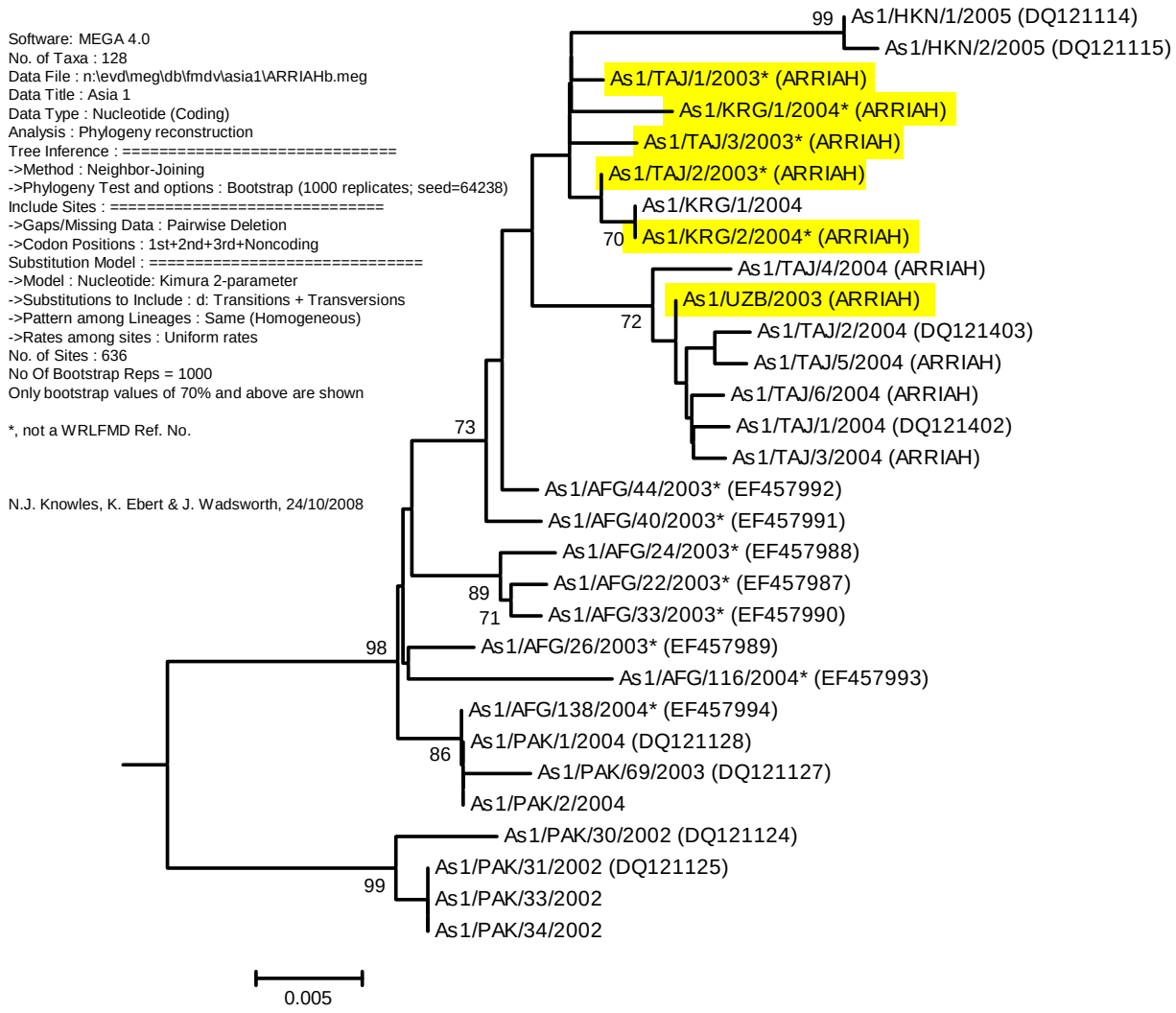



Fig. 11. FMDV type Asia 1 in Central Asia in 2003-2004.

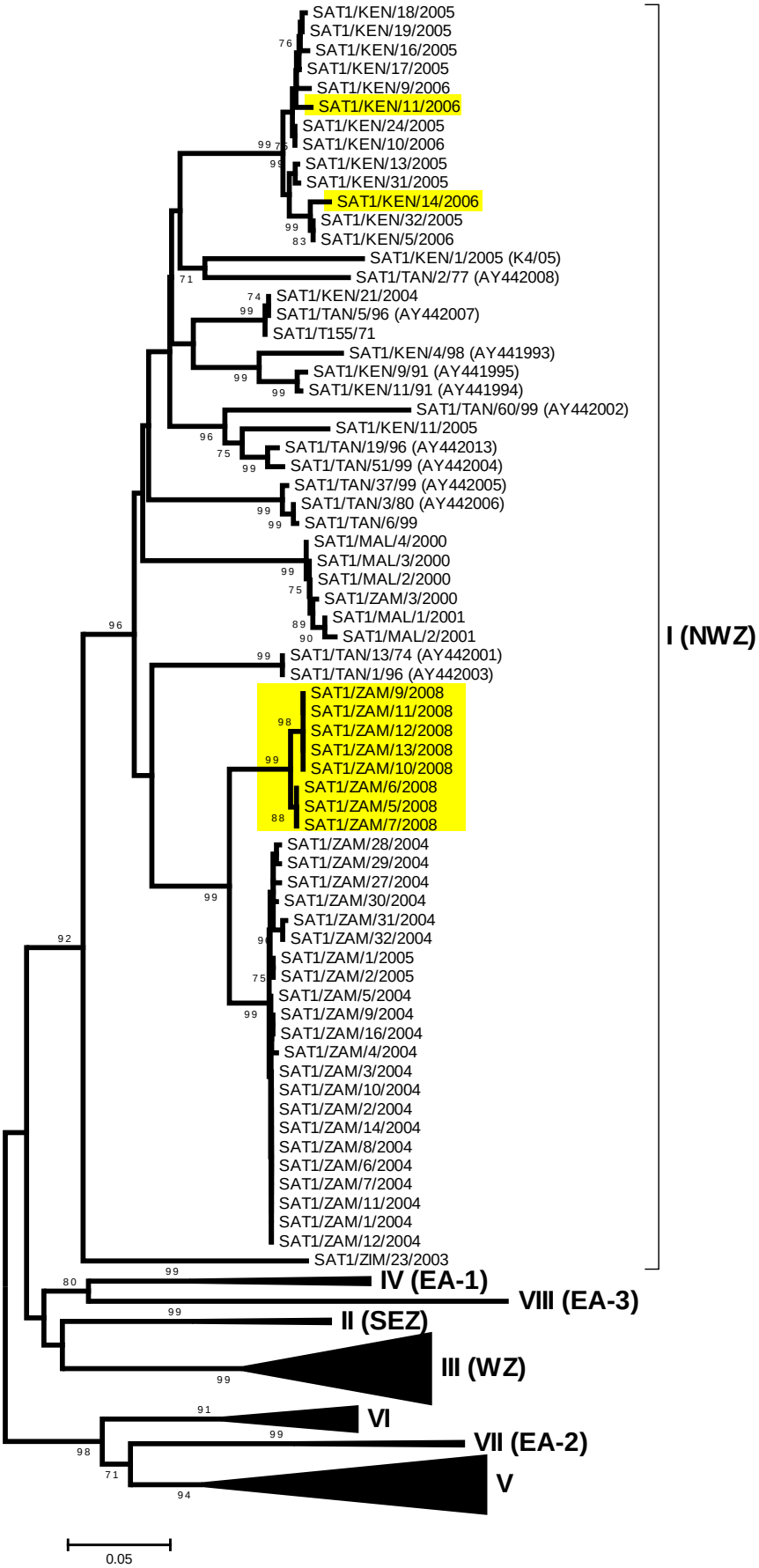



Figure 12. FMDV type SAT 1 in Kenya and Zambia.

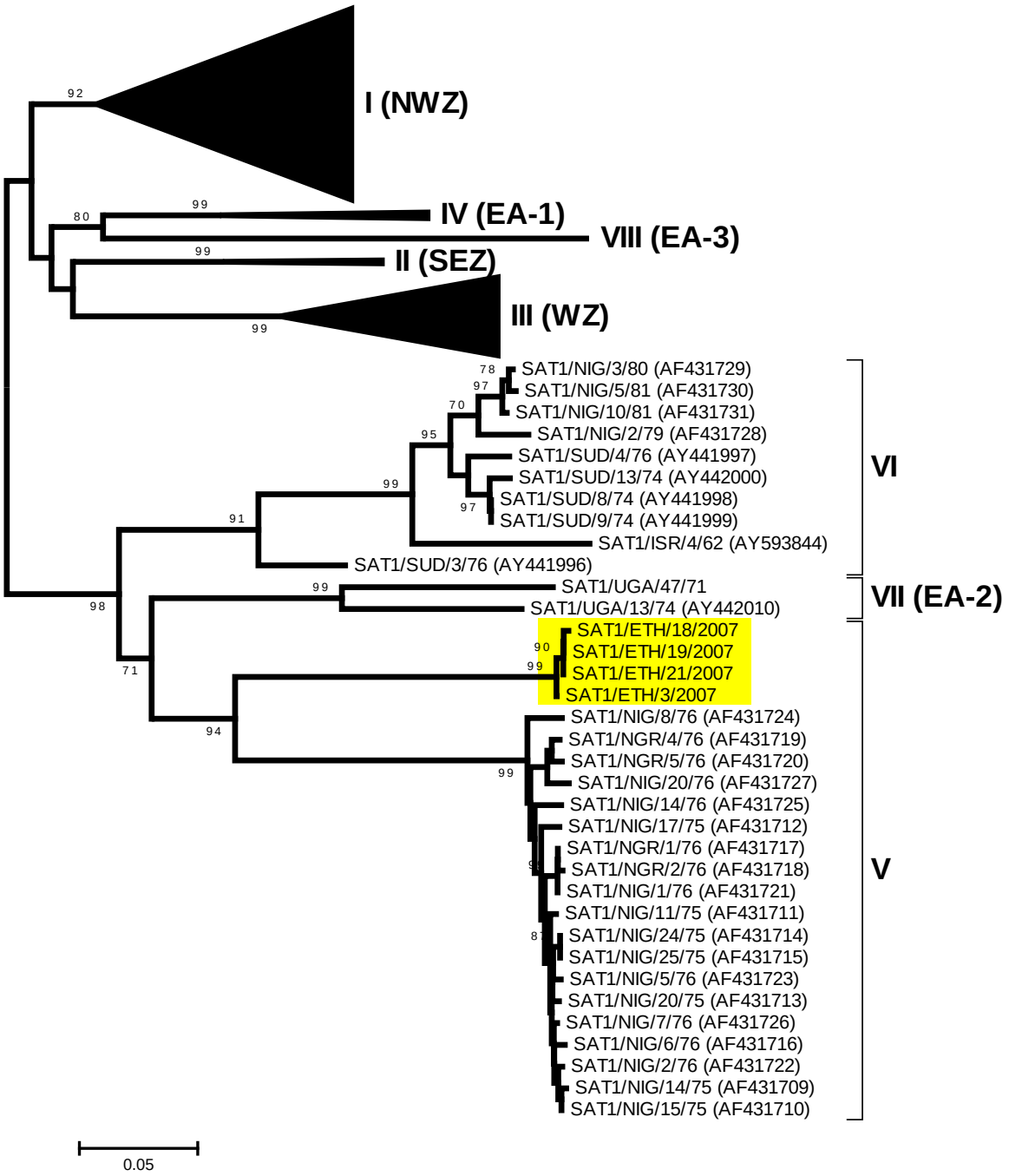



Figure 13. FMDV type SAT 1 in Ethiopia.

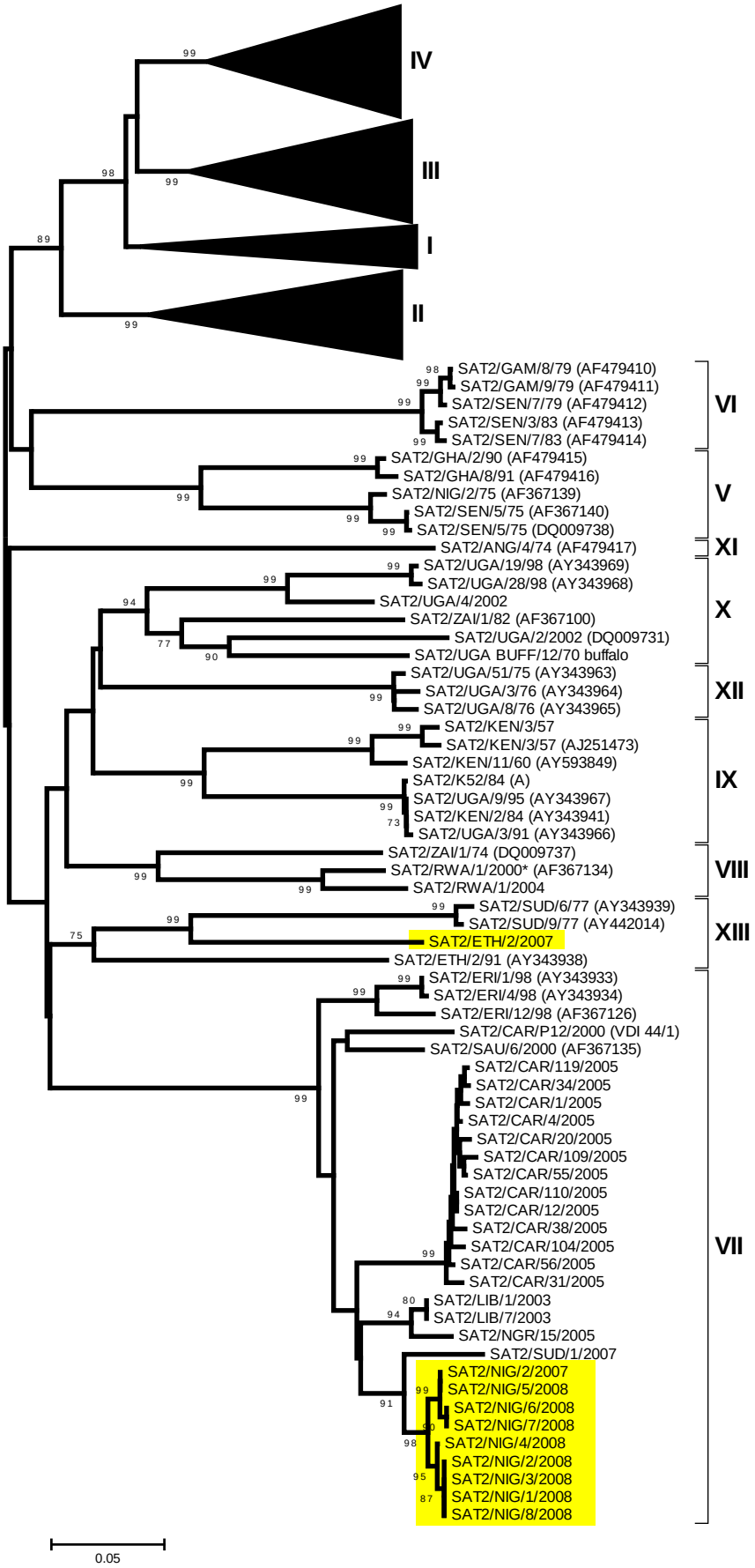



Fig 14. FMDV type SAT 2 in Ethiopia and Nigeria

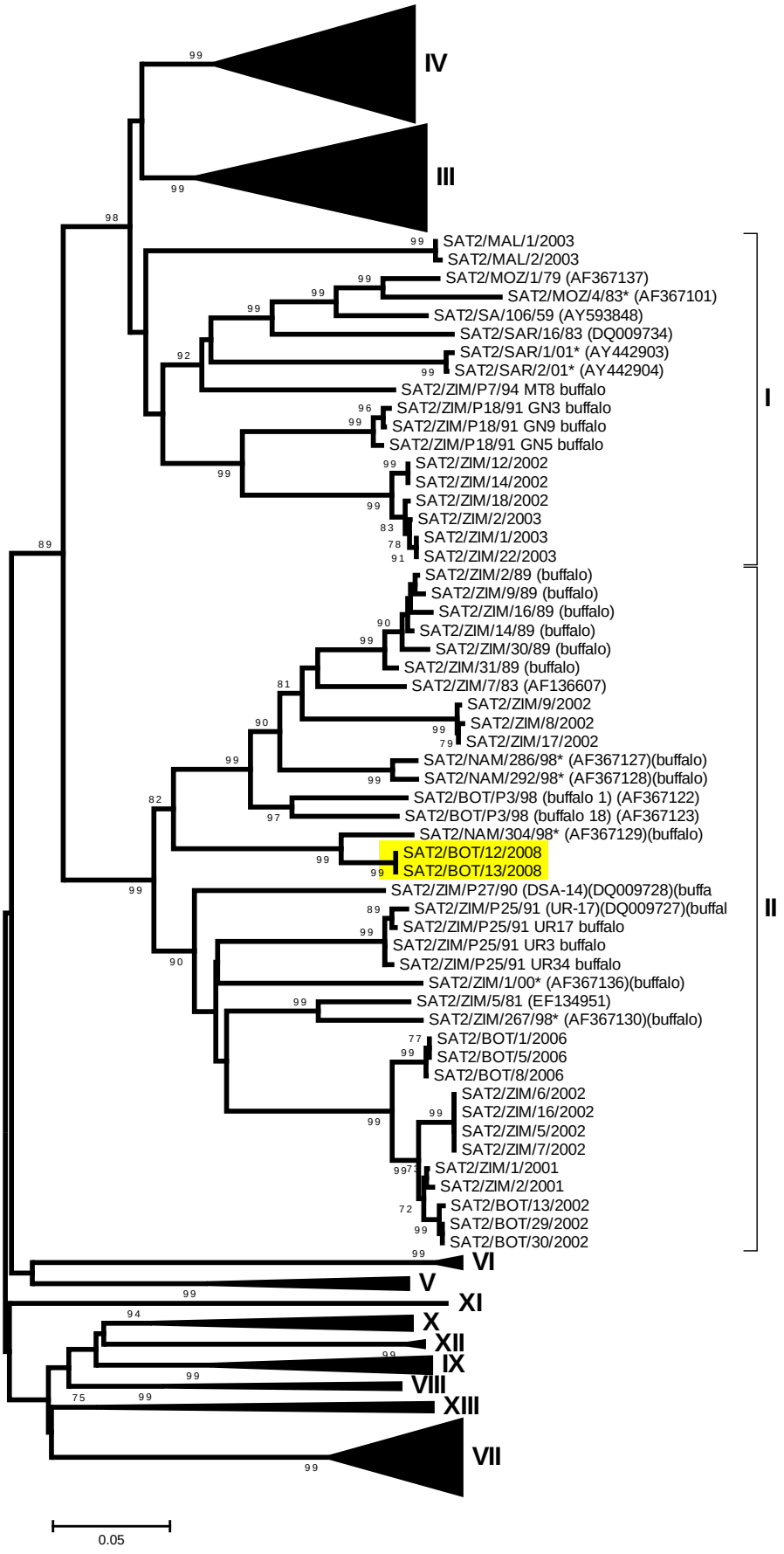



Fig. 15. FMDV type SAT 2 in Botswana.

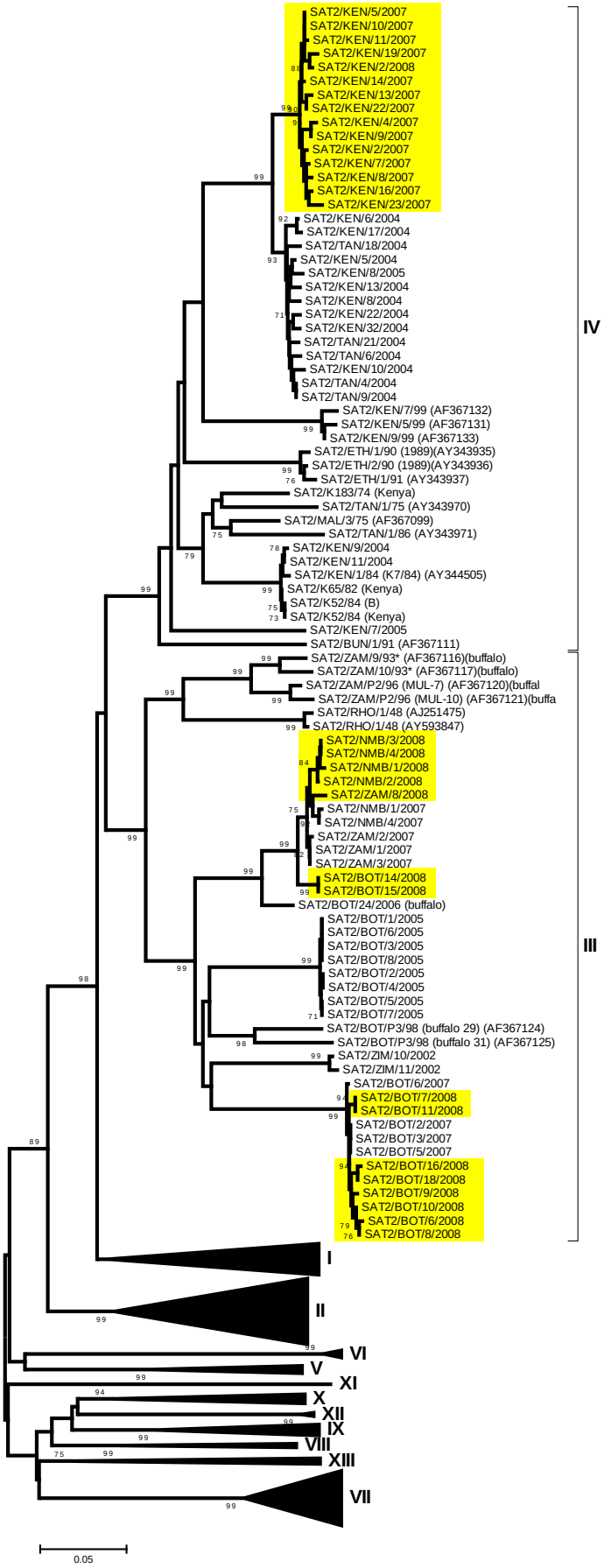



Fig. 16. FMDV type SAT 2 in Botswana, Namibia, Zambia and Kenya.

Fig. 17. Neighbour-joining tree comparing the complete VP1-coding sequences of type A FMDV collected in South America.

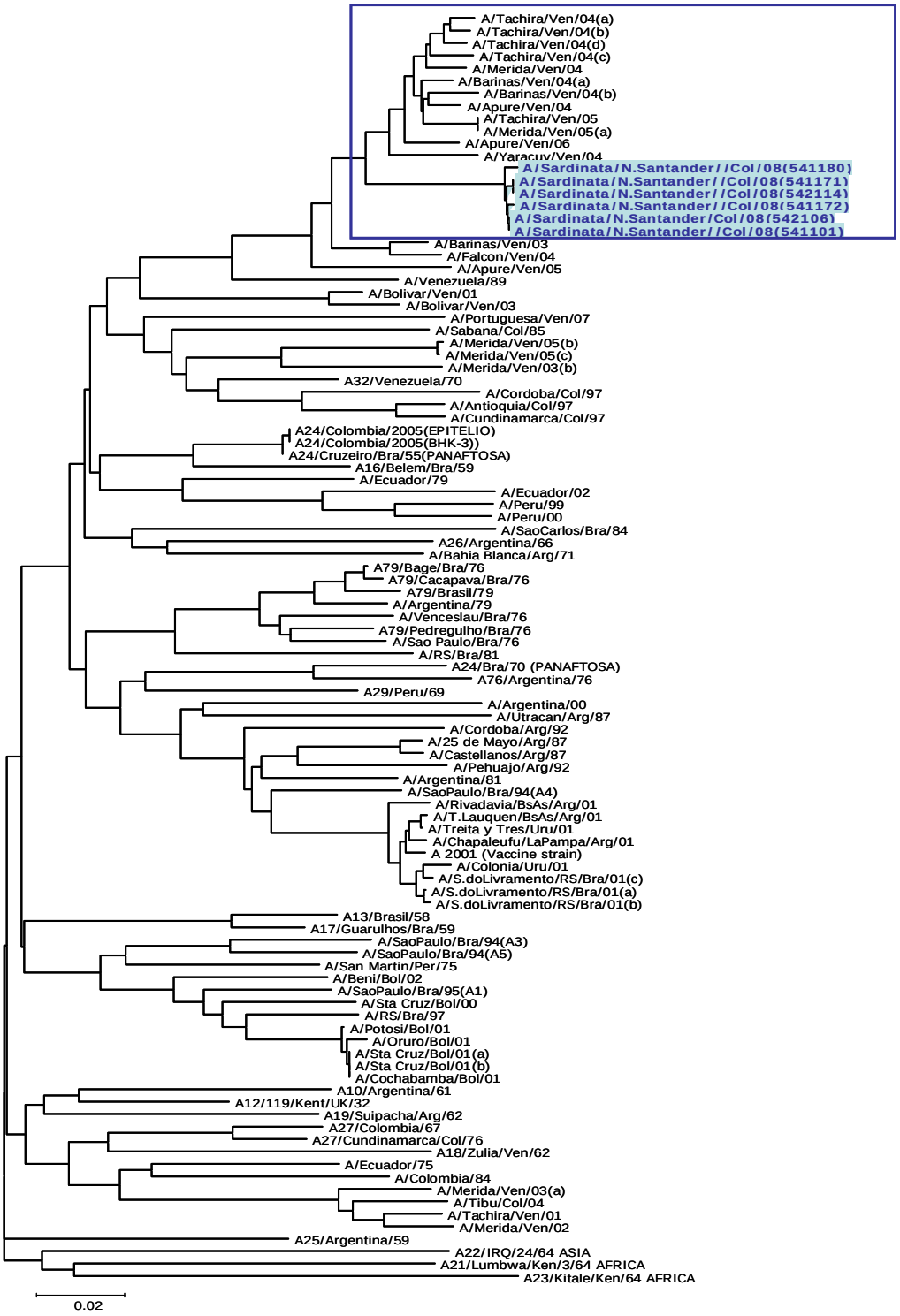


Fig 18. Neighbour-joining tree comparing the complete VP1-coding sequences of type O FMDV collected in South America.

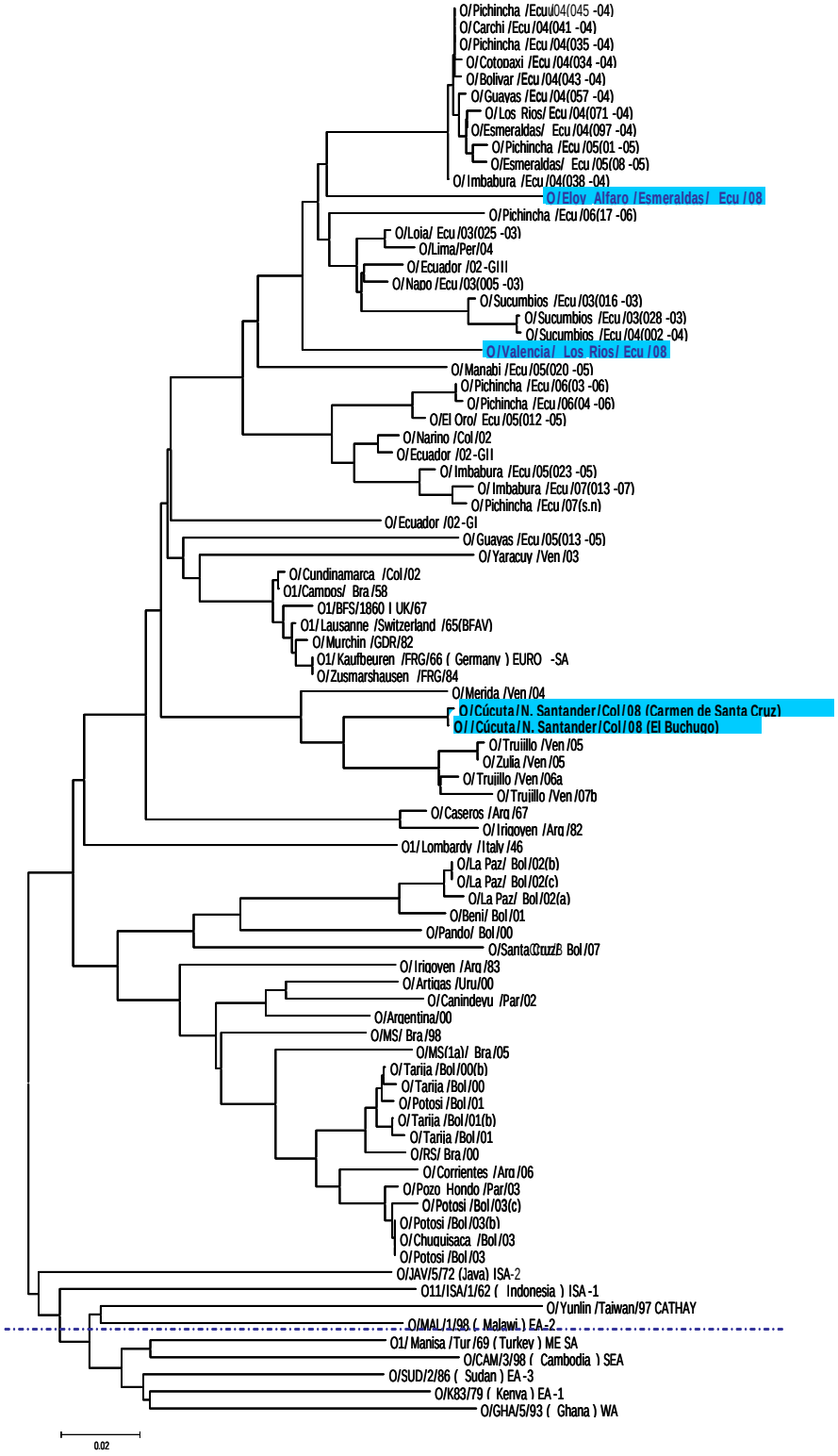


Fig. 19. Neighbor-joining tree (FGI-ARRIAH) showing the position of A/Kyrgyzstan/2007 field isolate. Based on complete VP1 sequences.

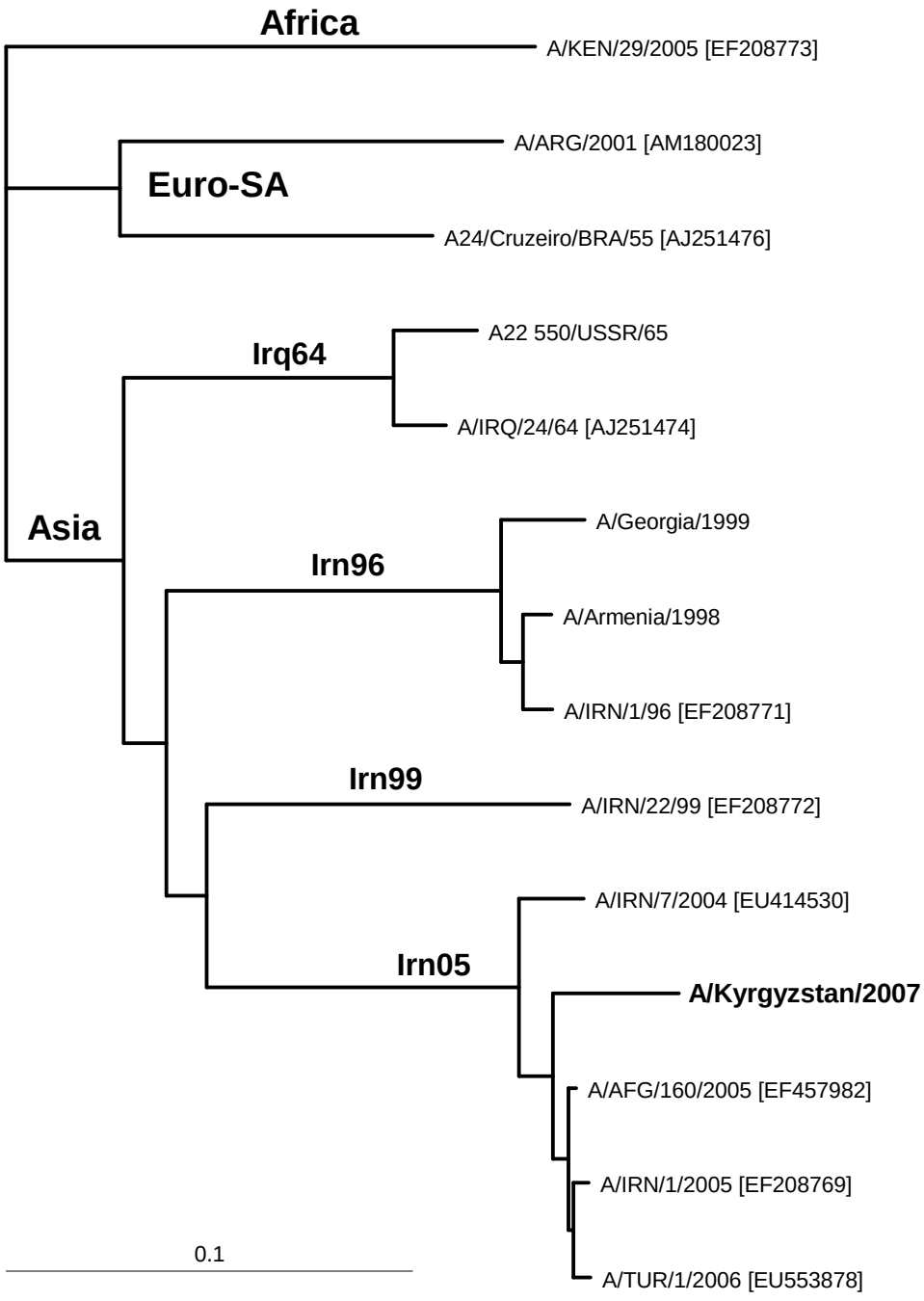
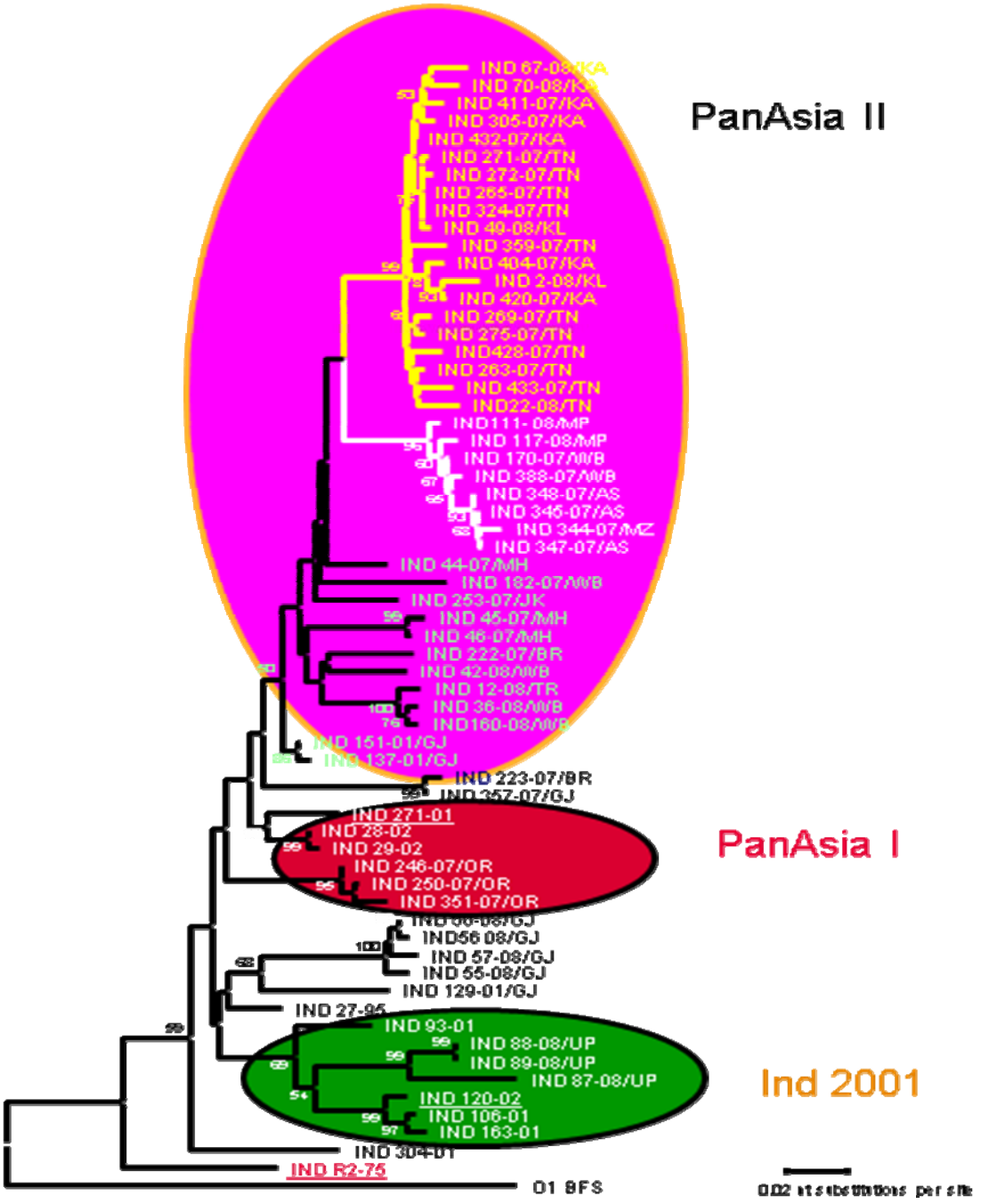


Fig. 20. NJ tree showing genetic relationships among the type O isolates at VP1 region recovered during 2007-08

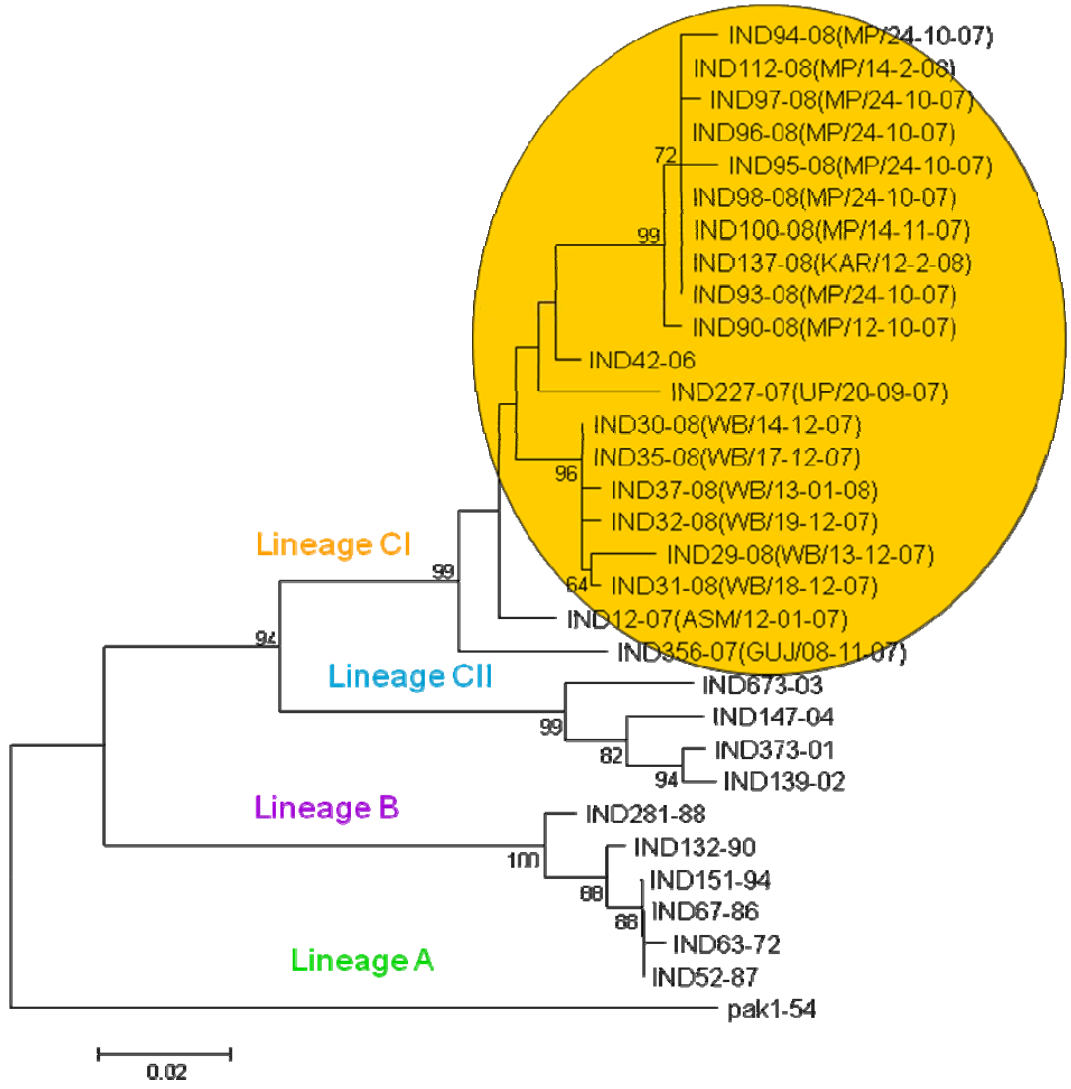
At present, two sublineages of PanAsia virus are co-circulating in the country, of which PanAsia II has dominated the type O outbreaks. This sublineage was responsible for severe FMD outbreaks in Tamilnadu and Karnataka during late 2007. The Ind 2001 strain which predominated in 2001 caused sporadic outbreaks in the Northern states. Comparison of Indian type O field isolates in relation to global type O viruses revealed the presence of PanAsia II strain in neighboring countries viz; Bhutan, Nepal, Pakistan and also in Malaysia.




***Compiled by RP Tamilselvani, 2008***

Fig. 21. NJ tree showing genetic relationships among the type Asia1 isolates at VP1 region.

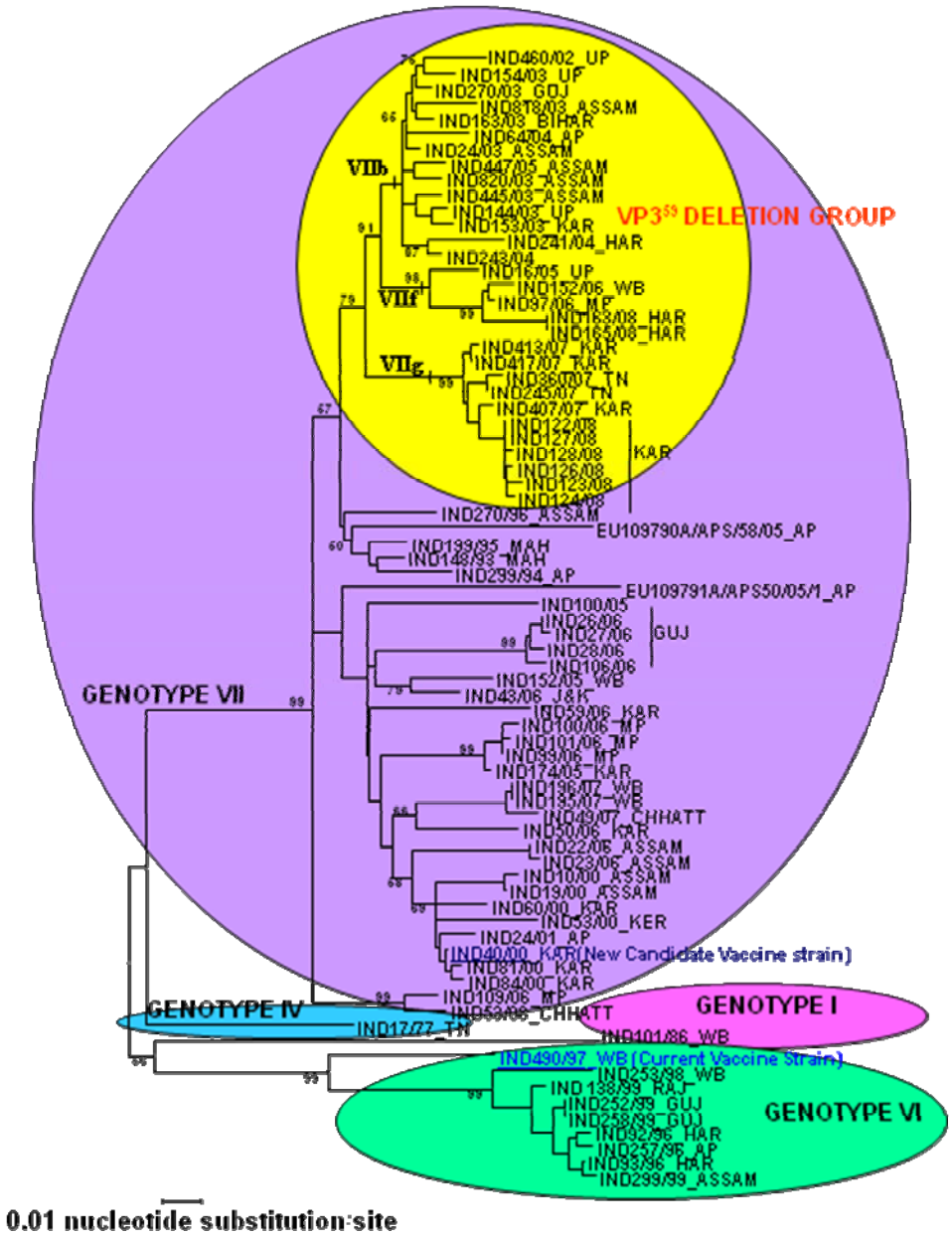
Isolates of lineage B (IND 63/72 group) disappeared since 1999. Lineage CI dominated Asia1 outbreaks since 1998. Divergent group lineage CII appeared in 2001 and dominated exclusively between 2002 and 2004. Lineage CI again reemerged in 2005 and dominating since then. Indian FMD Asia1 field isolates grouped separately from Asia1 isolates of other country.




***Compiled by S.Saravanan 2008***

Fig. 22 Neighbour-joining tree depicting phylogenetic relationship among type A isolates at 1D region

Four genotypes (I, IV, VI and VII) were identified in India with >15% nt divergence. There was endemic co circulation of VI and VII between 1990-2000 and disappearance of genotype I and IV since 1990. Genotype VI is non-existent in India since 2001. Deletion group within genotype VII appeared in 2003 and responsible for recent outbreaks. In 2007-08, there is exclusive incidence of lineage VII. 1D region based phylogeny revealed that this lineage is genetically diverging with time.




***Compiled by J.K.Mohapatra 2008***

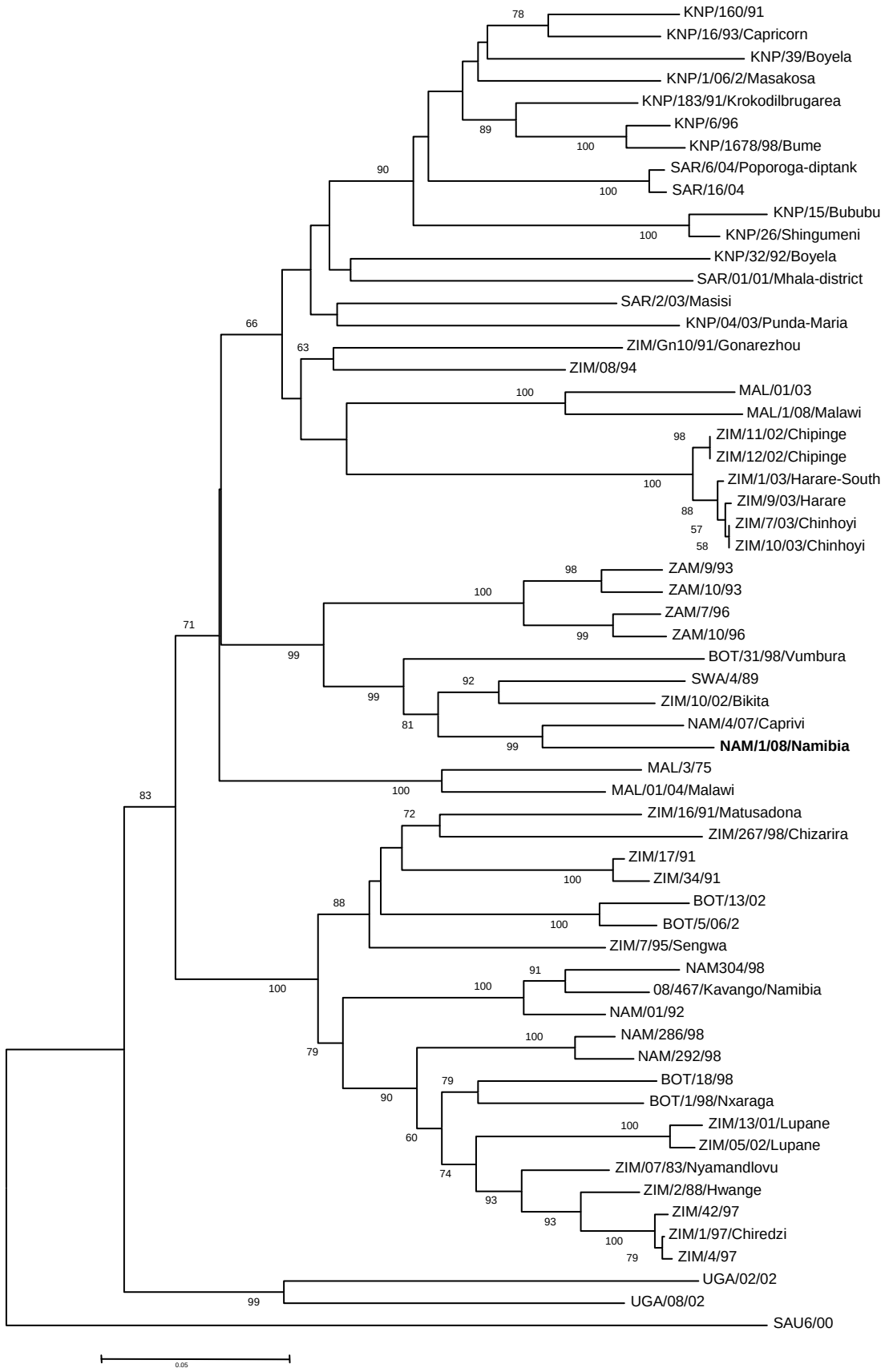



Fig. 23. Neighbor joining tree depicting the SAT 2 FMD outbreak strain from Namibia. The current strain (NAM/1/08) indicated in bold, clusters with the 2007 strain characterised from Namibia.

***Compiled by RM Dwarka and NTE Mtshali, 29 November 2008***

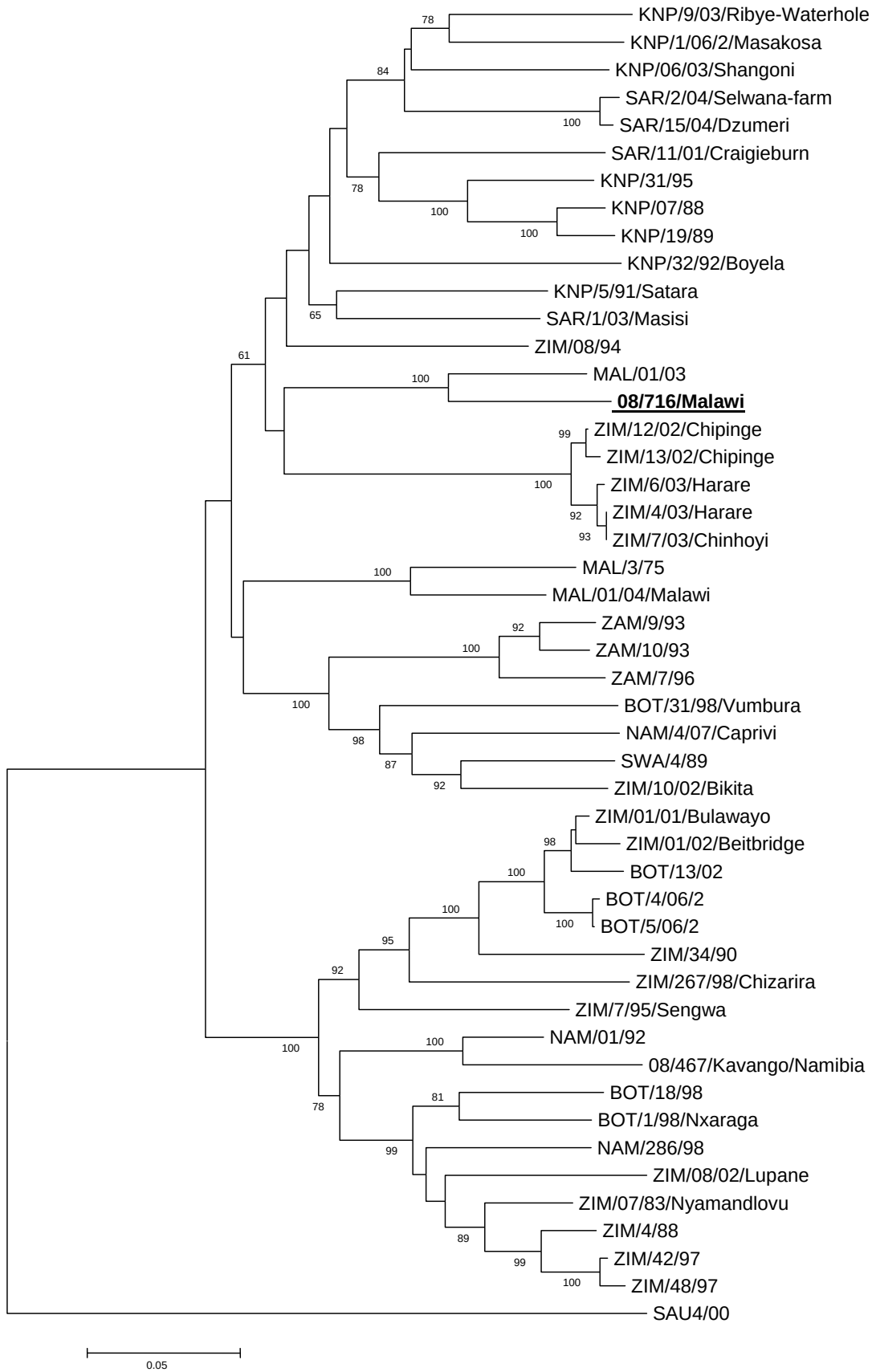



Fig. 24. Neighbor joining tree depicting the SAT 2 FMD outbreak strain from Malawi (indicated in bold). The current outbreak strain, designated 08/716, differs by 10% at nucleotide level from a SAT 2 outbreak strain characterised from Malawi in 2003.

***Compiled by RM Dwarka and NTE Mtshali, 29 October 2008***

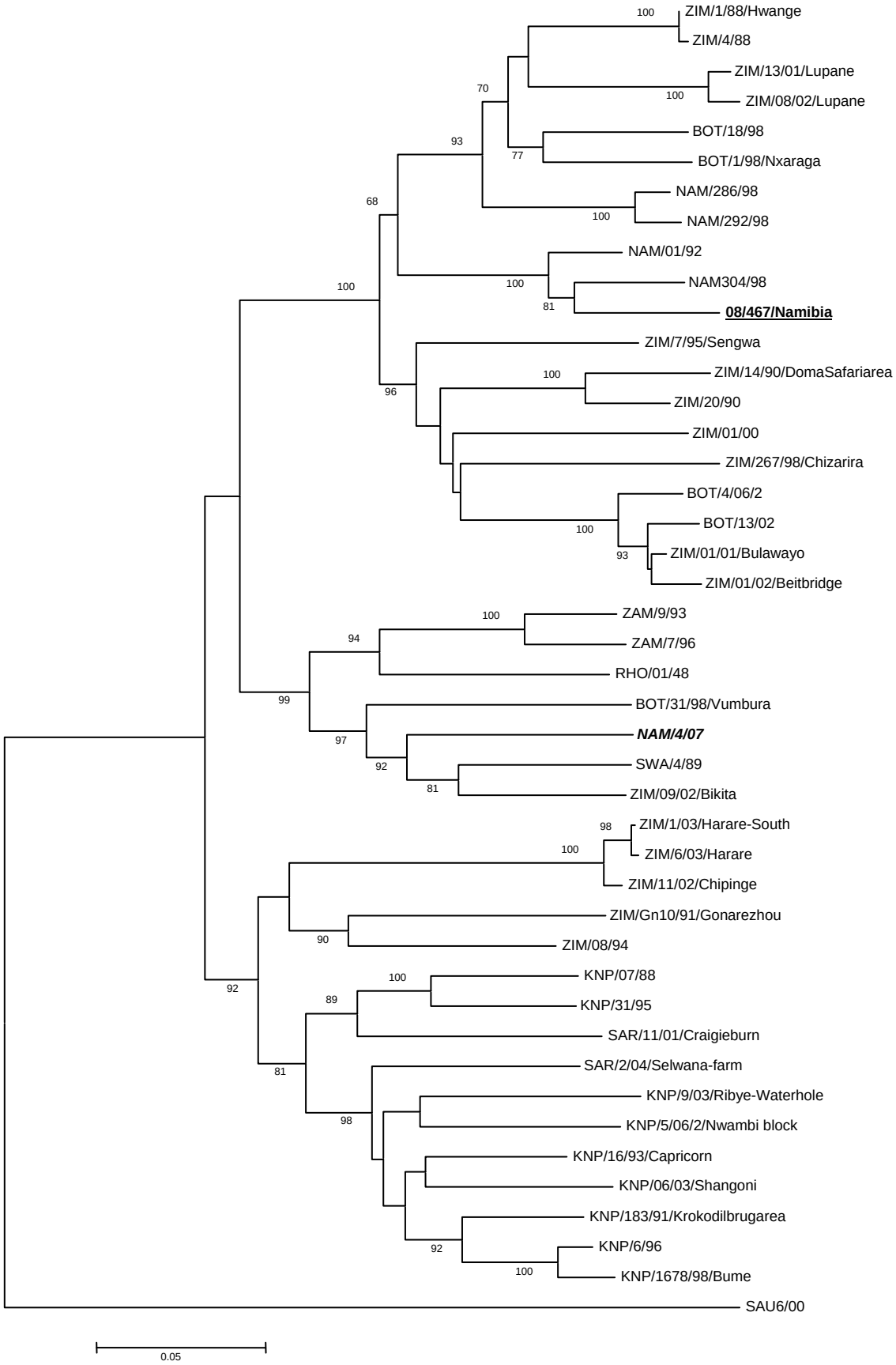



Fig. 25. Neighbor joining tree depicting the current SAT 2 outbreak strain characterised from Nambia **(08/467/Namibia**). This strain clusters with previously characterised SAT 2 strains from Namibia (NAM/304/98 and NAM/01/92) with an 8% difference at nucleotide level. The current isolate also differs by 28 % from the SAT 2 outbreak strain characterised in 2007 (NAM/4/07).

***Compiled by RM Dwarka and NTE Mtshali, 20 August 2008***

Fig. 26. FMDV serotype O collected in Israel

Neighbour joining tree depicting serotype O outbreak in Israel 2007. A wide comparison of the VP1 coding region with a total of 446 O isolates revealed that the cluster of the six Israel isolates is more closely related to the isolates from South-Asia, including Bhutan, Nepal and Malaysia than those from Middle East in Israel, Iran, and Turkey isolated in 2003 and 2004. Analysis performed at PIADC.

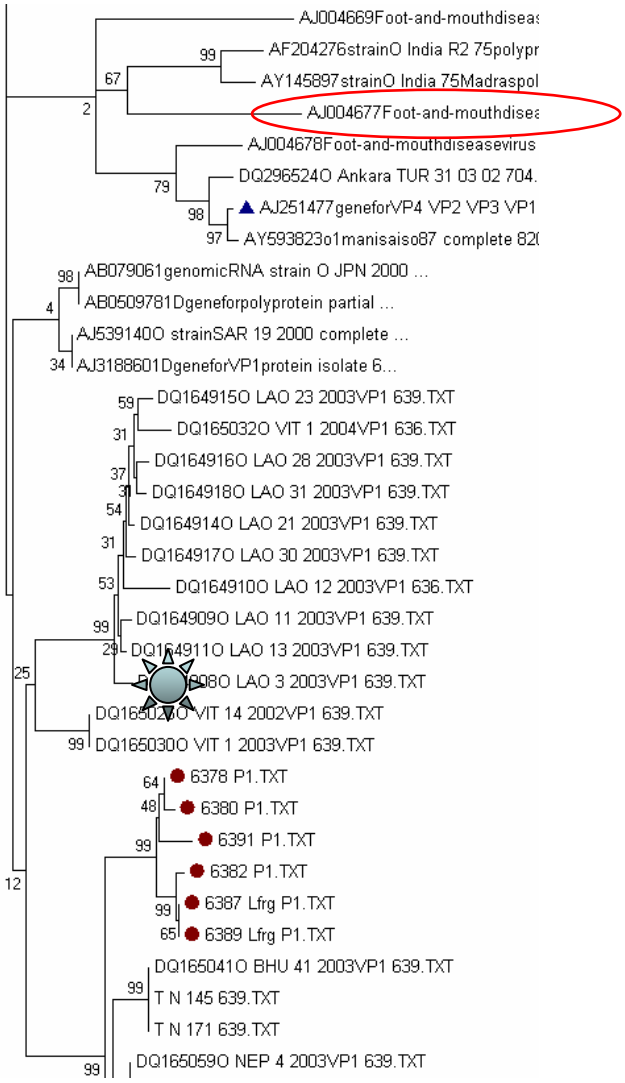


Fig. 27. FMDV serotype O collected in Israel.

Neighbour joining tree depicting serotype O outbreak in Israel 2007. P1 region sequence analysis of six isolates collected from six villages within 3 districts revealed that the isolates can be divided into 2 subgroups which may have arrived in Israel from different but related sources, or they may have arrived from the same source virus and subsequently diverged due to locality differences, host type and/or incubation period/conditions. Analysis performed at PIADC.