Foot-and-mouth Disease

Global and regional risks

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World Organisation for Animal Health
Founded as OIE

FMD Reference Laboratory

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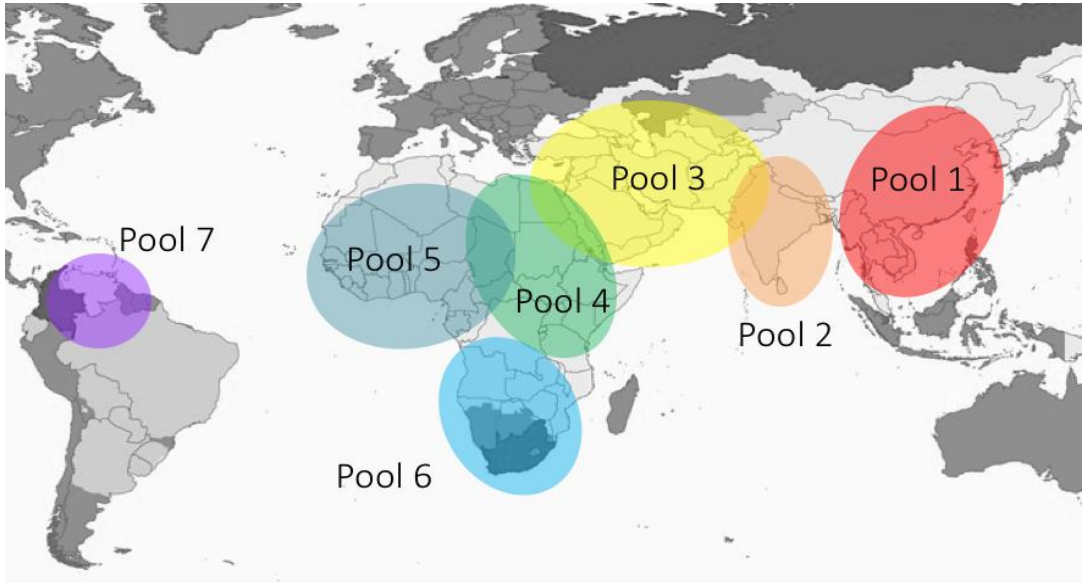
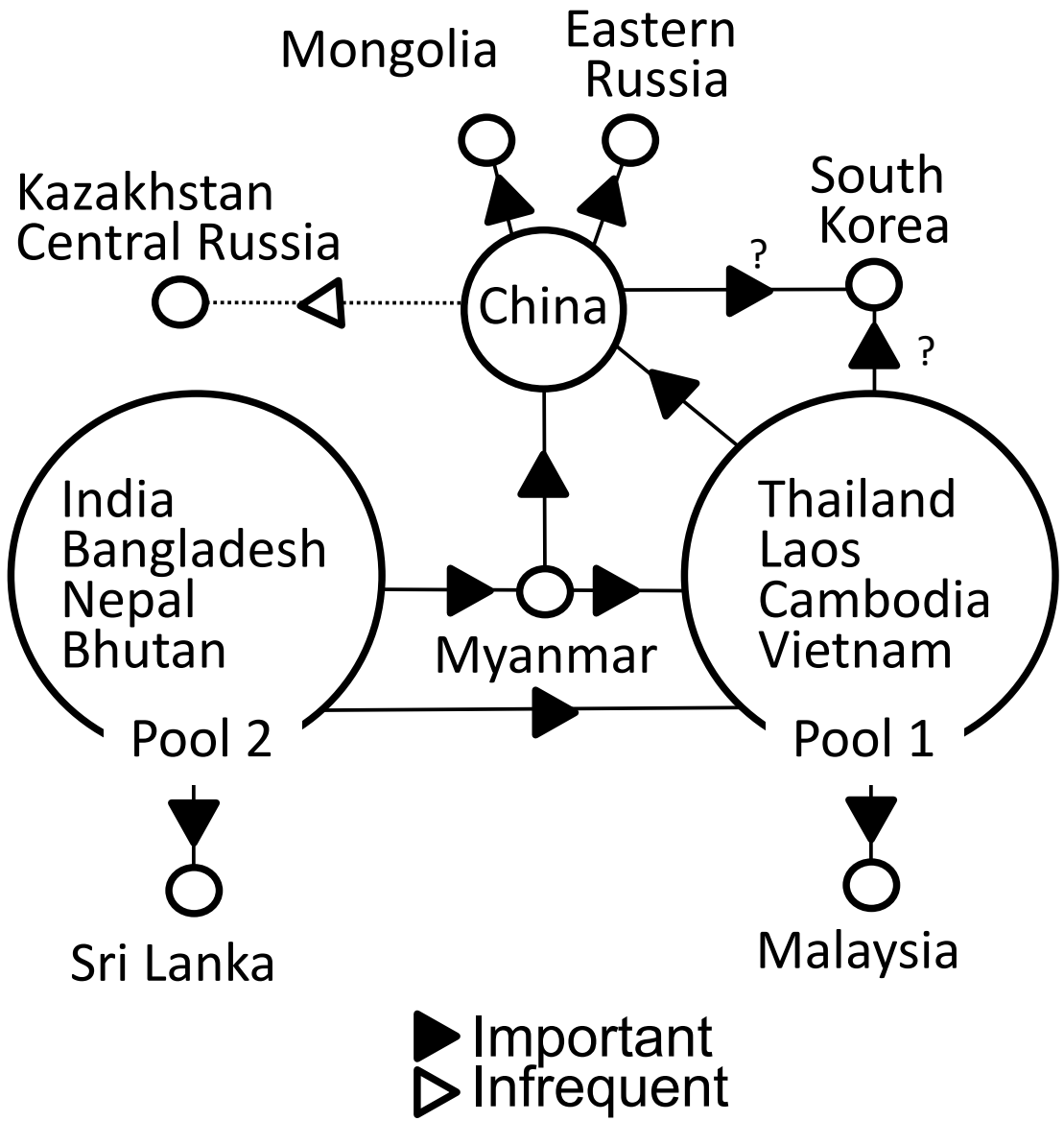
FMD epidemiology: global summary

- The epidemiology of FMD is dynamic; defined by:
  - Seven virus ecosystems (pools) that maintain specific FMDV strains requiring tailored diagnostics and vaccines
  - Six circulating FMDV serotypes with an unequal distribution (NB: Serotype C has not been detected globally since 2004)
  - Long-distance “trans-pool” movements of FMDV lineages which are often unpredictable
- **International partnerships are essential to collate, share and analyse data**

WOAH/FAO Foot-and-Mouth Disease Reference Laboratories Network



Conjectured FMDV connections: South Asia, Southeast/East Asia



Viral sequences highlight most frequent connections between countries (reflect trade and animal movements)

Potential risk pathways:

- Illegal imports
- Import of fodder
- Overseas workers
- Returning travellers
- Wildlife

Spread beyond Pool 2 – 10-year historical context

POOL 2

O

O/ME-SA/Ind-2001

>15 escapes

2013+
North Africa
Gulf States
Mauritius (2016 & 2022)

2015+
Mainland SEA

2015
Saudi Arabia, Türkiye, Iran, Armenia, Israel
(Bachanek-Bankowska et al., 2018 – EID)

A

A/ASIA /G-VII

Asia 1

2017
Myanmar
(Bo et al., 2019 – TBED)

SCIENTIFIC REPORTS

OPEN

Reconstructing the evolutionary history of pandemic foot-and-mouth disease viruses: the impact of recombination within the emerging O/ME-SA/Ind-2001 lineage

Katarzyna Bachanek-Bankowska[1], Antonello Di Nardo[1], Jemma Wadsworth[1], Valerie Mioulet[1], Giulia Pezzoni[2], Santina Grazioli[2], Emiliana Brocchi[2], Sharmila Chapagain Kafle[3], Ranjani Hettiarachchi[3], Pradeep Lakpriya Kumaravadu[4], Ibrahim M. Eldaghayes[5], Abdunaser S. Dayhum[5], Deodass Meenowa[6], Soufien Sghaier[7], Hafsa Madani[8], Nabil Abouchoaib[9], Bui Huy Hoang[10], Pham Phong Vu[10], Kinzang Dukpa[11], Ratna Bahadur Gurung[11], Sangay Tenzin[11,16], Ulrich Werner[12], Alongkorn Panthumart[13], Kingkarn Boonsuya Seeyo[13], Wilai Linchongsubongkoch[13], Anthony Relmy[14], Labib Bakkali-Kassimi[14], Alexei Scherbakov[15], Donald P. King[1] & Nick J. Knowles[1]

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DOI: 10.1111/tbed.14134

RAPID COMMUNICATION

WILEY

Foot-and-mouth disease viruses of the O/ME-SA/Ind-2001e sublineage in Pakistan

Syed M. Jamal[1] | Salman Khan[1] | Nick J. Knowles[2] | Jemma Wadsworth[2] | Hayley M. Hicks[2] | Valérie Mioulet[2] | Abdelghani Bin-Tarif[2] | Anna B. Ludi[2] | Syed Asad Ali Shah[3] | Muhammad Abubakar[4] | Shumaila Manzoor[5] | Muhammad Afzal[5] | Michael Eschbaumer[6] | Donald P. King[2] | Graham J. Belsham[7]

Received: 30 May 2022 | Revised: 6 June 2022 | Accepted: 6 June 2022
DOI: 10.1111/tbed.14607

RESEARCH NEWS

Transboundary and Emerging Diseases

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Foot-and-mouth disease in Kazakhstan

SB Tyulegenov[1] | A Zhakupbayev[2] | M Berdikulov[3] | T Karibayev[3] | GN Yessembekova[1] | AA Sultanov[4] | AM Perez[5] | SK Abdrakhmanov[1]

AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

Genome Sequence of a Foot-and-Mouth Disease Virus Detected in Indonesia in 2022

Nuryani Zainuddin,[a] Edy Budi Susila,[b] Hendra Wibawa,[c] Rosmalina Sari Dewi Daulay,[b] Putriani Endah Wijayanti,[b] Dini Fitriani,[b] Dewi Noor Hidayati,[b] Syafrison Idris,[a] Jemma Wadsworth,[d] Noemi Polo,[d] Hayley M. Hicks,[d] Valerie Mioulet,[d] Nick J. Knowles,[d] Donald P. King[d]

frontiers | Frontiers in Veterinary Science

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Check for updates

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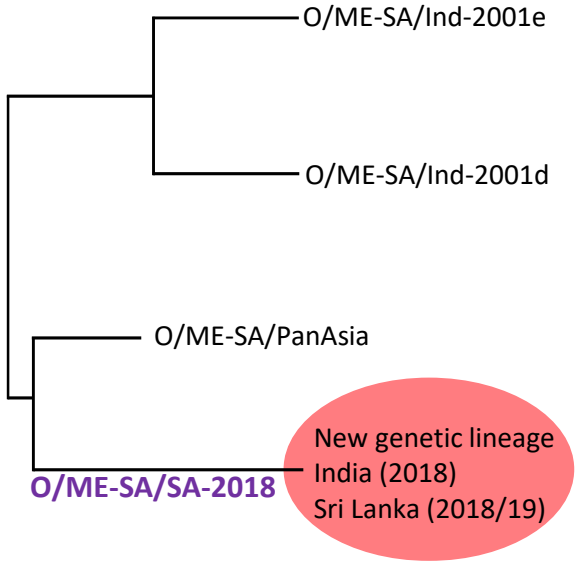
Re-emergence of foot-and-mouth disease in the Republic of Korea caused by the O/ME-SA/Ind-2001e lineage

Soyoon Ryoo[1], Hyeonjeong Kang[1], Da-Rae Lim[1], Jae-Myung Kim[1], Youngwoo Won[2], Ji Ye Kim[2], Donald P. King[3], Antonello Di Nardo[3] and Sang-Ho Cha[1]*

Brewing up the next serotype O virus lineage from Pool 2

- History tells us that pandemic serotype O lineages emerge from **Pool 2**

- O/ME-SA/SA-2018 lineage detected in Pool 2 (India, Nepal, Bangladesh and Sri Lanka)
- Lineage estimated to represent ~ 40% of serotype O cases in India
- Detected in Pool 3 (UAE and Oman) in 2021 in small ruminants (and perhaps also in Iran?)



https://www.thinglink.com/scene/451911993104793602

Emergence of O/ME-SA/SA-2018 in Pool 3

- 2023/4: further evidence for infection in Iran, Palestinian AT and Türkiye
- 2025: cases due to this lineage detected in Iraq and Israel
- Sequences from Palestine/Israel are distinct to those from Türkiye, Iraq and Iran (~4% nt dif.)
- Data support multiple recent introductions of this lineage from Pool 2
- **This lineage poses a risk for countries in Southeast Asia**

State of Palestine
Ministry of Agriculture

Vaccine Matching data is available for field isolates from the O/ME-SA/SA-2018 lineage

	O1-Manisa [BI]		O-TUR/5/09 [MSD]		O-3039 [BI]		O-Campos [BI]		O-PanAsia-2 [BI]		O-Campos [BB]	
Isolate	r1value	heterologous titre (log_{10})	r1value	heterologous titre (log_{10})	r1value	heterologous titre (log_{10})	r1value	heterologous titre (log_{10})	r1value	heterologous titre (log_{10})	r1value	heterologous titre (log_{10})
UAE/15/2021	0.56	2.15	0.69	2.32	0.75	1.94	0.28	2.19	0.47	2.30	0.51	2.63
UAE/9/2021	0.44	2.04	0.68	2.32	0.59	1.83	0.23	2.10	0.32	2.13	0.60	2.70
NEP/13/2022	0.63	2.33	1.00	2.32	1.00	2.02	0.40	2.28	0.57	2.35	0.51	2.65
NEP/26/2022	0.32	2.04	0.68	2.15	0.66	1.82	0.23	2.03	0.32	2.10	0.20	2.29
NEP/38/2022	0.98	2.45	0.89	2.29	0.84	2.00	0.45	2.17	0.50	2.31	0.66	2.71
NEP/13/2024	0.88	2.40	0.78	2.23	0.82	1.99	0.74	2.27	0.99	2.49	0.68	2.72
IRQ/10/2025	0.73	2.23	0.62	2.23	0.46	1.87	0.38	2.22	0.50	2.21	0.59	2.64
IRQ/21/2025	0.70	2.22	0.71	2.29	0.64	2.01	0.39	2.23	0.54	2.24	0.50	2.56
GER/1/2025	1.00	2.41	0.97	2.37	0.84	1.96	0.48	2.06	0.56	2.15	0.58	2.44

Pool 1: Status in 2025

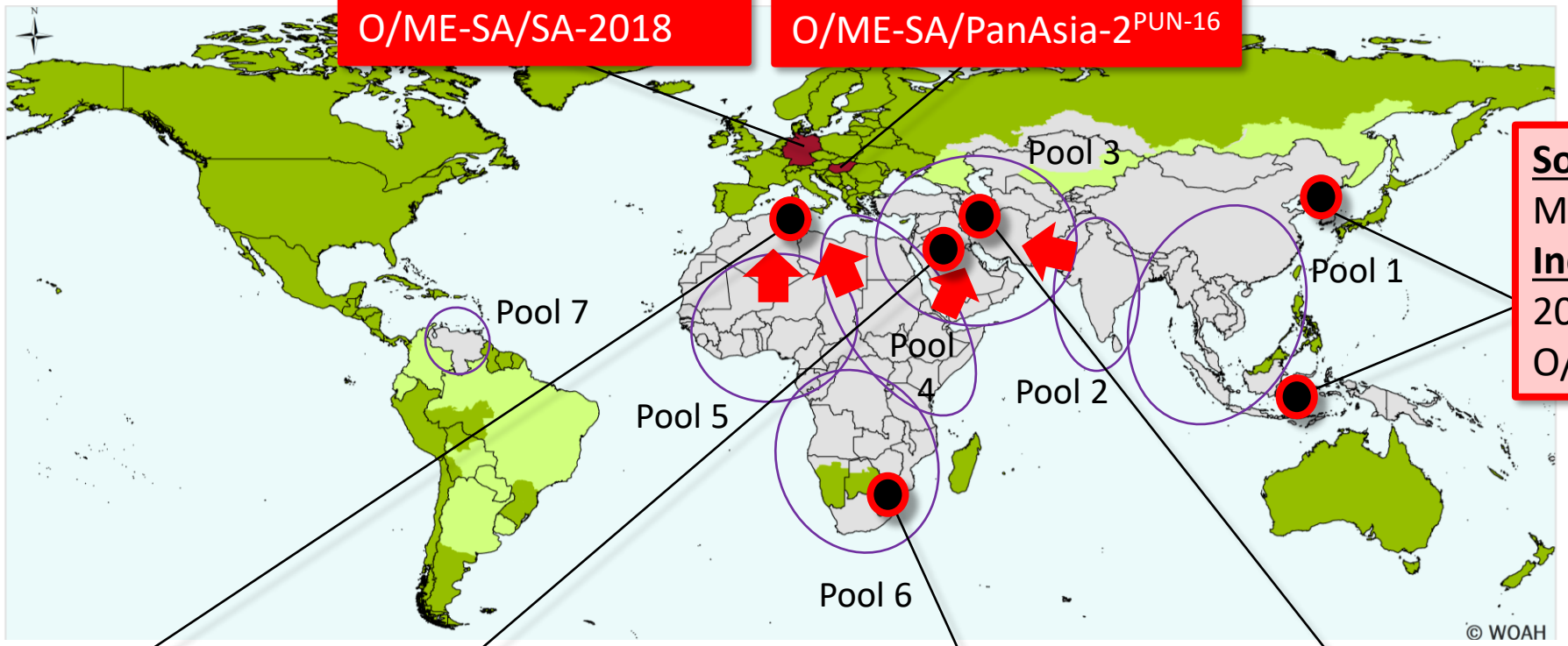
Characterisation of different FMD virus lineages

Based on data from WRLFMD, RRLSEA, the WOAH/FAO Lab Network, publications* and reported @SEACFMD

Country	O					A		Asia-1
	ME-SA/Ind-2001e	SEA / Mya-98	CATHAY	ME-SA / PanAsia	ME-SA/ PanAsia-2	ASIA / Sea-97	ASIA/Ind	
Cambodia	2024	2016		2024		2016		
Laos	2024	2017		2024		2018		
Malaysia	2024	2016	2005	2023	2009	2023		
Myanmar	2022	2021				2021	2010	2017
Thailand	2024	2018	2012	2019		2022		
Vietnam	2023	2024	2018	2024		2017		2007
PR China	2025	2020	2024	2019		2019		2009
Indonesia	2025							
Mongolia	2022	2018		2017		2016		

*Recent papers: Khanh et al., (2025)

Headline global status for FMD (September 2025)



Germany
Jan 2025
O/ME-SA/SA-2018

Hungary, Slovakia
Mar 2025
O/ME-SA/PanAsia-2^{PUN-16}

South Korea
March 2025
Indonesia
2024-25
O/ME-SA/Ind-2001e

Maghreb (2025)
O/EA-3

Algeria (2023/4)
SAT2/V

Middle East (2025)
SAT1/I

Middle East (2023)
SAT2/XIV

Southern Africa
Serotype SAT2
(and SAT1 & SAT3)

Eswatini
SAT2

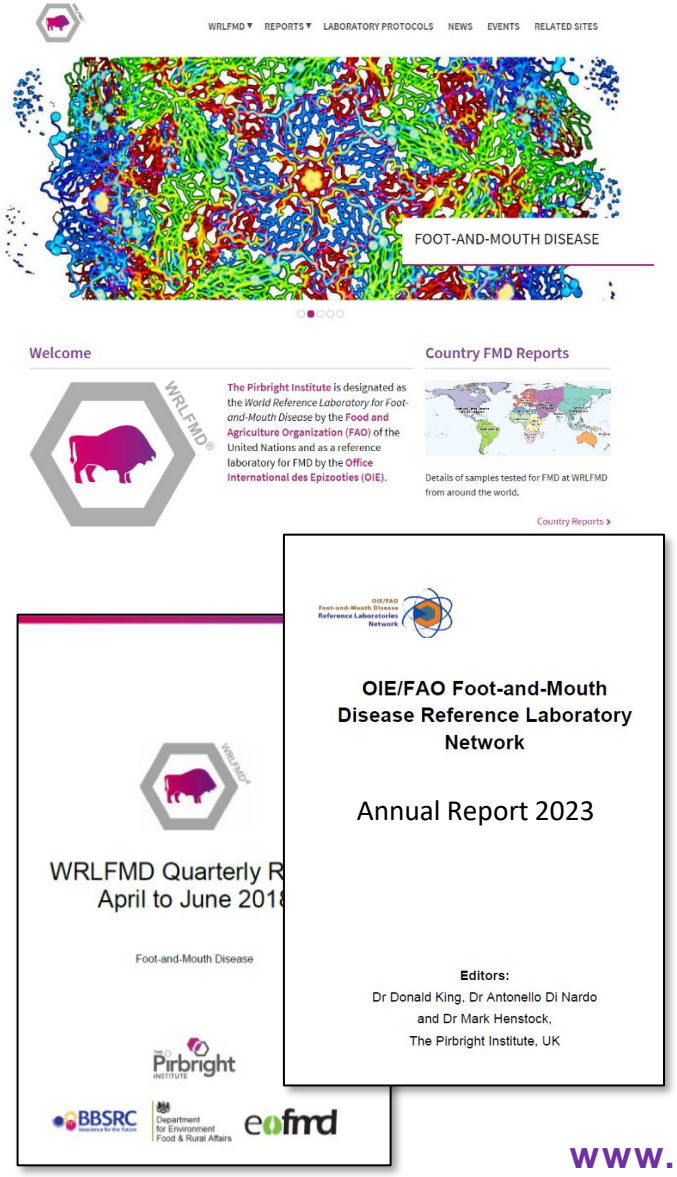
Iran, Iraq, Türkiye, Palestine, Israel
2023-2025
O/ME-SA/SA-2018

Talk summary

- Epidemiology of FMD is very dynamic
- New patterns due to virus incursions from East Africa and southern Asia
- Circulation of different FMD virus lineages impact the selection of appropriate vaccines to control outbreaks
- **New risks for countries in Southeast Asia**
- Sampling of field outbreaks is critical……
- WRLFMD and the WOAH/FAO Lab Network welcome sample submissions
  - Testing is free of charge
  - Contact: donald.king@pirbright.ac.uk
- Testing/evaluation of FMD vaccines is important
  - Vaccine matching
  - Heterologous testing
  - Small scale immunogenicity studies and evaluation of FMD vaccines in the field

Further information……

- FMD reports and lab testing (https://www.wrlfmd.org/ref-lab-reports)
    - *Genotyping reports*, *Vaccine matching* and *Serotyping reports*
- Other data sources:
    - Quarterly WRLFMD/EuFMD report (https://www.wrlfmd.org/ref-lab-reports)
    - Annual report of the WOAH/FAO FMD Laboratory Network (http://foot-and-mouth.org/)
    - OpenFMD (www.openfmd.org) – sequences, genotyping, vaccine selection and surveillance



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