



### Global Update -2018/19

#### on behalf of the OIE/FAO FMD Lab Network

Acknowledgements: Don King, Valerie Mioulet, Nick Knowles, Anna Ludi, Ginette Wilsden, Alison Morris, David Paton, Abid Bin-Tarif, Mehreen Azhar, Hannah Baker, Lissie Henry, Jemma Wadsworth, Clare Browning, Antonello Di Nardo, Bob Statham, Britta Wood, Ashley Gray, Beth Johns, Mark Henstock, Nick Lyons, Dexter Wiseman, Julie Maryan, Sarah Belgrave









# Enhanced surveillance via the OIE/FAO FMD Laboratory Network

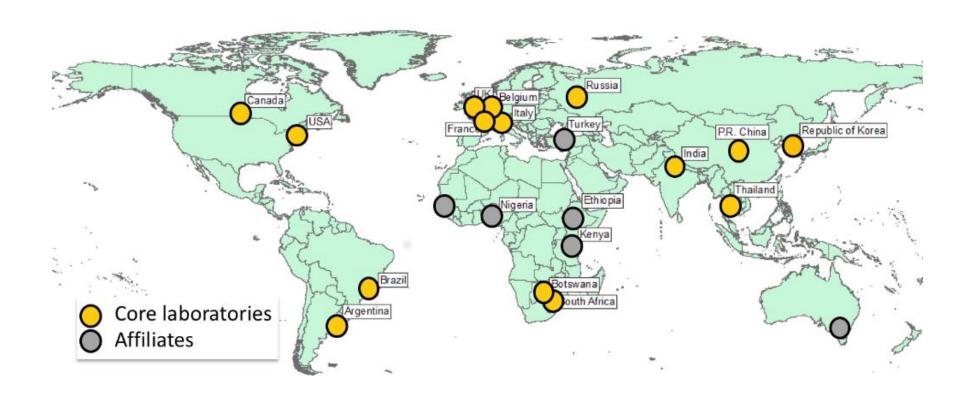


- Able to rapidly respond to changing events
- Global surveillance and changing patterns in risk
- Harmonised and improved lab capacity
- Established in 2004
- 15 Core OIE and FAO FMD Reference Laboratories
- New EU ref labs: Maisons-Alfort Laboratory for Animal Health, ANSES, France and Sciensano, Belgium
- Meeting and annual reports available: <a href="http://www.foot-and-mouth.org/">http://www.foot-and-mouth.org/</a>



### OIE/FAO FMD Laboratory Network - MoU

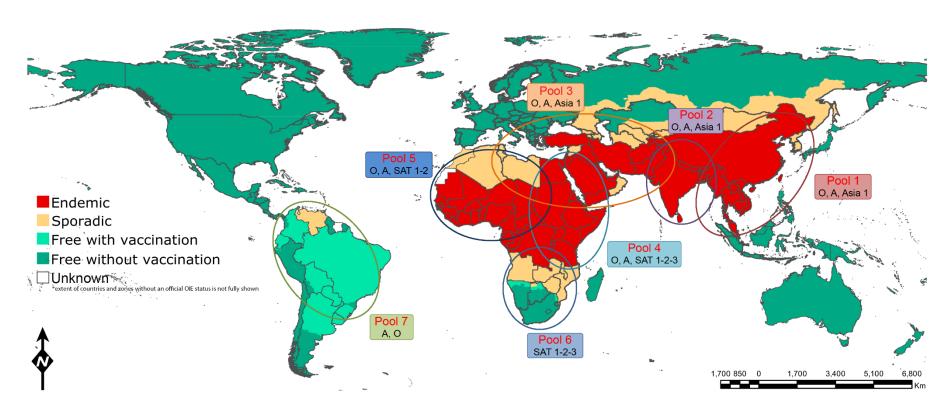
- Work collectively to freely share real-time unpublished data
- Confident of relationship between the "core" partners
- Acknowledge data sources in communications and reports



### Conjectured global status

#### Seven endemic pools

- Ecological niches that maintain specific FMD virus strains
- Control via (tailored) vaccination and supporting diagnostics

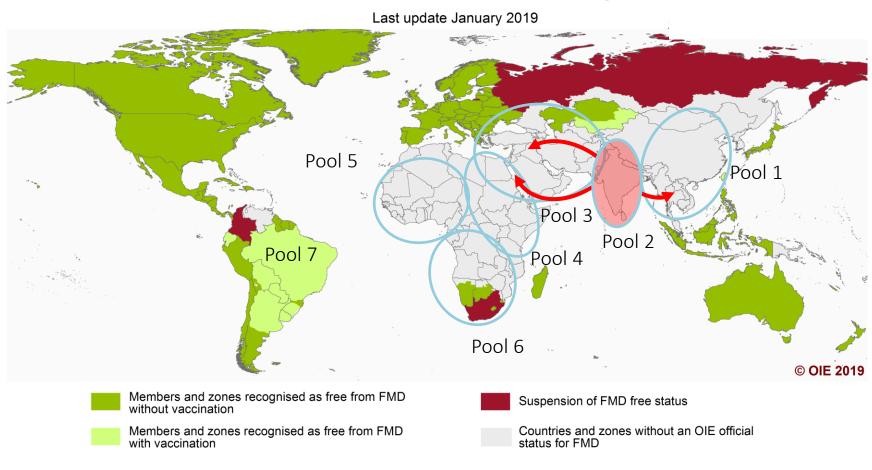


No reported serotype C outbreaks since 2004 (Kenya and Brazil)



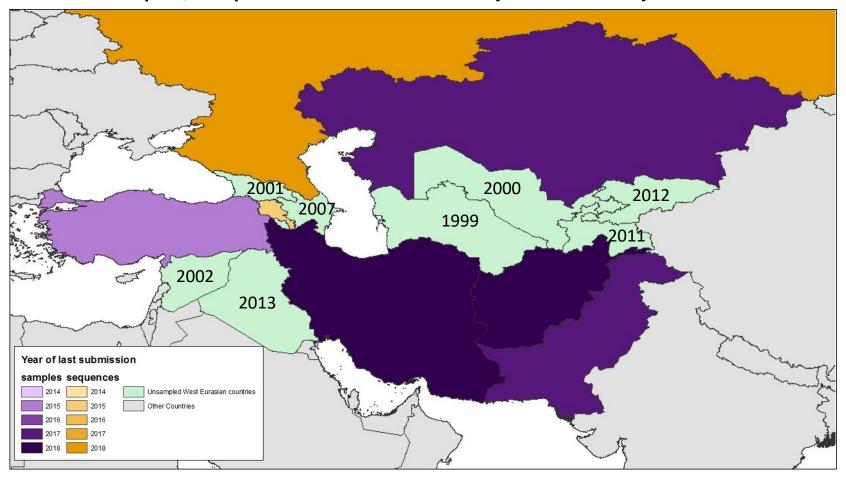
### **OIE Global status**

#### **OIE Members' official FMD status map**



### FMD surveillance within West Eurasia

WRLFMD sample/sequence submissions (2014-2018)



- All submissions shown (positive and negative samples)
- Detailed reports for all samples can be found at: www.wrlfmd.org

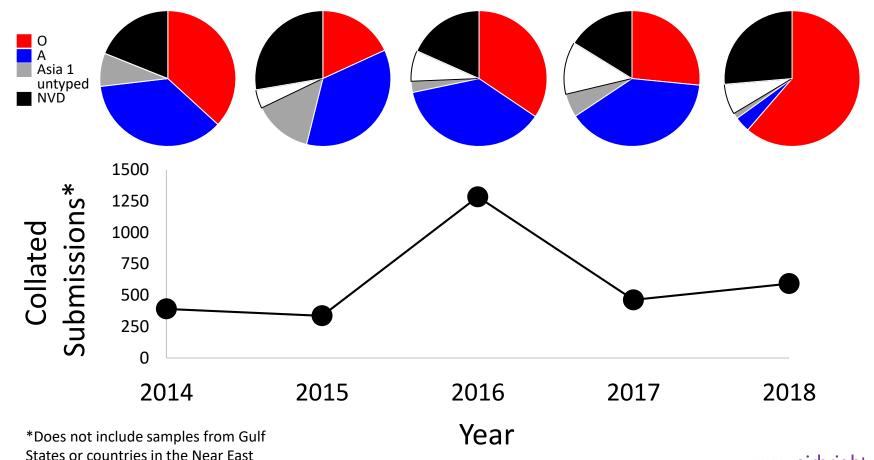
# Collated data for West Eurasia Roadmap countries (2014-18)\*





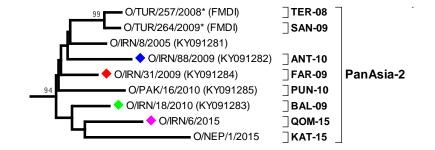


- Data from ARRIAH (Russia), ŞAP Institute (Turkey) and WRLFMD
- 2018 increased dominance of serotype O in the region



### O/ME-SA/PanAsia-2

- Sub-lineage nomenclature used to define different viral genotypes
- Some of these sub-lineages appear to co-circulate
- Sequence data provide evidence for east-west movements of these viruses
- Two active sub-lineages
- An additional O/ME-SA genotype in Pakistan, Iran and Russia (Bashkortostan – 2017)

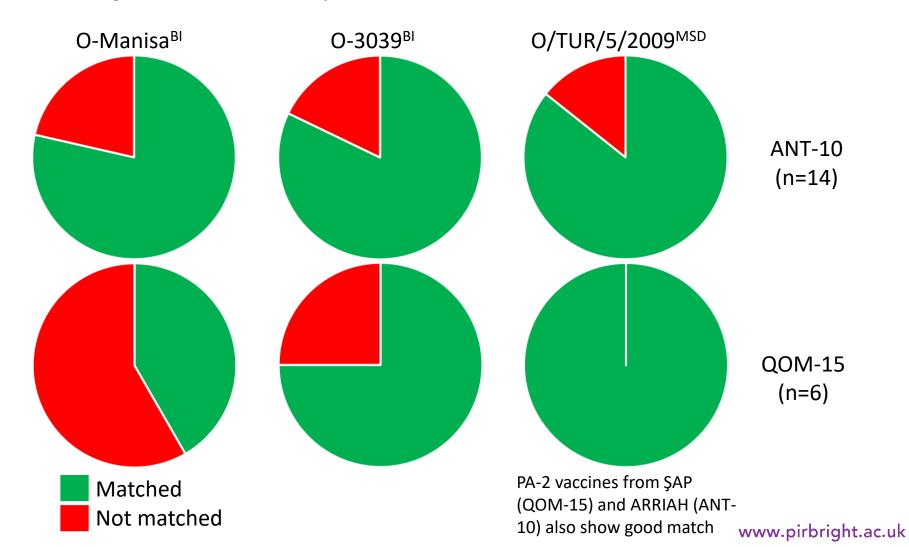


ANT-10	Country	2014	2015	2016	2017	2018	FAR-09	Country	2014	2015	2016	2017	2018
•	Afghanistan						•	Afghanistan					
•	Armenia							Armenia					
	Azerbaijan							Azerbaijan					
	Georgia							Georgia					
	Iran							Iran					
	Iraq							Iraq					
	Kazakhstan							Kazakhstan					
	Kyrgyzstan							Kyrgyzstan					
	Pakistan							Pakistan					
	Russia							Russia					
	Syria							Syria					
	Tajikistan							Tajikistan					
	Turkey							Turkey					
	Turkmenistan							Turkmenistan					
	Uzbekistan							Uzbekistan					
BAL-09		2014	2015	2016	2017	2018	QOM-15		2014	2015	2016	2017	201
_	Afghanistan						7	Afghanistan					
	Armenia						_	Armenia					
	Azerbaijan						_	Azerbaijan					
	Georgia						_	Georgia					
	Iran		*				_	Iran					
	Iraq						_	Iraq					
	Kazakhstan						_	Kazakhstan					
	Kyrgyzstan						_	Kyrgyzstan					
	Pakistan		*					Pakistan					
	Russia							Russia					
	Syria						_	Syria					
		1	1					Tajikistan					
	Tajikistan												
	Turkey							Turkey					
								Turkey Turkmenistan Uzbekistan					

<sup>\*</sup> These isolates were subsequently re-classified as OOM-15

### O/ME-SA/PanAsia-2: vaccine matching (2014-18)

 Quick and cost-effective laboratory assessment of the antigenic relationship between field and vaccine viruses

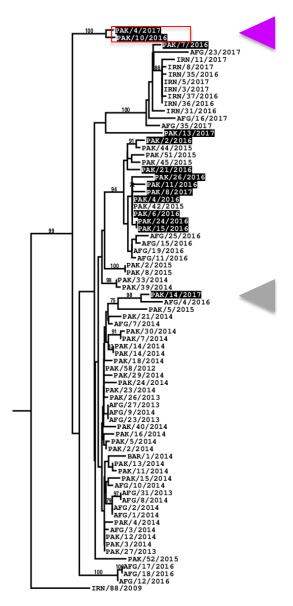


### A new (emerging) antigenic variant for serotype O?

- Two isolates in a new discrete genetic clade within O/ME-SA/PanAsia-2<sup>ANT-10</sup>
- Collected in Punjab, Pakistan (2016/17) from cattle and water buffalo
- No neutralization in VNT with BVS for O-Manisa, O-3039 or O-TUR-5-09

Vaccine-matching: r<sub>1</sub>-values

	O 3039	O Manisa	O TUR/5/2009	
O/PAK/14/2017	0.62	0.32	0.48	
O/PAK/10/2016	0	0	0	
O/PAK/4/2017	0	0.10	0	

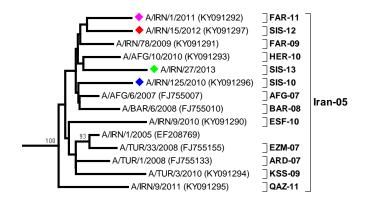


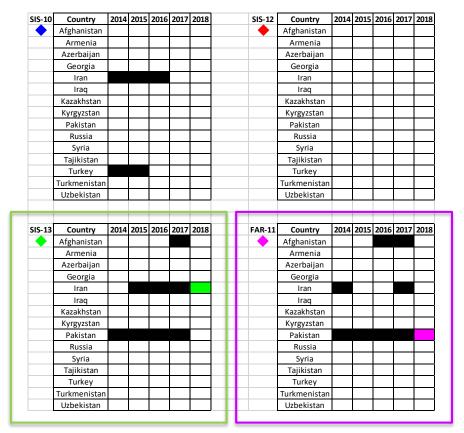
# What other FMDV lineages are circulating in the region?

	Viral lineage:	West EurAsia	Gulf States	
	O/ME-SA/PanAsia-2	<b>√</b>	<b>√</b>	<del></del> ,
	A/ASIA/Iran-05	✓	$\checkmark$	Vaccines:
	Asia-1	✓	√ 2011 Bahrain	Asia-1 Shamir Asia-1 Sindh-08
From Indian sub-	A/ASIA/G-VII	✓	<b>√</b>	Asia-1 TUR 14
continent	O/ME-SA/Ind-2001d/e		<b>√</b>	
From	O/EA-3		$\checkmark$	
From Africa	SAT 2 topotype VII		√ 2015	Oman
Airica	SAT 2 topotype IV		√ 2012	Bahrain

Spectrum of vaccines required to cover these different threats

### A/ASIA/Iran-05

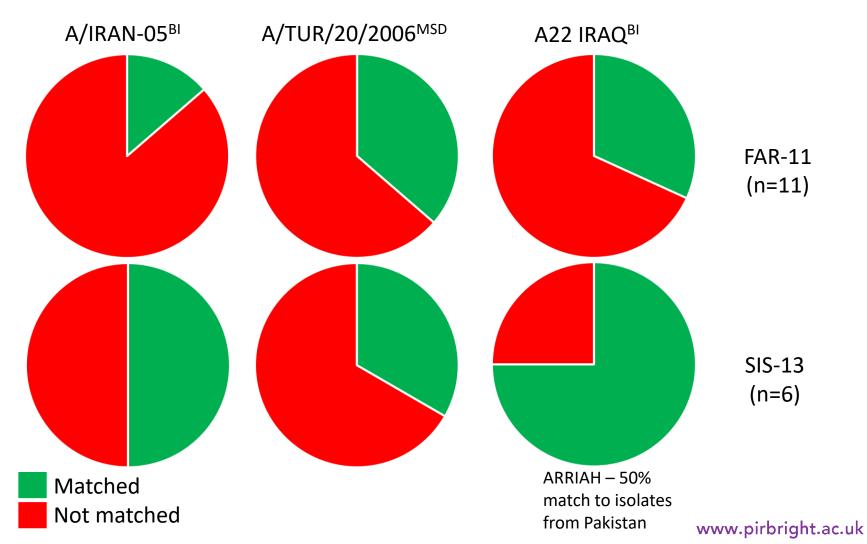




- Two active sub-lineages in 2018;
  - SIS-13
  - FAR-11
- SIS-12 sub-linage appears to have become extinct
- In many respects, eastto-west regional movements parallel O/ME-SA/PanAsia-2
- Since 2015, A/ASIA/G-VII has replaced
   A/ASIA/Iran-05 in Turkey

### A/ASIA/Iran-05: vaccine matching (2014-18)

 Reinforces the importance of good quality vaccines, booster regime with good coverage in target host populations



### Spread of A/ASIA/G-VII:

- Emerged in 2015 from Pool 2
- Rapid spread in a number of countries (Israel in 2017)
- Poor in vitro and in vivo responses for vaccines that are used in West Eurasia
- New tailored vaccine strains have been produced
- Are cases due to this lineage decreasing in the region?
- Is A/ASIA/Iran-05 now the most important serotype A lineage in the region?



	r-values:	A/SAU/1/2015	A/SAU/2/2015	A/IRN/8/2015	A/IRN/12/2015	A/IRN/25/2015
Vaccines	A-Iran-05	0	0	0	0	0
	A-Tur-20-06	0.03	0.06	0.01	0.15	0.01
	A-22	0.11	0.11	0.13	nd	0
	A-Iran-87	0	0.04	nd	nd	nd
	A-Iran-96	0.04	0.06	nd	nd	nd
	A-Iran-99	0.01	0.01	nd	nd	nd
	A-Sau-95*	0.20	0.19	0.26	0.16	nd
	A-May-97	0.14	0.23	0.15	0.23	nd
	A-Tur-11	0.01	nd	0.10	0.04	nd
	A-Tur-14	0	nd	0	0	nd
	A-IND-40-2000*	0.26	nd	0.03	0.24	nd

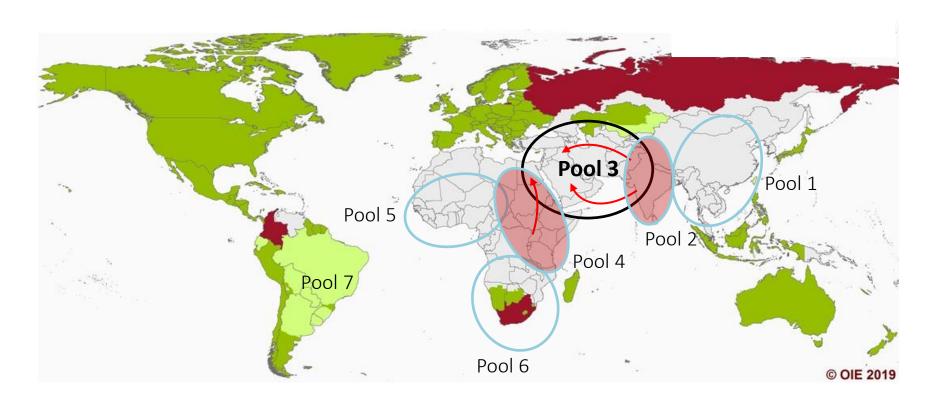








# Threats to the region: Via trans-pool viral movements



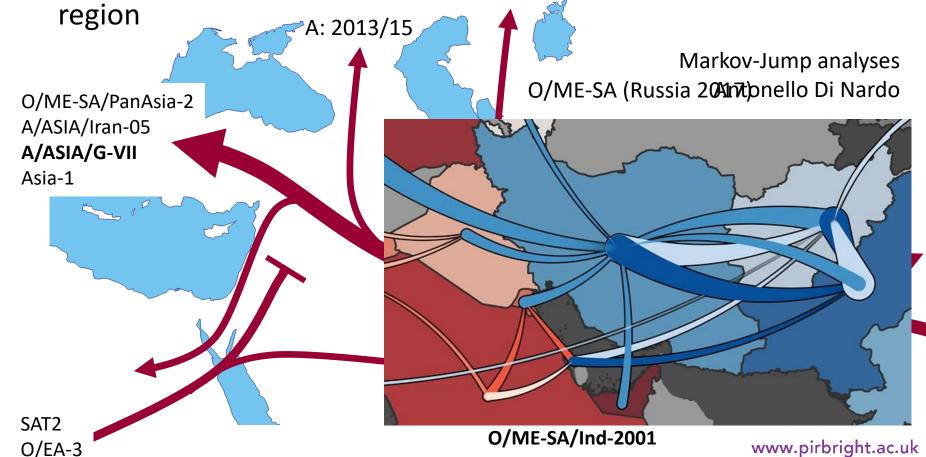
 Viruses from neighboring pools (Pool 2 [South Asia] and Pool 4 [East Africa])

O/ME-SA/Ind-2001: a risk for the region? Two sub-lineages (d and e) • Since 2013, full genomic sequence data indicates that there have been multiple "escapes" from Pool 2 (Bachanek-Bankowska et al., 2018) Pool 2 Saudi Arabia (2016) Myanmar (2015) Saudi Arabia (2015) UAE (2015) Myanmar (2017) Jordan (2017) Vietnam (2016) Tunisia Libya Thailand (2016) Algeria -(2013)Myanmar (2017) Morocco China (2017) Saudi Arabia (2013) Russia (2016) Bahrain (2015x2) Vietnam (2015) Mongolia (2015/17) **UAE (2014)** Laos (2015) South Korea (2017) Malaysia (2018) stituto Zooprofilattico Sperimentale Mauritius Sri Lanka (2014/13)(2016)www.pirbright.ac.uk

#### **West Eurasia**

Simplified summary and conjectured routes by which FMD spreads

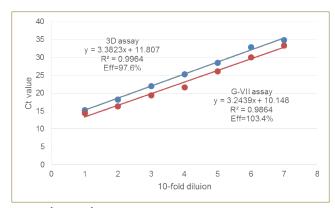
 Understanding transmission pathways helps identify future FMDV lineages that threaten the



# Development of tailored lineage-specific real-time RT-PCR assays for FMDVs circulating in Asia

- Real-time RT-PCRs designed to detect:
  - A/ASIA/Iran-05, A/ASIA/Sea-97, O/ME-SA/Ind-2001, O/ME-SA/PanAsia and PanAsia-2, O/SEA/Mya-98, O/EA-3 Serotype Asia 1 SAT 2/VII
- Single protocol used for all assays identical to pan-serotype rRT-PCR
- Validated with recent samples sent to WRLFMD from Pool 1, Pool 2 and Pool 3
- Represent a comprehensive panel of assays (<u>molecular toolbox</u>) for rapid characterisation of the FMDV lineages circulating in Asia at relatively low cost

Saduakassova et al. (2018) JVM Saduakassova et al., EuFMD OS-18



Analytical sensitivity comparison to 3D rRT-PCR



Mika Saduakassova and Kasia Bankowska

### **Proficiency Testing Scheme (PTS)**

- To assist FMD Reference Laboratories to develop/improve accurate and reproducible FMD diagnostic tests
- QA requirements to support ISO/IEC 17025
- Phase XXX
  - 71 FMD laboratories participated
- Phase XXXI (self-funded or supported by EU and EuFMD)
  - 15 Network lab participants
- Proposal for Phase XXXII (post-BREXIT):
  - Global PTS to complement PTS organised by EURL
  - Focus on endemic diagnostic challenges
  - Scenarios tailored PCP expectations for the participating labs

## Talk summary



- Epidemiology of FMD is very dynamic
  - New unpredictable patterns in Asia (East and West) and North Africa
  - Threats to FMD-free countries in Europe and Turkish Thrace
- Sampling of field outbreaks is critical
- Importance of an active FMD Reference Laboratory Network to facilitate sample collection from FMD outbreaks in the field—to feed real-time lab data back to FMD control programmes
- Impact upon selection and deployment of vaccines

### Reports and information

- New website (<u>wrlfmd.org</u>) launched in November 2018
- In addition to Genotyping reports, now contains Vaccine matching and Serotyping reports
- Other data sources:
  - EuFMD Monthly report
  - Quarterly WRLFMD report

#### Tools for FMDV sequences

- Priority for the FMD community
- FMDVTools: <a href="https://mallorn.pirbright.ac.uk">https://mallorn.pirbright.ac.uk</a>



# **Acknowledgements**

- Donald King for sharing slides
- Support for the WRLFMD and research projects
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   and field teams
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