The practice of innovation

Open Session of the Standing Technical and Research Committees of the European Commission for the Control of Foot-and-Mouth Disease

OS'16. Cascais, Portugal. 26th-28th October 2016

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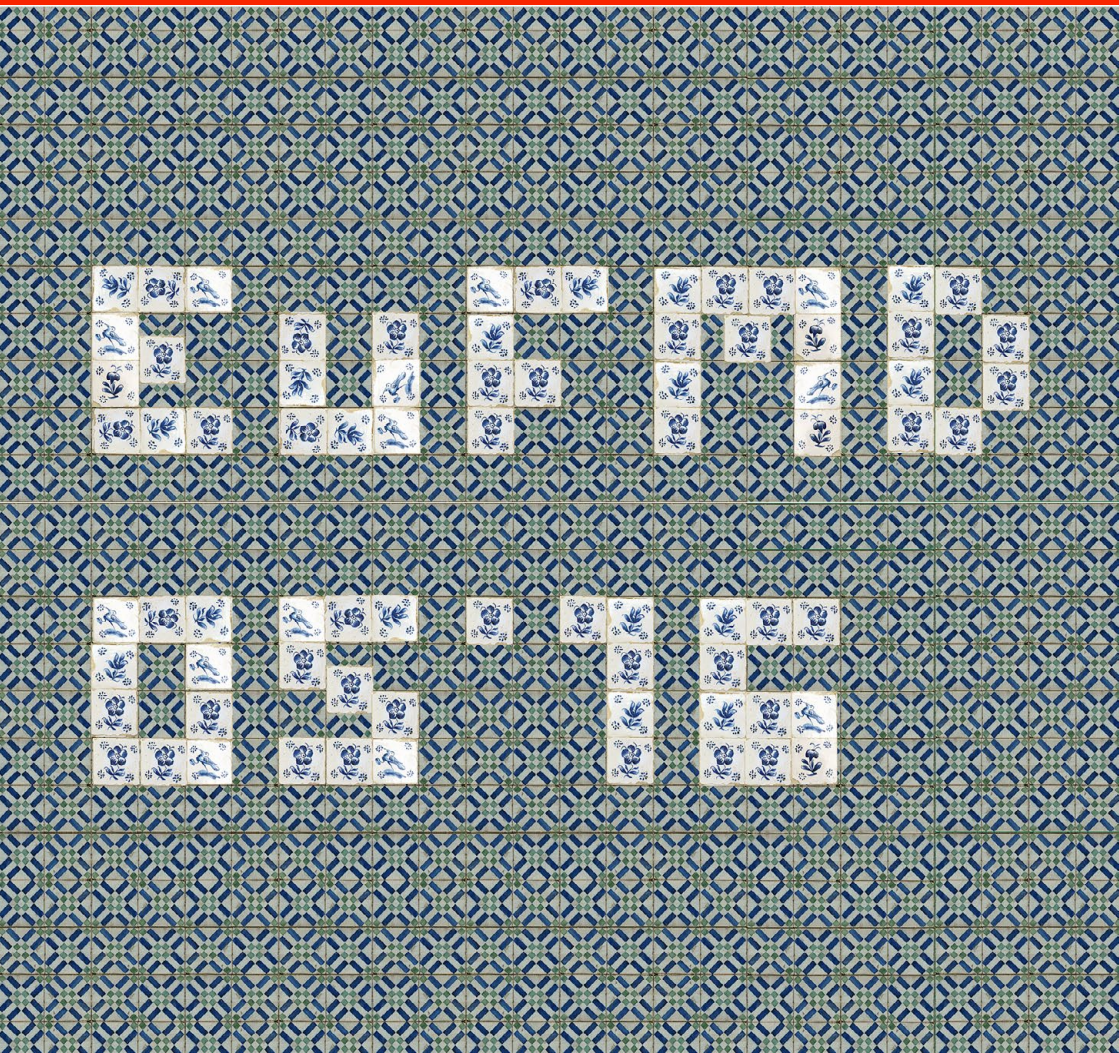

26 Oct.

INNOVATIVE IDEAS AND OPTIONS FOR FMD MANAGEMENT

PLENARY	P1
1. OPENING: Global situation. Frenkel	
2. The livestock sector and disease emergencies: Innovation and ideas	**P1.** Global progress against FMD
3. Higher health compartments: The way ahead?	**P2.** Vaccine efficacy (GFRA)
4. Vaccination as an option: What challenges remain?	**P3.** FMD Endemicity (GFRA)

27 Oct.

GLOBALIZING ACCESS TO SCIENCE AND INNOVATION: CONNECTING LIVESTOCK KEEPERS AND KNOWLEDGE LEADERS.

PLENARY	P1
5. Global and regional FMD surveillance	**P4.** New vaccines
6. New insights from epidemiology studies	**P5.** Improving current vaccines
7. Risk-based approaches: What have we learnt?	**P6.** Preventing FMD: Tools to assist decision making
8. Measuring impact of vaccination and other preventive measures	**P7.** Innovation in diagnosis

SOCIAL EVENTS

28 Oct.

P0	P1	P2	P3	P4
9. Innovations in Training and Knowledge exchange	**G1.** Modelling Network: Innovators and innovations looking for a place to practice	**G4.** Innovative surveillance options for field use	**G7.** FMD vaccination in endemic settings: Optimising schedules and vaccine efficacy trials	**G10.** New developments in wildlife (FMDV in African buffalo)
10. The way forward to FMD freedom; what are the tools and processes available?	**G2.** Contingency Planning and Emergency Vaccination Network: Our plans for the future	**G5.** Diagnostics: harmonisation of laboratory tests, and tools to share sequence data	**G8.** Closed Meeting on Licensing Novel Vaccines *Invitation only*	**G11.** Pathology and pathological basis of persistence
11. How can we change FMD management mindsets?	**G3.** The role of regional laboratory and epi networks in improving international surveillance for FMD	**G6.** Biocontainment of FMDV: challenges and solutions for laboratory biorisk management	**G9.** Vaccine quality assurance (VQA) initiative: what is proposed and how do we move it forward?	**G12.** Funding innovation: Q&A *To be confirmed at Session*

12. FINAL SESSION (Plenary room): Globalizing access to knowledge and innovation

CLOSURE.

This Book of Abstracts and the Report that follows this Session is dedicated to the memory of Bernd Haas, a man whose contributions over three decades to EuFMD Sessions and whose outstanding leadership of the group that led the revision of the EuFMD Laboratory Biorisk Management Standards have been an inspiration to so many and created a safer environment for many of us to work in.

Dear colleagues,

Foot-and-mouth disease (FMD) is feared by livestock owners and official veterinary services across the world for its ability to find gaps in biosecurity and immune defences, enabling variants to emerge as epidemics in endemic and free countries. The viruses involved have the ability to exploit niches, while maintaining their core business of persistence in the market, continually circulating, probing for new opportunities. Faced with such an innovative adversary, in many countries the virus has been winning for years - so far ahead of the prevention efforts that it seems to set its own pace. In other regions, notably Europe and South America, a common, zero tolerance policy to virus circulation has been a success, but maintaining this status requires a continual high level of vigilance and many risk pathways exist that might be breached, with severe consequences.

Necessity drives innovation, and the need for innovation to counter the FMDV challenge is enormous in endemic regions. Hundreds of millions of livestock owners cannot access quality FMD vaccines at all, although often willing to pay; worse still, they have little access to daily local information systems to inform them of what they could do. We live in an age where innovations are held in our hands in the form of networking tools formerly called phones, and we can share ideas and innovations across continents in seconds. But what are the innovations likely to change disease risk management? Who are the innovators? What are the practises we should adopt to speed the transfer of innovation? How will the change in livestock value chains across countries and continents change risk, and how much policy innovation is possible, while maintaining businesses at home and international trade?

This Session is dedicated to the daily innovators who contribute so richly to the FMD technical and policy fields. We are happy to welcome so many of them to this Session, to give an opportunity to share practice, and identify ways to support the entry into practice of those innovations which hold promise. We trust this Session brings you all new ideas and gives you opportunities to meet people of similar mind, open to innovation and keen to see it tested in the white hot seat of FMD management.

Innovators in FMD management, science and policy, thank you for getting together at OS'16!

Dr Keith Sumption
Executive Secretary
European Commission for the Control of Foot-and-Mouth Disease

Organization of the OS'16

STC - STANDING TECHNICAL COMMITTEE

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K.Schwabenbauer, Y.Ivanov, S.Zientara.

SCRPD - SPECIAL COMMITTEE ON RESEARCH AND PROGRAMME DEVELOPMENT

Pillar I

T. Alexandrov (BG). *Contingency planning, wildlife surveillance ;* Y. Ivanov (BG). *FMD research vaccine evaluation;* S. Mortensen (DK). *Crisis management, contingency planning, epidemiology*

G. Cáceres (SP). *Surveillance, risk management.*

Pillar II

L. Bakkali (FR). *FMD surveillance in REMESA, RESOLAB, European neighbourhood risk*

M. Bellaiche (IS). *FMD surveillance and management, Israel/Mid-East;* N. Bulut (TUR). *FMD surveillance in West Eurasia, vaccine quality and production;* G. Ferrari (IT). *FMD surveillance and epidemiology, FMD-PCP expert;* M.Masiulis (LT). *FMD surveillance in Eastern Europe.*

Pillar III

J. F. Valarcher (SWE). *FMD virology, vaccine QA, surveillance, epidemiology, global*; R. Bergevoet (NL). *Veterinary economist/FMD*; K. Stark (CH). *Veterinary epidemiology, surveillance, management;* S. Zientara (FR). *Epidemiology, surveillance systems, Europe/Africa/REMESA/ West Eurasia;* Nick Lyons (UK). *FMD epidemiology and vaccination effectiveness, Africa/Egypt.*

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HEAD OF THE BIORISK MANAGEMENT GROUP. K.Summermatter (CH).

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ACKNOWLEDGEMENTS

YOUR AGENDA

DAY 1 - PLENARY

1	OPENING GLOBAL SITUATION FRENKEL LECTURE (pag. 20)
9.00	OPENING
9.30	FRENKEL LECTURE (A. Dekker)
10.00	Keynote: UPDATE ON CURRENT GLOBAL SITUATION FOR FMD: NEW OUTBREAKS AND THREATS (D. King)
2	THE LIVESTOCK SECTOR AND DISEASE EMERGENCIES: INNOVATION AND IDEAS (pag. 21)
11.00	Keynote: CHANGE IN THE MANAGEMENT OF THE FMD DISEASES CONTROL TO AN PRIVATE-PUBLIC-PARTNERSHIP APPROACH (V. Schütz)
11.30	A 'READINESS RATING' FOR BALANCING BIOSECURITY PRIORITIES IN FMD PREPAREDNESS AND RESPONSE (R. Horwitz)
11.45	ORGANISATION OF RAW MILK COLLECTION DURING AN FMD OUTBREAK (Y. Tempelman)
12.00	ECONOMIC COSTS AND EFFECTS OF ACTIVITIES TO PREVENT FMD IN DENMARK (S. Mortensen)
12.15	COST AND RESPONSIBILITY SHARING ARRANGEMENTS IN THE EU TO PREVENT AND CONTROL NOTIFIABLE VETERINARY RISKS (R. H.M. Bergevoet)
3	HIGHER HEALTH COMPARTMENTS: THE WAY AHEAD? (pag. 26)
13.30	Keynote: NON-GEOGRAPHICAL APPROACHES TO FMD RISK MANAGEMENT (G. Thomson)
13.50	ADVANCEMENTS IN COMPARTMENTALIZATION AND REGIONALIZATION - OPPORTUNITIES, RELATIONSHIPS, INFORMATION AND CHALLENGES (E. Parker)
14.10	CAPABILITY ANALYSIS AND SCENARIOS OF RESOURCES POOLING IN CASE OF FMD EPIZOOTICS IN FRANCE AND TUNISIA (M. Marsot)
14.25	SPREAD OF FMD SEROTYPE O-PANASIA2 IN A DAIRY COMPLEX IN IRAN (C. Bartels)
14.40	A RISK BASED MODEL TO GUIDE DECISIONS ON ZONIFICATION TO STOP VACCINATION IN A FREE COUNTRY WITH VACCINATION (J. L. Gonzales)

P1	GLOBAL PROGRESS AGAINST FMD: SESSION ORGANISED BY THE FMD WORKING GROUP OF FAO AND OIE (pag. 38)
11.00	GLOBAL, REGIONAL AND NATIONAL PROGRESS OF FMD CONTROL (S. Metwally)
11.15	NATIONAL ACTIVITIES FOR FMD CONTROL IN KENYA (A. Sangula)
11.30	NATIONAL ACTIVITIES FOR FMD CONTROL IN THAILAND (TBD)
11.45	NATIONAL ACTIVITIES FOR FMD CONTROL IN AFGHANISTAN (G. Ferrari)
12.00	NATIONAL ACTIVITIES FOR FMD CONTROL IN KAZAKHSTAN (D. Imanbayeva)
12.15	DISCUSSION
P2	VACCINE EFFICACY (GFRA) (pag. 40)
13.30	Keynote: ADVANCES AND GAPS IN VACCINE MODELLING (R. Reeve)
13.50	SELECTION OF FMD VACCINES IN VIETNAM (D. Do Huu)
14.10	THE VALUE OF IN VITRO ANTIGEN MATCHING IN PREDICTING VACCINE PROTECTION (W. Vosloo)
14.20	CORRELATION OF SEROLOGICAL RESPONSE AFTER VACCINATION AGAINST FMDV AND PROTECTION AGAINST CHALLENGE IN PIGS (P. Eblé)
14.30	NOVEL MARKER FOOT-AND-MOUTH DISEASE VIRUS VACCINE MOLECULARLY BOUND TO NANOLIPOPROTEIN ADJUVANT (E. Rieder)
14.40	ANTIGENIC REFOCUSING OF A SAT2 FMD VIRUS THROUGH EPITOPE DAMPENING (T. Ramulongo)
14.50	Poster: ESTIMATE OF CROSS-PROTECTION PROVIDED BY AN FMDV O-BFS VACCINE IN THE TUNISIAN EPIDEMIOLOGICAL CONTEXT (E. Brocchi)

DAY 1 - PLENARY

4	VACCINATION AS AN OPTION: WHAT CHALLENGES REMAIN? (pag. 31)
15.30	ENCOURAGING THE USE OF VACCINATION-TO-LIVE AS A CONTROL STRATEGY FOR FMD OUTBREAKS: PERSPECTIVES AND ISSUES (K. De Clercq)
15.45	IMPROVING ACCESS TO EMERGENCY FMD VACCINE THROUGH A VACCINE BANK SHARING ARRANGEMENT (T. Smylie)
16.00	WHICH VACCINES ARE MOST IMPORTANT? A DECISION SUPPORT TOOL FOR FMD VACCINE BANK MANAGERS (M. McLaws) Via adobe
16.15	EARLY DECISION INDICATORS TO PREDICT THE SEVERITY OF AN FMD OUTBREAK (C. Cook)
16.30	EMERGENCY VACCINATION BENEFITS ERADICATION OF HYPOTHETICAL INTRODUCTIONS OF FMD INTO NEW ZEALAND (Z. Yu) Presented by K. Walker
16.45	A PROCESS MODELLING APPROACH TO ESTIMATE FMD DIAGNOSTIC CAPACITY FOR OUTBREAK MANAGEMENTDECISION-MAKING (K. Walker)
17.00	QUANTIFYING THE VALUE OF PERFECT INFORMATION IN EMERGENCY VACCINATION CAMPAIGNS FOR FMD (M. Tildesley)

DAY 2 - PLENARY

5	GLOBAL AND REGIONAL FMD SURVEILLANCE (pag. 55)
9.00	THE ORIGIN, EVOLUTION AND DIAGNOSIS OF SENECA VALLEY VIRUS, A NEW VESICULAR DISEASE-CAUSING PICORNAVIRUS OF PIGS (N. Knowles)
9.15	OUTBREAKS OF FOOT-AND-MOUTH DISEASE VIRUS IN THE MIDDLE EAST DURING 2015 AND 2016 DUE TO AN EXOTIC A/ASIA/G-VII (G-18) LINEAGE (J. Wadsworth)
9.30	FULL GENOME STUDY ON THE EVOLUTION OF THE FMD VIRUS O/ME-SA/IND-2001d LINEAGE: EVIDENCE OF RECOMBINATION (K. Bachanek-Bankowska)
9.45	GENETIC CHARACTERIZATION OF FMD VIRUSES IN BALOCHISTAN, PAKISTAN (S. M.Jamal)

P3	FMD ENDEMICITY (GFRA) (pag. 47)
15.30	Keynote: THE ROLE OF ASYMPTOMATIC CARRIERS IN FMD ECOLOGY; UNIFYING KNOWLEDGE FROM CONTROLLED LABORATORY EXPERIMENTS AND FIELD STUDIES (J. Arzt)
15.50	NEXT GENERATION SEQUENCING REVEALS NEW SOUTHERN AFRICAN TERRITORIES GENOTYPES BRINGING US CLOSER TO UNDERSTANDING THE HISTORY OF FMD VIRUS IN AFRICA (N. Knowles)
16.00	WAVES OF FMD IN EAST AFRICA AND ADVANCES IN PRACTICAL SURVEILLANCE (T. Lembo)
16.10	GENETIC AND ANTIGENIC VARIATION OF FOOT-AND-MOUTH DISEASE VIRUS DURING PERSISTENCE IN NATURALLY INFECTED CATTLE AND BUFFALO (J. K. Biswal)
16.20	MOLECULAR EPIDEMIOLOGY OF FOOT-AD-MOUTH DISEASE VIRUSES IN SOUTHERN AFRICA (C. Kasanga)
16.30	A NOVEL MODELLING APPROACH FOR ENDEMIC FMD IN SUB-SAHARAN AFRICA (M. Bronsvoort)
16.40	DISCUSSION

P4	NEW VACCINES (pag. 90)
9.00	A PRIME-BOOST VACCINATION STRATEGY IN CATTLE TO PREVENT SEROTYPE O FMDV INFECTION USING A “SINGLE-CYCLE” ALPHAVIRUS VECTOR AND EMPTY CAPSID PARTICLES (G. J Belsham)
9.15	VACCINE EFFICACY OF FMD VIRUS-LIKE PARTICLES PRODUCED BY THE BACULOVIRUS EXPRESSION SYSTEM (E. van den Born)
9.30	ENHANCED POTENCY AND IMMUNOGENICITY FOR CATTLE VACCINATED WITH FMD A SEROTYPE VACCINE ADJUVANTED WITH POLY (I:C) (S. Parida)
9.45	EFFECT OF THE ANTIGEN PAYLOAD, POLYVALENCY AND REVACCINATION IN THE PROTECTION CONFERRED BY FMD VACCINES AGAINST HETEROLOGUS CHALLENGE IN CATTLE (M. Pérez-Filgueira)

10.00	THE EPIDEMIOLOGICAL TREND OF FMDV IN PAKISTAN: A STEP FORWARD TO FUTURE PLANNING TO CONTROL FMD IN PAKISTAN (U. Waheed)
10.15	Poster: GENETIC CHARACTERIZATION OF THE 2016 FMD VIRUSES IN SOUTH KOREA (B. Kyung Ku)
10.19	Poster: CURRENT STATE OF FMD SURVEILLANCE IN SENEGAL (M. Moustapha)
10.23	Poster: GENETIC CHARACTERIZATION OF FMD VIRUS ISOLATED DURING CROSS SECTIONAL SURVEILLANCE STUDIES IN CATTLE FROM UGANDA DURING 2014-2015 (Z. Ahmed)
10.27	Poster: EPIDEMIOLOGY OF FMD IN GEORGIA (Z. Rukhadze)
10.31	Poster: INVESTIGATION OF FMD EPIDEMIC (OPANASIA2) IN CENTRAL REGION OF IRAN IN 2009 (J. Emami)
10.35	Poster: ANTIGENIC AND GENETIC CHARACTERIZATION OF FMD VIRUS SEROTYPE O CIRCULATING IN SOUTH-EAST ASIA (S. Upadhyaya, M. Mahapatra)
6	NEW INSIGHTS FROM EPIDEMIOLOGY STUDIES (pag. 66)
11.00	DETECTION AND MOLECULAR CHARACTERIZATION OF FMD VIRUSES FROM OUTBREAKS IN NORTHERN NIGERIA 2013-2015 (A.De Vleeschauwer)
11.15	ANTIGENIC AND EVOLUTIONARY ANALYSIS OF FMD VIRUSES FROM THE 2014-2015 OUTBREAKS IN THE MAGHREB REGION (G. Pezzoni)
11.30	CHARACTERIZATION OF FMD VIRUSES COLLECTED IN NIGERIA BETWEEN 2007 AND 2014: EVIDENCE FOR EPIDEMIOLOGICAL LINKS BETWEEN WEST AND EAST AFRICA (H. G. Ularamu)
11.45	SERO-EPIDEMIOLOGICAL STUDY OF FMD IN LIVESTOCK IN WEST LIBYA (A. S. Dayhum)
12.00	EPIDEMIOLOGICAL PARAMETERS FROM TRANSMISSION EXPERIMENTS: NEW METHODS FOR OLD DATA (S. Gubbins)
12.15	Poster: COMPLETE GENOME SEQUENCES OF THREE AFRICAN FMD VIRUSES FROM CLINICAL SAMPLES ISOLATED IN 2009 AND 2010 (K.De Clercq)
12.19	Poster: SURVEILLANCE OF FMD IN GEORGIA (M. Donduashvili)
12.23	Poster: THE ROLE OF SEASONAL MOVEMENT OF ANIMALS IN FMD CONTROL IN AZERBAIJAN (T. Aliyeva)
12.27	Poster: HORIZONTAL TRANSMISSIBILITY OF THE FMD VIRUS O/JPN/2010 AMONG DIFFERENT SPECIES OF ANIMALS (K. Fukai)

10.00	Poster: IMMUNE RESPONSES TO FOOT-AND-MOUTH DISEASE VIRUS IN GUINEA PIGS AFTER VACCINATION WITH CANINE ADENOVIRUS VECTOR (S. Lacour)
10.05	EU AUTHORISATION OF NOVEL VACCINES (M. Ilott)
10.20	DISCUSSION
P5	IMPROVING CURRENT VACCINES (pag. 95)
11.00	APPLICATION OF INDIRECT AND AVIDITY ELISA TESTS TO ASSESS ANTI-FMDV ANTIBODIES INDUCED BY VACCINATION IN BUFFALO AND SWINE SERUM SAMPLES (A. Capozzo)
11.15	DEMONSTRATION OF EARLY PROTECTION AGAINST FMD VIRUS SEVEN DAYS POST-VACCINATION (L. Mouton)
11.30	EFFICACY OF A FMD INACTIVATED VACCINE (AFTOVAXPUR DOE), ADMINISTERED AT A 1 ML DOSE TO SHEEP (C. Hamers)
11.45	FMDV EMERGENCY TYPE O VACCINES ARE EFFECTIVE AGAINST CHALLENGE WITH FMDV O/ALG/2013 (O IND 2001d) IN CATTLE (N. B. Singanallur)
12.00	PROTECTION IN SHEEP AGAINST HETEROLOGOUS CHALLENGE WITH SEROTYPE ASIA 1 FMD VIRUS USING HIGH POTENCY VACCINE (J. Horsington)
12.15	NO HETEROLOGOUS PROTECTION WITH FMD SAT2 SAU VACCINE AGAINST SAT2 BOT CHALLENGE (A. Dekker)

12.31	Poster: MOLECULAR EPIDEMIOLOGY OF FMD SUDANESE ISOLATES IN 2012 (I.Habiballa)
12.35	Poster: POSSIBLE ROLE OF CAMEL AS A RESERVOIR FOR FOOT AND MOUTH VIRUS: FIELD SERO-LOGIC COMPARISON WITH OTHER LIVESTOCK SPECIES (J.Emami)

7	RISK BASED APPROACHES: WHAT HAVE WE LEARNT? (pag. 77)
13.30	Keynote: PRIORITISATION OF RESOURCES FOR EARLY DETECTION OF DISEASE INCURSIONS (A. Cameron)
14.00	PREDICTED IMPROVED CONTROL OF FOOT-AND-MOUTH DISEASE TRANSMISSION BETWEEN FARMS BY USING PRECLINICAL DETECTION (N. Nelson)
14.15	DEFINING THE SPATIO-TEMPORAL SCALE OF FOOT-AND-MOUTH DISEASE VIRUS LINEAGES EMERGENCE IN THE MIDDLE EAST REGION (A. Di Nardo)
14.30	COMBINING LIVESTOCK MOVEMENT PATHWAYS WITH PHYLOGENETICS TO HELP UNDERSTAND THE SPREAD OF FMD IN SOUTH-EAST ASIA (Y. Qiu)
14.45	SERO-PREVALENCE AND RISK FACTORS FOR FOOT AND MOUTH DISEASE AMONG WILD AND DOMESTIC UNGULATES IN ISRAEL (E. Klement)
14.55	Poster: TRANSBOUNDARY HIGH RISK AREA COORDINATED EPIDEMIO-SURVEILLANCE PROGRAMME (THRACE) IN BULGARIA, GREECE AND TURKEY (T. Alexandrov)
14.59	Poster: FIRST REPORT OF FOOT-AND-MOUTH DISEASE VIRUS (FMDV) SEROTYPES O ISOLATION IN PUPPIES IN IRAN (D.Abdollahi)
8	MEASURING IMPACT OF VACCINATION AND OTHER PREVENTIVE MEASURES (pag. 84)
15.30	FMD VACCINATION AND POST-VACCINATION MONITORING IN AFGHANISTAN: ISSUES AND CHALLENGES (G. Ferrari)
15.45	COUNTRY SPECIFIC VACCINE CAN EFFECTIVELY CONTROL FMD IN ENDEMIC SETTING (M. Afzal)

12.30	Poster: SELECTION OF AN ADJUVANT TO RAISE POLYCLONAL ANTIBODIES TO FOOT-AND-MOUTH DISEASE VIRUS IN RABBITS AND GUINEA-PIGS (B. Sanz-Bernardo)
12.34	Poster: APPLICATION OF MOUSE MODEL FOR EFFECTIVE EVALUATION OF FMD VACCINE (J.H. Park)
12.38	Poster: DEVELOPMENT OF A VIRULENT FMD CHALLENGE MODEL IN SHEEP (L. Mouton)

P6	PREVENTING FMD: TOOLS TO ASSIST DECISION MAKING (pag. 104)
13.30	FMD IN TURKEY - LIVESTOCK MOVEMENTS AND MATHEMATICAL MODELLING (P. Dawson) Presented by M. Tildesley
13.45	THE U.S. ANIMAL MOVEMENT MODEL (USAMM), A BAYESIAN APPROACH TO MODELING OF A PARTIALLY OBSERVED CONTINENTAL SCALE LIVESTOCK MOVEMENT NETWORK (P. Brommesson)
14.00	ENSEMBLE MODELING FOR FMD (T. Lindström)
14.15	REAL-TIME BAYESIAN DATA ASSIMILATION AND PREDICTION FOR LIVESTOCK EPIDEMICS (C. Jewell)
14.30	REAL-TIME UPDATING IN EMERGENCY RESPONSE TO FMD OUTBREAKS (W. Probert)
14.45	HAEBOS, A HYBRID AGENT-AND EQUATION - BASED MODEL OF FMD IN VERMONT (A. Yoak)
15.00	Poster:REDUCING COMPUTING TIMES OF SPATIALLY EXPLICIT FMD MODELS (S. Sellman)
P7	INNOVATION IN DIAGNOSIS (pag. 111)
15.30	DEVELOPMENT OF A NOVEL VIRUS NEUTRALIZATION ASSAY USING QRT-PCR-BASED ENDPOINT ASSESSMENT FOR RAPID DETECTION AND TITRATION OF NEUTRALIZING ANTIBODIES AGAINST FOOT-AND-MOUTH DISEASE VIRUS (Z. Zhang)

16.00	EVALUATION OF ROUTINE VACCINATION AGAINST FMDV SEROTYPE A LINEAGE G-VII ON LARGE SCALE DAIRY FARMS IN SAUDI ARABIA (N. Lyons)
16.15	THE SEROLOGICAL RESPONSE INDUCED BY INACTIVATED FMD VACCINE IN ISRAEL – CLINICAL TRIALS IN A DAIRY FARM (E. Klement)
16.30	FARMERS'INTENTION AND PERCEPTIONS THAT INFLUENCE THEM IN IMPLEMENTING FOOT AND MOUTH DISEASE CONTROL IN ETHIOPIA (W. T. Jemberu)
16.45	THE CURRENT EPIDEMIOLOGY AND THE CONTROL STRATEGY OF FMD IN CHINA (Y. Li)
17.00	FMD DISEASE RISK ASSESMENT AND PROGRESS ON RISK BASEDCONTROL PROGRAM (N. Bulut)
17.15	Poster: SPATIO-TEMPORAL ANALYSIS OF FMD EPIDEMIC SITUATION AMONG FARM ANIMALS IN THE REPUBLIC OF KAZAKHSTAN FOR THE PERIOD OF 1955 - 2013 (S. K. Abdrakhmanov)
17.19	Poster: EPIDEMIOLOGY OF FMD IN VACCINATED DAIRY HERDS: TRANSMISSION DYNAMICS AND THE PERSISTENCE OF THE CARRIER STATE (K. VanderWaal)

16.00	COMPETITIVE LUMINEX IMMUNOASSAYS FOR THE DETECTION OF ANTIBODIES TO FMD AND VESICULAR STOMATITIS VIRUSES IN MULTIPLE SUSCEPTIBLE HOSTS (C. K. Nfon)
16.15	TAILED PRIMERS ENHANCE REAL-TIME RT-PCR DETECTION OF FMD VIRUS (D. Lefebvre)
16.30	DEVELOPMENT OF ONE-STEP MULTIPLEX RT-PCR ASSAY FOR DIFFERENTIATION OF FMDV SEROTYPES A, O AND SAT2 CIRCULATING IN EGYPT (A.A. Shehata)
16.45	GO PRIME: IN SILICO TESTING OF rRT-PCR PRIMERS AND PROBES FOR DIAGNOSIS OF FOOT-AND-MOUTH DISEASE (E. Howson)
17.00	Poster: DEVELOPMENT OF A REFERENCE FOOT-AND-MOUTH DISEASE VIRUS ANTIGEN PANEL FOR THE CONSISTENT VALIDATION OF DIAGNOSTIC ASSAYS (A. Morris)
17.04	Poster: ESTABLISHMENT AND VALIDATION OF TWO DUPLEX ONE-STEP REAL-TIME RT-PCR ASSAYS FOR DIAGNOSIS OF FMD (L. Bakkali-Kassimi)
17.08	Poster: EVALUATION OF ALTERNATIVE CELL LINES FOR THE ISOLATION OF FDMV (A. Gray)
17.12	Poster: AN IMPROVED APPROACH TO WHOLE GENOME SEQUENCING OF FMDV IN CLINICAL SAMPLES (T. Bowden)
17.16	Poster: COMPARISON OF TWO COMMERCIAL NSP ANTIBODY TESTS (PRIOCHECK® AND ID-VET®FMDV NS ELISAS) TO DETECT INFECTION IN VACCINATED ANIMALS (DIVA) (S. Parida)
17.20	Poster: DETECTION OF FMD VIRUS CARRIER CATTLE: DEVELOPMENT AND EVALUATION OF AN IGA ELISA KIT FOR O, A AND ASIA1 SEROTYPES (K. Parekh)
17.24	Poster: THE CHALLENGES OF USING IN-VITRO TESTS FOR VACCINE MATCHING (A. Bin-Tarif)
17.28	Poster: ISOLATION OF CAMELID NANOBODIES FOR COST EFFECTIVE DIAGNOSTICS OF FMDV IN UGANDA AND THE DEVELOPING WORLD (L. Loben)

DAY 3 - PRESENTATIONS

ROOM P0 - KNOWLEDGE EXCHANGE, GF-TADS

SESSION 9. INNOVATIONS IN TRAINING AND KNOWLEDGE EXCHANGE (p. 126)

9.00h "www. training": The who, what and where of building capacity for FMD control in the information age (J. Maud)

SESSION 10. THE WAY FORWARD TO FMD FREEDOM; WHAT ARE THE TOOLS AND PROCESSES AVAILABLE? (p. 128)

SESSION 11. HOW CAN WE CHANGE FMD MANAGEMENT MINDSETS? (p. 129)

13.30h Training for change or changing the training

ROOM P1 - MODELLING, CONT. PLANNING AND EPI NETWORKS

SESSION G1. MODELLING NETWORK: INNOVATORS AND INNOVATIONS LOOKING FOR A PLACE TO PRACTICE (p. 131)

SESSION G2. CONTINGENCY PLANNING AND EMERGENCY VACCINATION NETWORK: OUR PLANS FOR THE FUTURE (p. 132)

SESSION G3. THE ROLE OF REGIONAL LABORATORY AND EPI NETWORKS IN IMPROVING INTERNATIONAL SURVEILLANCE FOR FMD (p. 133)

ROOM P2 - INNOVATIVE SURVEILLANCE AND DIAGNOSIS

SESSION G4. INNOVATIVE SURVEILLANCE OPTIONS FOR FIELD USE (p. 134)

9.00h Evaluation of oral swabs for FMDV surveillance (P. Kirkland)

9.15h Use of lateral flow devices for safe and low cost shipment of FMDV suspected samples (S. Blaise-Boisseau)

9.30h Progress to develope practical field-based tools for detection of FMDV (V. Fowler)

9.45h Development of a successful surveillance model for FMD in Pakistan (M. Afzal)

SESSION G5. DIAGNOSTICS: HARMONISATION OF LABORATORY TESTS, AND TOOLS TO SHARE SEQUENCE DATA (p. 139)

11.00h Results of the 2015 Proficiency Testing Scheme (A. Ludi)

11.15h Vibasys and FMDV-tools: Practical resources for FMDV sequence analysis (P. Ribeca)

11.30h Poster: Antigen-detection ELISA performance vs virus evolution (V. Mioulet)

11.34h Poster: Do commercially available Lysis buffers inactivate FMDV? (B. Wood)

SESSION G6. BIOCONTAINMENT OF FMDV: CHALLENGES AND SOLUTIONS FOR LABORATORY BIORISK MANAGEMENT (p. 144)

13.30h A Contaminated environment is an efficient route of transmission for FMDV(C. Colenutt)

13.45h Evaluating the survival of FMDV in the environment (E. Brown)

14.00h The New Zealand national biocontainment laboratory project - Innovative approaches to meet testing requirements in the event of an FMD outbreak (R. P.Spence)

ROOM P3 - VACCINATION PROGRAMMES NETWORK

SESSION G7. FMD VACCINATION IN ENDEMIC SETTINGS: OPTIMISING SCHEDULES AND VACCINE EFFICACY TRIALS (p. 148)

SESSION G8. CLOSED MEETING ON LICENSING NOVEL VACCINES INVITATION ONLY (p. 148)

SESSION G9. VACCINE QUALITY ASSURANCE (VQA) INITIATIVE: WHAT IS PROPOSED AND HOW DO WE MOVE IT FORWARD? (p. 149)

ROOM P4 - WILDLIFE, PATHOLOGY AND PERSISTENCE

SESSION G10. NEW DEVELOPMENTS IN WILDLIFE (FMDV IN AFRICAN BUFFALO) (p. 150)

9.00h Serological and molecular surveillance of FMDV transmission events over time in an isolated African buffalo herd in the Kruger National Park (K. Scott)

9.15h FMDV persistence and transmission in African buffalo (E. Pèrez)

9.30h FMD in African buffalo (Syncerus caffer): differences in host responses between SAT 1, 2 and 3 in experimental and natural infection (B. Beechler)

9.45h Dynamics of fmd in African buffalo (Syncerus caffer):Calf-to-calf transmission alone is incompatible with disease persistence (A. Jolles)

10.00h Specificity of FMD surveillance in wild boards (Y. Ivanov)

10.15h Wildlife surveillance and control for Fmd (T. Alexandrov)

10.30h Longitudinal studies of FMD (short title). (M.T.Dhikusooka)

SESSION G11. PATHOLOGY AND PATHOLOGICAL BASIS OF PERSISTENCE (p. 157)

11.00h Pathological change of the development of the vesicular lesion in pigs experimentally infected witht the FMDV O/JPN/2010 (M. Yamada)

11.15h FMDV- Host interaction in a model of persistently infected bovine cells (S. Blaise-Boisseau)

11.30h Localization of FMD RNA and viral antigens in different tissues from apparently healthy cattle and buffalo under natural conditions in India (R. Ranjan)

SESSION G12. FUNDING INNOVATION: Q&A (p. 160)

PLENARY SESSION - FINAL SESSION

SESSION 12. GLOBALIZING ACCESS TO KNOWLEDGE AND INNOVATION (p. 162)

15.30h UK experience of modelling in support of FMD control, applying new approaches to knowledge transfer, and tackling the challenge of maintaining and making best use of global funding in support of research and innovation (N. Gibens)

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DAY 1

INNOVATIVE IDEAS AND OPTIONS FOR FMD MANAGEMENT

PLENARY SESSION		PARALLEL SESSION
1. Opening	9.00h	P1. Global Progress against FMD: Session organised by the FMD Working Group of FAO/OIE
2. The Livestock sector and disease emergencies:innovation and ideas	11.00h	P2. Vaccine efficacy (GFRA)
3. Higher health compartments: The way ahead?	13.30h	P3. FMD endemicity (GFRA)
4. Vaccination as an option: what challenges remain?	15.30h	

FRENKEL LECTURE

A. Dekker AVAILABLE UPON REQUEST

UPDATE ON CURRENT GLOBAL SITUATION FOR FMD: NEW OUTBREAKS AND THREATS

Donald P. King, Valerie Mioulet, Anna Ludi, Nick J. Knowles, Britta Wood, Ashley Gray, Barsha Thapa, Lissie Henry, Ginette Wilsden, Clare Browning, Mark Henstock, Bob Statham, Abid Bin-Tarif, Kasia Bachanek-Bankowska, Jemma Wadsworth, Antonello Di Nardo, Veronica Fowler, Alison Morris, Beatriz Sanz-Bernardo, Sarah Belgrave and Julie Maryan, on behalf of the OIE/FAO FMD Laboratory Network

WRLFMD, Vesicular Disease Reference Laboratory, The Pirbright Institute, Ash Road, Pirbright, GU24 0NF, UK

Data from FMD Reference Laboratories are used to monitor the transboundary movements of FMDV in Asia and Africa, and to also provide recommendations about the suitability of vaccine strains that can be used to control outbreaks. In addition to mapping epidemiological patterns in these FMD endemic settings, the OIE/FAO FMD Laboratory Network have also recently detected a number of exotic and unexpected incursions of FMD viruses into new areas that have potential for regional spread and pose increased onward risks to FMD-free countries.

From a European perspective, the emergence and spread of serotype O and A FMDV lineages in North Africa and Anatolia (Turkey) have raised the greatest concerns. During 2013-16, viruses from the O/ME-SA/Ind-2001 lineage have been detected in the Middle East (UAE, Saudi Arabia and Bahrain), and have spread in a westerly direction across North Africa from Libya into Tunisia, Algeria and Morocco. This viral lineage has also spread east into Southeast Asia (Laos, Vietnam and Myanmar) and has recently been identified as causing FMD outbreaks on the islands of Mauritius in the Indian Ocean. During 2015, another FMD viral lineage named A/ASIA/G-VII [G-18]) has also emerged from the Indian subcontinent to rapidly spread in some countries of the Middle East (currently in Saudi Arabia, Iran, Armenia and Turkey). Importantly, vaccine-matching data using in vitro tests indicates that established vaccines that are supplied by international and local manufacturers for use in the West Eurasia region (or are held in reserve by international vaccine banks) may not provide adequate protection against this viral lineage. New tailored vaccines (such as those rapidly produced in Turkey) are now being developed and deployed to address this situation.

There is probably no single factor that underpins these dynamic transboundary patterns; although these long distance and rapid movements of FMDV are probably exacerbated by the escalation of regional political crises, and migration of people in North Africa and the Middle East. These data reinforce the role played by the OIE/FAO FMD Laboratory Network to closely coordinate global surveillance to monitor the distribution of FMDV, and to recognise the emergence of new FMDV lineages that may require new vaccines for control.

CHANGE IN THE MANAGEMENT OF THE FMD DISEASES CONTROL TO AN PRIVATE-PUBLIC-PARTNERSHIP APPROACH

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Summary
The management of highly contagious livestock diseases like foot-and-mouth diseases should be focused much more on the structure of the added value chain and on new measurements. Crisis management structures should be changed from "public management" to involve public-private partnerships which will address the cross border nature of the "added value chain" in the EU. Furthermore decision making in crisis situation must use economic evaluation of options, with less emphasis on epidemic indicators as outcomes. The economic impact upon farmers of managing vaccinated animals in their herds must be recognised and the use of marker vaccines must be described in the European law.

References
Saatkamp, H. W., M. C. M. Mourits, G. E. Hop, T. Böcker and N. Buijs, 2015: Wirtschaftlich impfen – Final Report,

Keywords: economic effects of vaccination, private-public-partnerships, cross border solutions

A 'READINESS RATING' FOR BALANCING BIOSECURITY PRIORITIES IN FMD PREPAREDNESS AND RESPONSE

R. P. Horwitz

The American Studies Department at the University of Iowa and the Coastal Institute at the University of Rhode Island, USA, with support from the states of Rhode Island and Vermont, the New England States Animal Agriculture Security Alliance (NESAASA), the U.S. Department of Agriculture (USDA-APHIS), and the U.S. Food and Drug Administration (DHHS-FDA).

Introduction

Prior FMD outbreaks suggest that disease-free nations would be well served by improving strategies to balance potentially conflicting response objectives: to control disease and to sustain farms, to seal them off and to keep them in business. Biosecurity is the consensus key to such a balance, but scientific support for particular tactics is uneven. Among the most pressing needs are specific biosecurity benchmarks that stakeholders can trust and that responders can use, as in issuing permits for milk pick-up from uninfected dairy herds in a FMD Control Area. The objective of the present work is to research, develop and demonstrate such a tool – a "Readiness Rating" – for Incident Command to use in rapid, incident-appropriate decisions and to help producers prepare for them.

Materials and methods

Field techniques conventional in cultural anthropology were applied among State Animal Health Officials (SAHO) in New England as they assessed the FMD-vulnerability of dairy operations in their jurisdictions. About fifty criteria were identified and weighted to build a composite measure reflecting the consensus priorities of SAHOs and USDA-APHIS epidemiologist in determining if a farm would be "ready" – sufficiently biosecure – to permit milk pick-up.

Results

Ethnographic findings confirm remarkable consensus among animal-health officials in assessing biosecurity preparedness. The criteria that they endorse also fit national Secure Milk Supply (SMS) performance standards. About 70% of the licensed dairy farms (1,200 of 1,700) in New England have now been assessed, and all six states have agreed to share a single SMS plan that includes Readiness Ratings.

Discussion

Results of the present study indicate that the Readiness Rating could be a useful tool in promoting sustainabilty of dairy operations during a FMD outbreak. Its value includes compatibility with pragmatic, flexible and transparent preparedness and response strategies.

ORGANISATION OF RAW MILK COLLECTION DURING AN FMD OUTBREAK

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Introduction

The structures of the Swiss dairy market are complex and highly dynamic. There are many different and partially intertwined trade and transport routes for milk. FMD can potentially spread through milk trucks or circulate through contacts at milk collection centers or dairies. In an outbreak situation, it is challenging to find the right balance between protective measures and business continuity. Switzerland has developed a new concept for the raw milk collection during a FMD-outbreak.

Materials and methods

A working group including representatives of the Veterinary services, milk producers, milk transporters and the dairy industry has developed in 2014 a new approach for the milk collection during a FMD outbreak. Jointly, they elaborated a draft concept and submitted it to veterinary expert committees and the main national companies of the dairy industry. In January 2016, all involved partners tested the new approach locally during a tabletop exercise.

Results

The concept consists of a main principle with a choice of restrictive and protective measures. In the early stage of an outbreak situation, Switzerland will pronounce a total standstill. Milk collection will not be permitted in the restriction zones for at least seven days after the elimination of affected farms. Subsequently, milk collection will restart again under restrictive measures and supervision of the veterinary services. All stakeholders have agreed to this principle. Technical consequences including the safe elimination of milk on the farm are described in the concept.

Discussion

The new approach fits the overall strategy against FMD in Switzerland. Drastic measures are applied in the early stages of an outbreak in order to contain the disease rapidly. The first days are used to put in place most efficient control measures according the national FMD contingency plan. Common planning and close collaboration of public and private sectors prevent a total business disruption of the dairy industry.

ECONOMIC COSTS AND EFFECTS OF ACTIVITIES TO PREVENT FOOT AND MOUTH DISEASE IN DENMARK

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[1] University of Copenhagen. [2] Danish Agriculture & Food Council. [3] Technical University of Denmark.[4] Danish Veterinary and Food Administration.[5] SEGES- Knowledge centre for cattle production.

Introduction

Danish export of pigs, pork, cattle, beef and milk products is important for the national economy. It is estimated that a medium sized outbreak of foot and mouth disease (FMD) would cost around € 1 billion. The annual cost of preventing FMD, biosecurity on farms, surveillance, traceability-systems and the contingency plan against FMD in Denmark was estimated to € 32 million. The three most influential parameters for economic losses in an outbreak have been identified as: the duration of the HRP, the probability of local spread, and the probability of transmission from low-risk contacts. We studied how changes in resources allocated to the FMD related activities and the contingency plan may affect the costs of an FMD outbreak.

Materials and methods

The annual costs of FMD preventive activities were estimated by activity. The DTU-DADS (version 0.165) is a stochastic simulation model. This model was used to simulate how changes in activities affect the costs related to FMD outbreaks in nine alternative scenarios.

Results

Our results suggest that systematic follow-up on trucks and non-professional visitors to outbreak farms during outbreaks might reduce the size and costs of an FMD outbreak. In addition, simulations indicate that current resources allocated to depopulation and surveillance could be reduced without affecting the size and costs of an outbreak.

Discussion

There seems to be an economic potential in prioritizing resources to prevent introduction of FMD. By combining epidemiological modelling with economic analysis, an improved approach to prioritize investments has been developed.

COST AND RESPONSIBILITY SHARING ARRANGEMENTS IN THE EU TO PREVENT AND CONTROL NOTIFIABLE VETERINARY RISKS

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Introduction

Financing schemes related to the non-EU compensated part of animals that are compulsory culled and other costs related to the control and eradication costs differ between MS's. While some MS's finance the direct losses from the national budget (public funds), other MS's have set up some form of statutory public-private financing system.

The objective of this paper is to review the distinct features of a Cost and Responsibility Sharing Scheme (CRSS) enabled by a Public Private Partnership (PPP) to prevent and control veterinary risks.

Materials and methods

Based on an extensive literature review relevant topics related to implementing a CRRS are addressed.

Discussion

Items addressed are:

- An overview of possible compensation schemes and rationalizing public involvement of co-financing and distinctive governance models associated with PPP's .
- The role of a PPP is to raise more awareness, reduce risk exposure, provide incentives for rapid disclosure and increases support of control strategies if outbreaks occur.
- Reasons for farmers to participate in a CRSS is the responsibility sharing part.
- Advantages and disadvantages of CRSS.

Overall it can be concluded that MS's reveal a diverse and complementary views; some are more in favour of the more advanced options for reconsideration of the compensation system, whereas other MS's are more conservative. Determining an appropriate base for sharing is a highly complex matter and it is in their opinion unlikely there is to be a "one size fits all" solution to cost sharing but there is a need for a systematic approach.

NON-GEOGRAPHICAL APPROACHES TO FMD RISK MANAGEMENT

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Management of risk associated with any infectious disease is a function of at least three factors: (1) the epidemiology of the disease, (2) the ease and accuracy of detection and (3) availability of effective intervention measures (bearing cost and practicality in consideration). In the case of SAT serotype FMD, in southern Africa at least, a number of elements that comprise these factors differ on a statistically significant basis from those of the Eurasian lineage of FMDVs, viz.

- The unique co-evolution of SAT serotypes with and maintenance by African buffalo (Syncerus caffer);
- Differences in modes and rates of transmission of the two lineages, including the epidemiological significance of persistent infection;
- Frequency of mild disease and unapparent infection of both wildlife and livestock resulting from infection with SAT viruses;
- Vaccine efficacy that is compromised by greater antigenic diversity within SAT serotypes and also duration of vaccine-induced immunity, shown in some studies to be unusually ephemeral.
-

Therefore, the management of SAT infections – which in extensive rangeland systems often result in slow-spreading, low impact disease – as well as conditions for safe market access for commodities and products derived from cloven-hoofed animals, also need to be different. The implication is that conventional geographic approaches to FMD management are, in some circumstances, inappropriate. In southern Africa they can also be environmentally and/or economically catastrophic.
Fortunately, international standards and norms have begun to change in this respect but, so far, not fast enough nor with the level of international and regional acceptance necessary.

This paper will present these issues in the context of FMD management in southern Africa specifically and sub-Saharan Africa more generally and in the light of regional guidelines that are under development.

ADVANCEMENTS IN COMPARTMENTALIZATION AND REGIONALIZATION - OPPORTUNITIES, RELATIONSHIPS, INFORMATION AND CHALLENGES

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National and international discussions surrounding compartmentalization and regionalization (zoning) have increased in recent years. While the World Organisation for Animal Health (OIE) has introduced the concepts of both as well as the application of compartmentalization, in the Terrestrial and Aquatic Animal Health Codes for purposes of disease control and international trade, practical implementation and policy gaps remain. Technology innovations and scientific advances provide opportunities to successfully lessen some of the challenges. For example, improved next generation vaccine and differentiating infected from vaccinated animals (DIVA) diagnostic tools, and the ability to rapidly share real-time data from the field and between the private and public sectors. Policies and application of these innovations must stay abreast of their use and not be made in isolation. Quality control, verification, transparency and assurances of movement/exports of non-affected animals/ products is paramount. Private and public sector collaborative business continuity planning can also assist in effective implementation of compartmentalization and regionalization within countries and between countries, as these plans can include details of the multiple layers of mitigation required (e.g. biosecurity, surveillance, sanitation, traceability, diagnostic requirements, etc.) while in the context of "speed of commerce", legal business contractual obligations, specific sector and production models/ subpopulations needs, livelihoods, economic and animal welfare impacts. This presentation will focus on some recent examples of the above; opportunities and issues related to how the livestock sector might use compartmentalization/regionalization; and particularly explore the opportunity of new information tools that might contribute to enable effective compartments and more efficiently provide relevant information such as real-time animal health/mortality data to veterinarians, livestock owners and animal health authorities. Finally, successful advancement and use of these concepts will require focused collaborations at national and international levels between livestock owners, livestock value chain, veterinarians, scientific experts, animal health authorities and international bodies.

CAPABILITY ANALYSIS AND SCENARIOS OF RESOURCES POOLING IN CASE OF FOOT-AND-MOUTH DISEASE EPIZOOTICS IN FRANCE AND TUNISIA

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Introduction

FMD represents a major concern for developed countries, because of its impact on trade and the economic losses induced. Contingency plans provide several control measure in case of FMD epizootics, which could be adapted according to the spread of the disease. Resources can be a limitation to the implementation of control measures, especially in countries that are densely populated with livestock herds (Halasa and Boklund, 2014). The objectives of this study were to assess whether current surveillance capacity is sufficient to control a potential FMD epizootics in France and Tunisia, which have respectively a FMD-free status and a suspended status of endorsed official control program to control FMD since the epizootics in 2014.

Materials and methods

In this context, we identified and quantified resources needed to implement the surveillance and control measures against FMD (grid of necessary resources by tasks and skills needed for these tasks). Then capability surveys of local actors were conducted to evaluate the available resources at a local scale (for the management of one or several FMD outbreaks and the associated administrative management). We finally propose plausible scenarios of pooling resources in case of limitation of resources in a given location.

Results

The capability analysis has been conducted in 5 French departments and 7 Tunisian governorates. The first results indicated that active surveillance, by vets, of herds located inside the protection and surveillance zones, were not feasible with the resources available at a local scale. Moreover, the workload induced by administrative tasks appeared to have been strongly underestimated.

Discussion

At the end of the study, information regarding the identification and quantification of human and material resources necessary to FMD detection and control will allow the decision-makers to anticipate a potential FMD crisis in France and Tunisia, by identifying areas where resources are a limiting factor and proposing scenarios of resources mutualisation.

SPREAD OF FMD SEROTYPE O-PANASIA2 IN A DAIRY COMPLEX IN IRAN

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[1]European Commission for the Control of Foot-and-Mouth Disease, [2]Iranian Veterinary Organisation

Introduction

To lesser the burden of livestock industry in the living areas of Iranian villages, there was a policy to locate livestock holdings outside villages in complexes. With continuous buying and selling of livestock, these complexes act as important melting pots of FMD viruses. In the period between 12 February and 15 April 2010, a FMD outbreak with serotype O-Panasia2 ran through the Laban dairy complex in Qom province, Iran. An immediate animal movement standstill was imposed after the first sign of clinical FMD, which allowed to follow-through the spread of FMD between units based on local spread. This allowed us to estimate the reproduction number (Rnaught) between units. The Rnaught is an important parameter for infectious disease dynamics as it expresses the number of secondary units infected by a primary infected unit.

Materials and methods

Of 393 units, 127 units had live cattle housed with an average of 73 heads of livestock per unit. All units were observed daily for clinical signs with recording of the first day of clinical cases, number of heads of livestock affected per day and total duration of clinical FMD. The Rnaught was estimated using the exponential growth rate (Wallinga & Lipsitch), defined by the per capita change in number of new cases per unit of time. We used the deviance-based R-square statistic to guide the choice of the period in which the growth in the epidemic curve was exponential.

Results

The Rnaught for FMD between livestock units was estimated to be 1.6 (95% confidence interval 1.4-1.8).

Discussion

The Rnaught was estimated based on local spread only. Local spread referred to FMD virus transmission through people moving around, materials being used between units, fomites and through airborne FMD virus transmission. It indicated that biosecurity measures and contamination of the environment are important factors to consider when controlling clinical FMD.

A RISK BASED MODEL TO GUIDE DECISIONS ON ZONIFICATION TO STOP VACCINATION IN A FREE COUNTRY WITH VACCINATION

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Introduction

The Southern countries in South America are mainly free of foot-and-mouth disease (FMD) with vaccination. In Bolivia, 13% of the territory (in the western region) is already free without vaccination. The intention in the country is to gradually extend the free without vaccination zones in a risk based manner.

The objective of this study was to develop a model to quantify the risk of FMD re-emergence in zones where vaccination is discontinued and evaluate the efficacy of control measures to minimise this risk.

Material and methods

A scenario-tree model was developed where the main risks considered were: the movement of animals from vaccinated to non-vaccinated zones, the purpose of the movement (breeding or slaughter), the hypothetical prevalence (< 2%) in the zone of origin and the risk category of this zone (based on vaccination and surveillance coverage). Evaluated measures to minimise risk of movement of infected animals were: 1) Testing of animals at the farm of origin: clinical inspection or serological testing and 2) clinical inspections during movement. The basic scenario included clinical inspections during movement only.

Results

A zone was selected for evaluation and initial implementation of the model. This zone has a low cattle density and approximately 800 animals are introduced annually. If no controls were implemented, the probability p of introduction of an infected animal would be 0.005. Implementation of clinical inspection in origin would reduce p to 0.002. Seasonal changes in p to target higher risk periods for inspection were quantified. These results suggest that discontinuing vaccination in this specific zone would result in a low risk of re-emergence of FMD.

Discussion

The model developed here can be used to identify FMD-low risk zones where vaccination can be stopped and to guide the implementation of cost-effective measures to further minimise risks of FMD re-emergence.

ENCOURAGING THE USE OF VACCINATION-TO-LIVE AS A CONTROL STRATEGY FOR FMD OUTBREAKS: PERSPECTIVES AND ISSUES

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The use of vaccination-to-live as a control strategy for FMD after incursions in countries or zones previously free of FMD without vaccination is complicated by a range of uncertainties surrounding the impact of this policy on the subsequent process to regain official OIE FMD-free status and on the implications for external and internal markets. It is widely recognised that, across Europe, public tolerance for controlling FMD outbreaks by culling-alone has decreased. Countries or regions using sustainability or carbon counters for livestock production as a significant part of their marketing strategy are less likely to accept vaccination to kill as part of their FMD control strategy. The decision to vaccinate is time-sensitive, since the likelihood of a successful vaccination campaign is increased if vaccination is started promptly; therefore constraints to the use of vaccination-to-live should be identified in advance and addressed where possible. It is important to convince large food retailers that there is no impediment to the marketing and consumption of meat/milk from vaccinated animals. Different sectors of society will bear the costs and benefits of the various choices. Bringing stakeholders into the discussion can help to build awareness of what the implications are of vaccinating or non vaccinating, thereby increasing the likelihood of consensus if the decision needs to be made in the face of an outbreak. Specific guidelines emphasising the importance of data interrogation for NSP survey results are needed, especially in relation to detecting spatial clustering and the extent of positivity of surveillance samples. A six month waiting period following vaccination-to-live does not necessarily provide substantially more confidence in disease freedom in itself compared with a three month period; the quality of the vaccination strategy and post-outbreak serosurveillance, including post-vaccination monitoring, are likely to have a much more considerable effect on the actual probability of undetected FMD virus circulation than just an additional three months wait; criteria by which these elements can be evaluated are needed. Allowing countries a choice to provide either a comprehensive package of quality assurance data and an epidemiological analysis demonstrating that it had reached a high level of confidence in disease freedom after three months, or to wait an additional three months until the current six month period is reached, would offer a way to address one major constraint to the adoption of vaccination-to-live.

IMPROVING ACCESS TO EMERGENCY FOOT-AND-MOUTH DISEASE VACCINE THROUGH A VACCINE BANK SHARING ARRANGEMENT

Dr. Tom Smylie[1], Dr. Sam Hamilton[2], Dr. Jennifer Davis[2], Dr. Andre Van Haleren[3], Dr. Darrel Styles[4], Dr. Carlos Marin[5], Dr. Maria del Rocio Reyes[5]

[1]Canadian Food Inspection Agency (CFIA),[2]Australian Government Department of Agriculture and Water Resources (DAWR), [3]New Zealand Ministry for Primary Industries (MPI), [4]Animal and Plant Health Inspection Service of the United States Department of Agriculture (USDA-APHIS), [5]Mexican Secretariat of Agriculture, Livestock, Rural Development, Fisheries and Food (SAGARPA).

Introduction

In the past, most FMD vaccine banks were established to provide an emergency supply of foot-and-mouth disease (FMD) vaccine to be used as a last resort in the event of an inability to control an outbreak when following a strict stamping out policy. The Quads modelling group has shown that in large outbreaks, early initiation of a vaccination strategy assists in shortening the length of an outbreak, as well as reducing the number of infected premises. As a result, vaccination is no longer seen as a last resort option to control FMD outbreaks in many FMD-free countries.

Recognizing that access to sufficient number of FMD vaccine doses could be difficult through regional vaccine banks, an arrangement to share FMD Vaccine was signed between three FMD Vaccine banks on the margins of the World Organization for Animal Health (OIE) General Session on May 23 2016. The participants to this arrangement are the vaccine banks of: (1) North America (Canada, the United States and Mexico), (2) Australia, and (3) New Zealand.

Discussion

Participating countries have all recognized that current VAC holdings in regional vaccine banks may be insufficient to meet the demands in large outbreaks. In addition, it is recognized that the likelihood of all five signatory countries being affected by FMD at the same time is negligible. This non-binding arrangement supports the sharing of FMD vaccine by facilitating the rapid consideration of requests for additional vaccine doses, thereby allowing the affected country/countries to benefit from an increased number of available vaccine doses to improve their response capacity.

WHICH VACCINES ARE MOST IMPORTANT? A DECISION SUPPORT TOOL FOR FOOT AND MOUTH DISEASE VACCINE BANK MANAGERS

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European Commission for the Control of Foot and Mouth Disease (EuFMD)[1], WRLFMD The Pirbright Institute[2]

Foot and mouth disease (FMD) significantly constrains trade in animals and animal products, and most FMD-free countries invest considerable resources to prevent and prepare for possible incursions. As part of these efforts, multinational and national vaccine banks have been established to enable rapid implementation of emergency vaccination in the event of an outbreak. FMD is caused by a virus with 7 serotypes and multiple strains within serotypes, with no cross protection between serotypes and variable protection between strains within each serotype. Therefore, to be effective, the banks should hold vaccine strains suitable for protection against the virus strains most likely to cause an incursion.
We developed a semi-quantitative spreadsheet model to assist vaccine bank managers worldwide prioritize which antigens to hold in the bank. The tool combines two distinct considerations: 1) which strains pose the greatest threat of incursion into a given area (antigen risk score) and 2) the effectiveness of available vaccines to protect against each circulating strain (coverage score). The antigen risk score is derived by combining the relative importance of possible source regions (i.e. FMD endemic areas) with the relative prevalence of circulating strains in the source regions. These values are determined by expert elicitation. The relative importance of different source regions will vary according to the location of the vaccine bank, and will be influenced by proximity, connectedness of countries (e.g. by immigration and trade) and the prevalence of FMD virus. The coverage score is calculated for each combination of vaccine and virus strain according to the percentage of virus isolates that match the vaccine in question. Finally, the coverage score and the antigen score are combined to yield a vaccine score for each vaccine strain eligible for inclusion in the bank. This tool is being piloted by vaccine bank managers.

EARLY DECISION INDICATORS TO PREDICT THE SEVERITY OF AN FMD OUTBREAK

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Introduction

Foot and mouth disease (FMD) presents an ongoing threat to livestock industries in countries where the disease is non-endemic. For countries that are disease free without vaccination, potential outbreak size and duration have a large impact on trade restrictions and the final economic cost of an outbreak. Emergency vaccination, although increasingly recognised as a potentially important strategy for bringing FMD outbreaks under control, adds liabilities and cost. This study attempts to identify early decision indicators (EDIs) of outbreak severity which can then be used to inform the timing of the most effective and appropriate control methods.

Materials and methods

FMD models from Australia, New Zealand, Canada, USA, UK and Sweden were used to create a database of simulated FMD outbreaks for each country covering a range of starting conditions. Indicators known or available to disease mangers early in an FMD outbreak including farm, animal and human population density at the site of the index case and the number of IPs at days 7, 14 and 21, were assessed as predictors of final outbreak size and duration and the area under control.

Discussion

A reliable set of EDIs will allow decisions regarding FMD vaccination to be made with greater confidence, taking into account additional direct costs such as possible extended trade restrictions, additional serology surveillance requirements, managing a vaccination program and tracking vaccinated animals. In this presentation, we will discuss the performance of EDIs available at days 7, 14, and 21 of an FMD control program as predictors of final outbreak size, duration and the total area under control. We will also discuss the trade-off between the benefits from starting a vaccination control plan early in an outbreak, or postponing the decision until more information becomes available.

EMERGENCY VACCINATION BENEFITS ERADICATION OF HYPOTHETICAL INTRODUCTIONS OF FMD INTO NEW ZEALAND

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Introduction

Recognition that emergency vaccination could be a valuable adjunct tool when responding to FMD incursions prompted New Zealand to assess appropriate strategies, associated benefits and key influencing factors.

Materials and methods

InterSpread Plus (ISP) was used to simulate emergency vaccination as an additional response measure based on two variations of a stamping-out (SO) FMD eradication programme. Hypothetical introductions of FMD to three regions with different farming systems and incursion scenarios were used in this investigated. Vaccination implementation was varied by the deployment time, strategy, zone size, herd immunity settings and species. Results from 336 different scenarios were analysed to evaluate the benefits and influencing variables.

Results

Overall, vaccination reduced the epidemic size and, importantly, suppressed the probability of a run-away epidemic. The benefits of vaccination tended to be more pronounced with the more effective SO programme, for larger epidemics and when deployed earlier in the response. Larger vaccination zones produced marginally better results but with a dramatic increase in human resources and vaccine doses. The optimal vaccination strategy was identified as being a 3-5 km radius suppressive ring vaccination zone deployed between 11 – 16 days after first detection. Human resource requirements and a cattle-only vaccination option were also quantified in a subset of scenarios.

Discussion

The results indicated that emergency vaccination could augment SO programmes under New Zealand conditions, provided resources are available and vaccination is implemented timely and without compromising the effectiveness of SO activities. Areas for future studies to further support preparedness and response decision-making will be highlighted.

A PROCESS MODELLING APPROACH TO ESTIMATE FMD DIAGNOSTIC CAPACITY FOR OUTBREAK MANAGEMENT DECISION-MAKING

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Introduction

New Zealand's FMD Diagnostic Surveillance Strategy includes pre-determined testing algorithms and sampling rules for different farm risk situations (as presented at EuFMD OS'14). This strategy, along with a combination of process modelling and epidemic simulation modelling, is used to determine laboratory testing capacity for outbreak and proof-of-freedom surveillance in the New Zealand setting. The framework presented has useful applications for prioritising surveillance activity and for informing management decisions, such as vaccination policy, before and during an outbreak.

Materials and methods

Flowcharts detailing the diagnostic testing algorithms to be employed in the event of an FMD outbreak, and during proof-of-freedom surveillance, are entered into a process modelling application. Specifications such as time, resources, and personnel required, are attributed to each step. Input sample numbers and testing requirements are estimated from epidemic simulation modelling.

The most realistic daily laboratory testing capacity given the available resourcing is produced from the simulation model. Potential bottlenecks and resource shortages in the testing processes can be identified, and improvements to efficiency and capacity modelled. Alternate scenarios are tested against the capacity models to compare the effect on the efficiency of diagnostic surveillance and the implications for management of an outbreak.

Results

Knowledge of the laboratory testing capacity is used to:

- Inform prioritisation of diagnostic surveillance during an outbreak to align the submitted volume of samples with laboratory capacity;
- Approximate the time and resources necessary to complete proof-of-freedom surveillance and thus return to trade;
- Evaluate the likely effect of DIVA post-vaccination testing on the time and resources necessary to complete proof-of-freedom surveillance, thus informing vaccination policy.

Discussion

Having an understanding of the logistical constraints and timing involved with surveillance testing

provides valuable information for the management of an outbreak, particularly in decisions around adapting surveillance strategies during a response, and for factors impacting on proof-of-freedom testing.

QUANTIFYING THE VALUE OF PERFECT INFORMATION IN EMERGENCY VACCINATION CAMPAIGNS FOR FOOT-AND-MOUTH DISEASE

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Introduction

FMD outbreaks in non-endemic countries can lead to large economic costs and livestock losses but the use of vaccination has been contentious, partly due to uncertainty about emergency FMD vaccination. Whilst this uncertainty may be challenging to resolve during outbreaks, it is vital that vaccination is introduced rapidly and effectively in order to have maximum effect. Here we calculate the expected value of resolving uncertainty about vaccine efficacy, time delay to immunity after vaccination and daily vaccination capacity for FMD outbreaks.

Methods and Results

We use predictions of the impact of competing vaccination strategies for outbreaks of FMD in the UK to quantify the effect of uncertainty regarding the effectiveness of vaccination on decision-making. If it were possible to resolve all uncertainty prior to the introduction of control, we could expect savings of £55 million in outbreak cost and 221,900 livestock culled. All vaccination strategies were found to be preferable to a culling only strategy. However, the optimal vaccination radius was found to be highly dependent upon vaccination capacity for all management objectives. We calculate that by resolving the uncertainty surrounding vaccination capacity we would expect to return over 85% of the above savings, regardless of management objective.

Discussion

Formal incorporation of a policy to resolve uncertainty regarding management of epidemics can change the optimal control strategy and result in significant cost savings. Using a mathematical modeling approach, we concluded that, should it be possible to resolve the uncertainty regarding the number of doses of vaccination that could be implemented per day, significant cost savings could be made. It may be possible to resolving uncertainty about daily vaccination capacity before an outbreak, and this would enable decision makers to select the optimal control action via careful contingency planning.

GLOBAL, REGIONAL AND NATIONAL PROGRESS OF FMD CONTROL

Samia Metwally[1], Laure Weber-Vintzel[2], Nadège Leboucq[2], Eran Raizman[1], Silvia Kreindel[1], Gregorio Torres[2]
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Introduction

The past decade has been an exciting period for FMD control and its elimination efforts. The progressive control pathway for FMD (PCP-FMD) was developed to provide a stepwise methodology for a risk management and cost effective control approach followed by the development of the FAO-OIE Global FMD Control Strategy (2012). The PCP-FMD contributed significantly to the Global Control Strategy and represented the backbone for its implementation.

Materials and methods

FMD Global Control Strategy is applied at national level while the progress is assessed at regional level using roadmap platforms, which permit the formulation of harmonized programs and exchange of information on virus circulation, vaccination and other control initiatives. This approach has been proven to be best achieved by bringing together the Chief Veterinary Officers, national FMD experts, regional and international organizations, and development partners. At the regional roadmap meetings, countries are assessed and placed in their appropriate PCP Stage (0-3) based on their self-assessment, and reports of their control activities. The FAO and OIE FMD working group coordinates the activities at the global and regional levels and facilitates the development of guiding materials for national supports.

Results

Out of 87 FMD-affected countries, 57 nations belong to FMD virus pools 2-5 are currently engaged at various levels in the implementation of control measures using the PCP-FMD guidelines in the quest to reduce or eliminate FMD virus circulation by 2020-2025. Since 2012, countries continued to advance along PCP stages with clear shift to have more countries in PCP stages 1 and 2. A few countries progressively advanced to higher stages as of 2016.

Discussion

In this session, the achieved milestones, success stories and challenges in the implementation of the global FMD control will be discussed entitled “Global Program against FMD”. Countries at different stages of PCP will present their experience and advancement in FMD control.

NATIONAL ACTIVITIES FOR FMD CONTROL IN KENYA *A. Sangula*

NATIONAL ACTIVITIES FOR FMD CONTROL IN THAILAND *TBD*

NATIONAL ACTIVITIES FOR FMD CONTROL IN AFGHANISTAN *G. Ferrari*

NATIONAL ACTIVITIES FOR FMD CONTROL IN KAZAKHSTAN *D. Imanbayeva*

AVAILABLE UPON REQUEST

ADVANCES AND GAPS IN VACCINE MODELLING

R. Reeve

The Boyd Orr Centre for Population and Ecosystem Health, Institute of Biodiversity, Animal Health and Comparative Medicine, College of Medical, Veterinary and Life Sciences, University of Glasgow, UK
The Pirbright Institute, Ash Road, Pirbright, UK

Vaccine modelling takes many forms, including predicting vaccine potency and efficacy from live animal challenge experiments; modelling the relationship between serological responses to vaccination and protection both in experimental settings and in the field; predicting the cross-reactivity and cross-protection afforded by vaccines against heterologous viruses; modelling the effect of adding vaccines into epidemiological models; and estimating the effectiveness of vaccines as deployed in the field.
I will describe how foot-and-mouth disease research has investigated these and other aspects of vaccine modelling, and what refinements exist in other disease contexts. I will then discuss some potential future avenues that we ought to be considering to improve our ability to choose appropriate vaccines and predict their effectiveness in the field.

SELECTION OF FMD VACCINES IN VIETNAM

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Approximately 20 millions doses of foot and month disease (FMD) vaccines have been imported and used each year in Vietnam under the scope of the National FMD Control Programme (Phase 1: 2006-2010, Phase 2: 2011-2015, Phase 3: 2016-2020).

The choice of strains of FMD virus vaccines is based on: i) potency and ; ii) antigenic matching, i.e. the matching of representative field isolates from outbreaks to available vaccine strains.

For the period from 2010-2015, viruses serotype O were found dominant in the country with viruses serotype A being detected time to time. With support given by the WRLFMD at the Pirbright Laboratory on vaccine maching, selection of FMD vaccines in Vietnam has been done based on the r-values of virus neutralisation test (VNT).

This approach encountered some constrains in selection for the most appropriate vaccines to use in FMD control programmes in an endemic country like Viet Nam. First, in order to ensure that a field strain is representative for the country in a period of time, the surveillance capacity of the national Veterinary Services will be an issue. It might take some times to assess if the identified strains are the most dominant in the field. Secondly, commercial vaccine manufactors are often not willing to change the vaccine antigen should the strain is not widely spread. In case, the country would like to speed up the vaccine maching test by doing it with their national laboratories, they will not be able to access to the vaccine strains on order to conduct VNT.

In short, alternative approaches for vaccine matching are needed, especially for countries in endemic setting. In an effort to overcome these constrains, Vietnam is developing its own vaccines for FMD.

THE VALUE OF IN VITRO ANTIGEN MATCHING IN PREDICTING VACCINE PROTECTION

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Introduction

In the absence of live animal challenge studies, in vitro antigen matching is used to predict the ability of vaccine strains to protect against a field isolate. The standard method to measure the antigenic match is the virus neutralisation assay. However, reproducibility with this method is challenging, and results between operators and laboratories are often difficult to compare. The liquid phase blocking ELISA can also be used and provides more reproducible results, but does not determine the neutralising antibody response. With both assays, the current cut-off values may not be an accurate measure for protection, particularly when looking at heterologous challenge, which is the most likely field scenario.

Materials and methods

Several vaccine trials were performed in cattle, sheep and pigs. Animals were vaccinated with double oil emulsion vaccines of serotypes O, A or Asia-1 (>6 PD50) and challenged with heterologous viruses at 4, 7 or 21 days post vaccination (dpv). Clinical scores were recorded and viraemia and serological responses were measured.

Results

In most of the trials the vaccines provided protection against clinical disease, even when the in vitro antigen matching predicted vaccine failure. The protection was significantly improved when the challenge was performed once the immune response had been fully developed (21 dpv), compared to earlier time points. However, in most cases the protection was not sterile, and there was less protection observed in pigs.

Discussion

The current laboratory assays do not provide an accurate estimation of protection when using high-potency vaccines, especially when challenged with heterologous field strains. The assay results should be interpreted with care, and challenge trials may be needed to determine vaccine efficacy, unless improved laboratory based methodologies are developed. The use of quality vaccines, with high antigen payloads, administered using good vaccination practices, is essential to provide some guarantee of efficaciousness.

CORRELATION OF SEROLOGICAL RESPONSE AFTER VACCINATION AGAINST FMDV AND PROTECTION AGAINST CHALLENGE IN PIGS

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Introduction

Vaccination is one of the most effective ways to protect animals against infection with FMDV. For cattle, the correlation between antibody levels and protection against challenge has been studied extensively. For other species, these data are scarce. We used data of previously performed experiments in which vaccinated pigs were challenged with FMDV. We estimated whether the VNT titre after vaccination could be correlated with protection.

Materials and methods

We used data of previously performed experiments. Data for each pig (n=63) consisted of: the vaccine strain (O Taiwan or O Manisa), the challenge strain (O Taiwan or O Netherlands), the VNT titres (log10) against the vaccine strain, challenge method (intradermal inoculation, contact with (non-)vaccinated infected animals), type of challenge (homologous or heterologous to vaccine) and protection status.
The relationship between antibody titre and the probability of protection against either infection (virus excretion) or disease (clinical signs) was evaluated by fitting a binomial regression model where protection was the response variable and antibody titre was the explanatory variable. Additionally the effect of the type of challenge and the used challenge method on the probability of protection was evaluated by adding these variables in the model. The titre at which 50% protection of the vaccinated pigs is expected (VNT50) was calculated.

Results

The VNT titre elicited by vaccination had a significant association with protection. Neither the type of challenge nor the challenge method had a significant effect in the models.
The estimated VNT50 against infection was 1.8 (1.4–2.2). To protect against disease, a lower VNT50 was needed, 1.4 (1.0–1.7).

Conclusion

Two models were developed where the expected probability of protection for pigs against challenge with FMDV could be quantified. The antibody thresholds (VNT50) that were estimated could be used as correlates of protection to assess vaccine efficacy and or vaccination effectiveness.

NOVEL MARKER FOOT-AND-MOUTH DISEASE VIRUS VACCINE MOLECULARLY BOUND TO NANOLIPOPROTEIN ADJUVANT

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Foot-and-mouth disease (FMD) is considered an economical important disease of livestock, is an OIE notifiable disease and it remains a global threat to national and international trade in livestock and livestock products.

Control of FMD by means of vaccination, relies strongly on the chemical inactivation of complete viral particles. Improvements on FMDV vaccine and diagnostic assay are warranted on several fronts of development.

In this study, we engineered novel FMDV vaccines by an approach involving (1) mutant FMDV containing six histidine residues (6X-His) inserted into FMDV genome between the C-terminus of capsid protein VP1 and non-structural protein 2A (2) 6xHis FMDVs readily assembled into antigen: adjuvant complexes in solution with Ni2+-chelated nanolipoprotein and monophosphoryl lipid A adjuvant (MPLA:NiNLP). This marker 6xHis FMDV exhibited in vitro growth profiles, virus titers and neutralizing (r1) values similar to the parental virus. Concentration of the viruses by Co2+ affinity columns and ELISA assays confirmed the functional expression of His tags on the marker virus capsid surface. Electron microscopic imaging and biochemical assays showed that the mutant virus binds to a Ni-chelating nanolipoprotein monophosphoryl acid adjuvant (NiNLP-MPLA) in a concentration dependent manner.

Animals Immunized with BEI-inactivated 6xHis-FMDV:MPLA:NiNLP formulated vaccine acquired enhanced protective immunity against FMDV challenge compared to virions alone, using an experimental mouse model.

This technology has broad applications to facilitate antigen purification and to induce effective immune responses to other relevant picornaviruses.

ANTIGENIC REFOCUSING OF A SAT2 FOOT-AND-MOUTH DISEASE VIRUS THROUGH EPITOPE DAMPENING

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Introduction

The South African territory (SAT)-2 FMDV is the most prevalent and diverse of the SAT serotypes. The need to understand the antigenic diversity of these viruses remains essential towards new approaches in engineering of a vaccine seed strain that confers cross-protection within the serotype.

Materials and methods

Towards refocusing the antigenicity of SAT2/ZIM/7/83, two strategies were utilised, (1) replacement of predicted antigenic determinants to corresponding sites of the antigenic distant SAT2/EGY/9/2012 virus and (2) charge-dampening of previously identified epitope regions with alanine residues. The antigenic distance of refocused mutants was evaluated by (1) virus neutralisation assays using parental and heterologous convalescent sera and (2) through antigenic profiling with non-neutralising SAT2-specific monoclonal antibodies (mAbs).

Results

No significant shift in cross-reactivity was observed for the charge-dampened mutants compared to that of the parental virus against the homologous antisera. Nevertheless, a reduction in neutralisation titre was seen for epitope replaced mutant Site3, in VP1, with both the homologous and heterologous antisera. A significant increase in neutralisation was seen for the βG-βH loop and C-terminus replaced mutant with the heterologous sera confirming antigenicity of this region. Alanine dampening of mutation 2A, in VP2, showed the highest reduction (80%) in binding towards four of the mAbs, whilst mutation of Site4, in VP3 exhibited at least 35% reduction in binding to all mAbs.

Discussion

A high titre of antibodies directed against the highly variable Site3 region in VP1, evidenced the role it may play in misleading the immune response from conserved critical regions. Antigenic profiling of these mutant viruses with mAbs resulted in mapping of potential SAT2 antigenic determinants. Information gained from this study serves as a stepping stone towards better understanding of the antigenic regions of the diverse SAT2 serotype and will assists in novel approaches towards development of a cross-protective vaccine seed strain.

ESTIMATE OF CROSS-PROTECTION PROVIDED BY AN FMDV O-BFS VACCINE IN THE TUNISIAN EPIDEMIOLOGICAL CONTEXT

Parallel- 14.50h - Poster

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Introduction

Vaccination is one of the most important tools to combat FMD. Since immunity to FMDV is serotype-specific, and even within serotypes cross-protection between strains may be incomplete, the vaccine strain selection should be based on knowledge of threats from trade and from virus circulating regionally, in order to ensure a sufficient antigenic match between the vaccine and the field strain and provide a broad range of protection against multiple threats. The objective of this study was to predict the efficacy of an FMD vaccine based on the strain O-BFS in the Tunisian epidemiological context, despite its poor in-vitro matching with the type O-Ind 2001 virus responsible for 2014-15 outbreaks in the Maghreb region.

Materials and methods

The field vaccine trial was conducted in Tunisia. Two groups of animals, respectively naïve or previously vaccinated with the Tunisian vaccine (O Manisa + O Tunisia 1999), each composed by 40 cattle and 40 sheep, received a single vaccination with O-BFS vaccine. The level of virus neutralizing (VN) antibodies against the vaccine strain (O BFS) and the Tunisian field virus was determined before vaccination, 5 and 21 days post-vaccination (DPV).

Results

Assuming a VN titre of 1/128 as indicative of protection, the results showed that in previously vaccinated cattle and sheep a booster vaccination with O-BFS elicited a strong and fast increase of antibodies, with protective immunity achieved as soon as 5 DPV for both type O strains; antibody titres against O-BFS were on average only 2-fold higher than against the heterologous field virus.

In the groups of naïve animals, 21 DPV, the primary immune-response was 6-8-fold lower than in the groups that received a booster vaccination; furthermore, 30% sheep and 15% cattle did not achieve the protecting antibody level against the field virus, whilst all animals overcame the estimated threshold against the homologous vaccine strain O-BFS.

Discussion

In the Tunisian epidemiological context and considering the heterogeneity of the population immune status, the vaccination with FMDV O-BFS, despite the limited antigenic matching with the field virus (topotype O-Ind2001), is expected to induce a good immunity when administered to animals

THE ROLE OF ASYMPTOMATIC CARRIERS IN FMD ECOLOGY; UNIFYING KNOWLEDGE FROM CONTROLLED LABORATORY EXPERIMENTS AND FIELD STUDIES

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The carrier state of foot-and-mouth disease (FMD) continues to be a determinant of aggressive control policies based upon the perception that carriers may transmit FMD to susceptible animals. However, documented basis for this perceived threat remains limited and equivocal. In endemic settings the role of persistently infected animals in long term viral maintenance and emergence of new outbreak strains remains undefined. It has been definitively established that domestic ruminants and various wild ungulates are competent to remain infected with FMD virus (FMDV) for months to years after initial infection. These findings have been obtained through two main modalities of investigation: field studies that investigate naturally occurring FMDV carriers in endemic regions and experimental studies in which animals are inoculated with FMDV in containment laboratories and monitored through the development of persistent infection. The information generated from these distinct forms of research are sometimes similar, sometimes complimentary, yet sometimes contradictory. The purpose of this presentation will be to consider the similarities and differences between controlled experiments and field studies and how these distinct approaches contribute to the overall landscape of the current understanding of the FMDV carrier state. Specific issues to be considered include the duration of the carrier state, the concept of "FMDV shedding", the implications of isolating infectious virus versus viral RNA, anatomic sites of viral persistence, and the use of phylogenetics to investigate transmission patterns. Gaps in knowledge will be identified and prioritized. Options will be considered for modifying FMD response plans based upon (potentially) altered perceptions of the risk of contagion from carriers.

NEXT GENERATION SEQUENCING REVEALS NEW SOUTHERN AFRICAN TERRITORIES GENOTYPES BRINGING US CLOSER TO UNDERSTANDING THE HISTORY OF FOOT-AND-MOUTH DISEASE VIRUS IN AFRICA

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Introduction

Despite increased number of publicly available whole genome sequences, current foot-and-mouth disease virus (FMDV) genomic data are biased by the opportunistic nature of sampling, which makes it difficult to evaluate the real variability of FMDV. Using next generation sequencing we have generated full genome sequences of FMDV field isolates from a variety of hosts and geographical locations which will help to characterise the true sequence space of the FMDV genome.

Materials and Methods

Since whole genome sequences of Southern African Territories (SAT) genotypes are underrepresented, 50 SAT isolates collected from various locations in East Africa were sequenced using PCR-free protocol pioneered at The Pirbright Institute. Complete genome sequences were reconstructed de novo using optimised bioinformatics pipeline. Phylogenetic analysis such as maximum likelihood, detection of phylogeny violation and Bayesian analysis were applied to characterise these SAT isolates.

P3

Results

Sequencing of FMDV SAT 1-3 serotypes from East Africa revealed new distinct genotypes of SAT viruses. Phylogenetic analysis suggests that while the newly characterised SAT isolates are capable of recombination with both SAT and non-SAT viruses, these new genotypes did not arise from recombination but probably from geographical isolation of FMDV within Africa caused by the Great African Rinderpest Pandemic (1887-1897).

Discussion

While it is generally considered that FMDV originated in Africa, the Great African Rinderpest Pandemic led to a massive die-off of FMDV hosts (both domestic and wildlife) leading to the eradication of a number of FMDV genotypes in Africa. It is thought that many currently circulating FMDV O and A genotypes were re-introduced into Africa from Europe and Asia after 1900; however, SAT isolates probably re-emerged from remaining African buffalo (Syncerus caffer) herds. The newly identified SAT genotypes may represent virus lineages which existed before 1890s.

WAVES OF FMD IN EAST AFRICA AND ADVANCES IN PRACTICAL SURVEILLANCE

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Introduction

We have demonstrated that foot-and-mouth disease (FMD) considerably impacts traditional livestock systems in northern Tanzania, and that infection is driven by livestock- rather than wildlife-related factors. Demand for prevention of infection in livestock through vaccination is high amongst government- and community-level stakeholders. However, such an approach is constrained by the complex antigenic and genetic landscape and the lack of effective polyvalent vaccines.

P3

Methods

We investigated spatial and temporal patterns of FMD infections in northern Tanzanian cattle over a three-year period (2010 – 2014), combining (1) information on FMD viruses (FMDVs) responsible for outbreaks (2) virus neutralisation testing (VNT) data and (3) outputs of Bayesian models developed to ascertain retrospectively the serotype causing outbreaks from serology. From the literature, spatio-temporal serotype-specific FMDV information was also available for southern Kenya.

Results

The Bayesian model showed that serotypes SAT1 and then O were the most dominant ones prior to the availability of virus typing data. Consistent with the serotype O inferences, in 2011 the highest proportion of animals were VNT positive for serotype O (93.3%, [95% CI:77.9-99.2%]), followed by SAT1 (37.5%[21.2-56.3%]), A (34.4%[18.6-53.2%]) and SAT2 (0.0%,[0.0-10.8%]). Virus isolation data showed that O outbreaks were followed by SAT2 (early 2012), A (late 2012/early 2013) and finally SAT1 (late 2013 to 2015) outbreaks. This latter sequence of outbreaks was inversely related to antibody levels. The patterns of FMD serotype dominance in northern Tanzania and southern Kenya were consistent over time.

Discussion

This suggests a predictability to circulation of FMD serotypes in relation to space, time and herd immunity and is consistent with serotype-specific waves of infection spreading across East Africa. Research is ongoing using lateral-flow device technology to enhance surveillance in these communities. If these patterns are consistent and predictable, cattle vaccination using monovalent vaccines, which are much more readily available than polyvalent, could target predicted outbreaks.

GENETIC AND ANTIGENIC VARIATION OF FMD DISEASE VIRUS DURING PERSISTENCE IN NATURALLY INFECTED CATTLE AND BUFFALO

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Introduction. There is a need to improve the understanding of FMDV natural ecology and epidemiology in endemic regions to provide the basis for effective control strategies. The possible role of FMDV persistently infected ruminants in initiating new outbreaks remains controversial and the inability to quantify the real risk posed by such animals could preclude control of FMD in India. This report reflects collaborative research activities between USDA-ARS Foreign Animal Disease Research Unit at PIADC, USA and the ICAR-Directorate of FMD, Mukteswar, India. Here we report genetic and antigenic variations of FMDV serotype O/ME-SA/Ind2001d lineage that have been analyzed in consecutive isolates recovered over a period of 14 months from cattle and buffalo with natural persistent infection.

P3

Materials and methods. In a privately managed, organized dairy farm, where FMD outbreak was recorded during January 2014 , oesophageal-pharyngeal fluid (OPF) samples were collected from convalescent (n=32) and asymptomatic (n=22) cattle and buffaloes at 2-3 months interval from March 2014 for a period up to 14 months. Viruses were recovered from the OPF in LFBK-$\alpha V\beta 6$ cells and the entire capsid coding (P1) sequences were determined from the cell culture supernatant at low passage level (3-4).

Results and Discussion. Analysis of the P1 sequences from acutely infected animals (n=4), convalescent carriers (27 sequences from 19 animals) and asymptomatic carrier (10 sequences from 8 animals), revealed point mutations that represented fixation of mutations at the rate of 1.816 x 10-2 substitution/site/year (s/s/y) with a 95% credible interval of 1.362-2.31 x 10-2 s/s/y. Two codons in VP1 (138 and 148) and one codon each in VP2 (78) and VP3 (76) was found to be under positive selection with statistical significance. Though fixation of nucleotide and amino acid changes were observed at some position, majority were not conserved in consecutive isolates. Between different animals, mean dN/dS (β) value of the entire capsid coding region varies from 0.076 to 0.357, which indicates that the selection pressure acting on viral genomes differ between individual animals. From the statistical parsimony analysis, it was evident that all the virus isolates from carrier animals were originated from acute virus except six isolates. This may be attributed to either silent re-introduction of virus or very high rate of mutation in some individual animals or coexistence of heterogeneous populations in which variants evolve independently of each other. The antigenic relationship value as determined by 2D-MNT assay indicates fluctuation of antigenic variants in some of the carrier animals. The genetic and antigenic variations observed in the carrier viruses differ largely between individual animals. Our study indicates evidence of viral activity in the persistently infected animals under field scenario and probable role of host factor in shaping their evolution

MOLECULAR EPIDEMIOLOGY OF FOOT-AD-MOUTH DISEASE VIRUSES IN SOUTHERN AFRICA

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Background

FMD is endemic in most countries in Africa. The control of FMD outbreaks in endemic settings requires better understanding of the epidemiology of the disease and molecular characteristics of FMD virus (FMDV) involved. The epidemiological factors and virus characteristics that contribute to the sporadic outbreaks of FMD in different locations in Africa have not clearly been investigated. In this study, the genetic characteristics of FMDV detected from cattle and buffalo in Southern Africa were investigated.

Methodology

Livestock samples from Tanzania between 1967 and 2013 plus probang samples collected during 2011 from buffalo in game parks and neighbouring cattle populations in Tanzania, Zambia, Malawi and Mozambique were investigated. From the latter group, 10 isolates from buffalo and livestock around Marromeu NP in Mozambique were studied in greater depth. The investigation was undertaken using virus isolation, RT-PCR, VP1 and whole genome sequencing, and phylogeny.

Results

Phylogenetic reconstructions showed that Tanzanian type O viruses clustered into the EAST AFRICA 2 (EA-2) topotype, type A viruses into the AFRICA topotype (genotype I), type SAT 1 viruses into topotype I and type SAT 2 viruses into topotype IV. They were all genetically related to contemporary lineages and topotypes that occur in the East African region. The phylogenetic analysis of 5 isolates collected from buffalo in Marromeu NP provided evidence for the presence of novel lineages for all three FMDV SAT serotypes which were distinct from the topotypes previously described in the region. The complete polyprotein analysis of one SAT 1 isolate (SAT1/MOZ/BUF-B16/2010) showed closest nucleotide identity (94%) to SAT1/RHO/5/66 isolated from cattle in southeast Zimbabwe in 1966.

Conclusion

This RT-PCR and whole genome sequencing strategy could be deployed to study the extent of diversity in FMDV lineages and understand mechanisms that impact upon viral evolution and factors that influence FMDV endemicity in Africa. This information is necessary for recommending rational FMD control method(s) in the region.

P3

A NOVEL MODELLING APPROACH FOR ENDEMIC FOOT-AND-MOUTH DISEASE IN SUB-SAHARAN AFRICA

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Introduction
Modelling endemic foot-and-mouth disease has many challenges. Unlike in settings where individual animal movements and farm locations are known, the situation in much of SSA is such that very little is known about the circulating strains and animal movements. Furthermore, the extensive grazing systems mean many modeling frameworks developed to date, do not suit the scenarios found in SSA. We therefore explore the use of other potential frameworks such as gravity models for their utility for disease modelling in these settings.

Materials and Methods
VPI FMDV sequences from cattle in Cameroon and publically available sequences from other regions of SSA, including Kenya and Tanzania were used to infer the transmission network between countries for serotypes A and SAT2 by phylogeographic methods employing time resolved Bayesian phylogenetics with discrete trait models.

P3

Results
For serotype A, we found a clear divide between strains circulating on the eastern side of Africa since the 1950s, and those circulating between Central, Western and Northern areas. For SAT2 we found a similar Central, Western and Northern pattern but with a greater diversity of strains circulating between Eastern and Southern Africa.
To investigate the transmission patterns further we also performed more detailed analyses at local scales within Cameroon, Kenya and Tanzania using regions as the discrete traits, making use of the Generalised Linear Modelling (GLM) framework within the BEAST software. to estimate the relative importance of cattle density, human density, distance between regions, and accessibility of regions as predictors of the transmission pattern in a phylogenetic GLM. By combining the predictors in several ways; for example cattle density at source, human density at destination divided by distance, we can also test whether and to what extent different gravity models are predictive of the observed transmission patterns.

Discussion.
We propose that this approach gives the first modeling frame work to study continent wide FMD spread and circulation in a spatially explicit manner.

DAY 2

GLOBALIZING ACCESS TO SCIENCE AND INNOVATION: CONNECTING LIVESTOCK KEEPERS AND KNOWLEDGE LEADERS

PLENARY SESSION		PARALLEL SESSION
5. Global and regional FMD surveillance	9.00h	P4. New vaccines
6. New insights from epidemiological studies	11.00h	P5. Improving current vaccines
7. Risk-based approaches: What have we learnt?	13.30h	P6. Preventing FMD: tools to assist decision making
8. Measuring impact of vaccination and other preventive measures	15.30h	P7. Innovation and diagnosis

DAY 2

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THE ORIGIN, EVOLUTION AND DIAGNOSIS OF SENECA VALLEY VIRUS, A NEW VESICULAR DISEASE-CAUSING PICORNAVIRUS OF PIGS

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Introduction

Seneca Valley virus (SVV) is a picornavirus belonging to the species Senecavirus A in the genus Senecavirus. SVV was first isolated from pigs in North Carolina in March 1988. From about 1997, SVV was occasionally associated with idiopathic vesicular disease (IVD) in pigs. Recently, there has been an increased incidence of the isolation of SVV from cases of porcine IVD and occurrence of both the virus and the disease in Canada, Brazil and China. Experimental infection of pigs with SVV has recently been shown to result in vesicular lesions (Montiel et al. 2016; Emerg. Infect. Dis. 22:1246-1248).

Materials and methods

Genome sequences were determined using Illumina MiSeq technology and phylogenetic analyses performed using MEGA and BEAST. Using a collection of historical SVV samples a new real-time RT-PCR (rRT-PCR) assay developed at Kansas State University was validated to establish testing capacity within WRLFMD and to allow differentiation from other vesicular diseases.

Results

We determined the genome sequences of seven porcine SVVs isolated between 1988 and 2001 in the US. These were compared to the genome sequences of over 20 SVV's that available on GenBank. Phylogenetic analyses showing that all currently identified SVV's belong to a single lineage which has a common ancestor dating to around 1985. The new rRT-PCR assay detected all currently available SVV isolates with no cross-reactivity with foot-and-mouth disease, vesicular stomatitis or swine vesicular disease viruses.

Discussion

These results suggest that SVV probably entered the US pig population in a single event around 1985 from an unknown source and has spread throughout the country and then later to other countries (Canada, Brazil and China). The source could have been from pigs from another country or from a different host species. SVV may have already entered Europe and we need to be vigilant for this emerging pig virus.

OUTBREAKS OF FOOT-AND-MOUTH DISEASE VIRUS IN THE MIDDLE EAST DURING 2015 AND 2016 DUE TO AN EXOTIC A/ASIA/G-VII (G-18) LINEAGE

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Introduction

Phylogenetic analyses of foot-and-mouth disease virus (FMDV) VP1 sequence data has made a major contribution to our understanding of the distribution and evolution of the viruses in different geographical regions. Serotype A is endemic in the Indian sub-continent and the A/ASIA/G-VII (aka G-18) lineage has been reported as the only type A lineage circulating in the country since 2001. FMD viruses collected from recent outbreaks in Saudi Arabia and Iran were identified as belonging to the A/ASIA/G-VII lineage.

Materials and methods

FMD viruses were collected from outbreaks of FMD in Saudi Arabia and Iran in 2015 and 2016, and the sequences of the genome region coding VP1 were obtained using standard methods. Phylogenetic analyses including sequence data from recent outbreaks in Turkey and Armenia as well as publically available sequences of the A/ASIA/G-VII lineage circulating in India were performed.

Results

Viruses from the outbreaks in Saudi Arabia were found to belong to the A/ASIA/G-VII (G-18) lineage and grouped together with sequences obtained from 2015 outbreaks in Turkey (F. Özyörük, personal communication, 2015) and Armenia (A. Mischenko and A. Scherbakov, personal communication, 2015) as well as a recent VP1 sequence from India (J. Biswal and B. Pattnaik, personal communication, 2015). Sequences obtained from individual farms in Saudi Arabia could be distinguished and revealed amino acid differences in antigenic site 1. Phylogenetic analyses indicated close evolutionary relationships between VP1 sequences from viruses collected in Iran, Turkey and Armenia. Genome sequences were also determined for a number of the Saudi Arabian and Iranian viruses.

Discussion

The A/ASIA/G-VII lineage has apparently spread from the Indian sub-continent, where it is normally endemic, to the Middle East. This stresses the importance of close and careful surveillance and development of tailored diagnostic methods as well as highlights the complexity of application of robust FMDV control measures.

FULL GENOME STUDY ON THE EVOLUTION OF THE FOOT-AND-MOUTH DISEASE VIRUS O/ME-SA/IND-2001d LINEAGE: EVIDENCE OF RECOMBINATION

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Introduction

The foot-and-mouth disease virus (FMDV) type O topotype MIDDLE EAST-SOUTH ASIA (ME-SA) occurs mainly in southern Asia, the Middle East and Southeast Asia. Since 2013, repeated introductions of viruses belonging to the O/ME-SA/Ind-2001d sub-lineage, endemic to the Indian subcontinent, have been recorded in the Middle East and North Africa. The outbreaks in North Africa, initially recorded in Libya in 2013, continued to spread westwards to Tunisia and Algeria and cases were reported in Morocco in 2015 (Bachanek-Bankowska et al., 2016) after 16 years of FMD absence. Recently, O/ME-SA/Ind-2001d was also detected in Sri Lanka, Laos and Vietnam.

Materials and methods

Representative viruses from recent field outbreaks due to the O/ME-SA/Ind-2001d sub-lineage in the Middle East, North Africa and Southeast Asia as well as viruses from historic outbreaks within the Indian sub-continent were selected for whole genome sequencing (WGS). Sequences were determined using an Illumina MiSeq according to an established protocol (Logan et al., 2014) and analysed using Bayesian evolutionary methods.

Results

Bayesian evolutionary analyses of WGS confirmed the origin of the O/ME-SA/Ind-2001d sub-lineage within the Indian sub-continent and estimated the time of its emergence in the early 2000s. Independent and phylogenetically unrelated introductions of viruses belonging to the O/ME-SA/Ind-2001d were confirmed to have taken place in the Middle East, North Africa and Southeast Asia. Genome recombination analyses also revealed an outbreak of due to a chimeric virus in Bahrain in 2015.

Discussion

These data highlight the important role of FMD viruses emerging from the Indian sub-continent on the epidemiology of FMD in the Middle East and Southeast Asia. WGS provides high resolution tool to investigate the origin of outbreaks FMDV outbreaks but virus genome recombination events can significantly impact analyses and lead to false interpretations. Genome sequence data exchange is required for better understanding of FMDV evolutionary events.

GENETIC CHARACTERIZATION OF FOOT-AND-MOUTH DISEASE VIRUSES IN BALOCHISTAN, PAKISTAN

Asad Ullah [1,2], Syed M. Jamal [3,], Aurore Romey [4], Kamila Gorna [4], Muhammad Azam Kakar [5], Ferhat Abbas1, Jamil Ahmad [2], Stephan Zientara [4], Labib Bakkali Kassimi [4]*

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Introduction

Various studies have been conducted on genetic diversity of FMDVs circulating in Pakistan. However, similar information on FMDV in Balochistan province of Pakistan is very scare. Balochistan is the largest province of the country that shares borders with Iran and Afghanistan. Thus geographical location of this Province has importance in both formal and informal trade of animals among Pakistan, Iran and Afghanistan and spread of transboundary animal diseases including FMD. This study reports characterization of foot-and-mouth disease virus (FMDV) in samples collected from Balochistan, Pakistan.

Materials and methods

Oral swab samples were collected from clinically suspected cases of FMD in Balochistan Province, Pakistan. These samples were subjected to virus isolation, antigen-ELISA and both pan-FMDV and serotype-specific real time RT-PCR assays. The complete VP1 coding region of the selected samples were sequenced. The sequence data generated were analysed with other sequences from GenBank and phylogenetic trees were constructed.

Results and discussion

FMDV was detected by pan-FMDV real time RT-PCR in 31 samples (epithelial and oral swabs) collected from clinical suspect cases. Of these, 29 samples were serotyped by serotype-specific real time RT-PCR assays and were confirmed by sequencing the VP1 coding region. Sixteen samples were found positive for serotype A and 8 for serotype Asia-1, whereas, 5 samples were found positive for both serotypes A and Asia-1. Two serotype A positive samples were found positive for two different strains of serotype A FMDV each. Phylogenetic analyses of serotype A FMDVs showed circulation of at least three different sub-lineages within the A-Iran05 lineage. These included two earlier reported sub-lineages, A-Iran05HER-10 and A-Iran05FAR-11 and a new sub-lineage, designated here as A-Iran05BAL-11. This shows that viruses belonging to the A-Iran05 lineage are continuously evolving in the region. Viruses belonging to the A-Iran05FAR-11 sub-lineage showed close identity with the viruses circulating in 2009 in Pakistan and Afghanistan. However, viruses belonging to the A-Iran05HER-10 detected in Balochistan, Pakistan showed close identity with the viruses circulating in Kyrgyzstan, Iran and Kazakhstan in

2011 and 2012, respectively, showing that viruses responsible for outbreak in these countries have a common origin. Serotype Asia-1 FMDVs reported in this study all belonged to the earlier reported Group-VII (Sindh-08), which is currently a dominant strain in the West EurAsian region. Detection of two different serotypes of FMDV or/and two different strains of the same serotype in one animal/ sample shows complexity in epidemiology of FMD.

THE EPIDEMIOLOGICAL TREND OF FMDV IN PAKISTAN IN PAST: A STEP FORWARD TO FUTURE PLANNING TO CONTROL FMD ENDEMIC SETTINGS OF PAKISTAN

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Introduction

Foot-and-mouth disease (FMD) is a viral disease that affects cloven-hoofed domestic and wild ungulates. The disease is caused by FMD virus (FMDV), is positive sense ssRNA virus of genus Aphthovirus and Picornaviridae family. The disease has serious impact upon food security, rural income and significant economic consequences for FMDV endemic countries. The basic part for the control strategy of viral infections lies in epidemiological tracing of virus transmission that can be achieved with the application of molecular and phylogenetic methods.

Materials and Methods

We have used VPI sequences of prevalent FMDV types previously submitted to GenBank from Pakistan to assess the phylogeny of the virus types separately by using appropriate bioinformatics software.

Results

We have found that FMDV type O has changed itself to very much from its appearance in 1994 and 1998 in Pakistan. Presently the virus which is prevalent in Pakistan is having a changed nucleotide sequence since 2005 to now. It is clearly observed that the circulating strains belong to PanAsia lineage of FMDV type O. The same viruses with minor changes are the cause of the disease each year. The same is true for FMDV type A, that presently circulating viruses are different from Iran and Indian lineages. FMDV type A are also emerging with minor nucleotide changes in the field over a period of time. Further there are also evidences of viral recombination when analyzed on the basis of whole genome sequences of available sequences of FMDV types O, A and Asia 1, that may change the scenario of disease in field in the days to come.

Discussion

Constant surveillance and looking of previous molecular epidemiology is the key to control FMD in endemic settings of Pakistan. This study adds to the knowledge-base of FMD epidemiology in Pakistan.

GENETIC CHARACTERIZATION OF THE 2016 FMD VIRUSES IN SOUTH KOREA

Plenary 10.15h - Poster

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Introduction

In January 2016, an outbreak of foot-and- mouth disease O serotypes occurred in South Korea. The outbreaks continued for a period of 79 days and affected 21 farms. To establish the possible relationship with the virusesv causing the December 2014- May 2015 epizootic in Korea, a genetic characterization and phylogenetic analysis was performed using 20 field isolates.

Materials and methods

Viral RNAs were extracted from clinical epithelium or vesicular fluid samples using a MagnaPure96 system (Roche). The VP1 region was amplified using a one-step RT-PCR kit (Qiagen). PCR products were purified with ExoSAP-IT (USB) and directly sequenced on an ABI 3130 genetic analyzer (Applied Biosystems) using a Big Dye Terminator Kit v3.1 (Applied Biosystems). Phylogenetic tree which was based on the complete VP1 nucleotide sequence (639bp) estimated using the neighbor-joining method in MEGA-6.

Results

The sequence data obtained for the VP1 gene indicated that the O type virus isolated belongs to the topotype Southeast Asia, genotype Mya-98. Although all isolates exhibited high homology to serotype O viruses which had occurred previously in 2014 and 2015, the phylogenetic tree classified into two different groups. It is possible that these groups evolved into two branches from a same ancestor.

Discussion

The outbreak of FMD O serotype in Korea in 2016 is considered to have originated from previously isolated viruses 2014 and 2015. These findings raises concerns regarding the recurrence of FMD, suggesting that the control efforts should focus primarily on reducing FMDV circulation around the outbreak area.

CURRENT STATE OF FOOT AND MOUTH DISEASE SURVEILLANCE IN SENEGAL

Pleuary 10.19h - Poster

Lo MM[1]; Seck Ismaila[2], Diop Mariame[1]; Sall Baba[2]; Seck MT[1] and Lo Mb[2]

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Introduction

Until year 2013 there was a clear gap in our knowledge concerning FMD virus strains circulating in Africa. This was particularly evident in western Africa region. According to EuFMD December 2013 report, there were only four serotypes found (O, A, SAT1 and SAT2) in Senegal. In light of addressing these gaps, it was critical to sample and characterise the FMD field serotypes causing outbreaks in western Africa. To address the issue, the Directorate of Veterinary Service of Senegal in collaboration with the National Veterinary Laboratory conducted a survey to estimate the prevalence of three diseases: Rift Valley Fever, Contagious Bovine Pleuropneumonia and Foot and Mouth Disease.

Materials and methods

In order to identify circulating serotypes in Senegal, 1735 bovine sera were collected from cattle in fourteen regions and analysed by kit FMDV Antigen detection Elisa serotyping of FMDV O, A and SAT2 (IZSLER: Brescia, Italy)

Results

473 samples were FMD group positive. From FMD group positive, 367 are known serotypes; 106 samples have not been serotyped yet. The prevalence for serotype O was 49 (47%), for A - 45 (24%) and for SAT2 - 19 (3%). Between regions, we found that the south is more infected by SAT2 whereas the central and western parts of country are more infected by O and A. Kedougou region, which shares the borderline with Guinea, was not infected with any serotype.

Discussion

More research is necessary to better understand molecular epidemiology of FMD and the impact of transhumance. We plan to serotype all FMD positive groups and identify other potential serotypes circulating via transboundary trade; test hypothesis that links spreading disease to susceptible animal movement; test viral population for genetic characterization and selection of vaccine candidates; develop tools allowing detection of circulating strains; and to propose control strategy at the regional level based on virology and epidemiology study results.

GENETIC CHARACTERIZATION OF FOOT AND MOUTH DISEASE VIRUS ISOLATED DURING CROSS SECTIONAL SURVEILLANCE STUDIES IN CATTLE FROM UGANDA DURING 2014-2015

Pleuary 10.23h - Poster

Zaheer Ahmed[1,4], Frank Mwiine[2], Julius Lutwaama [3], Kim VanderWaal[4], Andres Perez[4], Luis Rodriguezl, Elizabeth Rieder[1]

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Foot and Mouth Disease (FMD) virus causes an acute and the most contagious vesicular disease of livestock. The causative agent is a virus of the Aphthovirus genus in the Picornaviridae family. This disease in endemic in Uganda. This cross sectional study was designed to monitor and isolate FMDV serotype(s) circulating in the country divided into 4-regions namely Northern, Western, Central and Eastern. A total of 25 representative districts from all the regions of Uganda were selected for FMDV surveillance. A total of 1300 oral-pharyngeal fluid samples received at Plum Island Animal Disease Center were tested by rRTPCR and virus isolation (VI) using LFBKaVB6 cell line followed by PI sequencing to determine the FMDV serotypes. FMDV serotype O was isolated from Northern and Eastern regions while serotype SAT 2 was isolated from Western region of Uganda during samples collected in 2014. However, FMDV serotype SAT 1 (from the same region) and O were isolated in oral-pharyngeal fluid samples collected in 2015. The phylogenetic analysis of the PI sequences for the viruses isolated in relation to geographical distribution of FDMV serotypes isolated during 2014-2015 in Uganda will be discussed. This information could be useful for the improvement of disease control strategies and for vaccine strain selection for Uganda in the future.

EPIDEMIOLOGY OF FMD IN GEORGIA

Pleuary 10.27h - Poster

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Introduction

Foot and mouth disease (FMD) is endemic in Georgia where the last clinical outbreak occurred in 2002. Since 2002, no clinically confirmed cases have been reported. Results of FMD virus sero-surveys indicate that the virus is still circulating in Georgia. Georgia has several specific FMD control activities including: annual risk assessment; epidemiological/surveillance systems; lab diagnostics proficiency testing for laboratory workers; public awareness campaigns; and communication/cooperation

activities with public/private sector stakeholders. Also, twice yearly, all large and small ruminants throughout Georgia are vaccinated against FMD using a high potency trivalent (A-Iran05, A G-VII; O-PanAsia2; Asia1-Shamir) vaccine.

Materials and methods

In this study, we summarize the vaccination plan in 2015 through the first half of 2016. Via a joint OIE-FAO program, animals were vaccinated across Georgia using the approved State Program, as recommended by the European Commission for the Control of Foot-and-Mouth Disease (EuFMD) committee.

Results

In 2015, 2,438,051 animals (1,521,932 cattle, and 916,116 small ruminants) were vaccinated. In 2016, the Georgian livestock population susceptible to FMD was estimated by the NFA to be 1.2 million large cattle, 800,000 small ruminants, and 250,000 pigs. In 2016, using the existing vaccine with the addition of the vaccine for the A G VIII strain, 679,609 cattle and 729,637 small ruminants are being vaccinated.

Discussion

A significant portion of the Georgian GDP is based on the livestock trade. Both commercial animal husbandry and nomadic husbandry systems exist in Georgia. Seasonal pastures are generally located in areas bordering countries with unreliable FMD surveillance. In the event of a FMD outbreak, there is a significant threat of rapid spread among a large population of susceptible animals. As Georgia is a bridge between Asia and Europe, FMD outbreaks will have a negative impact on transit potential of Georgia and will pose a disease threat for EU countries.

INVESTIGATION OF FMD EPIDEMIC (OPANASIA2) IN CENTRAL REGION OF IRAN IN 2009

Plenary 10.31h - Poster

S.M. Baranil[*,1], K. Mirzaie[2], H. Mahravani[3], N. Rasouli Beirami[1],A.Bahonar4,H.Jafari[1],J.Emami[2]

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Introduction

It was reported FMD outbreaks due to Opanasia2 strain in Iran and in Laban dairy complex in central region of Iran for the first time in last months of 2009 in Qom province. This study was conducted to investigate new FMDV serotype clinical manifestations.

Materials and methods

A questionnaire was prepared and pretested and completed in all dairy farms and data were analysed. The chi-square test used for analysis of data.

Results

There were 127 dairy farms with independent management with 9245 cattle and 3214 milking cows with mean milk production of 29 liters/day. There was a regular vaccination program every 4 months with Merial tetravalent FMD vaccine and the last vaccination have been conducted 40 days before mentioned outbreaks.In spite of all preventive measures to control of outbreaks, all farms were affected by FMD. Different FMD clinical signs include 100% oral lesions, 88.1% myocarditis, 78.7% (CI95% 71.5-85.9) interdigital space lesions, 62.2% (CI95% 53.6-70.7) teat lesions and 51.9% (CI95% 43.1-60.7) abortion. FMD outbreaks period in dairy complex was 83 days and mean disease period in every farm was 29.7(CI95% 27.7-31.7) days. Mean morbidity rate was 77 %(CI95% 74.3-95.4) and the highest affected age group was 4-12 months. Mortality rate was 5.7 %(CI95% 4.9-6.5%). Mean daily milk drop was 9.6 litres/cow % in the period of disease.The cost of disinfectant per animal was 455$ and the cost of drugs per animal was 9.67$.

Discussion

There were two main points in this epidemic: First, in spite of all control and preventive measures all farms affected by FMD due to virulence of new FDMV serotype. Second, High prevalence of myocarditis showed good tropism of new FMDV serotype to myocardium. High morbidity and mortality in 4-12 months calves showed high sensitivity of this age group due to myocarditis.

ANTIGENIC AND GENETIC CHARACTERIZATION OF FOOT-AND-MOUTH DISEASE VIRUS SEROTYPE O CIRCULATING IN SOUTH-EAST ASIA

Plenary 10.35h - Poster

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Introduction

Foot-and-mouth disease (FMD) is one of the economically important livestock diseases with a global distribution. The disease is endemic in Asian continent including South East Asia. Although three of the seven known FMDV serotypes (A, O, and Asia 1) are circulating in South East Asia (SEA) most of the outbreaks are caused by serotype O. Although vaccination is mainly considered to control the disease, vaccine strains used in the region are either old or do not match. Here we report the genetic and antigenic characterization of serotype O FMD viruses circulating in SEA with an aim to recommend

suitable vaccine strain for use in the region.

Materials and methods

The vaccine matching was carried out by 2D virus neutralisation test (VNT) using five different bovine post-vaccinal sera including four current vaccine strains and one putative vaccine strain and 90 FMD serotype O viruses circulating in eleven SEA countries and results represented as antigenic relationship (r1) values. In addition, full capsid sequence data was generated for all the viruses to investigate the genetic basis of antigenic variation in the isolates.

Results

Phylogenetic analysis carried out using the capsid nucleotide sequence indicated three different topotypes (ME-SA, SEA and Cathay) of FMD serotype O viruses circulating in SEA. Preliminary vaccine matching results indicate PanAsai-2 vaccine strains to be broadly protective with all the three topotypes SEA serotype O FMD viruses.

Discussion

The serology and capsid sequence data will now be analysed further to predict the vaccine match. This may lead to identification of sequence motifs contributing to the loss of cross-reactivity with the antisera that can be tested in a reverse genetics system to study their impact on the antigenicity of the virus.

DETECTION AND MOLECULAR CHARACTERIZATION OF FOOT AND MOUTH DISEASE VIRUSES FROM OUTBREAKS IN NORTHERN NIGERIA 2013-2015

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Introduction

Data on the circulating foot and mouth disease (FMD) virus (FMDV) serotypes/strains in Nigeria is scarce, due to lack of diagnostic capacity and under-reporting of FMD cases. Resulting, targeted control measures for FMD have not been implemented.

Materials and methods

In 2013-2015 FMD outbreaks from four Northern Nigerian States reported to the National Veterinary Research Institute (NVRI), Nigeria were investigated. Blood and epithelial samples were collected from clinically affected cattle and the single affected sheep and blood was collected from in-contact sheep. In the framework of the OIE Twinning laboratory project between the NVRI (Nigeria) and CODA-CERVA (Belgium) samples were shipped to Belgium for laboratory analysis by NVRI staff during technical and scientific trainings with the objective of capacity building for the FMD diagnosis at NVRI.

Results

Seventy-three % of cattle (131/178) and 64% (47/73) of sheep sera were antibody-positive against FMDV NSPs. Using solid phase competition Elisa on NSP-antibody positive sera, predominantly antibodies against FMDV serotypes O (C: 101/127, S: 13/26) , A (C: 43/127, S: 8/26) and SAT2 (C: 66/127, S: 14/26) were detected. Using rRT-PCR, FMDV genome was detected in 97.3% (73/75) of the epithelial tissues and from 29/75 samples FMDV could be isolated. Isolates belonged to serotypes O, A and SAT2. Phylogenetic analysis of the virus isolates revealed that two serotype O topotypes, East Africa-3 (EA-3) and West Africa (WA), were circulating, as well as FMDV strains belonging to the Africa genotype (G-IV) of serotype A and FMDV SAT2 topotype VII strains.

Discussion

This study provides evidence of co-occurrence of FMDV serotypes and topotypes in West, Central, East and North Africa and this has implication for control. The findings may help fill the knowledge gap of FMDV dynamics in Nigeria and West Africa sub-region to support local and regional control plans.

ANTIGENIC AND EVOLUTIONARY ANALYSIS OF FMD VIRUSES FROM THE 2014-2015 OUTBREAKS IN THE MAGHREB REGION

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Introduction

FMD outbreaks were reported in the Maghreb region from April 2014 to November 2015, after 15 years of disease absence, and FMDV isolates collected to date were shown to belong to the Ind-2001d lineage within the Middle East-South Asia (ME-SA) topotype. The objective of the present work was to extend the study of genomic and antigenic features to more isolates from this region, in order to provide more insights into virus evolution and epidemiological relationships between outbreaks.

Materials and methods

FMD Viruses from Libya (n. 7), Tunisia (n. 12), Algeria (n. 12) and Morocco (n. 1) were included in the study. When possible, the full genome sequences (FGS) were produced by MiSeq instrument (Illumina, USA). A Bayesian evolutionary analysis, either based on VP1 and on FGS, was performed with BEAST software. A panel Monoclonal Antibodies (MAbs) was used in order to evaluate the antigenic profile of the isolates.

Results and Discussion

A nearly complete genome sequence of 8076 nucleotides in length was obtained from available isolates.

Phylogenetic analyses indicate that a unique introduction of FMD virus occurred in Libya in 2013, from which all the viruses later detected in the small Maghreb have evolved. In fact, all the Maghreb isolates were shown to derive from a unique putative common ancestor, estimated to be present since beginning of 2014. The Tunisian isolates evolved in three main branches, geographically consistent with animal movements in the country. Two different introductions from Tunisia to Algeria have likely occurred, in 2014 and 2015 respectively; the Moroccan isolate derived from viruses of the 2015 Algerian outbreaks, with which it shares a common ancestor.

Finally, the antigenic profile obtained with MAbs showed limited variation among isolates, restricted to neutralizing MAbs, and consistent with the low number of nonsynonymous mutations observed.

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CHARACTERIZATION OF FOOT-AND-MOUTH DISEASE VIRUSES COLLECTED IN NIGERIA BETWEEN 2007 AND 2014: EVIDENCE FOR EPIDEMIOLOGICAL LINKS BETWEEN WEST AND EAST AFRICA

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Introduction

Foot-and-mouth disease (FMD) is an endemic transboundary animal disease that affects livestock health across most of sub-Saharan Africa. Since the first official report of FMD in Nigeria in 1924, serotypes O, A, SAT 1 and SAT 2 have been documented within the country (Fasina et al, 20013; Lazarus et al., 2012; WRLFMD 2010; WRLFMD 2014)). Molecular epidemiology has been used to trace the origin of FMD outbreaks in the case of animal movement, inter-species transmissions and trans-continental introductions (Samuel et al., 1999; Sangaré et al. 2004). Therefore, the aim of this study was to characterize the FMD viruses circulating in Nigeria from 2007-2014 in order to understand the epidemiology in the region and to assist policy makers with decisions for effective disease control.

Materials and methods

Epithelial and oesophageal/pharyngeal (probang) samples were collected from 104 suspect cases of FMD in cattle between 2007 and 2014. Both tissue supernatant and probang samples were used for tissue culture isolation (ZZ-R 127). Total RNA was extracted from the cell culture isolates using RNeasy® kit (Qiagen Ltd, Crawley, West Sussex, UK). The VP1 region of the FMDV genome was amplified using a one-step RT-PCR kit (Qiagen), as described previously (Knowles et al., 2009).

Results

In this study, 104 suspect FMDV samples, collected from 14 different Nigerian states, were analysed for the detection and typing of FMDV. FMDV genome was detected and serotypes were determined for 45 epithelium samples (yielding 47 unique sequences when accounting for mixed infections) from eight different states

Discussion

VP1 sequences were used to establish the relationships among the virus serotypes isolated in Nigeria. However, the 2009 and 2011 isolates were more closely related to each other, than the 2007 isolate. These data support two separate introductions of serotype O/EA-3 viruses into Nigeria, as well as the persistence of this topotype in country from 2009-2011.

SERO-EPIDEMIOLOGICAL STUDY OF FMD IN LIVESTOCK IN WEST LIBYA

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Introduction

In Libya, FMD is endemic in many parts of the country. This study aimed to establish an accurate comprehension of the epidemiology of FMD, and the outcome might be employed in the surveillance and the development of a risk-based strategy plan (RBSP) of FMD, to help Libya to progress to PCP-FMD stage 2.

Methods

A cross-sectional sero-survey including a questionnaire on putative risk factors was undertaken for small (SR) and large ruminants (LR) in West Libya (Zliten and Tripoli cities). Ten percent of small ruminants' herds with 100 or more animals were randomly selected, sampling 48 animals per herd from different age groups (< 1 year, 1 year-2 year, and > 2 year). Ten percent of cattle herds were selected randomly, sampling a maximum of 5 animals. A total of 1590 SR (34 herds) and 435 LR (87 herds) were tested for the present of Non-Structural Proteins for FMD using a PrioCHECK® FMDV NS. Several risk factors at animal and herd level were analysed using logistic and poisson regression models.

Results

Individual animal prevalence was 37% and 16%, herd prevalence was 97% and 71% and the median within-herd prevalence was 10% and 20% for SR and LR respectively. Statistically-significant factors related to testing positive for NSP Abs were 'level of biosecurity', 'sales' and 'manure treatment' for SR and 'city' for LR.

Discussion

The results of this survey underlined the endemicity of FMD virus circulation in livestock high-density regions of Libya and supported the development of the RBSP.

EPIDEMIOLOGICAL PARAMETERS FROM TRANSMISSION EXPERIMENTS: NEW METHODS FOR OLD DATA

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Introduction

Small-scale challenge experiments are widely used to estimate key epidemiological parameters for foot-and-mouth disease virus (FMDV). Interpreting the results of these experiments is not straightforward, however, and often requires strong assumptions to be made about when animals become infected and when they are infectious.

Materials and methods

We have developed a suite of Bayesian methods that allow us to avoid the need to make assumptions when analysing the results of transmission experiments. In particular, these methods infer the times at which animals become infected rather than assuming when they do. Furthermore, the methods allow us to determine directly when animals are infectious and how infectious they are rather than relying on proxy measures of infectiousness. We apply the methods to data from transmission experiments for FMDV in sheep, pigs and cattle.

Results

Using our new methods we obtain similar estimates for the transmission of FMDV in sheep, though we are also able to show that the latent period is different for inoculated and in-contact lambs. Rapid spread to all contact animals means that the old methods perform poorly when analysing the transmission of FMDV in pigs, but our new methods allow us to estimate parameters. Finally, we are able to infer directly when cattle are infectious using challenge data. Comparison with virus isolation data shows that viral titres in nasal fluid are a robust proxy for infectiousness, but viral titres in blood or in oesophageal-pharyngeal fluid are not.

Discussion

Bayesian methods facilitate the analysis of the outcome of transmission experiments while making minimal assumptions. As well as providing estimates for key epidemiological parameters the methods allow insights into transmission processes. In addition, they quantify the uncertainty in the estimates in a manner suitable for incorporating in regional scale models for spread and control.

COMPLETE GENOME SEQUENCES OF THREE AFRICAN FOOT-AND-MOUTH DISEASE VIRUSES FROM CLINICAL SAMPLES ISOLATED IN 2009 AND 2010

Plenary 12.15h - Poster

Steven Van Borm[1], Toon Rosseel[1,] Andy Haegeman[2], Mpolokang Elliot Fana[3], Latoa Seoke[3], Joseph Hyera[3], George Matlho[3], Frank Vandenbusschel, Kris De Clercq[2]*

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Introduction

To evaluate the feasibility of complete genome sequencing from clinical samples using unbiased RNA sequencing methods, three FMDV strongly positive epithelial samples from symptomatic cattle from Zambia and Namibia were selected using real-time RT-PCR.

Materials and methods

The original clinical samples were homogenized in PBS, pretreated by 0.45 M size selective filtration and nuclease, and RNA was extracted. cDNA was synthesized using Super-Script III reverse transcriptase and random hexamer primers. Sequencing libraries were prepared using 1 ng of cDNA and the Nextera XT kit (Illumina), quantified and fragment length distribution was verified using the Bioanalyzer with the high-sensitivity DNA kit. Sequencing was performed using a MiSeq reagent kit version 3 with 2 X 300-bp paired-end sequencing. Twenty-three libraries were multiplexed using standard Illumina indexing primers. The quality of the sequences was checked with FastQC. Stretches containing unidentified nucleotides were trimmed using Cutadapt prior to quality trimming using Sickle (Q score, <30; length, <50 bp). De novo assembly was performed using Newbler.

Results

The complete genome sequences of SAT2/ZAM18/2009 and O/ZAM14/2010 were obtained, with average coverages of 2,151X and 732X, respectively. These FMDV genomes contain a single open reading frame of 7,008 (SAT2/ZAM18/2009) and 6,999 nucleotides (O/ZAM14/2010) encoding a polypeptide precursor protein, and they share high nucleotide homology with AF540910 and HM191257, respectively. The contig representing SAT1/NAM01/2010 contains a single 7,020-nt ORF (polypeptide precursor protein) and shares a high nucleotide homology with AY593842. As only a limited number of FMDV reads were available for the latter sample, two gaps were closed using PCR amplification and Sanger sequencing, while the average coverage was <10X.

Discussion

These data demonstrate the feasibility of direct sequencing of complete FMDV coding sequences from samples from symptomatic animals (CT range of 14.63 to 16.18) using an unbiased cDNA sequencing approach. However, targeted approaches using FMDV-specific cDNA synthesis primers or PCR amplification may result in a better sensitivity for whole-genome sequencing.

SURVEILLANCE OF FOOT AND MOUTH DISEASE (FMD) IN GEORGIA

Plenary 12.19h - Poster

Marina Donduashvili[,1], Ketevan Goginashvili[1], Tamar Tigilauri[1], Ana Gulbani[1], Lali Cheishvili[1], Marina Saponjian[1]*

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Introduction

Foot and Mouth Disease (FMD) is an acute contagious disease affecting animals, which poses serious economic impacts. It is an important transboundary disease, therefore surveillance is important for Georgia and neighboring countries; especially those involved in animal import/export.

The international community is attempting to control/eradicate FMD through the FAO Progressive Control Pathway (PCP). Georgia is a stakeholder in this program and surveillance is part of the State program; disease free status is projected in Georgia by 2020. Laboratory testing at the Laboratory for the Ministry of Agriculture (LMA) is essential due to recent increases in animal export from Georgia to Asian countries. This study reviews data from FMD testing at LMA from 2014-2016.

Materials and methods

Testing for FMD virus at LMA follows the World Organization for Animal Health algorithm, using serological testing, antibody serotyping (liquid phase blocking ELISA), and molecular biology techniques to identify viral nucleic acids.

Results

Of the 1,823 samples tested in 2014, 11.5% were positive for anti-FMD virus antibodies; of the 10,769 samples tested in 2015, 360 (3.3%) were positive. From January–June 2016, a total of 2,040 samples were collected at regional laboratories across Georgia; 67 (3.3%) were positive, testing is ongoing. The Veterinary Department of the National Food Agency will continue testing throughout the year.

Discussion

Serological results show the presence of anti-FMD virus antibodies, which supports that FMD is circulating in Georgia, although clinical and tissue samples were not provided for direct virus identification by PCR. Data suggests a downward trend for the incidence of FMD, however, the region-to-region analysis suggests that the overall prevalence of FMD remains the same from 2012-2016. Continuing surveillance followed by eradication of positive animals, as well as the enrollment of Georgia in PCP activities, is important due to increases in the export of animals from Georgia.

THE ROLE OF SEASONAL MOVEMENT OF ANIMALS IN FMD CONTROL IN AZERBAIJAN

Plenary 12.23h - Poster

T. Aliyeva[1], K.Asadov[2], J.Aliyev[2]

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Introduction

Azerbaijan, due to geographical location and type of animal husbandry is an area of high risk of introduction and spreading of FMD. Risk based analysis is identified seasonal animal movement as risk hotspots, which can play important role in virus circulation.

Objectives

The objective of the study was to indicate role of seasonal animal movement in circulation of FMD virus in country.

Materials and methods

Detailed analysis of animals seasonal movement were carried out. Blood samples have been tested (NSP) in districts, closed to migration routes.

Results

Distance pasture rearing farm management is typical for Azerbaijan. Seasonal pastures are high risk zones, because of large density of susceptible animals. Animals migration to summer pastures starts at the end of April, and in October move back to winter pastures. Most of animals are vaccinated before the migration, but due to the lack of strict control during migration, there is the risk of spreading the virus, since the mixing of animals from areas with different immune status. Some pastures are close to Georgia and Iran, in several places there is no border fences, and animals from both sides share the pastures. According to serosurveys results, great number of villages with NSP high level are close to seasonal pastures and migration routes. Using the data obtained, there were identified animal routes, and mapped.

Discussion

Animals seasonal movement plays important role in circulation of FMD virus in country. All seasonal migrating herds should be clinically checked prior and during the migration. Checkpoints, vaccination of animals (at least 3 weeks before the start of migration) in villages, located close to migration routes is crucial. Serosurveys at the pastures is necessary.

HORIZONTAL TRANSMISSIBILITY OF THE FOOT-AND-MOUTH DISEASE VIRUS O/JPN/2010 AMONG DIFFERENT SPECIES OF ANIMALS

Pleuary 12.27h - Poster

K. Fukai[1], T. Nishi[1], N. Shimada[1], K. Morioka[1], M. Yamada[1], K. Yoshida[1], R. Kitano[1], R. Yamazoe[1], M. Yamakawa[1]
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Introduction

Horizontal transmissibility of the foot-and-mouth disease virus (FMDV) O/JPN/2010, which was isolated in the 2010 epidemic in Japan, has been analyzed among the same species of animals such as cows, goats and pigs in previous studies. The O/JPN/2010 transmitted horizontally to all contact animals. In this study, horizontal transmissibility of the O/JPN/2010 among different species of animals was analyzed in order to elucidate transmitted situations of FMDV in flocks and regions that different species of animals are raised together.

Materials and methods

Four cows, four goats and four pigs were inoculated via an intradermal route with 106 TCID50¬ (measured in the IB-RS-2 cells) of the O/JPN/2010. Each animal was then raised individually with different species of animals in different cubicles. Clinical signs, virus excretion and antibody responses of the animals were observed for approximately 2 weeks.

Results

All the animals inoculated with the O/JPN/2010 were infected and excreted viruses into salivary and nasal discharge. Vesicular lesions were observed in the inoculated cows; however, apparent lesions were not observed in the inoculated goats. Although 3 of 4 goats raised with the inoculated cows and 3 of 4 pigs raised with the inoculated cows were infected, the former were infected earlier than the latter. One of 2 contact cows raised with the inoculated goats was infected; however, all 4 contact pigs were not infected. Experimental infections using inoculated pigs and different species of animals raised with the inoculated pigs are ongoing.

Discussion

Horizontal transmission of the O/JPN/2010 occurred completely among the same species of animals; however, the transmission did not occur completely among different species of animals. The O/JPN/2010 could transmit easier among the same species of animals than among different species of animals. Appearance of vesicular lesions may be involved in horizontal transmissibility of the O/JPN/2010 in animals

MOLECULAR EPIDEMIOLOGY OF FMD SUDANESE ISOLATES IN 2012

Plenary 12.31h - Poster

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Introduction

In this study molecular epidemiology have been investigated for Foot and mouth disease virus, three serotypes circulating in Sudan which include serotypes O, A and SAT2.

Material and methods

11 suspected samples were collected during 2009-2011 from different outbreaks in Sudan were tested by laboratory assays virus isolation, antigen detection ELISA, real time PCR, RT PCR and VP1 sequencing in WRL Pirbright.

Results

5 of this samples were typed using Ag ELISA as serptype A while the reminder of the viruses comprised either serotype O (n=5) and SAT2 (n=1).

Phylogenatic analysis have been carried out for the three serotypes, 5 serotype A show big identity with the Sudanese archive isolates with 99% identity, 97.97% similarity with Egyptian isolates and 94% with Eritrian isolates. For type O Sequences showed that the Sudanses isolates were all classified as belonging to the East Africa -3(EA-3) topotype .

4 of the samples with exception of a single isolate from Mwelain Omdurman in 3/3/2011 is more related to the Eritrian isolates with identity 95,62% .

The phylogenetic analysis of Sudanses SAT2 is classify within SAT2 topotype and genotype ALX-12.

SAT2/EGY/2012 has nucleotide sequences identity with 95.83% and after that come SAT2/SAU from Saudia Arabia with 92% identity. Some viruses from west africa (Lybia, Senigal and Camiron) have a relation similarity respectivily 90.12, 89.97 and 89.81% identity.

Discussion

The results obtain from the phylogentic analysis give us clear picture about the circulating viruses inside the Sudan and the viruses in neighbor countries. The similarity between the viruses could be due to the trade between borders or smuggling also could be a reason because there will not be a quarantine mearturments if the animals were infected. The movement and migration of Numads also could be a threat and the can spread the disease between the countries in East Africa.

POSSIBLE ROLE OF CAMEL AS A RESERVOIR FOR FOOT AND MOUTH VIRUS: FIELD SEROLOGIC COMPARISON WITH OTHER LIVESTOCK SPECIES

Pleuary 12.35h - Poster

*S.M. Barani[*1], K. Mirzaie[2], H. Mahravani[3], N. Rasouli Beirami[1],J.M.C.Bartels4 ,R.Hasanzade[5],M.Torabigodarzi[6],H. Jafari[1],J.Emami[2]*

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Introduction

Camels may play a possible role in the transmission of FMDV, and may carry FMDV over significant long distances including crossing the border to neighboring countries. The aim of this study to investigate the serological evidence of natural exposure of camels to FMDV, and evaluate the possible role of camels as reservoirs for this virus, in comparison with cows, sheep, and goats.

Materials and methods

All sixteen villages which had camel population were included in this study and 10% of the animal within each villages were chosen to be sampled. The blood samples were taken randomly. The ELISA (IZSLER) test was carried out to assess the presence of FMDV.

Results

In this study, 827 animals (405, 194, 228 camels, cattle and sheep and goat respectively) were sampled. Out of 4000 camels, 405 camels were randomly selected. Furthermore, 228 sheep and goat in contact with camel herds were sampled. The sampled sheep and goat flocks were from 15 herds and 11 villages. Out of 405 tested camels, only 10 camels were identified to have significant detectable positive non-structural antibodies (NSP) and out of 16 villages, 5 villages were seropositive and the prevalence of seropositive against FMD based on villages was determined as 31.25% (95% CI: 8.54-53.96). Comparison of the prevalence of non-structural antibodies in camel (2.47%; 95% CI: 0.96-3.98), sheep and goats (31.14%; 95%CI: 25.13-37.15), and cattle populations (71.13%; 95%CI: 64.76-77.51), indicates that prevalence in sheep and goats population is about 13 times and in cattle population 29 times more than the prevalence in camel herds. No statistically significant relationship due to FMD occurrences among them were found.

PRIORITISATION OF RESOURCES FOR EARLY DETECTION OF DISEASE INCURSIONS

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Early detection of incursions of exotic disease is one of the key purposes of surveillance. Other areas of surveillance, such as demonstration of freedom or measuring the prevalence of disease have been extensively studied to produce quantitative guidelines relating to sample size, frequency etc., but much less guidance is available to support resource allocation decisions related to early detection surveillance.

Following the FMD outbreaks in Tunisia, Algeria and Morocco in 2014 and 2015, an approach was required to support decisions on resource allocation. A new framework was developed based on the consideration of three factors: the probability of incursion of disease, the probability of failure to rapidly detect disease after an incursion, and the consequences of the incursion, measured in terms of secondary outbreaks.

A theoretical economic model was developed, based on these inputs, to inform national-level decisions about the level of total investment in disease prevention. However some of the parameters are very difficult to estimate, so this higher level model may be of limited value. A second model was developed to quantify risk for different population compartments and regions. Inputs for this simple model can be relatively easily estimated to provide clear guidance on the prioritisation of expenditure of available budget in different sectors.

PREDICTED IMPROVED CONTROL OF FOOT-AND-MOUTH DISEASE TRANSMISSION BETWEEN FARMS BY USING PRECLINICAL DETECTION

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Introduction

During an outbreak of foot and mouth disease (FMD) rapid detection and removal of infected animals is important to successfully control further spread. This study examines the potential for preclinical detection of infected animals during reactive surveillance to stop between herd transmission.

Materials and methods

A series of pair-transmission experiments were performed using FMDV O UKG.34/2001 to infect cattle. Following a contact period with inoculated calves, contact calves were removed to clean rooms and monitored for infection and disease progression for 8 days.

Daily nasal, saliva, probang, and blood samples (clinical samples) as well as air samples measuring ambient and directly exhaled air were taken. All samples were tested for viral RNA using qPCR. The degree of virus shedding was evaluated and the diagnostic sensitivity (Se) of the different samples during the preclinical phase of infection was quantified. The Se values were used in a mathematical model to evaluate the impact of preclinical surveillance on controlling between herd transmission. This effect was measured as reduction in the between-herd reproduction ratio (Rh) and, in particular, whether it was below one.

Results

With the exception of serum, the Se of all clinical samples was higher than 85%. A lower Se was obtained for air samples. Results from the mathematical model suggested that using any clinical sample for preclinical surveillance reduced Rh to less than one when sampling 10 animals per farm per week. For the air samples daily (ambient) sampling was required to obtain Rh<1.

Discussion

The study demonstrates that FMD can be diagnosed with high Se before clinical signs are observed in infected cattle. The results suggest that preclinical surveillance could reduce Rh sufficiently to control transmission between farms. Preclinical surveillance represents a suitable control alternative during epidemics, potentially minimising the need for pre-emptive culling of uninfected herds.

DEFINING THE SPATIO-TEMPORAL SCALE OF FOOT-AND-MOUTH DISEASE VIRUS LINEAGES EMERGENCE IN THE MIDDLE EAST REGION

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Introduction

Studying the genetic signals that underpin the historical emergence, dispersal and expansion of foot-and-mouth disease virus (FMDV) populations could help in understanding the principles and processes that drives the evolutionary fitness and geographical structure of FMDV lineages in endemic systems, as well as the virus adaptation and virulence evolution in response to resistance variability among host populations.

Materials and Methods

A total of 2509 FMDV VP1 coding sequences belonging to serotype O PanAsia2 lineage (n=1185), serotype A Iran-05 lineage (n=771) and serotype Asia-1 (n=553) were obtained from the WRLFMD database. Middle East region-wide analyses were performed using Bayesian phylogeographic methods in order to reconstruct, for each FMDV lineage, i) the transmission events in space-time, ii) the geographical structure of the phylogenetic clusters and iii) the dynamics of the viral populations.

Results

Evolutionary trajectories were reconstructed for each FMDV lineages, where different phylogenetic clusters were defined across time and space. At the geographical level, O/PanAsia2 and A/Iran-05 lineages were found to diffuse within the very same regional extent. Genetic diversity estimates for each serotype revealed cyclical dynamics which might reflect periodicity of FMDV transmission within the Middle East and, although multiple lineages belonging to different serotypes can be detected within the same time-period, single FMDV lineages most often predominate at time intervals.

Discussion

The circulation of multiple serotype and/or genotype within the Middle East could be a result of complex competition dynamics of co-existing FMDV lineages acting at the same host population level. This might lead to an evolutionary geographical structure and cyclical phases of co-evolving FMDV lineages. Understanding the evolutionary drives of FMD diffusion at geographical and temporal scales might be translated into effective intervention and prevention strategies, in order to support the Middle East regional progression towards FMD control in line with global efforts.

COMBINING LIVESTOCK MOVEMENT PATHWAYS WITH PHYLOGENETICS TO HELP UNDERSTAND THE SPREAD OF FMD IN SOUTH-EAST ASIA

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Introduction

Phylogenetic inference from molecular sequences of isolated viruses can make a significant contribution to investigating the evolutionary and spatial pathways underlying FMD epidemics. Matching data on livestock movement with molecular epidemiology can enhance our understanding when reconstructing the spread of the virus between geographical regions, which is important for the development of effective FMD control strategies.

Materials and Methods

The phylogenetic analysis was performed with the VP1 sequences of 59 field isolates of FMD virus serotype O and 74 field isolates of serotype A, collected in South-East Asia from 2012 to 2015. The QGIS 2.12 was used to depict spatial distribution of isolates from the same phylogenetic cluster.

Results

The FMD serotype O viruses were grouped in eight clusters, and FMD serotype A viruses were grouped in six clusters. Viruses of the same cluster can often be found in various neighboring countries. For example, isolates of O/SEA/Myanmar98 lineage, cluster 1, were first detected in Thailand during the first half of 2014, with subsequent detections in Lao PDR and Cambodia in the following 6 months and more recently in Viet Nam in 2015. While differences between the effectiveness of disease detection and reporting among countries may explain these observed trends, the virus spread patterns are consistent with the cattle movement pathways in the region. OIE animal movement studies have shown that large numbers of cattle and buffalo are passing through Thailand every year to cross Lao PDR or Cambodia, destined for high-value markets in Viet Nam and China.

Discussions

Our study demonstrates good agreement between the pathways of FMD virus dissemination and animal movements in South-East Asia, pointing to animal movements as a significant risk parameter. This fact reinforces the need for strong official controls on cross-border animal movements, as well as for enhancing multinational cooperative measures on FMD control.

SERO-PREVALENCE AND RISK FACTORS FOR FOOT AND MOUTH DISEASE AMONG WILD AND DOMESTIC UNGULATES IN ISRAEL

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Introduction

Foot and mouth disease (FMD) occurs in Israel almost every other year despite routine vaccination of livestock. The incidence of FMD varies among different livestock and management systems. This serological study was aimed to characterize the driving factors of FMD dynamics in Israel.

Materials and methods

The study included about 5000 sera collected from dairy, beef, and feedlot cattle, sheep and goats, as well as 207 samples from wild ungulates during the last two decades. Sera were examined by a commercial ELISA kit for the detection of antibodies against non-structural proteins (NSP). NSP Sero-prevalence was calculated for each livestock sector and wildlife species and risk factors for infection were examined.

Results

Sero-prevalence in beef, dairy, and feedlot cattle, and small ruminants was 13.2% (CI95% = 10.8 - 15.8%), 2.7% (CI95% = 2 - 3.6%), 0.4% (CI95% = 0 - 2.2%) and 3.7% (CI95% = 3.0% -4.5%), respectively. In beef cattle high sero-prevalence was associated with age and the occurrence of previous outbreaks in the herd, while in dairy cattle, proximity to other outbreaks and to the border were significant risk factors. In small ruminants sero-positive samples were scattered over the entire country. Proximity to an FMD outbreak in cattle was a significant risk factor, while grazing and large herds had a lower risk for infection. Sero-prevalence among wild animals was 7.7% (4.4-12.1%). However, almost all of the positive samples were obtained from wild boars in one year (2007).

Discussion

FMD is endemic in small ruminants in Israel, but their importance in the disease spread is probably negligible, especially due to the current vaccination regimen of livestock. Higher attention should be directed to beef cattle. Increasing intensity of surveillance and vaccination of beef cattle (primarily in high risk zones like the Golan Heights) may be beneficial for reducing FMD incidence.

TRANSBOUNDARY HIGH RISK AREA COORDINATED EPIDEMIO-SURVEILLANCE PROGRAMME (THRACE) IN BULGARIA, GREECE AND TURKEY

Plenary 10.15h - Poster

A. Skrypnyk[1], M. Masiulis[1], A. Zdravkova[1], S. Khomenko[2], T. Alexandrov[3], A. Bulut[4], S.-E. Antoniou[5], A.-M. Baka[1], C. Fouki[1], F. Rosso[1], K. Sumption[1]

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Introduction

The Thrace region of Bulgaria, Greece, and Turkey is considered a high-risk area for the introduction of FMD and other TADs into Europe. By coordinating activities and taking a risk-based approach to surveillance, greater confidence can be achieved in the FMD-free status of the region. THRACE programme aimed to provide continuous evidence of FMD freedom and detect possible incursion of FMD and other TADs at early stage.

Materials and methods

A co-ordination framework established between Bulgaria, Greece, and Turkey to implement the programme, share the results of activities and facilitate communication and a risk-based surveillance designed and implemented by local veterinary consultants. Calculation of FMD confidence of freedom is based on deterministic model, which uses quantitative analysis of risk-based surveillance, combination of evidence from surveillance activities and Bayesian accumulation of historical surveillance evidence.

Results

The epidemiological data was collected from three countries and entered into database developed for THRACE using Google Fusion software which provides geographical location. It allows creating "heat maps" showing density of susceptible animals population by species and epi-units visited most frequently. Database includes possibilities for new infections (TADs) to be entered and used for models to calculate the confidence of freedom.

Discussion

THRACE programme showed high efficiency of co-ordinated surveillance network in maintaining the confidence on FMD freedom in Thrace region. Based on combination of surveillance activities, the targeted risk-based surveillance resulted in FMD confidence of freedom for over 33 months with the 99% probability (as of 1st cycle 2016). Google Fusion database is fast, user friendly, robust and permits online update of surveillance data. It is powerful tool to combine capabilities of database with mapping of surveillance activities and can be effectively used for visualization of work conducted by field consultants, thus allowing timely modification of the surveillance strategy and activities.

FIRST REPORT OF FOOT-AND-MOUTH DISEASE VIRUS (FMDV) SEROTYPES O ISOLATION IN PUPPIES IN IRAN

Pleuary 14.59h - Poster

D. Abdollahi[1], R. Hassanzedeh[2], M. Hosseini[3], H. R. Parishni4, D. Jahanpeyma[1]

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Foot-and-Mouth-Disease (FMD) is one of the most important animal diseases in the regions that outbreaks mostly occurring in cattle & sheep population. However, during 2015-2016 outbreaks in Iran, there were reports of dead puppies in two Epidemiological Units with FMD outbreaks in sheep and Goat population. Further investigation show that Studies show that the puppies have been fed from heart of FMDV affected lambs.

Hart samples collected from one dead poppy and two lambs and sent to CVL in Tehran. All samples were positive in PCR, ELISA for FMDV serotype O. The samples submitted to WRL and FMDV serotype O isolation confirmed by WRL in puppy sample. Further investigation ongoing in WRL.

This appears to be the first report of evidence of FMDV isolation in dog in Iran and the regions.

Key words: Puppy, ELISA, foot-and-mouth-disease (FMD)

EVALUATION OF ROUTINE VACCINATION AGAINST FMDV SEROTYPE A LINEAGE G-VII ON LARGE SCALE DAIRY FARMS IN SAUDI ARABIA

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Introduction

A new serotype A lineage (A/ASIA/G-VII) has recently emerged from the Indian sub-continent causing outbreaks in Saudi Arabia, Turkey, Armenia and Iran. The results of in vitro vaccine matching have demonstrated relatively poor antigenic match to commonly used strains. There is some evidence that a polyvalent vaccine containing A Saudi-95 may provide protection although large-scale farms in Saudi Arabia routinely vaccinating with this strain have reported outbreaks.

Materials and methods

This study investigated outbreaks of A/ASIA/G-VII on four large-scale dairy farms in Saudi Arabia. Data were extracted from farm records and FMD incidence was analysed by affected group and putative risk factors. Additionally, serum samples were taken from a related farm using an identical vaccination schedule with no history of FMD. Samples were tested for NSP antibody and neutralising titres to the homologous vaccine strains and a heterologous A/ASIA/G-VII strain from an affected farm.

Results

One outbreak has been analysed so far affecting six groups of heifers in a spatially restricted region of the farm. Group level incidences ranged from 1.5-19.8% (mean 8.4%). On the unaffected farm, the percentage of animals NSP seropositive was high in the 1-2 year age group indicating likely previous exposure. However, neutralisation titres indicated this was not due to A/ASIA/G-VII. The mean log10 reciprocal titres for A Iran-05, A Saudi-95 and the A/ASIA/G-VII field strain were 2.84 (95%CI 2.77-2.92), 2.87 (95%CI 2.82-2.93) and 2.48 (95%CI 2.40-2.55) respectively and were not affected by age.

Discussion

Analysis so far reveals partial protection to A/ASIA/G-VII using a >6.0PD50 polyvalent vaccine containing the A Saudi-95 strain. This is despite satisfactory heterologous titres obtained in the same age group on a similar farm with implications for assumed protective thresholds in this farming system. There is also evidence of subclinical virus circulating in farms using routine vaccination in endemic settings.

THE SEROLOGICAL RESPONSE INDUCED BY INACTIVATED FOOT AND MOUTH DISEASE VACCINE IN ISRAEL – CLINICAL TRIALS IN A DAIRY FARM

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Introduction

In Israel, outbreaks of Foot-and-Mouth disease (FMD) in vaccinated dairy farms, usually affect calves, not cows. The aim of this study was to determine the dynamics of antibodies to FMDV, elicited by vaccination in different age categories of cattle. Additionally, we estimated the association between vaccination timing of calves and protective coverage.

Materials and methods

Ninety-nine dairy cows of different ages and FMD vaccination statuses were followed for two years. Further, forty-four calves of different ages were vaccinated four times and followed for 70 weeks. During these periods, blood samples were collected regularly. From these, the neutralizing antibody titres against four serotypes included in the used FMDV vaccines were determined using Serum-Neutralization-Tests. Dynamics of these SNT titres for the different age categories were compared.

Results

In cows that were vaccinated up to 3 times before the beginning of the trial, there was a significant increase of the antibody titre after vaccination, followed by a rapid decrease. However, in cows vaccinated more than 3 times before the beginning of the trial, the antibody titre remained high and consistent throughout the study period but there was only minimal immunological response to new vaccination. In calves younger than 3 months, in the presence of maternally derived antibodies, only minimal antibody response was elicited by vaccination and the time of protective coverage provided by vaccination during the period between ages of 6 and 18 months was significantly lower than in calves vaccinated after the age of three months.

Discussion

Differences in antibody dynamics between cows and calves may explain the differences in susceptibility to natural FMD infection. Additionally, too early vaccination of calves may result in a prolonged reduction in protective coverage against FMD, even if repeated vaccinations are administered. Continuing vaccination after administration of five doses can be re-considered.

FARMERS' INTENTIONS AND PERCEPTIONS THAT INFLUENCE THEM IN IMPLEMENTING FOOT AND MOUTH DISEASE CONTROL IN ETHIOPIA

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Introduction

Motivation to implement livestock disease control measures is influenced by the perceptions of farmers about a disease and its control measures. The objectives of this study was to explore farmers' intentions to implement foot and mouth disease (FMD) control, and identify perceptions that significantly influence the intentions to implement FMD control measures using the Health Belief Model (HBM) framework.

Material and methods

Data were collected using questionnaires from 293 farmers in the pastoral, crop-livestock mixed (CLM) and market oriented cattle production systems. The influence of perceptions on the intention to implement control measures were analyzed using multivariable binary logistic regression, and the effect of socio-demographic and husbandry variables on those perceptions that significantly influence intentions were analyzed using multivariable ordinal logistic regression.

Results

Farmers' intention to implement vaccination free of charge was high (>90%) and this intention decreases significantly if vaccination was to be given at their own cost specially in the CLM system (<30%). The intentions to implement animal movement restriction both during outbreak and all time were low specially for pastoral and CLM systems. Among the HBM perception constructs, perceived barrier (cost of vaccination) was found as significant predictor of intention to implement vaccination. Perceived susceptibility (frequency of outbreak), perceived benefit (effectiveness of movement restriction) and perceived barrier (difficulty of movement restriction) were the significant predictors of the intention for movement restriction measures. The type of production system and age of farmers were the most important factors that significantly modify the relevant perceptions for intention to implement FMD control measures.

Conclusions

The results of this study suggest that disease control promotion programs designed to increase farmer participation in FMD control by vaccination and movement control should give more attention to the barriers of control measures and should take into account differences in perceptions among the production systems.

THE CURRENT EPIDEMIOLOGY AND THE CONTROL STRATEGY OF FMD IN CHINA

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Introduction

The FMD is endemic in China. The Chinese National/OIE Reference Laboratory for FMD has been monitoring the epidemiology of the disease and the genetic evolution of the FMD virus. A national immunization and surveillance programme are in place.

Results and Discussion

The FMD epidemiology in recent years is described. The national control strategy for FMD including immunization and surveillance programme will be briefly introduced. Constrains and challenge of the control of the disease will be discussed.

FMD DISEASE RISK ASSESMENT AND PROGRESS ON RISK BASED CONTROL PROGRAM

N. Bulut

AVAILABLE UPON REQUEST

SPATIO-TEMPORAL ANALYSIS OF FOOT-AND-MOUTH DISEASE EPIDEMIC SITUATION AMONG FARM ANIMALS IN THE REPUBLIC OF KAZAKHSTAN FOR THE PERIOD OF 1955 - 2013

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Introduction

This research is dedicated to the analysis of spatio-temporal patterns of foot-and-mouth disease (FMD) outbreaks among the agricultural livestock in the Republic of Kazakhstan (RK) using historical national data for the period of 1955 - 2013. The goal of the study was to illustrate the effect of vaccination on the formation of local FMD epidemics within the study period.

Materials and methods

Total of 5260 FMD outbreaks of serotypes A, O, and A22 among cattle, small ruminants and pigs were recorded during this period in the RK. The method of spatio-temporal cluster analysis using Kulldorff scan statistics has been employed in order to identify local epidemics.

Results

We revealed 35 statistically significant clusters of serotype A outbreaks with the duration of 95 ± 46 days, 41 cluster of the serotype with the duration of 116 ± 92 days, and 13 clusters of the serotype A22 with the duration of 76 ± 59 days. The within-cluster rate of the disease spread was assessed by means of spatio-temporal incidence rate, which is the average number of new focuses per 1,000 km2 within 1 month. This rate was estimated at 0.42 ± 0.30 for all three FMD serotypes. We also calculated the prevalence values in infected herds by serotype and species. Cattle, being the most affected population, demonstrated 3.9% (95% CI: 3.7 – 4.2), 4.6% (4.4 – 4.7) and 2.8% (2.4 – 3.3) prevalence of FMD serotypes A, O and A22 respectively.

Discussion

The analysis shows that clustering of FMD types A and O, which in sum amount to about 95% of all outbreaks, was interrupted in 1969. This finding is consistent with the fact of the start of mass preventive vaccination in the country since the late 1960s, which allowed eliminating the development of local epidemics and led to a sharp decline in FMD cases reporting in the RK.

Keywords: foot and mouth disease, livestock, Kazakhstan, spatio-temporal clusters, vaccination.

EPIDEMIOLOGICAL MODELLING OF FMDV IN ENDEMIC AND EPIDEMIC SETTINGS: A REVIEW OF RESEARCH AT THE UNIVERSITY OF MINNESOTA

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Introduction

Epidemiological models are useful tools to enhance understanding of FMDV transmission in endemic and epidemic contexts. We will present projects conducted during the past two years at the University of Minnesota College of Veterinary Medicine. In endemic settings, we highlight investigations of the spatial distribution of FMDV in Uganda, transmission at the buffalo-cattle interface in Kenya, and within-herd dynamics of FMDV in vaccinated dairy herds in India. For FMDV-free contexts, we focus on models that inform risk analyses in the USA.

Materials and methods

The spatial distribution of FMDV in Uganda was investigated using clustering analysis and heat maps. Buffalo-cattle transmission was investigated using serological and molecular epidemiological approaches. Transmission rates of serotype O in a vaccinated population were estimated using SEIR models and maximum likelihood approaches, whereas the extinction of the carrier phase following an outbreak in Indian dairy farms was investigated using longitudinal sampling and survival analysis. In FMDV-free contexts, simulation modeling was used to assess within- and between-farm spread of FMDV in US swine.

Results

Spatial clusters of high FMDV-risk in Uganda were identified in northeastern and eastern regions, along the Kenyan border. Within Kenya, seroprevalences of >75% and >90% were found in wild African buffalo and sympatric cattle, respectively. Within-farm dynamics of FMDV in India revealed transmission coefficients of 0.021 (0.018-0.025), and the carrier stage persisted for ~13 months. In the context of a US outbreak, we demonstrate that the size and duration of an outbreak could be reduced if control zones were expanded by 50%.

Discussion

The models and analyses presented here are useful for estimating factors associated with endemicity and quantifying spatiotemporal variation in risk across multiple contexts. The information provided by these models can be used to enhance biosecurity in free areas and control strategies in infected regions.

A PRIME-BOOST VACCINATION STRATEGY IN CATTLE TO PREVENT SEROTYPE O FMDV INFECTION USING A "SINGLE-CYCLE" ALPHAVIRUS VECTOR AND EMPTY CAPSID PARTICLES

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Introduction

Foot-and-mouth disease (FMD) remains one of the most economically important infectious diseases of production animals globally. Vaccination can help to control this disease, however, current vaccines based on chemically inactivated FMDV, are imperfect and there is a need for new, safe and effective vaccines to control FMD. There is no cross protection between the 7 serotypes but serotype O is the most abundant globally.

Material and methods

The FMDV capsid protein precursor (P1-2A) of strain O1 Manisa has been expressed with the FMDV 3C protease (3Cpro) using a "single cycle" packaged alphavirus self-replicating RNA based on Semliki Forest virus (SFV). Purified O1 Manisa empty capsid particles (ECs) have been prepared using a recombinant vaccinia virus expression system. Cattle have been vaccinated with the SFV-FMDV vectors and boosted subsequently with the ECs and then challenged with serotype O FMDV. The immune response against FMDV achieved by vaccination and infection status following challenge has been determined.

Results

In cattle vaccinated once with these rSFV-FMDV vectors alone, anti-FMDV antibodies were elicited but the immune response was insufficient to give protection against FMDV challenge. However, the vaccination with these vectors resulted in a much stronger immune response against FMDV post-challenge than in naïve animals. In subsequent experiments, cattle were sequentially vaccinated with the rSFV-FMDV followed by recombinant FMDV empty capsid particles prior to challenge. Animals given a primary vaccination with the rSFV-FMDV vector and then boosted with FMDV empty capsids showed a strong anti-FMDV antibody response prior to challenge. Following challenge with serotype O FMDV, the cattle were protected against disease and no FMDV RNA was detected in their sera.

Discussion

This prime-boost system, using reagents that can be generated outside of high-containment facilities, offers significant advantages to achieve control of FMD by vaccination.

VACCINE EFFICACY OF FMD VIRUS-LIKE PARTICLES PRODUCED BY THE BACULOVIRUS EXPRESSION SYSTEM

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Introduction

There is room for improving the stability of conventional killed foot-and-mouth disease virus (FMDV) vaccines. Also, the time to market should be improved in case of new outbreaks. Finally, vaccine production is currently carried out in high containment manufacturing facilities, resulting in very high production costs and lack of production capacity. To address these issues, a system to express FMDV virus like particles (VLPs) was developed. The possibility of producing VLP-based FMD vaccines in conventional facilities greatly increases the flexibility and significantly lowers costs of commercial manufacturing. The utility of VLPs can be further enhanced by improving their thermostability and pH sensitivity by introducing amino acid changes in the VLPs.

Materials and Methods

VLPs were expressed in insect cells using the baculovirus expression system. The proper expression and assembly of the VLPs was evaluated by several techniques, including Western blotting, ELISA, and electron microscopy. Vaccines containing VLPs were formulated with an appropriate adjuvant. Guinea pigs were vaccinated with these vaccines and the virus neutralising antibody titres (VNT) were measured. Vaccine efficacy will also be determined in vaccination-challenge cattle experiments.

Results

Selected FMDV sequences have been analysed in silico to predict mutations that might enhance VLP thermostability. These mutations have been introduced into the target virus sequences that have been cloned into baculovirus expression constructs and VLP expression was confirmed. Guinea pig immunisation studies have been performed with these VLPs, and VNT data obtained demonstrated that the vaccines were of high potency. Cattle experiments are planned to demonstrate vaccine efficacy.

Discussion

Virus-like particles is one of the few technologies currently available with the potential to be a commercially viable alternative to conventional killed vaccines. We have demonstrated that VLPs can be efficiently produced in baculovirus-infected insect cells, and that VLP-based vaccines can be produced with high potency.

ENHANCED POTENCY AND IMMUNOGENICITY FOR CATTLE VACCINATED WITH FMD A SEROTYPE VACCINE ADJUVANTED WITH POLY (I:C)

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Introduction

Virus neutralizing (VN) antibody is important for protection of animals against foot-and-mouth disease (FMD) but antibody titres are not fully predictive of protection. We have shown that FMDV vaccines that induce similar levels of VN antibodies can have different levels of T-cell responses and confer different degrees of protection against FMDV infection. We have shown a positive correlation between IFN-β response and vaccine induced protection and persistence of FMD virus and further showed that CD4+ T-cells are the major proliferating phenotype and IFN-β producing cells.

Materials and methods

Immunogenecity and potency of conventional FMD A serotype vaccine was tested in cattle incorporating 4 new adjuvants in addition to oil-in-water (ISA 206) adjuvant.

Results

Incorporating a molecular adjuvant (Toll like receptor [TLR] 3 agonist polyinosinic:polycytidylic acid [Poly I:C]) in to the existing formulation of FMD vaccine (serotype) we have demonstrated enhanced CD8+ and CD4+ T cell responses. In addition, all the vaccinated animals were protected in this group, whereas the conventional vaccine formulated with an oil-in-water adjuvant did not protect fully following challenge. Similarly, a significant increase in VN antibody titer (VNT) was observed for the poly I:C group in comparison to other TLR adjuvant groups including the conventional vaccine group (ISA-206). To measure the protective effect of adjuvant in these experiments we had reduced the antigen pay load from 10 µg to 2.5 µg in each experimental group.

Discussion

From our above recent work it is evident that incorporation of poly I:C as an adjuvant into the existing FMD vaccine formulation, the potency and immunogenecity can be significantly increased. In conclusion, we have identified a molecular adjuvant for FMD vaccine that enhances potency and immunogenicity. In a follow on BBSRC grant, we are currently investigating the longevity of immunity provided by new vaccine formulation.

EFFECT OF THE ANTIGEN PAYLOAD, POLYVALENCY AND REVACCINATION IN THE PROTECTION CONFERRED BY FMD VACCINES AGAINST HETEROLOGUS CHALLENGE IN CATTLE

Parallel - 09.45h

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Introduction

The wide antigenic diversity of FMD virus (FMDV) may hamper the implementation of vaccine strategies during an outbreak due to poor cross-protection among different strains, even within the same serotype. For this reason, it is essential to understand the mechanisms and variables underlying the generation of heterologous protection.

Materials and methods

Groups of steers (n = 5 each) were vaccinated with (1) 1 dose of 40 µg of A24/Cruzeiro; (2) 1 dose of 10 µg of A24/Cruzeiro; (3) 1 dose of trivalent A24/Cruzeiro (10 µg), O1/Campos (20 µg) and C3/Indaial (10 µg), and (4) 2 doses from 10ug of A24/Cruzeiro vaccine (at 0 and 15 DPV, 4). Two unvaccinated steers were used as controls. All the animals were infected at 30 DPV with the heterologous strain A/Arg/2001 (104TCID50% by IDL route) and followed for FMD symptoms during 7 days. Blood and serum samples were taken at different times before and after viral challenge, to characterize the adaptive immunity.

Results

Groups 1 and 2 showed FMD clinical signs in 1 and 2 steers, respectively. Animals in group 3 did not show clinical symptoms, despite having the same antigen payload as those from group 1 (40 µg/dose). Similarly, none of the revaccinated animals (4) showed signs of disease at 7 DPI. Mean titers for LP-ELISA, VNT, Ig isotypes, avidity or IFN-β production against (A/Arg/2001) were similar between groups at 30 DPV. Avidity index was higher in protected than in non-protected steers ($p<0.05$). Animals with low A/Arg/2001 LP-ELISA (below the EPP 75% threshold) but with high avidity indexes resulted protected to the heterologous challenge.

Discussion

Our results suggest that protection against heterologous strains may be favoured by high antigenic payloads and by enhancing the antigenic diversity in the vaccine. Avidity resulted the best predictor for the humoral protective response against the heterologous strain.

IMMUNE RESPONSES TO FMD VIRUS IN GUINEA PIGS AFTER VACCINATION WITH CANINE ADENOVIRUS VECTOR

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Introduction

Vaccination is a key element in the control of foot and mouth disease (FMD). A recombinant canine adenovirus-based FMD vaccine, Cav-P1/3C, expressing the P1 precursor along with the non-structural protein 3C protease of FMDV, was evaluated as a novel vaccine against FMD. Guinea pigs were used as experimental model for the determination of the immunogenicity and vaccine efficacy afforded by this recombinant virus.

Materials and methods

A non-replicative canine adenovirus vector expressing the FMDV capsid polyprotein P1 and the 3C protease for its cleavage (Cav-P1/3C) using coding sequences of FMDV strain O/FRA/1/2001 was developed. Four groups of four guinea pigs were vaccinated intramuscularly twice with a three week interval. Three weeks after the last vaccination, all guinea pigs were challenged intradermally with guinea pig-adapted O1 Manisa/Turkey/1969 strain. Body weight, attentiveness and the appearance of foot and tongue lesions were monitored daily after challenge. FMD viral RNA were sought in serum and internal organs using a one-step real-time RT-PCR for the FMDV 3D gene. Antibodies elicited against FMDV following immunization of guinea pigs were examined in a direct solid phase competitive ELISA and quantified by a Luminex-based immunoassay. In addition, serum samples were tested for the presence of FMDV-specific virus neutralizing antibodies.

Results

A humoral immune response was elicited in guinea pigs following immunization with Cav-P1/3C. The Cav-P1/3C recombinant vaccine protected guinea pigs from FMD to a similar extent as did a high potency double-oil-emulsion O1 Manisa vaccine.

Discussion

These results show that Cav-based vector can express immunogenic FMDV antigens in rodents, offer protection against FMD in guinea pigs and suggest that Cav-P1/3C can be considered to be a potential marker vaccine against FMD.

EU AUTHORISATION OF NOVEL VACCINES

M. ILOTT

AVAILABLE UPON REQUEST

APPLICATION OF INDIRECT AND AVIDITY ELISA TESTS TO ASSESS ANTI-FMDV ANTIBODIES INDUCED BY VACCINATION IN BUFFALO AND SWINE SERUM SAMPLES

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*# Both authors equally contributed to this publication, *Presenting author*

Introduction

Simple high-throughput methods easily adaptable to any new strain are needed to replace currently used Liquid Phase Blocking ELISA (LPBE) and the virus neutralization test (VNT). We developed single-dilution indirect and avidity ELISAs ("IE" and "AE", respectively) to assess anti-FMDV-antibodies (Ab) in buffalo and swine serum samples; and isotype ELISAs for swine samples. We evaluated the concordance between the ELISAs and VNT to assess the level of protective antibodies against FMDV; and followed humoral responses to primo-vaccination.

Materials and methods

Concordance and accuracy between ELISAs and VNT was first analysed with 91 buffalo serum samples with different VNT titers. Then, a group of 45 buffaloes received one dose of commercial vaccine and Ab were followed up to 210 post-vaccination (dpv). Fifteen weaned piglets (2 months old) were vaccinated with a single dose of commercial vaccine (n=12) or PBS/Adjuvant (n=3). Serum samples were taken at 0, 10, 21 and 60 dpv and assessed by the different tests.

Results

Buffalo´s samples could not be categorized solely based on a single ELISA test. However, combining IE and AE that assess total Ab and their avidity, an excellent concordance with VNT was achieved. High levels of anti-FMD antibodies were detected up to 210 dpv. All vaccinated piglets elicited anti-FMDV antibodies from 10 dpv that continued to increase up to 60 dpv. IgG2 was induced in higher levels than IgG1, with maximum values observed at 60 dpv.

Discussion

We have standardized simple serological high-throughput techniques to evaluate anti-FMDV immunity in vaccinated pigs and buffalos. These ELISAs provide similar diagnostics results than VNT but without the need of using cell culture and live virus. This is the first study analysing the diagnostic accuracy of traditional and novel serological tests for indirect assessment of herd immunity against FMDV using buffalo serum samples.

DEMONSTRATION OF EARLY PROTECTION AGAINST FOOT-AND-MOUTH DISEASE VIRUS SEVEN DAYS POST-VACCINATION

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Introduction

Foot-and-Mouth Disease virus (FMDV) can spread very rapidly, and vaccination is mostly the best tool to control the disease. In the face of outbreaks, the ideal vaccine should have a rapid onset of immunity. The present work was designed to assess the efficacy of AFTOVAXPUR DOE vaccine in eliciting protection 7 days post-vaccination (dpv).

Materials and methods

Ten cattle were vaccinated with a commercial double-oil-emulsion FMDV vaccine containing O1 Manisa antigen. Another group of 10 cattle was left unvaccinated. All animals were challenged , twice 1-hour apart, by nebulization of 2.5 ml diluted challenge virus per nostril. Each cattle received in total 10 000 BID50 of FMDV type O1 Manisa. FMD lesions were scored under sedation on 4, 8 and 14 days post-challenge (dpc). Blood samples were taken up to 11dpc for titration. Mouth swabs were taken daily for 8 days.

Results

All controls developed FMD lesions on all feet whereas none of the vaccinated cattle presented foot lesions over the 14 days period. Virological testing revealed a complete protection against viremia in the vaccinated group, whereas all controls became viremic. FMDV was detected in mouth swabs of 7 cattle in the vaccinated group, but in all controls. The duration of FMDV detection in mouth swabs was significantly shorter and lower in intensity in the vaccinated cattle compared to the controls.

Discussion

Clinical protection against intra-nasal O1 Manisa challenge was demonstrated 7 dpv, with prevention of foot lesions. Virological testing also revealed a complete protection against viremia in the vaccinated group. Although FMDV was isolated in the mouth swabs of some cattle likely due to local replication, virus excretion was highly reduced in the vaccinated animals. The present study thus demonstrates a rapid onset of immunity as soon as 7 days post vaccination with inactivated AFTOVAXPUR DOE vaccine.

EFFICACY OF AN FMD INACTIVATED VACCINE (AFTOVAXPUR DOE), ADMINISTERED AT A 1 ML DOSE TO SHEEP

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Introduction

While not always specifically indicated as such in vaccine labels, FMD vaccines are frequently administered to sheep at half the dose recommended for cattle in field practice. The main reasons supporting this practice are: i) a lower susceptibility of sheep to FMD infection ii) the relative vaccine cost as compared to the value of a sheep.

The study presented aimed at assessing vaccination of sheep with half of the recommended dose (1 mL) of an AFTOVAXPUR DOE, in comparison with a full (2 mL) dose.

Materials and methods

Two groups of 10 sheep were vaccinated once with either 1 or 2 ml of an AFTOVAXPUR DOE trivalent (O1 Manisa, A22 Iraq, SAT2 SAU) vaccine, formulated at low antigen payload. Blood samples were collected on a regular basis and tested for neutralizing antibodies against all antigens included in the vaccine. The antibody response was statistically compared between the 1 ml and 2 ml vaccinated groups. In addition, the vaccinated group was challenged 28 days post-vaccination with FMD O1 Manisa virulent cattle adapted virus, together with a third group of non-vaccinated naïve sheep (controls). After challenge, these 2 groups were monitored for clinical signs, FMD lesions and viraemia.

Results

Serological results demonstrated non-inferiority of the antibody response against both A22 Iraq and SAT2 SAU of the 1 ml vaccinated group compared to the 2 ml vaccinated group. Despite the lower serological response observed against O1 Manisa, protection against challenge was demonstrated through a significant reduction of clinical disease and a complete prevention of detectable viraemia in the 1 ml vaccinated sheep.

Discussion

Efficacy of the vaccine with low antigen content was demonstrated at a 1 mL dose, through clinical and virological protection against virulent challenge (O1 Manisa) and comparison with the serological response obtained with a 2 mL dose (A22 Iraq, SAT2 SAU) .

FMDV EMERGENCY TYPE O VACCINES ARE EFFECTIVE AGAINST CHALLENGE WITH FMDV O/ALG/2013 (O IND 2001d) IN CATTLE

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Introduction

The efficacy of two high potency vaccines was compared in cattle, against challenge with a variant of FMDV O/IND/2001d lineage, at either 7 or 21 days post vaccination (dpv).

Materials and Methods

Two groups of cattle calves (A and B; n=5) were vaccinated intramuscularly with 2 ml dose of monovalent O-3039 vaccine while two other groups (C and D; n=5) received 2 ml dose of bivalent O-3039 and O1 Manisa vaccine. Groups A and C were challenged at 21 dpv and groups B and D at 7 dpv by intra-dermolingual inoculation with 105 pfu (equivalent to 104 CID) with cattle derived O/ALG/3/2014. Three naive infection controls were included.

A thorough clinical inspection was performed at 4 and 7 days post challenge (dpc). Blood, oral and nasal swabs were collected daily until 7 dpc and 11, 14, 18, 21, 25, 28, and 33 dpc. Oropharyngeal fluid were collected on 11, 14, 18, 21, 25, 28, and 33 dpc.

Results

All cattle in groups A and C, three in group B and four in group D, did not develop lesions on their feet. Viraemia was absent in all vaccinated cattle, but pronounced in the naïve infection control group. Oral and nasal swabs tested positive for FMDV between 1 and 7 dpc only. A number of probang samples tested positive at 11 dpc with RNA/virus detected intermittently until 33 dpc in some vaccinated animals, while RNA/virus was consistently detected in one of three infection control animals.

Discussion

The monovalent O-3039 vaccine performed equal to the bivalent O-3039/O1 Manisa combination and both vaccines can be used to protect cattle against challenge with FMDV strains of the O/IND/2001d lineage, with some cattle protected as early as 7 dpv. The protection provided at 7 and 21 dpv was not statistically significant different (P=0.2105, Fisher's exact test).

PROTECTION IN SHEEP AGAINST HETEROLOGOUS CHALLENGE WITH SEROTYPE ASIA 1 FMD VIRUS USING HIGH POTENCY VACCINE

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Introduction

Asia 1 is prevalent in countries considered high risk to Australia and has recently been responsible for a number of outbreaks. In vitro vaccine matching has identified a number of contemporary strains with poor or no match to Asia 1 Shamir. Therefore it was important to test the ability of the Asia 1 Shamir vaccine to protect sheep from challenge with a recent, heterologous strain at different days post-vaccination (dpv), including in an emergency vaccination scenario (challenge 4 or 7 dpv).

Materials and methods

Sheep (5 per group) were challenged with the Asia-1/PAK/19/2014 isolate by intranasopharyngeal instillation 21 (V21), 7 (V7) or 4 (V4) dpv with high potency (>6 PD50) Asia-1 Shamir vaccine. Five sheep were mock-vaccinated with adjuvant only (antigen-free preparation) 4 days prior to challenge (AO), and five unvaccinated (UV) control sheep were also challenged. Samples (blood, saliva and nasal swabs) were collected daily for 10 days, then weekly to 35 days post-challenge. Probang samples were collected weekly to 35 days post-challenge.

Results

All V21 and V7 sheep and 80% of V4 sheep were protected from clinical FMD. 80% of V21 sheep and 40% of V7 sheep developed sterile immunity, however all V4 sheep became systemically infected. Vaccination reduced excretion of virus in nasal and oral secretions but had no effect on the development of persistence. All AO and UV sheep developed clinical FMD, however, overall the severity of disease and duration of excretion of FMDV in saliva was greater in the UV group.

Discussion

The high potency Asia 1 Shamir vaccine will protect against disease should an outbreak of contemporary Asia 1 viruses occur. Intranasopharyngeal instillation is an effective challenge method for use in vaccine efficacy studies in sheep. It would be of interest to examine the innate immune response to infection in the AO animals compared to the UV animals.

NO HETEROLOGOUS PROTECTION WITH FMD SAT2 SAU VACCINE AGAINST SAT2 BOT CHALLENGE

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Introduction

Recent studies on heterologous protection of foot-and-mouth disease (FMD) vaccines show that when good potency vaccines are used the protection against heterologous challenge is often better than was expected based on serological homology. These heterologous protection studies were limited to serotype A and O, no information is available on SAT2 vaccines. In the current study we tested in several experiments the protection by a high potency SAT2 SAU vaccine against both homologous and heterologous challenge.

Materials and methods

In total 4 PD50 studies were performed with SAT2 SAU vaccine. In 3 studies homologous challenge was used and in a 4th study SAT2 BOT virus was used as challenge strain. In each PD50 study, 5 cattle were vaccinated with a full dose, 5 cattle with a ¼ dose and 5 cattle with a 1/16 dose (in one study using homologous challenge also 5 cattle with a 1/64 dose were included). The cattle (including 2 control cattle) were challenged 4 weeks after vaccination and checked regularly for development of foot lesions till the end of the experiment 8 days after challenge. The antibody response at the day of challenge was analysed by linear mixed regression analysis (experiment as random variable). Protection by challenge was tested by logistic regression (R version 3.2.5, lme4 version 1.1-12).

Results

The antibody response in the cattle was correlated to the volume of vaccine injected. Based on the model 10 times more vaccine will result in approximately 0.6 higher antibody titre. The best predictors for protection were challenge strain and antibody titre. For heterologous protection approximately 1 log10 higher antibody titre was necessary, compared with homologous challenge.

Based on the logistic regression model the potency of the final formulation of SAT2 SAU vaccine against homologous challenge was 94 PD50 per dose. But a similar formulation failed to protect against a heterologous SAT2 BOT challenge (estimated heterologous potency 0.8 PD50 per dose).

Discussion

For FMDV serotype A and O often heterologous protection can be found when a high potency vaccine is used, despite the serological differences between strains (low r1 values). Therefore a very limited number of A and O strains are necessary to be able to control FMD in various regions. The current study shows that for FMD serotype SAT2 the differences between both strains used in the experiments are huge and no heterologous protection is found. The low protection was expected as the VP1 nucleotide

identity between BOT/5/2009 and SAU/6/00 is only 70% (BOT/5/2009 and SAU/6/00 are strains with available sequence data, www.wrlfmd.org, isolated from the same countries in the same year). The result shows that more SAT2 vaccine strains should be made available for vaccine banks as well as for use in the region.

SELECTION OF AN ADJUVANT TO RAISE POLYCLONAL ANTIBODIES TO FOOT-AND-MOUTH DISEASE VIRUS IN RABBITS AND GUINEA-PIGS

Poster

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Introduction

Raising good quality monoclonal and polyclonal antibodies is an essential requirement for the production of diagnostic reagents. These reagents require that animals are immunized to generate specific antibodies. The use of animals in research continuously raises concerns about their welfare within the general public and the scientific community, and therefore refining methods must be explored to minimize the pain and discomfort that animals may suffer.

Polyclonal antibodies for Foot-and-Mouth disease virus (FMDV) diagnostics have been historically produced in rabbits and guinea-pigs (GP) using Freund's adjuvant. Freund's is known to be a potent adjuvant which delivers good titers of antibodies however, its use has been questioned on several occasions as it has been associated with painful adverse effects, and therefore the use of alternative adjuvants are encouraged. An experiment has been designed to evaluate three different adjuvants as an alternative to Freund's in their ability to raise polyclonal antibodies to purified FMDV in GP and rabbits.

Materials and methods

Three candidate adjuvants Titremax-Gold, Montanide ISA-50V2 and Stimune will be evaluated in eighteen rabbits and eighteen GP, each divided in 3 groups of 6 animals for each adjuvant. Each group will be inoculated subcutaneously with an emulsion of sucrose-density gradient purified FMDV_A22_IRQ24/1964 (5 µg in GP and 15 µg in rabbits), followed by a boost on day 28. Inflammatory reactions at the site of the inoculation and data on individual health will be recorded, and the antibody titers will be measured by specificity ELISAs. Comparisons between groups will be evaluated to select the adjuvant with the highest titer and the least adverse effects.

Results

Not applicable. The study will finish end of August 2016.

Discussion

This study may provide some valuable data to select commercially available adjuvants that produce good quality antisera while have minimum adverse effects in rabbits and GP.

APPLICATION OF MOUSE MODEL FOR EFFECTIVE EVALUATION OF FMD VACCINE

Poster

S.Y. Lee[1,2], M.K. Ko[1], K.N. Lee[1], J.H. Choi[1], S.H. You[1], H.M. Pyo[1], M.H. Lee[1], B. Kim[1], J.S. Lee [2], J.H. Park[1]

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Introduction

Efficacy evaluation of foot-and-mouth disease (FMD) vaccines has been conducted in target animals such as cows and pigs. The lack of a laboratory animal model has resulted in inconvenience when it comes to using target animals for vaccine evaluation, bringing about increased cost, time and labor for the experiments. The FMD mouse model has been studied, but most FMD virus (FMDV) strains are not known to cause disease in adult mice.

Materials and methods

In the present study, we created a series of challenge viruses that are lethal to adult C57BL/6 mice. FMDV types O, A, and Asia1, which are related to frequent FMD outbreaks, were adapted for mice and the pathogenesis of each virus was evaluated in the mouse model. The O Jincheon/SKR/2014, A Malaysia 97, and Asia1 MOG/2005 viruses were passaged three times in ZZ-R cells, and 105.0 TCID50/0.1 ml of the viruses were inoculated intraperitoneally (IP) in 8-week-old C57BL/6 mice(n=2). The serum was collected at 2 days post infection (dpi) and filtered through a 0.2 μm syringe filter. The filtered serum was inoculated back to ZZ-R cells for two passages. A cycle of in vivo and in vitro passages for preparation of challenge virus was repeated five times.

Results

Challenge experiments after vaccination using in-house and commercial vaccines demonstrated vaccine-mediated protection in a dose-dependent manner. If such viruses are used in evaluations for the newly produced vaccines, they may enhance the reliability of vaccine evaluation.

Discussion

Emerging FMDVs that are lethal for mice will be used as challenge viruses in vaccine evaluation. What is more, the study findings obtained from mouse experiments can often be harmonized with the results obtained from experiments on the target species. Therefore, the mouse model can help to successfully predict the immune response to FMDVs in cows and pigs.

DEVELOPMENT OF A VIRULENT FMD CHALLENGE MODEL IN SHEEP

Poster

C. Hamers[1], L. Mouton[1] , M. Besset[1], A. Dekker[2], M. Bleijenberg[2], B. Van Schaijk[1], J. Coco-Martin3, M. Curet[1], S. Goutebroze[1]

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Introduction

Unlike Foot-and-Mouth Disease (FMD) in pigs and cattle, FMD in sheep is frequently mild and inapparent. Challenge experiments described in the literature confirmed inconsistent clinical expression.
The purpose of this study was to assess, in sheep, the ability of 3 different challenge strains of FMD to induce clinical signs and viremia, using the dose and route of inoculation considered suitable for cattle.

Materials and methods

Six female sheep, of 10 months of age, were randomly allocated to 3 groups of 2 sheep. Three virus suspensions, containing 10.000 cattle ID50 per 0.2 ml of FMD virus stock of either A22 Iraq, O1 Manisa or SAT2 SAU serotype were prepared. In each group, both sheep were intradermally inoculated into the tongue with one of these virus suspensions.
For all sheep, rectal temperature and clinical signs of FMD were recorded daily for 8 days. Blood samples were taken up to 7 days post infection (dpi) for viremia. FMD specific lesions were scored 4dpi and 8dpi.

Results

Some transient and moderate hyperthermia was observed in all sheep from 1 to 4 dpi. All sheep infected with O1 Manisa and SAT2 SAU presented feet lesions 4dpi. In sheep infected with A22 Iraq, 1 sheep presented similar feet lesions while the other did not present any FMD lesions. At necropsy (8dpi), all sheep from all groups showed tongue lesions together with FMD lesions of at least 3 feet. All sheep became viremic shortly after challenge.

Discussion

The study results demonstrated that A22 Iraq, O1 Manisa and SAT2 SAU strains are able to consistently induce FMD clinical lesions and viremia in sheep. This study further demonstrated that the intradermal tongue challenge route is suitable for sheep, at least for these 3 strains. Furthermore the induced infection resulted in more severe clinical lesions compared to field observations.

FMD IN TURKEY - LIVESTOCK MOVEMENTS AND MATHEMATICAL MODELLING

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Introduction

Mathematical models of livestock disease are being increasingly used as tools to aid policy makers. These models can be used to test out a variety of control measures and help to reduce FMD disease burden. However, such models are typically utilized in disease-free regions, either retrospectively to analyse historical outbreaks, or prospectively, to develop contingency plans. In this paper, we present a model to simulate the spread of FMD in Turkey, a country that experiences regular waves of FMD cases nationwide. The model is fitted to historical outbreak data and the effectiveness of intervention strategies are considered.

Methods and Results

The model utilises movement records supplied by TurkVet and reported outbreak data. A community detection approach is used to analyse the livestock movement network to determine regions of high risk for disease transmission. We parameterise the model in a Bayesian framework that allows for priors informed by expert opinion. We then investigate the impact of intervention strategies upon reducing disease burden.

Analysis of the movement network indicates a strong spatial and temporal variation in transmission risk. Livestock movements exhibit strong spatial clustering, with communities most likely to form between farms in close proximity to one another. The mathematical model indicates that targeted movement control can have an effect upon future FMD burden in Turkey, with results suggesting that a district level movement ban can dramatically reduce the spread of disease at the national scale.

Discussion

Analysis of the livestock movement in Turkey can provide information regarding high risk regions that should be targeted for surveillance to reduce future disease burden in the country. The results of our model can be used to assist with guidance on intervention strategies that can be implemented in Turkey to reduce the impact of FMD in the future.

THE U.S. ANIMAL MOVEMENT MODEL (USAMM), A BAYESIAN APPROACH TO MODELING OF A PARTIALLY OBSERVED CONTINENTAL SCALE LIVESTOCK MOVEMENT NETWORK.

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Introduction

Movement of livestock between farms poses a risk of spreading pathogens over large distances. Upon detection of foot and mouth disease (FMD), a movement ban would typically be put in place, and the primary risk of animal movement occurs during the silent spread phase. However, policy could also consider regionalized movement bans.

The importance of animal movements necessitates appropriate modeling of such contacts in mathematical models used to inform policy about FMD. EU legislations require states to keep records of animal movements between farms, and such databases can be used to parameterize models. However, many countries, including the US, which we focus on here, lack detailed and accessible information on livestock movement.

Materials and methods

We have developed the United States Animal Movement Model (USAMM). It uses a kernel approach to model movements between counties and implement Hierarchical Bayesian methods for data fitting. We incorporate multiple data sources, primarily a unique 10 % sample of all Interstate Certificates of Veterinary Inspections (ICVI) from May 2010 to September 2011. We also accounted for spatiotemporal heterogeneity, as well as livestock industry covariates. ICVIs only register interstate movement, and we extrapolated from these movements to estimate intrastate movements. For improved reliability, we also used expert opinions on the amount of intrastate shipments.

Results

We identified important spatiotemporal heterogeneity in the movement networks, and found that by considering relevant covariates, model accuracy was improved. Expert opinions regarding intrastate shipments had little effect on the results, mainly because expert disagreed in their estimates.

Discussion

USAMM allow us to capture important aspects of large scale animal movements. It is a promising approach to inform epidemiological models about animal movements, circumventing limitations of incomplete data. USAMM can thus enhance models used to inform policy decisions regarding FMD control, and hopefully increase the use of such models.

ENSEMBLE MODELING FOR FMD

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Introduction

Stochastic simulation models are powerful tools for epidemiology. However, all models are based on underlying assumptions about the disease and transmission process. As a consequence, models may vary in their predictions, and in the recommendations they provide for policy makers. Ensemble modeling offers the ability to combine multiple model predictions and has improved model predictions in other fields.

Materials and methods

Here we present the Bayesian Reliability Ensemble Average method (BREA) for use in epidemiological forecasting and the application of this method to foot and mouth disease (FMD) outbreak. The BREA methodology provides a platform for addressing planning and preparedness questions, and could be used as a response tool during an outbreak. Working with four FMD simulation models, which have been used in policy around the world, we explored the use a multi-model ensemble in a response situation. Focusing primarily on the UK 2001 outbreak, we seeded models with data from early in the outbreak to simulate an ongoing epidemic. We also addressed control questions, providing ensemble estimates of how different the outbreak would have been under alternative control.

Results

We find that the ensemble prediction captures the dynamics of the outbreak and does better than any single model alone.

Discussion

These results suggest that ensemble modeling could be a powerful tool for responding to and planning for disease outbreaks. Additionally, ensemble models can reduce the confusion caused by multiple models with differing predictions, and present a single, interpretable prediction. Ensemble modeling therefore has the potential to improve our ability to make epidemiological predictions and communicate them with policymakers.

REAL-TIME BAYESIAN DATA ASSIMILATION AND PREDICTION FOR LIVESTOCK EPIDEMICS

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Introduction

Bayesian methods provide a principled way to fit epidemic models to observed field data during an outbreak. By accounting for undetected, or occult, infections, they provide unbiased estimates of the importance of various transmission mechanisms, daily situation summaries of the extent of an outbreak, and predictions of disease spread with fully quantified uncertainty. However, the computational complexity of the algorithms is at odds with the need to provide fast, reliable information during an outbreak.

Methods

This paper focuses on the 2001 UK and 2010 Japan foot and mouth outbreaks. An MCMC algorithm is designed to fit a stochastic, spatial susceptible-infected-detected-culled model to case observations from each outbreak. The algorithm is accelerated using general-purpose Graphics Processing Unit (GPU).

Results

GPU-accelerated Bayesian analysis of national-scale epidemics is able to provide fully quantitative daily nowcast and forecast results. Maps are provided to visualise the probability of each presumed-uninfected farm having occult infection status, together with a ranked list of high risk farms to facilitate targeted surveillance. Information on how the spatial scale of transmission changes over time is provided in order to inform decisions on control regions. FMD vaccine efficacy in Japan is tracked, and estimated to be 81% [64%, 95%] by the end of the epidemic.

Discussion

Rigorous Bayesian fitting for epidemic models is now possible on a rapid, overnight timeframe conducive to providing timely nowcasting and forecasting information. Importantly, this speed of fitting opens up further possibilities to critique data and goodness of fit quickly, so as to provide an honest appraisal of results and not overstate the validity of the underlying modelling assumptions. Code is provided as an R package, ensuring reliable, repeatable results.

REAL-TIME UPDATING IN EMERGENCY RESPONSE TO FMD OUTBREAKS

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Introduction

At the start of an outbreak, there is often significant uncertainty regarding the behaviour and extent of the epidemic, which may limit the ability of epidemiological models to inform policy. As an outbreak progresses, more information is garnered and therefore more informed decisions may be made. However, during an outbreak situation, decision-makers do not generally have the luxury of waiting for information to accrue.

Materials and Methods

We combine recent methods for parameter estimation and a widely cited and validated forward simulation model to simultaneously estimate transmission parameters, the spatial distribution of undetected infections, and the rank performance of candidate interventions at several weeks throughout a historical outbreak of foot-and-mouth disease. By comparing policy recommendations based only on information available at a particular point in time with policy recommendations given complete data from the outbreak we can isolate the effect of information accrual.

Results

The optimal control policy is predicted accurately from an early stage in an outbreak despite highly uncertain projections of the size and duration of the epidemic. The best control action depends largely on the specific realisation of the outbreak.

Discussion

Our results give support for trusting models in the early stages of an outbreak when generating intra-model comparisons of control strategies and also highlight the necessity of generating state-dependent control strategies that may change as additional information arrives.

HAEBOS, A HYBRID AGENT - AND EQUATION - BASED MODEL OF FOOT AND MOUTH DISEASE IN VERMONT

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Introduction

Reporting behavior by livestock producers with infectious disease outbreaks on their premises can substantially affect outbreak size for pathogens with lengthy 'silent spread' periods.

Materials and methods

We created a hybrid model which combines the advantages of equation-based compartmental disease models with agent-based stochastic interactions between farms to investigate the effects of producer behavior on a hypothetical foot-and mouth disease outbreak originating in the northeastern US. We have investigated the influence of index premises production type, overall producer behavior, and the clustering of behaviors on outbreak size, makeup, and duration. This model is highly flexible and can allow for different diseases, locations, and input datasets.

Results

Preliminary results show substantial model output variability between outbreaks, even with identical starting conditions, with the number of infected farms ranging from 1 to 214 and duration ranging from 8 to over 800 days. The average outbreak lasts 146 days and results in the destruction of approximately 28 premises.

Discussion

Local area spread and milk-truck borne infection seem to be the major driver of pathogen spread in this area.

REDUCING COMPUTING TIMES OF SPATIALLY EXPLICIT FMD MODELS

Poster

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Introduction

Spatially explicit simulation models are powerful tools to inform policy. However, computation time quickly becomes a limiting factor, especially when considering large scale outbreaks. We present two methods that can reduce computation time by partitioning the landscape of farm locations into grids, without introducing truncations or approximations. We also provide an optimization method for how to split the given landscape into the grid configuration that minimizes computation time.

Materials and methods

The point pattern landscape of farms is divided into a grid of squares, and the simulation is split into two steps: 1) Does the infection possibly enter any of the grid-squares? 2) If yes, which farms within the squares are actually infected? By calculating an overestimated probability in step one, the methods circumvents further kernel evaluations if a grid is not entered. The computation time saved depend on the grid size. For small squares, many kernels have to be evaluated in step one. For large squares, the algorithm will often proceed to step two for evaluation of all farms. We formulate an equation that approximates the expected number of kernel evaluations for a particular grid configuration, providing a way to identify the configuration that minimizes computation time.

Results

With the proposed methods, calculation time can be reduced to one percent of the time required when evaluating each infected-susceptible farm pair directly. The improvement was found to be sensitive to grid size, the spatial configuration of farms, and outbreak size. Our method was effective in finding the grid configuration that optimized computation speed for both simulated and real farm locations (Sweden, US, and UK.)

Discussion

Fast computation of FMD models is crucial in order to allow modelers to test a wider range of parameters and control strategies. Our solution provides a promising approach towards this goal.

DEVELOPMENT OF A NOVEL VIRUS NEUTRALIZATION ASSAY USING QRT-PCR-BASED ENDPOINT ASSESSMENT FOR RAPID DETECTION AND TITRATION OF NEUTRALIZING ANTIBODIES AGAINST FOOT-AND-MOUTH DISEASE VIRUS

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Introduction

Foot and mouth disease (FMD) is a highly contagious disease affecting cloven-hoofed animals. Virus neutralization test (VNT) is the most recommended method for vaccine matching test of FMD virus (FMDV) and to measure the serological response to FMDV infection and vaccination, but currently traditional VNT is time-consuming, rate-limiting and easily affected by man-made factors. In order to improve upon its technical limitations, we have developed an alternative VNT using qRT-PCR-based endpoint assessment (qRT-PCR-VNT) for FMDV serotype Asia 1.

Materials and methods

FMDV serotype Asia 1/serum mixtures were incubated for one hour at 37oC and then transferred to IBRS-2 cell monolayers in a 96-well plate. The reduction in FMDV replication in the cells resulting from neutralizing antibodies in sera to be tested was quantified using one-step qRT-PCR with primers and a probe targeting a conserved region of FMDV 3D gene.

Results

A qRT-PCR-VNT was successfully developed for rapid detection of neutralizing antibodies against FMDV Asia 1. In this assay, the neutralization titer was defined as the highest serum dilution necessary to achieve equal to or great than 107 copy number of FMDV RNA per well at 20hpi, which was observed in virus control wells in the absence of neutralizing antibodies. The feasibility of measuring virus neutralization using qRT-PCR-based endpoint assessment at 20hpi was evaluated using sera (n=25) collected from experimentally-infected and healthy animals. This endpoint at 20hpi was found to be in agreement with traditional VNT in each serum sample tested.

Discussion

Compared with traditional VNT, the developed qRT-PCR-VNT was robust with respect to assay duration (20 hours vs.72 hours) and have inherent properties conducive to reducing intra-and inter-laboratory variability while affording suitability for automated high-throughput uses. In addition, our experimental approach may be broadly applicable for other FMDV serotypes.

COMPETITIVE LUMINEX IMMUNOASSAYS FOR THE DETECTION OF ANTIBODIES TO FMD AND VESICULAR STOMATITIS VIRUSES IN MULTIPLE SUSCEPTIBLE HOSTS

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Introduction

Foot-and-mouth disease (FMD) affects cloven-hoofed animals. Vesicular stomatitis (VS) affects horses, mules, cattle and swine. The clinical signs and lesions seen in swine and cattle due to FMD and VS are indistinguishable. Consequently, laboratory tests are essential to distinguish between the two. Competitive ELISAs for FMD and VS exist and can be adapted to the Luminex platform with the advantage of improved sensitivity, utilisation of small sample volumes and the possibility of multiplexing. The aim of this project was to develop competitive Luminex immunoassays (cLIAs) for FMDV and VSV.

Materials and methods

For FMD, mouse anti-3B monoclonal antibody (MAb) and Baculovirus - derived recombinant 3ABC antigen coated to MagPlex beads were used. The beads were mixed with equal volumes of anti-3B MAb and test sera. Antibodies in serum inhibited binding of anti-3B MAb to epitopes on 3ABC to various degrees. Phycoerythrin conjugated anti-mouse detection antibody was added, and mean fluorescence intensity which was inversely proportional to the amount of FMDV antibodies in the serum was determined on a Luminex Magpix. Results were expressed as percentage of inhibition. The design was identical for VSV New Jersey, using mouse polyclonal anti- VSV antibodies and recombinant VSV glycoprotein.

Results

The cLIAs successfully detected antibodies to FMDV and VSV in sera from infected animals. The performance of the cLIA was comparable to the corresponding cELISAs, with preliminary data indicating potentially high diagnostic sensitivity and specificity.

Discussion

These assays would be useful additional tools for serological diagnosis of FMD and VS. A competitive format reduces the problem of non-specific binding to beads since inhibition of the murine antibodies is due to antibodies to specific antigenic sites. Furthermore, with a multiplex cLIA, the two agents can be assayed at the same time, reducing time and amount of serum required.

TAILED PRIMERS ENHANCE REAL-TIME RT-PCR DETECTION OF FMD VIRUS

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Introduction

The detection of FMD viral RNA is routinely performed by using the 3D and 5UTR real time RT-PCRs from Callahan et al. (2002) and Reid et al. (2002) alone or in parallel (King et al., 2006). Our aim was to improve the robustness and overall performance of both assays.

Materials and methods

Short A/T rich 5'-tails were incorporated into the primer sets (Afonina et al., 2007). A panel of 50 FMDV strains was tested in parallel with the original non-tailed primers and with the modified tailed primers. For each assay the underlying mechanism was investigated.

Results

In the 5UTR assay fluorescence accumulated faster and to higher levels in reactions with tailed primers. This effect was more pronounced for SAT serotype strains and at lower target concentrations. Tailed primers significantly delayed the formation of PCR artefacts that are known to reduce amplification efficiency and restored the sigmoidal shape of the curves. Further, tailed primers altered the utilization patterns of the degenerate primers and increased the number of primer variants that participate in the reaction.

In the 3D assay the effect of tailed primers was less pronounced but for 5 FMDV strains of 4 serotypes the Cq values were markedly lower (3.43 ± 0.11) with tailed primers. Sequence analysis revealed several mutations in the inter-primer region that extend an existing hairpin structure immediately downstream of the forward primer binding site. Stabilization of the forward primer with a tail sequence restored the sensitivity of the assay, suggesting that the enhancing effect is due to a more efficient extension of the forward primer.

Discussion

Our results show that primer tailing can alter amplification through various mechanisms that are determined by both the assay and target region. The enhancing effect also depends on the viral isolate and the target RNA concentration.

DEVELOPMENT OF ONE-STEP MULTIPLEX RT-PCR ASSAY FOR DIFFERENTIATION OF FOOT AND MOUTH DISEASE VIRUS SEROTYPES A, O AND SAT2 CIRCULATING IN EGYPT

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Introduction

Egypt is endemic with three serotypes of FMDV (A, O and SAT2). Circulation of these different serotypes requires rapid and accurate detection of circulating strains in the country in order to implement the appropriate control measures. The difference in the circulating strains of FMDV from region to another gives the necessity to develop region specific molecular diagnostics for specific detection of these strains so a multiplex RT-PCR assay was developed and validated for typing of FMDV serotypes A, O and SAT2 in Egypt.

Materials and Methods

Serotype specific primers were designed in (VP1-2B) region to give the following amplicon sizes: 750, 666 and 283 bp for serotypes A, SAT2 and O respectively. A panel of archival FMDV samples from the three serotypes A, O and SAT2 and two negative bovine epithelial suspension and BHK-21 cell culture were used for assay validation. For assay evaluation, 45 recent clinical samples were tested by the developed assay and Ag ELISA then confirmed by nucleotide sequencing.

Results

The multiplex RT-PCR assay showed accurate and specific differentiation of the serotypes A, O and SAT2 in both archival and current clinical samples but Ag ELISA detected FMDV in only 19 samples. The results of nucleotide sequencing confirmed the typing by the developed multiplex RT-PCR assay. No cross reactivity and /or non-specific amplification were observed.

Discussion

Egypt is endemic with 3 different serotypes A, O and SAT2 and different topotypes and / or lineages from 2 endemic pools (Jamal and Belsham, 2013). The developed Multiplex RT-PCR assay successfully detected and differentiated the three different FMDV serotypes circulating in the country. It is more sensitive than Ag ELISA so the implementation of this method in diagnostic laboratories will not only improve the diagnosis of FMD but also will save time, money and effort.

GoPrime: IN SILICO TESTING OF rRT-PCR PRIMERS AND PROBES FOR DIAGNOSIS OF FOOT-AND-MOUTH DISEASE

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Introduction

PCR is an essential tool for molecular diagnostics and is considered as a gold-standard detection method for foot-and-mouth disease virus (FMDV). However, the high natural sequence variability and mutation rate of FMDV poses challenges to ensure PCR primer/probes remain fit for purpose. Traditionally, assay validation is carried out via rigorous laboratory testing, which can be timely and expensive. However, with the increased availability of published sequence data, we have developed 'GoPrime' as a novel in silico primer/probe analysis program which can accommodate sequence alignments, and which has been calibrated using empirical real-time PCR (rPCR) data.

Materials and Methods

To evaluate the impact of nucleotide mismatches (individually or in combination), rPCR analysis was performed on 90 varying synthetic DNA constructs designed around FMDV 3D (Callahan et al., 2002). The effects of mismatches in primer/probe binding regions were quantitatively investigated, looking at the increase in C_T (from a perfect match), rPCR efficiency and limit of detection (LOD). The data was used to parameterise the underlying mathematical model in 'GoPrime', which takes any given set of primer/probes, searches target genomes for potential matches and predicts an expected increase in C_T.

Results

Primer/probe-template mismatches resulted in a variety of effects, ranging from major (3'- end mismatches) to minor (5'β-end mismatches) impact on CT values and LOD but did not affect rPCR efficiency. 'GoPrime' was able to accurately predict the change in CT for naturally occurring nucleotide variations, suggesting the impact of primer/probe-template mismatches on rPCR follow a consistent and predictable pattern.

Discussion

PCR diagnosis relies upon the optimal design of primers/probes. 'GoPrime' offers a solution to rapidly predicting the sensitivity and specificity of primer/probe sets in silico. By ensuring confidence in current rPCR assays, 'GoPrime' will be used to predict the ability of FMDV rRT-PCR assays in distinguishing between different viral lineages.

DEVELOPMENT OF A REFERENCE FOOT-AND-MOUTH DISEASE VIRUS ANTIGEN PANEL FOR THE CONSISTENT VALIDATION OF DIAGNOSTIC ASSAYS

Poster

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Introduction

Foot-and-mouth disease (FMD) is highly contagious and has a significant economic impact on the international livestock trade. Foot-and-mouth disease virus (FMDV) is highly diverse, consisting of seven immunologically distinct serotypes: O, A, C, Asia 1 and Southern African Territories (SAT) 1, SAT 2 and SAT 3, and numerous sub-lineages.

Laboratory-based diagnostics play a pivotal role in the control and eradication programmes by accurately confirming the FMD status of animals with suspect clinical signs. However, the formal assessment of diagnostic sensitivity for these tests is complicated by the extent of sequence and antigenic variability that exists for naturally occurring field isolates of FMDV. Thus, the aim of this project is to prepare a reference panel suitable for the validation of existing and novel FMDV diagnostic assays.

Method & Results

Currently the panel consists of 102 isolates, covering all seven serotypes: O (n=39), A (n=21), C (n=5), SAT 1 (n=11), SAT 2 (n=13), SAT 3 (n=5) and Asia 1 (n=8). The panel represents the global diversity of FMDV by incorporating genetically and geographically distinct evolutionary lineages (topotypes), as determined by phylogenetic data generated by the World Reference Laboratory for FMD (WRLFMD). Each virus isolate was propagated in BHK-21 cells, and observed for cytopathic effect (CPE). CPE positive samples were harvested and the supernatant was tested by the ISO/IEC 17025 accredited polyclonal antigen ELISA in use at WRLFMD. Thus far, this panel has been used to assess the performance of two different antigen detection ELISAs.

Discussion

This panel will be a valuable asset, providing consistent and representative samples for assay validation exercises and inter-laboratory concordance testing. The long-term goal is to provide this panel (or a subset of these samples) as inactivated viruses, therefore eliminating the biosafety restrictions associated with shipping and handling live FMDV.

ESTABLISHMENT AND VALIDATION OF TWO DUPLEX ONE-STEP REAL-TIME RT-PCR ASSAYS FOR DIAGNOSIS OF FOOT-AND-MOUTH DISEASE

Poster

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Introduction

This study reports on the modification of two established rtRT-PCR methods to develop and validate two internally controlled one-step duplex rtRT-PCR protocols for Pan-FMDV detection.

Materials and methods

Each RT-PCR test consists of a ready-to-use master mix for simultaneous detection of the well established 3D or IRES FMDV targets and the host β-actin mRNA as an internal control target, in a single-tube assay.

Results

The two real-time RT-PCR 3D/β-actin and IRES/β-actin tests are highly sensitive and able to detect up to 7 TCID50/ml of FMDV and 10 copies/1 µl of viral RNA. In field samples, the diagnostic sensitivity was 100% (95% CI; 91–100%) for the 3D/β-actin test and 97% (95% CI; 87–100%) for the IRES/β-actin test. The diagnostic specificity was 100% (95% CI; 95–100%) for both RT-PCRs. In addition, both protocols proved to be robust, showing inter-assay coefficients of variation ranging from 1.94% to 6.73% for the IRES target and from 2.33% to 5.42% for the 3D target for different RNA extractions and RT-PCR conditions.

Discussion

The internally controlled one-step real-time RT-PCR protocols described in this study provide a rapid, effective and reliable method for the detection of FMDV and thus may improve the routine diagnosis for foot-and-mouth disease.

EVALUATION OF ALTERNATIVE CELL LINES FOR THE ISOLATION OF FDMV

Poster

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Introduction

The World Reference Laboratory (WRL) for Foot-and-Mouth disease (FMD) at The Pirbright Institute routinely utilises two cell lines in order to carry out virus isolation from clinical samples. Primary bovine thyroid (BTY) cells, prepared fresh every week, are the most sensitive cell line used for this purpose. However, these cells can vary from batch to batch, and preparation is labour intensive and requires trained staff. In addition to these logistical issues, BTY cells are a mixture of FMDV-sensitive epithelial cells and refractory fibroblasts, with the fibroblasts eventually outcompeting the epithelial cells. A continuous porcine kidney cell line, IB-RS-2, are used in conjunction with the BTY cells in order to isolate viruses from pig origin. However, IB-RS-2 cells are persistently infected with classical swine fever virus (CSFV), and as such their use is complicated by the requirement of biosafety facilities. Thus, the aim of this project is to identify alternative cell lines for FMD virus diagnosis with similar sensitivity to primary BTY cells.

Methods

An attempt was made to separate BTY epithelial cells from the fibroblasts in order to eventually generate a new continuous cell line that could be used for the isolation of FMDV. The stability and sensitivity of the cell line was evaluated after several passages using various serotypes of FMD virus and compared with freshly prepared primary BTY cells, IBRS-2 cells and ZZ-R foetal goat tongue cells.

Discussion

While primary BTY cells are the most sensitive to FMD virus isolation, ensuring their availability is laborious and expensive. In an outbreak or an endemic setting, it might also be difficult to procure thyroids from FMD-free calves. Novel continuous cell lines provide a more convenient diagnostic tool for FMD detection, provided their sensitivity is comparable to current established cell lines.

AN IMPROVED APPROACH TO WHOLE GENOME SEQUENCING OF FMDV IN CLINICAL SAMPLES

Poster

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Introduction

Next-generation sequencing (NGS) is a widely accepted tool for determining the consensus genome sequence and heterogeneity of viral populations within a single sample. However, direct sequencing of FMDV RNA in clinical samples, such as saliva and nasal swabs, particularly when the concentration of viral RNA is low, has proved challenging without prior enrichment by isolation and propagation of virus in cell culture. Here we report a target-enrichment strategy that enables direct sequencing of FMDV in clinical material, thereby avoiding the potential bias caused by inadvertent selection of viral variants that are better adapted to replication in vitro.

Materials and methods

NGS libraries were prepared from total RNA isolated from oral, nasal and rectal swabs, collected from naïve or vaccinated pigs that were subsequently challenged with O/VIT/2010 (Mya-98 lineage) or A/VIT/2005 (SEA-97 lineage), and were indexed to allow multiplexed sequencing for higher throughput. Lockdown capture probes, comprising 120-mer biotinylated DNA baits, were used to capture FMDV-specific cDNA. The hybridised probes were immobilised on magnetic beads, enabling contaminating host nucleic acid to be removed by washing prior to sequencing the FMDV-enriched NGS libraries.

Results

Following development and optimisation of the protocol using concentrated inoculum, for which the proportion of O/VIT/2010-specific sequences increased from 1.5% to 97.8% of the total reads, after enrichment, sequencing was undertaken on clinical samples containing variable concentrations of viral RNA. Full-length genome sequences were obtained from 22 of 24 serotype O samples and 12 of 15 serotype A samples, while near full coverage was obtained for the remaining 5.

Discussion

We have demonstrated proof of concept for obtaining high quality full-length FMDV genome sequence data from clinical samples. Such data will provide further insights into, and enhance our understanding of, the infection dynamics and evolutionary processes of this highly varied and complex viral pathogen.

COMPARISON OF TWO COMMERCIAL NSP ANTIBODY TESTS (PRIOCHECK® AND IDVET®FMDV NS ELISAS) TO DETECT INFECTION IN VACCINATED ANIMALS (DIVA)

Poster

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Introduction

NSP antibody tests are used to differentiate infection in vaccinated animals (DIVA). In cattle, the NSP tests (targeting the NSP 3ABC) that provide the highest sensitivity can detect up to 90% of vaccinated animals that become carriers after exposure to infection, with a specificity of 98-99%. Due to insufficient diagnostic sensitivity and specificity, detection of a low level of infection is difficult at the population level with a high degree of confidence. The low level nonspecificity response can be overcome by retesting samples scored positive using a second confirmatory test which should have at least comparable sensitivity to the first test. We previously reported results of a preliminary evaluation of a new commercial 3ABC NSP test (IDvet®FMDV NS ELISA) that provides good diagnostic sensitivity and specificity. Therefore, the main aim of this study is to validate and compare the diagnostic performance of both PrioCHECK® and IDvet®FMDV NS commercial ELISAs. Further we have accessed the benefits of using these two assays as screening and confirmatory tests to increase the diagnostic specificity and sensitivity.

Materials and methods

To determine the diagnostic specificity 991 naïve cattle sera and 130 vaccinated cattle sera are used. To determine the diagnostic sensitivity, serum samples from several experimental FMD vaccine/challenge studies (O, A, Asia1 and SAT serotypes) in cattle consisting of unvaccinated infected-recovered, unvaccinated infected-carriers, vaccinated infected-recovered and vaccinated infected-carriers animals are used. Further a published panel of 36 bovine sera from vaccinated and subsequently infected cattle and a set of 159 field sera from vaccinated known clinically infected Turkish cattle are also tested.

Results and discussion

Both PrioCHECK® and IDvet® (long and short incubation) MDV NS commercial ELISAs revealed 100% sensitivity and greater than 99% specificity for unvaccinated infected cattle. In vaccinated animals the detection was lower (80-85%) with similar level of specificity (>99%). Both the commercial tests detect 91.67% infection for panel samples and 97-100% infection for known clinically infected field samples with a specificity of >99%. The sensitivity and specificity of detection of infection further increased when both the commercial tests are used as screening and confirmatory tests. In conclusion both the commercial tests have enough sensitivity and specificity to detect infection in vaccinated as well as unvaccinated infected cattle.

DETECTION OF FMD VIRUS CARRIER CATTLE: DEVELOPMENT AND EVALUATION OF AN IGA ELISA KIT FOR O, A AND ASIA1 SEROTYPES

Poster

Krupali. Parekh[*] and Satya Parida[1]

[1]The Pirbright Institute, Ash Road, Pirbright, Woking, Surrey GU24 0NF, UK

Introduction

Since carriers may be considered a risk for transmitting infection, they should be identified by post-vaccination serosurveillance to substantiate freedom from infection and to regain the FMD-free status for the purpose of international trade. Assays against non-structural proteins (NSP) are used to differentiate between vaccination and infection. Recently we have reported that, NSP tests do not exclusively detect the carrier animals as they also detect the animals that were recovered from both clinical and sub-clinical FMD infection. In contrast, we have shown IgA antibody as an indicator of oro-pharyngeal replication of FMD virus and therefore IgA test detects only the present infection. In our previous reports we have developed IgA tests for O and A serotypes. In this present study we further detect the carrier cattle that were infected with Asia1 serotype FMD virus. Finally, we have developed and validated a single IgA ELISA kit for O, A and Asia1 serotypes that has been validated with large number of samples. A comparison has been made between inactivated FMD virus antigens and recombinant FMD empty capsids in the IgA assay for all the three serotypes.

Materials and methods

600 naïve cattle saliva/nasal fluids were tested for IgA test to detect the specificity of the assay. Several thousand saliva and nasal samples from vaccinated infected cattle from 7 homologous and 5 heterologous potency tests covering O, A and Asia1 serotypes and several hundred saliva/nasal samples from field outbreaks were evaluated in IgA ELISA kit. Further we have replaced the inactivated FMD virus antigen with recombinant FMD empty capsid in the IgA assay for all the three serotypes which facilitate to carry forward the assay outside the containment. Wherever possible, a comparison (ROC analysis) was made between the performances of detecting carrier animals by different tests viz; mucosal test, NSP test and antigen test (PCR + virus isolation).

Results and Discussion

The IgA ELISA kit is developed and evaluated for O, A and Asia in a single plate. We have evaluated inactivated antigen verses empty capsid in the kit and found similar level of carrier detection. All the three serotypes IgA ELISA performed well to detect the carrier animals in these experiments and comparable to VI and PCR results.

Acknowledgements

Funding from Defra, UK through SE 1128 is acknowledged.

THE CHALLENGES OF USING IN-VITRO TESTS FOR VACCINE MATCHING

Poster

Abdelghani (Abid) Bin-Tarif[1], Bob Statham[1], Anna B. Ludi[1], Donald P. King[1]

[1] The Pirbright Institute, Ash Road, Pirbright, Woking, UK, GU24 0NF on behalf of partner laboratories in the EURL, OIE/FAO FMD networks

Introduction

The Pirbright Institute is the OIE, FAO and EU Reference Laboratory for Foot-and-Mouth Disease (FMD). The Serum Assay Unit carries out vaccine matching tests for international samples received by the World Reference Laboratory (WRL), to characterise the antigenic relationship (r1-values) between circulating field strains and vaccines.

Materials and Methods

The method carried out is the two-dimensional virus neutralisation test for strain differentiation as described in the OIE Manual of Diagnostic Tests and Vaccines for Terrestrial Animals (Chapter 2.1.8). Efforts are being made within the OIE/FAO Network to collate and exchange representative reagents for a range of different vaccines (available from international suppliers and local vaccine producers). This network specifies that the vaccinal sera used is monovalent, non-boosted, 21-28 days post vaccination and a pool of five cattle with individual titres mid-range.

Results

The poster highlights the vaccine matching that has been carried out, with emphasis on O/ME-SA/Ind-2001 and A/ASIA/G-VII. These two lineages highlight the continuous antigenic evolution in the Middle East and the role of using r1-values in selecting a heterologous vaccine candidate when a vaccine within the same lineage is not available.

The data will be analysed according to the seven endemic pools and serotypes. More than 195 samples from approximately 38 countries have been tested.

FMD Serotype	Samples Tested	Vaccine used
A	51	A/IRN-05, A22-IRQ, A/TUR/06, A/MAY/97
O	97	O/3039, O/Manisa, O/TUR/5/2009
SAT1	11	SAT1/RHO
SAT2	24	SAT2/ERI, SAT2/ZIM
Asia1	12	Asia1/Shamir

Discussion

In the future the WRL along with international reference laboratories of the OIE/FAO Network is working to harmonise and improve the robustness and repeatability of the vaccine-matching test.

ISOLATION OF CAMELID NANOBODIES FOR COST EFFECTIVE DIAGNOSTICS OF FMDV IN UGANDA AND THE DEVELOPING WORLD

Poster

Sigal Gelkop[1], Shlomit Fedida-Metula[1], Ariel Sobarzo[1], Julius Lutwama[2], Elizabeth Rieder[3], Zaheer Ahmed[3], Victoria Yavelsky[1,2] and Leslie Lobel[1,2]*

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Foot-and-mouth disease (FMD) is caused by infection with foot-and-mouth disease virus (FMDV), a picornavirus, and is a serious threat to food supplies and economies. Seven different serotypes of FMDV have been identified. Development of a simple, rapid and sensitive DIVA diagnostic remains a challenge given that most affected animals are in the developing world. To develop inexpensive and economically sustainable diagnostic kits for the developing world we focused our efforts on developing such kits for Uganda. Most efforts toward control of the disease in Uganda have been hampered by lack of economical diagnostics for detection of local isolates of the virus as well as effective vaccine matching.

To ameliorate this situation, we are developing a diagnostic based on camelid monoclonal single chain antibodies, also known as nanobodies. Nanobodies have the major advantage of greater thermostability and can be produced in bacteria. As such, they are ideal for cost constrained environments and when the cold chain might also be a barrier to dissemination. Our work is aimed at producing nanobodies against FMDV NSP proteins; FMDV-3ABC and FMDV-3D recombinant proteins for production of DIVA diagnostics. We have thus far generated a large library of camelid nanobodies specific to 3ABC and 3D proteins that were expressed in Escherichia coli and purified. Sequence analysis of the nanobodies revealed that we possess five classes of nanobodies against FMDV-3ABC and five classes of nanobodies against FMDV-3D. Initial characterization of these nanobodies' affinity and specificity revealed that they have relatively high apparent affinity and recognize their respective target proteins with detection sensitivity in the ng/ml range in indirect, sandwich or competition ELISA. They are being further evaluated for specificity and sensitivity of binding to different viral strains and Ugandan isolates for the selection of the most optimal reagents for production of FMDV diagnostic assays.

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DAY 3

GLOBALIZING ACCESS TO SCIENCE AND INNOVATION: CONNECTING LIVESTOCK KEEPERS AND KNOWLEDGE LEADERS

SESSIONS

	room*	room*	room*	room*
9.00h	G1. Modelling Network: Innovators and innovations looking for a place to practice	G4. Innovative surveillance options for field use	G7. FMD vaccination in endemic settings: Optimising schedules and vaccine efficacy trials	G10. New developments in wildlife (FMDV in African buffalo)
11.00h	G2. Contingency Planning and Emergency Vaccination Network: Our plans for the future	G5. Diagnostics: harmonisation of laboratory tests, and tools to share sequence data	G8. Closed Meeting on Licensing Novel Vaccines *Invitation only*	G11. Pathology and pathological basis of persistence
13.30h	G3. The role of regional laboratory and epi networks in improving international surveillance for FMD	G6. Biocontainment of FMDV: challenges and solutions for laboratory biorisk management	G9. Vaccine quality assurance (VQA) initiative: what is proposed and how do we move it forward?	G12. Funding innovation: Q&A
15.30h				

* Will be notified during the conference / Session 12: Plenary Room

INNOVATION IN EDUCATION AND KNOWLEDGE EXCHANGE: LAUNCHING THE PROGRESSIVE CONTROL PRACTITIONERS' NETWORK

Organisers: Jenny Maud and Chris Bartels (EuFMD)

Summary

This session will cover

- Ideas and plans for identifying the training and capacity building needed for improved control of FMD.
- Using technology for networking and training; experiences, advantages, ideas and challenges.
- The launch of a new network for knowledge exchange on progressive control of FMD.

Background

The progressive control of FMD requires improvements in the knowledge and skills of all those involved in disease control, from the livestock keeper, to the local veterinary services, veterinary managers or decision maker. All of these diverse groups can be considered potential "Progressive Control Practitioners". In this session we seek your experiences and ideas for new ways to train and connect to these global practitioners. Who are they, what do they need to learn, and how can we best train them?

Who is the session aimed at?

Those interested in:

- Building capacity for FMD control, particularly in non-free countries.
- New ways of translating research findings into practical solutions for those "practitioners" on the front line of disease control.
- How practitioner networks may help channel bottom-up demand for information and technical innovations

Format

The session will consist of a number of short presentations interspersed with guided brainstorms and discussions.

We will

- Share experiences of innovative approaches to training;
- Hear directly from "Progressive Control Practitioners" around the world, who will join us in person and by online link to discuss the training needs and solutions for their regions.

Aim of the session

This session is intended to be a catalyst for a new online network for peer-to-peer knowledge exchange on progressive control of FMD. The outcomes of our discussions will feed directly into the development of the network.

"WWW.TRAINING" : THE WHO, WHAT AND WHERE OF BUILDING CAPACITY FOR FMD CONTROL IN THE INFORMATION AGE

Jenny Maud, Chris Bartels, Keith Sumption, Magdalena Gajdzinska, Karima Ouali and Gunel Ismayilova

European Commission for the Control of Foot and Mouth Disease, Animal Health Service, Food and Agriculture Organization of the United Nations, Rome, Italy.

Introduction

The European Commission for the Control of Foot and Mouth Disease (EuFMD) has a broad remit to improve preparedness for FMD outbreaks amongst its Member States, and to assist the Progressive Control of FMD in the European neighbourhood and globally. The Commission's activities increasingly involve the provision of training. Faced with large audiences requiring training on a broad range of topics, and limited resources, EuFMD has conducted needs assessments across its membership and neighbourhood in order to identify key audiences for training, and prioritise the knowledge and skills most needed by these audiences. EuFMD has extensively trialled the use of e-learning and virtual networking as a method of cost effective training of geographically distant professionals, many of whom share common training needs.

Methods

A questionnaire based training needs assessment was sent to focal points in 37 EuFMD Member States and 20 countries in the European neighbourhood. Questions included assessment of perceived competencies of veterinary services and stakeholders in a range of areas relating to FMD preparedness and control, and details of languages spoken and technology availability. Online training courses have been provided to over 2500 veterinarians in 7 languages, in over 40 countries. Participants complete an assessment and feedback survey at the end of the courses.

Results

Training needs assessments have identified a number of priority areas and personnel groups for training, which will be detailed during our presentation. Feedback for online courses is good with 75% of respondents rating the course as "excellent". Courses provided in local languages lead to particularly high levels of interaction.

Discussion

Online training and networking is one of a number of tools which can be used effectively to assist capacity building for FMD control. Our discussion at the Open Session will focus on the next steps to extend these initial activities to broader audiences.

THE WAY FORWARD TO FMD FREEDOM: WHAT ARE THE TOOLS AND PROCESSES AVAILABLE?

Organisers: FMD Working Group of GF-TADs (OIE and FAO)

Summary

This session will cover

- The existing tools (PCP – Progressive Control Pathway; PVS - Performance of Veterinary Services; PVM - Post Vaccination Monitoring guidelines; RBSP Template)
- The existing processes (Regional roadmaps including the regional assessment of PCP-FMD stages; the OIE procedure for official recognition of FMD freedom)
- The way forward

Background

In the past decades, some regions and sub-regions of the world have managed to control or even eradicate FMD. However, around 100 countries still do not have an FMD-free status. The Global Strategy has been designed and adopted in 2012 to improve FMD control in regions where the disease is still endemic or sporadic, thereby protecting the free status gained by other regions of the world. Since 2012, a set of tools and processes have been used to implement the Global strategy.

The objective of the session is thus to present those tools and processes and to explore further how best could the Global Strategy be implemented at national, regional and global level.

Who is the session aimed at?

Those interested in:

- Controlling FMD in their country
- Being involved in the overall process of FMD control and eradication at regional or global level
- Supporting countries in controlling FMD

Format

After a brief presentation on the existing tools and processes, the session will propose guided discussions on the following questions:

- Is FMD control achievable by 2027? (= all countries at least in PCP-FMD Stage 2)
- How best implement the Global FMD Control Strategy?
- How committed countries could be best supported?
- How countries that are not yet committed to FMD control could engage in this global strategy?

Aim of the session

The conclusions will assist with GF-TADs FMD Working Group in further engaging and supporting countries to FMD control.

HOW WOULD YOU CHANGE THE MANAGEMENT MINDSET OF A VETERINARY ORGANIZATION TO INCORPORATE A RISK-ORIENTED APPROACH TO FMD CONTROL?

Organizers: Chris Bartels (EuFMD)

Summary

This session will cover

- Why introducing risk-oriented approach to FMD management matters
- What problems are met in changing current management norms found in countries in lower PCP stages
- How changes in management could be introduced
- What forms of individual or group training make a difference in equipping people for change management

Background

The PCP approach to FMD control is a risk-based, and similar to the HACCP approach, requires monitoring and evaluation with regard to the principal risks and control points, during implementation and to evaluate impact. For many country situations, this approach requires a change to the management mindset of the veterinary organization. Such organizations currently often have independently-operating departments, each playing a role in implementation of parts of the critical control points of programmes. The effective management of risks , such as in PCP Stage 2 and above, involves organizations monitoring and acting upon information from the combined efforts of multiple departments. Delivering effectively may require change from organization administering the distribution of vaccines to the field, to evaluation of the effectiveness of vaccination campaigns delivered by public and private actors.

Who the session is aimed at

Those interested in change management, and the associated area of training.

Format

After a short introductory presentation, and depending on numbers, we will have facilitated group discussions on propositions relevant to change management and risk-orientation.

Aim of the session

We like to discuss this need for change management in particular in relation to building sufficient epidemiologic competence for FMD control. We wish to share experience and discuss how changes to the organizational mind set to incorporate a risk-oriented approach for developing FMD control may be introduced.

From these discussions, we hope to draw conclusions on how we can further improve our approaches to training on PCP-FMD, and identify those interested to work together more on this area in future.

TRAINING FOR CHANGE OR CHANGING THE TRAINING

Dr Chris J.M. Bartels, Dr Jenny Maud, Dr Keith Sumption
European Commission for the Control of Foot-and-Mouth Disease

Introduction

Over the course of time, the approach of EuFMD has changed from direct support to FMD control through the provision of diagnostic kits and vaccines, to an array of training and coaching activities with the focus to change FMD control management. Through our collaboration with national veterinary services, private and public stakeholders such as dairy cooperatives and university docents, and with primary producers, EuFMD has come to understand that there is a great need to support mechanisms that facilitate the changes needed. These changes are needed at different dimensions and with different time horizons.

For the diagnostic laboratories, the changes are from diagnostic services to surveillance of FMD to support understanding of FMD occurrence. For FMD control, there is a change from mass vaccination campaigns to a risk-based approach based on understanding the transmission and impact of FMD virus while acknowledging that resources such as time, people and money are limited.

With different approaches in the technical fields of disease management, we observe the need for changes in infrastructure and organisations of disease management. For one, complete, accurate and timely data on FMD occurrence and livestock populations need to be available at central level in a non-aggregated manner. Digitalisation of data to support its seamless flow, validation and analysis is possible with new technologies. However, the veterinary services are often not ready for these changes as they have rigid vertically-organised departments with little interaction between departments. Integrated disease management such as FMD control (or the combined control of FMD and LSD, FMD and PPR), there is need for a multi-disciplinary team or task force. Additionally, and possibly the most important need is for the veterinary services is to become a competent authority that oversees, supervises and monitors FMD control while other stakeholders such as private veterinarians, semi-public organisations are to implement FMD control.

Discussion

EuFMD is anticipating these needs for changes by establishing networks and offering an array of e-training modalities (see other presentations). We are well aware that training in its own right may change the attitude and practice of individuals. However, it is far from having changes made at an institutional level. In this presentation we further discuss the need for additional tools to motivate countries to adopt a different disease control strategy including going through an institutional change.

MODELLING NETWORK: INNOVATORS AND INNOVATIONS LOOKING FOR A PLACE TO PRACTICE

Summary

Organisers: Mark Hovari (EuFMD) and members of the EuFMD Special Committee for Research and Programme Development

This session will cover

- Discussions on how models can help disease managers in practice.
- Discussions on how to bring modelers (supply) and model users (demand) closer together.

Background

The objective of this session is on one side to bring together modelers to a common platform to exchange thoughts on how to accelerate the update of modelling innovations into practice in decision support on planning for disease management. On the other hand, this session also aims to enable the interests and needs of the public services, risk managers and contingency planners to be shared with the modelers so that progress on innovation can be discussed and the needs of different parties clarified.

Who is the session aimed at?

This session is mainly intended for epidemiologic and economic modelers, people involved in contingency planning and emergency preparedness and staff of veterinary services.

Format

The session will start with a presentations and then be followed by participative small group discussions or guided discussions.

We wil

- Present the CroBoDiMo project and discuss further possibilities.
- Discuss experience on obtaining data held by public services (e.g on animal movements) for modelling.
- Follow up the major innovations identified in sessions P6 on Preventing FMD on day 2.
- Identify issues of particular importance can then be prioritised for support.

Aim of the session

This session is intended to guide the future development of the modelling network and its relationship to the emergency management network. Topics or issues of particular importance can then be prioritised for support in the workplans for 2017.

CONTINGENCY PLANNING AND EMERGENCY VACCINATION NETWORK: OUR PLANS FOR THE FUTURE

Organisers: Mark Hovari (EuFMD) and members of the EuFMD Standing Technical Committee

Summary

This session will cover

- Discussion on the tools developed by EuFMD on supporting emergency preparedness of countries
- Discussion on vaccination to live issues
- Discussions on how countries could support each other to increase emergency preparedness

Background

The objective of this session is to bring together people involved in emergency preparedness for FMD. Although focussed on Europe, the issues are probably common to all regions and the session is open to all.

Countries free of FMD without vaccination generally put a lot of effort to maintain adequate level of emergency preparedness in case of an unexpected FMD outbreak. Several tools are available to ensure preparedness such as training, contingency planning and simulation exercises. As FMD by nature is a disease that forces veterinary services to see the big picture, an optimal level of preparedness can only be achieved by developing and maintaining relationships with other stakeholders. This big picture then further expands to neighbouring countries and entire regions, as the decisions made by one have an influence on many.

Therefore, this session is aimed at discussion on the recent changes experienced by countries and how regions with developed preparedness can aid those still making the first steps.

Who is the session aimed at?

This session is mainly intended for people involved in contingency planning and emergency preparedness, staff of veterinary services and modelers interested in this topic.

Format

The session will start with presentations and then be followed by participative small group discussions or guided discussions

We will

- Demonstrate examples of National training courses conducted.
- Present the knowledge bank, the Contingency Planning on-line self-assessment tool and the Handbook for the planning and preparation of simulation exercises.
- Introduce the economic calculator.

- Discuss the future of the practical management series.
- Discuss Vaccination to live policy issues in practice.
- Discuss how regions developing their emergency preparedness be supported by other countries.
- Follow up the major innovations identified in sessions 2 Livestock sectors and disease emergencies and session 4 Vaccination as an option on day 1.

SESSION G2

Aim of the session

This session is intended to guide the future development of the emergency preparedness network. Topics or issues of particular importance can then be prioritised for support in the workplans for 2017.

THE ROLE OF REGIONAL LABORATORY AND EPI NETWORKS IN IMPROVING INTERNATIONAL SURVEILLANCE FOR FMD

SESSION G3

Organisers: K. van Maanen and D. King

Summary

The session will cover

- An introductory talk about activities and challenges of the currently existing FMD laboratory and epi networks in pools 3, 4 and 5 and the involvement of EuFMD.
- Discussion about critical success factors for these networks and major issues experienced.
- Discussion about ways forward to empower these networks and to improve critical aspects of active and passive surveillance e.g. timely outbreak investigation, sample collection, sample transport, diagnostic testing, data collection and data sharing.

Background

Foot-and-mouth disease (FMD) is an economically devastating disease. It is highly contagious and has the potential to spread widely and rapidly, affecting cloven-hoofed animals, such as cattle, swine, sheep, goats, and deer. A widespread outbreak of the disease in any country would create disastrous economic consequences. Many countries in Africa, West Eurasia and Asia are still endemically infected with FMD. The virus circulates mainly within so-called pools, but also regularly jumps between pools. Therefore it is of utmost importance that passive and active surveillance is carried out in a cost-efficient and risk-based manner and that reliable laboratory and epidemiological data are produced and shared. Active regional networks can play a crucial role in the coordination and implementation of surveillance systems and will contribute to transparency and mutual trust.

Who is the session aimed at?

All laboratory scientists, representatives of OIE, FAO and National Reference Laboratories and epidemiologists interested in FMD surveillance in endemically infected countries and regions

INNOVATIVE SURVEILLANCE OPTIONS FOR FIELD USE

Organiser: Labib Bakkali-Kassimi (ANSES) and members of the EuFMD SCRPD

Summary

This session will cover

- Recent developments in field applicable penside/rapid diagnostic test systems.
- Issues remaining to be resolved.
- Discussions on how to improve participation of livestock owners and veterinarians in improved passive surveillance.

Background

Rapid, robust, accurate confirmation and typing of FMDV is a vital part of decision making in FMD emergencies in free countries. In endemic countries, there are also many potential uses, with typing of the virus in the field important to determine the serotype to be included in vaccination, and also for detection of antibody (e.g. for post-vaccination response). As many laboratories do not process many samples, and may not be equipped for live virus manipulations, tests conducted in the field or in field laboratories may potentially assist decisions that are required to be made at field level. Robust tests may also have a role in reducing operator error associated with complex lab based biological assays. In addition, new work indicates that some penside tests media can be used to transport FMDV RNA in a safe form that could reduce risks and costs of transport to labs. Potentially lateral flow devices (LFD) and other such media may act as a first screening in the field, and if adequate virus for a positive result, these could be sent for more advanced typing tests (including sequencing, even transfection to recover live virus) , a potential revolution in submission of samples to reference centres.

Who is the session aimed at?

Those interested in:

- The potential of field based and rapid robust tests in surveillance
- Those involved in field surveillance projects, or interested to support increased levels of typing in endemic regions

The session will consist of a number of short presentations followed by guided brainstorms and discussions.

We will

- Hear from leaders in the field
- Discuss the most promising new results and methods, and how these may be brought to the field
- Identify how the new technologies may assist to make surveillance more useful to those that need to act on the results

- Identify priorities for work needed to progress the concept of "biosafe transport of FMDV from the field"

Aim of the session

This session is intended to share progress in this field and to identify priorities for future support to improve the uptake of new methodologies, and to reduce the difficulty of submission of samples for specialised reference centre services. Passive reporting of FMDV has many constraints and the aim is also to help technology developers understand what other factors matter for improving reporting and sampling.

EVALUATION OF ORAL SWABS FOR FMDV SURVEILLANCE

P.D. Kirkland[1], R.J. Davis[1], B. Haas[2], K. Wernike[2] P.L.Eble[3], A. Dekker[3] and M. Beer[2].*

[1] Elizabeth Macarthur Agriculture Institute, Menangle NSW, Australia; [2] Institute of Diagnostic Virology, Friederich Loeffler Institute, Insel Reims, Greifswald, Germany; [3] Central Veterinary Institute of Wageningen UR (CVI), Lelystad, The Netherlands

Introduction

Clinical signs in sheep can be vague or difficult to detect. There is need for a laboratory method to support large scale surveillance. The objectives of this project were to apply high through-put qRT-PCR to detect FMDV in oral fluid and to estimate the level of sample pooling that is possible.

Materials and methods

Oral swab samples from sheep experimentally infected with either Asia 1 or O Manissa viruses were tested. After virus inactivation, total nucleic acid was purified using a magnetic bead based kit. The 3D qRT-PCR protocol was followed. To assess detection of FMDV in pooled samples, individual samples taken at either the onset or near the end of the virus detection period were diluted in pooled oral fluid collected from uninfected sheep.

Results

The qRT-PCR assay detected FMDV in almost all oral swabs in the first 10 days after infection and 65% of samples were positive at 30 days post infection. The qRT-PCR was more sensitive than virus isolation. Sample pooling studies showed that it was possible to detect a single positive sample in a pool of ten samples during the early stages of infection and to detect one positive in a pool of at least 5 samples one month later.

Discussion

Collection of oral swabs and testing by high throughput qRT-PCR adds a new dimension to the detection of FMDV in sheep and will facilitate surveillance. As virus levels in sheep are low compared to cattle and pigs, it is expected that this sampling strategy can also be readily applied to monitoring of these species.

USE OF LATERAL FLOW DEVICE FOR SAFE AND LOW COST SHIPMENT OF FMDV SUSPECTED SAMPLES

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Université Paris-Est, Anses, Laboratoire de Santé Animale, UMR1161 Virologie, 14 Rue Pierre et Marie Curie, 94700 Maisons-Alfort, France.

Introduction

Identification of circulating strains is an essential step towards the global eradication of FMD. However, the cost of sending FMD samples due to shipping conditions is an obstacle to submission of samples to Reference Laboratories. We developed a low cost and safe method for shipment of FMD samples.

Materials-methods

7 FMDV strains (representative of the 7 serotypes) were deposited onto penside tests (LFD, Svanodip®). After 30 min, LFDs were soaked in 0.2% citric acid bath for 15 minutes. Strips were disassembled and grounded. IBRS-2 and ZZ-R127 cells were incubated with the supernatant for 48 hours. In parallel, viral RNA was extracted from the supernatant. Real-time RT-PCRs targeting FMDV genome (3D-IRES) were performed. In addition, extracted RNA was transfected into cells monitored for CPE. The same method was evaluated on 9 positive field samples.

Results

After treatment of positive LFDs in a 0.2% citric acid bath, FMDV was inactivated. Viral RNA was however detected by 3D and IRES rtRT-PCR. Live virus was rescued after transfection of RNA extracted from inactivated positive LFD. Similar results were obtained (i) after incubation of the LFD at 37°C, (ii) from positive LFD soaked in a 5% citric acid bath, (iii) and on 9 field samples. However, FMDV live virus was rescued only from 2/9 RNA samples from field.

Discussion

After live FMDV collection on LFD and chemical treatment, FMDV is inactivated but viral RNA is detectable by rtRT-PCR and live virus is rescued after RNA transfection. Evaluation and validation of this process on field samples will be continued, particularly by improving transfection method.

PROGRESS TO DEVELOP PRACTICAL FIELD-BASED TOOLS FOR DETECTION OF FOOT-AND-MOUTH DISEASE VIRUS

V. L. Fowler[1], E. Howson[1,2], V. Mioulet[1], N. Lyons[1], S. Cleaveland[2], T. Lembo[2], D. P. King[1]

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Introduction

Accurate, timely diagnosis is essential for control of foot-and-mouth disease (FMD). Samples are currently tested at reference laboratories, transport to which delays critical decision making. We have recently compared three rapid, molecular field based assays [mobile rRT-PCR, rRT-loop mediated isothermal amplification (rRT-LAMP) and rRT-recombinase polymerase amplification (rRT-RPA)] and simple sample preparation methods (QIAamp®, Manual Magmax, dilution in water, chelex 100™, Acrodisc syringe and Ag-Lateral Flow Device elution wash), for molecular detection of FMD virus (FMDV) and benchmarked their performance against the "gold-standard" laboratory-based real-time reverse transcription-PCR (rRT-PCR) and extraction methods (Automated MagMax).

Materials and Methods

Analytical sensitivity was determined using an FMDV RNA standard and diagnostic sensitivity was determined using RNA extracted from a panel of clinical samples (n=32). Dilution series of FMDV spiked into a) epithelial suspension, b) serum and c) oesophageal-pharyngeal (OP) fluid were used to validate simple sample preparation methods. The final protocols were field tested in endemic settings in Kenya and Tanzania.

Results

The analytical sensitivity of rRT-PCR (mobile and gold standard), rRT-LAMP and rRT-RPA was 10^1, 10^1 and 10^2 RNA copies, respectively. The use of field applicable QIAamp® and manual Magmax extraction maintained analytical and diagnostic sensitivity of all tests comparable to automated extraction results, all other sample preparation methods resulted in loss of analytical sensitivity. However, for mobile rRT-PCR and rRT-LAMP this loss was only one log and still permitted the accurate detection of positive clinical cases within endemic settings.

Discussion

This study is the first standardised comparison of the diagnostic performance of a range of field based tests and associated simple sample preparation protocols. Results indicate that we can use simple sample preparation methods to confidentially and rapidly confirm FMD clinical cases in situ using both rRT-PCR and RT-LAMP; however at present these methods require further work for confirmation of negative cases.

DEVELOPMENT OF A SUCCESSFUL SURVEILLANCE MODEL FOR FOOT AND MOUTH DISEASE IN PAKISTAN

M. Hussain, M. Afzal, E. Khan, J. Arshad, N. Panhwar and A. Ahmad

FAO Project GCP/PAK/123/USA Progressive control of foot and mouth disease in Pakistan, Islamabad

Introduction

Although Pakistan has a vast network of veterinary service in the country, surveillance system for transboudary livestock diseases is weak. Only a few outbreaks of FMD are reported annually. In the absence of an effective surveillance system, it was not feasible to develop a strategy for the control of FMD in the country. Therefore, efforts were made to develop an effective surveillance system for FMD in the country.

Materials and Methods

A FMD Surveillance Model was developed with main focus on (i) FMD awareness seminars for livestock farmers (ii) training workshops for field veterinary staff (iii) provision of sample collection kits to the trained veterinary staff (iv) cover expenditure of sample collection and dispatch to a diagnostic lab (iii) respond back with outbreak handling; and (vi) report back to field staff on lab findings. Existing staff of the veterinary service undertook actual implementation of the field activities.

Results

Implementation of this surveillance model resulted in large number of FMD outbreaks from all areas of Pakistan. 7579 outbreaks of FMD were reported and controlled in the country in 3.75 years. During outbreak handling, 10,862 sick animals were treated and ring vaccination covered 241,039 animals. A total of 143 awareness seminars for 5928 farmers and 80 training workshops for 1994 veterinarians and 447 veterinary assistants were held during the project. Serotype and genotype data of the FMD outbreaks in Pakistan was generated.

Discussion

Application of surveillance model significantly improved FMD outbreak reporting in the country. Results assisted in determining pattern of the disease as well as hot spots in the country. Based on the findings of the project a Risk-based Control Strategy (RBCS) was developed. RBCS was approved by the Government of Pakistan and a national program based on the strategy is under active consideration.

DIAGNOSTICS: HARMONISATION OF LABORATORY TESTS, AND TOOLS TO SHARE SEQUENCE DATA

Organisers: D. King and K. van Maanen

Summary

Brief background

- FMD diagnostic laboratories need to be able to respond to suspect cases of FMD. FMDV is a highly variable and constantly evolving virus, and different diagnostic systems are employed in different laboratories for routine diagnostic purposes. The annual proficiency test (organised by WRLFMD/EU-RL for FMD) assesses the performance of laboratories and is central to the implementation of QA systems. This session will review results from the most recent proficiency testing scheme and will discuss factors that influence the performance of diagnostic tests (particularly focussing on antigen ELISAs for FMDV).
- Exchange of viral sequence data is becoming increasingly important and WRLFMD is working towards the implementation of a bespoke sequence database for FMDV. It is anticipated that this systems will be made available to the FMD community and during this session, feedback is welcome to consider and prioritise features that should be included in these new web-based tools.

The session will cover

- Results from the proficiency testing exercise
- Feedback on the performance of diagnostic assays
- Viral inactivation protocols
- Laboratory capacity and outbreak management
- New web-based tools to analyse FMD virus sequence data

Who is the session aimed at?

All laboratory scientists, representatives of OIE, FAO and National Reference Laboratories and epidemiologists (particularly molecular epidemiologists!)

After the talks – discussion will focus on approaches that can be used to analyse and exchange FMD viral sequence data. There will be opportunities to collect feedback regarding the design of new open access web-based tools and to highlight priorities for specific features and tools that are needed by the FMD community.

RESULTS OF THE 2015 PROFICIENCY TESTING SCHEME

Anna B. Ludi[1], Ginette Wilsden[1], Lissie Henry[1], Valerie Mioulet[1], Britta Wood[1], Ashley Gray[1], Barsha Thapa, Bryony Armson[1], Julie Maryan, Sarah Belgrave[1], Donald P. King[1]

[1] The Pirbright Institute, Ash Road, Pirbright, Woking, UK, GU24 0NF on behalf of partner laboratories in the EURL, OIE/FAO networks

Introduction

The Pirbright Institute as the OIE, FAO and European Union Reference Laboratory for Foot-and-Mouth Disease (FMD) carries out an annual proficiency testing scheme for laboratory tests. National EU Reference Laboratories, OIE and FAO Reference Laboratory as well as regional laboratories from all FMD endemic pools were asked to participate. Laboratories have received their individual feedback and the final report with recommendations. The purpose of this presentation is to provide an overview of the scheme for the 2015 exercise (Phase XXVIII) and introduce the new scheme for 2016 (Phase XXIX).

Materials and Methods

During 2015, three panels were made available to each laboratories:

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

Panel 2: Non-infectious materials originating from pigs and cattle with a vesicular condition for FMD antigen and virus genome detection.

Panel 3: Non-infectious materials from vaccinated or non-vaccinated cattle for FMD serological.

The particular diagnostic methods that the laboratories utilise were not specified; rather, it was up to each laboratory to use the appropriate tests.

Results

Seventy-eight countries participated in the 2015 PTS. This included twenty-seven EU member states, eight EuFMD member states (non-EU), eight neighbouring EU countries and ten Global Network Laboratories. The presentation highlights the tests laboratories are using and the overall performance of assays.

Discussion

Changes will be made to the 2016 PTS which will place greater emphasis on outbreak response. These changes will be highlighted during the presentation.

VIBAsys AND FMDV-Tools: PRACTICAL RESOURCES FOR FOOT-AND-MOUTH DISEASE VIRUS SEQUENCE ANALYSIS

J. Kim [1], L. Ferretti[1], K. Bachanek-Bankowska[1], N. Knowles[1], D.P. King1, P. Ribeca[,1]*

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Introduction

The FAO World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD), located at The Pirbright Institute, has collected and characterised thousands of samples from field outbreaks of foot-and-mouth disease virus (FMDV). These samples are routinely sequenced (using protocols to amplify VP1) and thanks to high-throughput sequencing technologies, a progressively larger fraction of this collection is being sequenced at the full genome level.

Materials and methods

New in-house information systems have been implemented in order to manage and track samples and sequence data. A robust, normalized and efficient abstract database scheme powers a flexible LIMS system and facilitates curation of the WRLFMD collection, as well as access to customised pipelines for bioinformatic analyses. The web interface is designed to be user-friendly and enable reproducible and accurate generation of scientific results.

Results

We present VIBASys (Virus Information and Bioinformatics Analysis System) and FMDV-Tools, practical resources for FMDV sequence management, comparison and analysis. These systems allow semi-automatic production of reports for the WRLFMD, as well as user-driven generation of sequence annotation and phylogenetic classification in a web-based format. They have been designed to be fully scalable (from VP1 to full genome) and can accommodate large number of sequences.

Discussion

VibaSys and FMDV-Tools are flexible resources that can be adopted by any Reference Laboratory both for internal and external use and adapted to different viruses. We believe they provide a significant step forward towards the improved sharing and democratization of FMDV sequence data between reference laboratories and among the FMDV research community.

ANTIGEN-DETECTION ELISA PERFORMANCE VS VIRUS EVOLUTION

Poster - P2

V.Mioulet, A.Morris, B.Wood, B.Thapa, A.Gray, L.Henry, N.J.Knowles, J.Wadsworth, D.P.King

The Pirbright Institute, Ash road, Pirbright, Woking, Surrey, GU24 0NF, UK.

Introduction

Foot-and-mouth disease (FMD) virus is a rapidly changing virus. As such, one of the most important ongoing challenges for diagnostic assays is to ensure that they continue to be matched to circulating field strains of the virus. The serotyping antigen-ELISA (Ferris and Dawson 1988) in current use at the World Reference Laboratory for FMD relies on polyclonal guinea-pig and rabbit antisera raised against purified viral antigens, some of which were originally isolated as far back as 1968. Although this is a reliable and robust assay recent changes in the virus now appear to be challenging this assay.

Materials and methods

Ag-ELISA data was examined and sample results were collated which could not be serotyped via this method or which gave rise to high cross-reactivity and required additional testing in order to assign a serotype with a sufficient degree of confidence. Alternative antigen detection ELISAs utilising monoclonal antibodies and recombinant integrin were used to define serotype, when this was not possible using the polyclonal assay system.

Results

Sample sets were identified and examined against their corresponding VP1 sequencing reports. The starkest example is the O/CATHAY topotype where signal strength in of the Ag-ELISA has been steadily decreasing so that now contemporary isolates are not detected with this test.

Discussion

While the challenges posed by the changing nature of FMDV is more obvious in the case of molecular assays, it is also now becoming more apparent in assays that utilize antibody reagents. Next generation assays are either in development or already commercialised but vigilance should be retained. It is hoped that a validation panel currently in development (Rand, Eu-FMD 2016) will assist with the validation of future assays.

DO COMMERCIALLY AVAILABLE LYSIS BUFFERS INACTIVATE FMD VIRUS?

Poster - P2

B. A. Wood, V. Mioulet, L. Henry, B. Thapa, A. Gray and D. P. King

World Reference Laboratory for Foot-and-Mouth Disease, The Pirbright Institute, Ash Road, Pirbright, Woking GU24 0NF, UK

Introduction

Given the strict biosecurity regulations associated with the handling of foot-and-mouth disease virus (FMDV), it is critical that lysis buffers used for molecular assays are capable of effectively inactivating the virus. Thus, the purpose of this study was to determine whether commercially available reagents are able to lyse/inactivate FMDV, as indicated by the lack of cytopathic effect (CPE)/virus replication in cell culture.

Methods

The three lysis buffers included in these experiments, all of which are used in the World Reference Laboratory (WRL) with field samples prior to nucleic acid extraction, were as follows: lysis binding solution from the MagMAX™-96 Viral RNA Isolation Kit (Ambion, Life Tech), NM1 lysis buffer from the MagVet Universal Isolation Kit (LSI, Life Tech), and RLT buffer from the RNeasy Mini Kit (Qiagen). The cells selected in these experiments were primary bovine thyroid cells (BTY) and porcine cells (IB-RS-2), both of which are highly sensitive and routinely used to propagate FMDV field strains in the WRL. Initial experiments were conducted to determine the dilution at which each lysis buffer was no longer cytotoxic; this was found to be 1:128 dilution of the sample:lysis buffer ratio as per manufacturer. High titre virus suspensions (≥7.0 TCID50) were added to each lysis buffer according to manufacturer recommendations and then diluted 1:128. FMDV-lysis buffer was then added to cells (incubated 37°C with rotation) and observed for CPE for up to 3 days. Where no CPE was observed by day three, the supernatant was harvested, blind-passed onto fresh cells and incubated for an additional three days of observation.

Discussion

Viruses from all seven FMDV serotypes will be included in these experiments, as well as swine vesicular disease virus, which is clinically indistinguishable from FMDV.

OIE/FAO FMD REFERENCE LABORATORY NETWORK WG ON VIRUS CLASSIFICATION AND NOMENCLATURE: DEFINING AND NAMING SOUTHERN AFRICAN TERRITORIES TOPOTYPES DO COMMERCIALLY AVAILS?

Poster - P2

K. Bachanek-Bankowska

AVAILABLE UPON REQUEST

BIOCONTAINMENT OF FMDV: CHALLENGES AND SOLUTIONS FOR LABORATORY BIORISK MANAGEMENT

Organiser: E. Ryan and the EuFMD-STC

Summary

This session will cover

- Presentations on contemporary FMDV biocontainment issues
- Discussions on common risk areas
- Proposals for an EuFMD biorisk management network to connect people and facilitate discussions

Background

The EuFMD minimum standards for laboratories working with FMDV sets out certain principles which are to be followed. However, the issues faced by laboratory biorisk managers vary across a range of areas, and it can be challenging to find solutions which mitigate the risk sufficiently while also being practical. The EuFMD intends to establish a network for FMDV biorisk managers to help facilitate discussions and to harmonise solutions to common problems.

Who the session is aimed at

Those who are interested in laboratory containment and biorisk management of FMDV; laboratory workers, biosecurity officers, regulators, contingency planners and policy makers.

Format

There will be a number of presentations followed by a facilitated group discussion on biorisk management and laboratory containment. This will also function as the launch event for the new EuFMD biorisk management network.

Aim

The objective is to bring together those involved in FMDV biorisk management, to strengthen and build on relationships, and to spread awareness of how the EuFMD biorisk management network can help people to effectively manage the challenges they face.

A CONTAMINATED ENVIRONMENT IS AN EFFICIENT ROUTE OF TRANSMISSION FOR FOOT AND MOUTH DISEASE VIRUS

Claire Colenutt[1], Emma Brown[1], Noel Nelson[2], Jose Gonzales[3] and Simon Gubbins[1]
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Introduction

Foot and Mouth disease virus (FMDV) is a contagious pathogen of cloven hooved animals, which can be transmitted via numerous routes. Transmission through direct contact with infected animals is the most common route of spread of FMDV, but can be prevented by implementation of control measures, such as culling and movement restrictions. The role of indirect contact and fomite transmission is less well understood and more complex to apply blanket control measures to. This study used a series of challenge experiments to determine and quantify the risk of FMDV transmission posed by environmental contamination.

Methods

A series of FMDV transmission experiments were performed in high containment facilities. Seven environmental challenges were undertaken with pairs of calves exposed for 24 hours to environments previously housing FMDV-infected calves. This included one challenge room in which the infected calves were housed only during their incubation period. Samples were taken from the contaminated rooms during challenge to assess the level of potential exposure.

Results

Five out of seven environmental challenges resulted in successful transmission of FMDV, including the challenge using an environment contaminated by preclinical, infected calves. In one case where environmental transmission did not occur, no infectious virus was isolated from environmental samples. The second unsuccessful environmental challenge used a contaminated room that was unoccupied for 24 hours between holding clinically diseased calves and the challenge of naïve calves.

Conclusions

The outcome of these challenge experiments suggests that the environment is an efficient route of transmission for a short period of time. Consequently, an appreciable proportion of transmission within a farm could occur via a freshly contaminated environment in addition to direct contact. Our results highlight the need for effective on farm biosecurity to reduce transmission through environmental routes and thorough decontamination and disinfection of premises prior to restocking with FMDV-susceptible livestock.

EVALUATING THE SURVIVAL OF FMD VIRUS IN THE ENVIRONMENT

E. Brown[1], C. Colenutt[1], N. Nelson[2], J.L. Gonzales[3], P. Eble[3], A. Dekker[3] and S. Gubbins[1]

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Introduction

Foot and mouth disease virus (FMDV) can survive outside of the animal host for extended periods of time. The duration of survival is a very important determinant of the risk of transmission via the environment. The objective of this study was to measure virus survival in a naturally contaminated environment to help assess the risk of transmission of FMDV.

Materials and methods

A series of ten indirect contact transmission experiments were carried out in high containment facilities, whereby pairs of naïve calves were exposed to environments that had previously held infected calves. Following challenge, nine rooms were left unclean and environmental samples were taken from the rooms for seven days post challenge. Relative humidity and temperature in the rooms were kept around 60% and 19°C respectively. Swabs from the floor, walls and food trough, as well as excreta (mostly faeces) samples were collected daily to measure the virus survival in the environment.

Results

Live virus could be detected on all surfaces. On the first day post challenge, the highest virus concentration was measured in excreta (2.2 log10 pfu/ml) and the lowest on the walls (0.4 log10 pfu/ml). Virus survived the longest in excreta, from where it was recovered for nearly a week. The estimated virus half-lives in and on excreta, floor, wall and feed troughs were 3.3 days, 2.1 days, 3.1 days and 2.3 days, respectively.

Discussion

The results of this study indicate that virus can persist in a naturally-contaminated environment for around one week. They also show that virus survival might be shorter than previously suggested from survival studies based on spiking different matrices with virus in a laboratory. This information is important to assess the relationship between the level of contamination in the environment and the risk of indirect transmission of FMDV.

THE NEW ZEALAND NATIONAL BIOCONTAINMENT LABORATORY PROJECT - INNOVATIVE APPROACHES TO MEET TESTING REQUIREMENTS IN THE EVENT OF AN FMD OUTBREAK

R. P. Spence, J. O'Keefe*

Animal Health Laboratory, Investigation and Diagnostic Centres and Response, Ministry for Primary Industries, 66, Ward Street, Upper Hutt, 5140, New Zealand.

Introduction

In October 2015 the Ministry for Primary Industries (MPI) in New Zealand began construction on the National Biocontainment Laboratory (NBL), a state of the art, 3400 square metre high containment laboratory facility to replace its current enhanced physical containment level 3 laboratory facility. Although New Zealand is free from FMD and many high priority animal diseases this facility is an important contingency to support diagnostic testing for such diseases.

Design considerations to meet FMD testing requirements

A number of critical factors had to be addressed when designing the NBL and considering FMD testing in New Zealand:

1. The NBL will be the only enhanced physical containment level 3 facility in New Zealand and as such should be resilient and provide continual service.
2. The NBL should be seismically resilient to minimise any potential impacts of a major earthquake on the facility and its integrity.
3. The NBL should offer a highly flexible work environment.
4. The NBL should provide the ability to meet surge testing capacity.
5. The NBL should provide sufficient space without being too big or expensive to operate.
6. The NBL should be able meet current and future international standards for work with FMD including meeting the requirements of the EU FMD guidelines.

Discussion

A range of innovative design approaches are being employed to address the above considerations such as use of modelling to understand testing capacity requirements, the ability to convert PC2 laboratory space to enhanced PC3 space to increase surge capacity and full base isolation to provide seismic resilience. This presentation will focus on the innovation being employed in the NBL and how it will improve MPI's readiness in the unlikely event of an FMD outbreak.

FMD VACCINATION IN ENDEMIC SETTINGS: OPTIMISING SCHEDULES AND VACCINE EFFICACY TRIALS

Organiser: N. Lyons (EuFMD Special Committee for Research and Programme Development, SCRPD)

Summary

This session will cover

This workshop session will discuss these issues in particular the types of studies that are required to address the needs of countries using vaccination in their control strategy.

Background

FMD vaccines are used extensively in countries with endemic disease including countries within EuFMD and bordering the EuFMD member states. The aim of vaccination is to reduce the impact of disease or circulation of virus and represents a significant cost of control . However, much of the knowledge we have about FMD vaccines is based on experimental challenge studies and focuses on their use in reactive scenarios relevant to FMD-free countries. These challenge studies generally only consider the effect of a single dose of vaccine and no not consider the range of exposures that are likely to be encountered in field conditions. Moreover a single challenge study is typically statistically underpowered to demonstrate efficacy. Demonstration of field efficacy for FMD vaccines is not typically required for regulatory agencies in contrast to many other vaccines used in livestock and humans.

Who is the session aimed at?

It is aimed at people who have experience of FMD in endemic settings and an interest in epidemiological aspects of vaccine efficacy studies.

SESSION G7

CLOSED MEETING ON LICENSING NOVEL VACCINES

(INVITATION ONLY)

SESSION G8

VACCINE QUALITY ASSURANCE (VQA) INITIATIVE: WHAT IS PROPOSED AND HOW DO WE MOVE IT FORWARD?

Organisers: A. Dekker (EuFMD Special Committee for Research and Programme Development, SCRPD) and other SCRPD members

Summary

This session will cover

- Why VQA matters
- Current VQA concepts, practise and issues
- VQA and the new Vaccination and Post-Vaccination Monitoring Guidelines (OIE/FAO)
- Use of serology to assess vaccine potency
- How to increase access to services to undertake serology for vaccine potency and PVM

Background

Hundreds of millions of doses of FMD vaccine are used annually across the world, with little in the way of data available to demonstrate the immunological or protective response to vaccines used. How to use field data on the effectiveness of vaccines is covered in Session G6. This session addresses the question of vaccine quality, with a focus on potency, and after a review of the current concepts behind use of serology for assessing vaccine potency, outlines some options for:

- Increasing the uptake of the serology methods in countries using FMD vaccines
- Use of specialised facilities/reference centres to undertake serological tests on samples collected pre/post vaccination.

The constraints to improving uptake of the serology tests will be discussed, and practical actions and priorities identified which can be carried out in the coming years.

Who is the session aimed at?

This session is mainly intended for people involved in purchase and delivery of FMD vaccine for use in the field, in preventive vaccination programmes, those involved in national reference centres for FMD whose tasks may include measuring the immune response to FMD vaccines, and those involved or interested in monitoring the impact of vaccination programmes.

Format

The session will start with a presentation and then be followed by facilitated group discussions.
We will

- Identify key gaps to be addressed and feasibility to address them
- Identify centres or experts willing to undertake such services in the near future and discuss how the supply of such services and key biological reagents could be provided (consortia of reference centres, individual supplier laboratory centres, ...)" for only the current validated strains

Aim of the session

This session is intended to identify key people and parties that are willing to put greater effort into this area, and guide the workplans of EuFMD and other parties, for training, advocacy and/or other forms of support in the period 2017-18.

SEROLOGICAL AND MOLECULAR SURVEILLANCE OF FMDV TRANSMISSION EVENTS OVER TIME IN AN ISOLATED AFRICAN BUFFALO HERD IN THE KRUGER NATIONAL PARK

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Introduction

In Africa, buffalo appear to be the primary FMDV maintenance host and carrier without obvious symptoms. Previously, buffaloes isolated for 24 years showed that FMDV can perpetuate long-term without re-introduction. However, experimental studies using defined challenge in an isolation facility showed virus recovery decreases and is cleared over 15-months. Ecological and evolutionary mechanisms contributing to FMDV transmission and persistence in buffalo are unknown. The objective of the study was to investigate antibody dynamics in naïve animals with waning maternal immunity exposed to new infections and in previously infected animals.

Material and methods

The ongoing study involves an established FMDV-positive breeding herd of 50 buffalo in a 300-hectare enclosure surrounded by double game fencing housing buffalo in isolation from other herds in the Kruger National Park (South Africa). The entire herd has been monitored for two years, allowing us to define FMD infection dynamics over the susceptible calf cohorts. Probang, tonsil swab and blood were sampled every 2 months for serological, molecular and viral isolation analysis.

Results

SAT-serotype antibody responses were assessed in each animal of the herd. PCR and virus isolation were used to confirm viral presence from esophageal-pharyngeal tissue. This data was used to track the status of each animal from maternally protected, susceptible, infected or carrier/recrudescence status. Statistical analysis has highlighted antibody dynamics of waning maternal antibodies and the timing of new FMDV infection; and uncovering broad variability in previously infected animals.

Discussion

These findings, together with other analyses such as stress, co-infections, immune status and contact periods of each animal studied can be combined to test models, which provide theoretical validation for each of the hypothesized transmission scenario as a basis for FMDV persistence. Understanding FMDV transmission and persistence in African buffalo will improve control measures when evaluating FMDV risk at the wildlife-livestock interface.

FMD VIRUS PERSISTENCE AND TRANSMISSION IN AFRICAN BUFFALO

Eva Perez-Martin[1], Fuquan Zhang[1], Francois Maree[2], Katherine Scott[2], Simon Gubbins[1], Julian Seago[1], LinMari de Klerk-Lorist[3], Louis van Schalkwyk[3], Anna Jolles4, Brianna Beechler5, Nicholas Juleff[1] and Bryan Charleston[1]

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Introduction

African buffalo is considered the main reservoir of the three Southern African Territories (SAT) FMDV serotypes, SAT1, SAT2 and SAT3, and the only ruminant described so far able to transmit the virus to naïve during the carrier state. Our group has recently described that there is a direct correlation between virus persistence in buffalo and cell killing capacity in vitro (Maree and de Klerk et al., 2016). In the present study, we used the same viruses described in this recent publication to determine their capacity of being transmitted from persistently infected buffalo to naïve.

Material and methods

Three groups of African buffalo, each containing 4 animals/group, were experimentally infected with SAT1 KNP/196/91, SAT2 KNP/19/89 or SAT3 KNP/1/08 FMDV isolates, respectively. Forty-five days later, buffalo were screened for the presence of FMDV in the oropharynx and divided into 2 identical groups, each group containing 2 FMDV persistently infected buffalo per serotype, totalling 6 carrier buffalo/group. Six new naïve animals were then introduced in each group and transmission from carrier to naïve was evaluated over five months.

Results

In contrast with previous published studies where transmission from carrier animals does not readily occur, we observed at least 3 transmission events (2 for SAT1 and 1 for SAT3) occurred from carrier to susceptible animals by day 17 post contact. Moreover, 2 additional SAT1 transmission events were observed at late time points, 3 and 4 months after contact, respectively. No transmission was observed from SAT2 carrier animals.

Discussion

Our recent findings, together with our previously published results (Maree and de Klerk et al., 2016) allow us to conclude that the capacity of FMDV to persist and transmit appears to be influenced at least in part by viral factors. Understanding FMDV transmission and pathogenesis from African buffalo will contribute towards FMD control in livestock.

FMD IN AFRICAN BUFFALO (SYNCERUS CAFFER): DIFFERENCES IN HOST RESPONSES BETWEEN SAT 1, 2 AND 3 IN EXPERIMENTALLY INFECTED AND CONTACT INFECTED INDIVIDUALS

Brianna Beechler[1], Eva Perez[2], Bryan Charleston[2], Caroline Glidden[1], Nick Juleff[2], LinMari de Klerk-Lorist[3], Francois Maree4, Katherine Scott4, Louis van Schalkwyk[3], Fuquan Zhang[2], Anna Jolles[1]

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Introduction

In sub-Saharan Africa, African buffalo act as maintenance host for FMDV, yet seemingly exhibit few clinical signs and suffer few disease consequences. Yet a comprehensive investigation into the correlation between host clinical signs, viremia and inflammatory response to FMDV infection has not been performed in African buffalo.

Materials and methods

We conducted an experimental study with 12 buffalo experimentally infected with FMDV (4 with SAT 1, 4 with SAT 2, 4 with SAT 3), which were allowed to mingle with 12 susceptible buffalo and monitored after infection for clinical signs, viremia and serological inflammatory immune responses - including serum amyloid A, haptoglobin, fibrinogen, TNF alpha and IFN gamma - for 30 days post-infection.

Results

Buffalo developed very mild clinical signs with a short-lived fever response but developed a systemic inflammatory response that lasted for 7-24 days post infection with FMDV. This response varied between SAT 1,2 and 3 with SAT 1 generally inducing a stronger inflammatory response. Experimentally infected buffalo and buffalo infected by natural contact had very different responses to infection – with experimentally infected generally mounting a stronger inflammatory response.

Discussion

During acute FMDV infection buffalo develop an active infection but limited mucosal lesions – unlike what is seen in cattle. Additionally, the response varies between SAT 1, 2 and 3 – indicating that the three types may have different effects on the host. The differences noted between experimentally infected and individuals infected by contact emphasize the importance of considering the dynamics in natural populations, as it may be different than what is expected from experimental results.

DYNAMICS OF FOOT-AND-MOUTH DISEASE IN AFRICAN BUFFALO (SYNCERUS CAFFER): CALF-TO-CALF TRANSMISSION ALONE IS INCOMPATIBLE WITH DISEASE PERSISTENCE

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Introduction

In sub-Saharan Africa, African buffalo act as maintenance host for FMD, complicating disease control. However, surprisingly little is known about the dynamics of FMDV transmission in its maintenance host. We estimated the transmission and recovery rates, and the basic reproductive number (R0) for FMD in buffalo from empirical data, and used a mathematical model to test the idea that the virus might be maintained as a typical "childhood" infection, circulating through each year's population of new susceptible calves.

Materials and methods

We conducted an experimental study to estimate the transmission and recovery rates from acute FMDV infection; and a cohort study to assess the timing of births in a herd of buffalo in Kruger National Park, South Africa. These data allowed us to parameterize a stochastic, individual-based mathematical model representing the transmission dynamics of acute FMDV infection in African buffalo.

Results

FMD was transmitted readily from acutely infected animals to naïve hosts, and recovery occurred within 4-6 days, resulting in estimates for R0 of 2.3 (SAT3), 3.5 (SAT2), and >3.5 for SAT1. Births occurred predominantly between November and March, giving an inter-birth interval of 5 months. Our models suggest that calf-to-calf transmission alone is highly unlikely to support persistence of FMDV in buffalo populations: simulated viral transmission almost invariably burned out in less than a year for realistic herd sizes.

Discussion

If the loss of maternal immunity in calves is very variable, viral persistence due to calf-to-calf transmission becomes more likely for large populations. Our team is investigating the timing of loss of maternal immunity to FMDV to evaluate this possibility. However, for small buffalo populations, other mechanisms of FMDV transmission are likely to be important for viral persistence.

SPECIFICITY OF FMD SURVEILLANCE IN WILD BOARS

P4

Yanko Ivanov; Tsvyatko Alexandrov
Bulgarian Food Safety Agency

The specific characteristics of FMD surveillance in wild boars are presented in relation to biology, age and social structure, reproduction, mortality and population dynamics, habitat, population density, herd immunity etc., as well as the human impact like hunting, vaccination, agriculture etc. Identification of wild animals by DNA barcoding of samples obtained by some non-invasive methods and trapping of wild boars are commented as alternatives or complementary of hunting, which is currently the main tool of surveillance in wild animals. It is stressed that hunting is practiced as a hobby and its goals are fundamentally different from the goal of surveillance namely to collect samples for disease control and eradication. Moreover, it is performed only in a limited hunting season, and is prohibited in national parks, protected areas and game reserves. Another shortcoming is that the hunted wild animals are not representative for the population in terms of age and sex. Furthermore, the individual hunting groups have preferred places and days for hunting. Therefore developing new approaches to capturing surveillance data should be encouraged.

WILDLIFE SURVEILLANCE AND CONTROL FOR FMD – WORKSHOP: PRACTICAL TRAINING FOR THE BALKAN COUNTRIES

P4

Keith Sumption[1], Anna Zdravkova[1], Artem Skrypnyk[1], Marius Masiulis[1], Klaas Dietze[2], Tsviatko Alexandrov[3]
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Introduction

A Workshop: Practical training for wildlife surveillance and control of Foot-and-Mouth Disease (FMD) was carried out in the State hunting ground "Vitoshko-Studena", in Bulgaria, in February 2016 for experts on contingency planning/wildlife from the Balkan countries aiming to improve the FMD preparedness for wildlife management, disease surveillance and control and to promote alternative diagnostic method - non-invasive sampling.

The training

THEORETICAL PART:

- Wildlife management - developing strategy and building capacity to address animal health issues at the wildlife-livestock-human interface. The Bulgarian experience with the FMD epidemics in 2011 with focus on wild boar surveillance and reinstatement of free status when wildlife was involved;
- Telemetry studies in Bulgaria for spatial and social interactions in wild boar population and the role of wild boar in FMD epidemiology;
- Non-invasive sampling for FMD and baits for alternative sampling methods following ANIMO principle (active, non-invasive management of outbreaks).

PRACTICAL EXERCISES:

- Distribution and collection of baits for non-invasive sampling of wild boar;
- Presentation of different trapping systems for wild boar;
- Clinical investigation, dissection and sampling of wild boar for contagious animal diseases
- Biosecurity in game collection center.

Discussions

- Wildlife management and surveillance should be incorporated as part of the Contingency plans;
- Common approaches for control of animal contagious diseases in wildlife are needed in the region;
- Biosecurity manual during game processing is needed and communication with the hunter associations should be addressed;
- Non-invasive sampling should be considered as first indicator method for the early detection of FMD introduction. Further development of ANIMO principle is needed.

LONGITUDINAL SURVEYS OF FOOT-AND-MOUTH DISEASE VIRUS IN CATTLE AT THE LIVESTOCK-WILDLIFE INTERFACE AREAS AROUND QUEEN ELIZABETH NATIONAL PARK IN UGANDA (2011-2014). IMPLICATIONS FOR THE FMD CONTROL

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Summary

In order to study how FMD is maintained at wildlife-livestock interface of Queen Elizabeth National Park in Uganda, We sampled three categories of animals, the community herds, the sentinel herd and the buffalo in the same location. These studies involved young, unvaccinated cattle (6-24 months) from community herds, two sets of 20 newly introduced FMD free sentinel cattle and buffalosthat interacted at this livestock wildlife interface. Six hundred nineteen young community cattle were sampled during six visits in a two year period (2011-2013), at intervals of 4-5 months. The sentinel cattle were followed for a period of up to 400 days and 35 buffalos sampledfrom the same area. Anti-FMDV antibodies were analyzed using PrioCHECK® FMDV NS kit, Solid Phase Blocking ELISA, and Virus Neutralization Tests, while FMDV RNA was determined by real-time PCR, virus isolation and sequencing.

Serological results from the community herds showed that cattle were occasionally exposed to serotypes O, and SAT-1, with a few cases of SAT-2 and SAT-3. The sentinel herd showed evidence of contact with serotypes O, SAT-1, SAT-2 and SAT-3. A SAT-3 virus was isolatedfrom cattle despite the absence of clear clinical signs. The buffalo samples demonstrated exposure to SAT-1, SAT-2 and SAT-3. A SAT-2 virus was isolated from buffalo. Comparison of the VP1 coding sequences of the cattle SAT-3 and the buffalo SAT-2 isolates demonstrated big genetic differences from the previous cattle and buffalo isolates from this area. This study shows that non clinical FMDV infections occur in cattle at different times of the year and that cattle may be having a significant role in the maintenance of FMDV. It seems that the FMDVs that cause disease in cattle are different from those existing in the buffalodespite the small numbers of isolates so far recovered. Further research to investigate the possibility of FMDV transmissionfrom the buffalo to cattle in this region is required.

Key words: Foot-and-mouth disease, livestock-wildlife-interface, cattle, non clinical FMDV, and control.

PATHOLOGICAL CHANGE OF THE DEVELOPMENT OF THE VESICULAR LESION IN PIGS EXPERIMENTALLY INFECTED WITH THE FOOT-AND-MOUTH DISEASE VIRUS O/JPN/2010

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Introduction

There are a limited number of reports on pathology in pigs infected with Foot-and-mouth Disease Virus (FMDV) within Southeast Asia (SEA) topotype. To deepen our understanding of pathogenesis of FMDV SEA topotype in pigs, we examined pathological changes in acute stage of infection in pigs experimentally infected with FMDV isolated from the 2010 epidemic in Japan via the intraoral routes.

Materials and methods

Six pigs aged four-weeks-old were inoculated orally with 106 TCID50 of FMDV O/JPN/2010 isolate. Each three pigs infected were examined clinically and euthanized at 1 and 3 days post inoculation (dpi). Clinical samples of sera, saliva and nasal swabs were collected. At necropsy, tissue samples were collected from each pig, homogenated for virus isolation and RT-PCR analysis and fixed in 10% neutral buffered-formalin for histology. Paraffin-embedded tissue sections were stained with hematoxylin and eosin and with immunohistochemistry using monoclonal anti-FMDV antibody (NIAH).

Results

Immunohistochemically, viral antigens were detected at first in the perivascular prickle cell in the upper layer of the stratum spinosum in the tongue. However, the epithelial lesion seemed to start on the single necrosis of the prickle cell in the middle to bottom layer of the stratum spinosum in the tongue. Small vesicles seemed to be fused together and develop large vesicles in the tongue. On the other hand, massive necrosis with prominent viral antigen was observed as primary lesion in the epidermis of the coronet and heel. The epidermal lesion developed further into vesicles by separation of the epithelium from the underlying tissue and filling of the cavity with vesicular fluid.

Discussion

In this study, it was appeared that pathological processes of the development of vesicular lesion in the epidermis of the coronet and heel were different from those in the epithelium of the tongue in pigs inoculated with FMDV O/JPN/2010 isolate.

FMDV- HOST INTERACTION IN A MODEL OF PERSISTENTLY INFECTED BOVINE CELLS

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Introduction

Underlying mechanisms of Foot-and-mouth disease virus (FMDV) persistence remain unclear. Several studies have shown evidence for cell/virus co-evolution during virus persistence as well as a modulation of cell innate immune response. In the framework of the "Transcriptovac" ANIHWA project, we aim to study host-FMDV interaction during persistent infection in bovine cellular models namely by identification of virus and cell gene signatures of persistence.

Materials and methods

MDBK were persistently infected with FMDV type O. Persistent viruses (FMDVOp) were collected. FMDV-host protein interaction map was performed by using the yeast two-hybrid (Y2H) system to screen MDBK cDNA prey library with viral bait-proteins. FMDV infection of primary bovine dorsal soft palate (DSP) and alveolar pneumocytes (AP) cells were performed to verify results obtained with MDBK.

Results

Y2H screening using 13 FMDV proteins as "bait" identified 313 interactions corresponding to 18 candidate interacting bovine proteins. Gene expression analyses of MDBK persistently infected cells are ongoing and FMDV infected DSP and AP cells have been characterized. Phenotypic characterization of FMDVOp viruses recovered from MDBK has been initiated and genetic studies are ongoing.

Discussion

Candidate cellular host genes interacting with FMDV proteins have been identified. These Interactions will be confirmed by biochemical or functional analysis. Further work will then investigate if such interactions are modulated during a persistent infection. Finally, these results will be confronted to those obtained with DSP and AP infected with FMDV.

LOCALIZATION OF FOOT-AND-MOUTH DISEASE RNA AND VIRAL ANTIGENS IN DIFFERENT TISSUES FROM APPARENTLY HEALTHY CATTLE AND BUFFALO UNDER NATURAL CONDITION IN INDIA

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Introduction

Following recovery from the acute form of FMD virus (FMDV) infection, a variable, yet substantial proportion of ruminants become persistently infected i.e. carriers. The potential role of persistently infected animals in initiating new outbreaks remains highly controversial and the inability to quantify the real risk posed by such animals could preclude control of FMD in India. The current study was envisaged to determine tissue-specific localization of FMDV in different tissues obtained from apparently healthy cattle and buffaloes under natural condition to provide the basis for effective control strategies.

Materials and methods

Eleven tissues per animal [Middle tongue (MTNG), ventral soft palate (VSP), dorsal soft palate (DSP)1 , DSP2*, palatine tonsil (PTON), dorsal nasopharynx (DNP)1**, DNP2**, middle retropharyngeal lymph node (MRPLN), submandibular lymph node (SMLN), right popiliteal lymph node (RPOP) and heart] were collected from apparently healthy cattle (n=22) and buffaloes (n=70) at slaughterhouses. Tissues were stored in 50% (v/v) buffered glycerin for virus isolation (VI) and genome detection (GD), and in OCT for pathological studies. Routine histopathological examination (H&E), as well as FMDV antigen detection by immunohistochemistry (IHC) and indirect fluorescence assay (IFA) were performed on 5 µm cryosectioned tissues with suitable positive, negative and isotype controls. FMDV antigen was detected by use of rabbit anti-FMDV serotype O-specific, polyclonal antibody (dilution 1: 2000 in blocking buffer) as primary antibody and goat anti-rabbit IgG-HRP and goat anti-rabbit IgG (H+L) Alexa Fluor® 594 conjugate for IHC and IFA, respectively, as secondary antibody.

Results and discussion

Infectious FMDV was not isolated from any tissues samples. Overall, 25 of the 1012 tissue samples were found to contain FMDV genomic RNA by both RT-PCR and RT-LAMP; 21 of these tissues were from buffalo, whilst 4 were from cattle. No considerable changes were observed in any tissues at microscopic level by light microscope except respiratory epithelium thickening and number of crypts was found more in buffaloes DSP than cattle. Amongst all tissues examined, positive signal for FMDV antigen was detected by IHC/IFA in 1-VSP, 5-DSPI, 8-DSP2, 3-DNPI, 5-DNP2 and 3-PTON while no signal were observed in its isotype and negative control. Interestingly, all these samples are of

buffalo origin, thereby suggesting a higher incidence and/or longer duration of persistence of FMDV in buffaloes than cattle. Among these tissues, samples with highest prevalence of detection of FMDV by immunomicroscopy were DSP2 followed by DSP1, DNP2, then DNP1 and PTON. Therefore, DSP and DNP are considered to be the principal sites of persistence of FMD virus in apparently healthy buffaloes under natural conditions.

SESSION G11

FUNDING INNOVATION : Q&A

SESSION G12

This session will be confirmed during the conference

Summary

This session will involve

- 10-15 minute presentations from international funding agencies and research funding coordinators.
- Understanding the viewpoint of the funders.
- An opportunity for questions and answers with each.

The areas to cover in moderated discussion include

- What changes can we expect in the next few years, in drivers or in funding?.
- How do funding organisations co-ordinate over priorities?.
- How do priorities get set? what are the information gaps that funding agencies need to make their decisions?.
- What areas or innovations in funding (or funded work) are considered by FUNDERS to show most promise, that we should all learn from?.
- How do we keep informed, move forward?.

Format and estimated time-schedule

Short presentations followed by question and answers:

- 13.30h Introduction – Keith Sumption, EuFMD Fund for Applied Research (FAR Fund)
- 13.35h International co-ordination of research funding; the work of STAR-IDAZ (Luke Dalton, DEFRA)
- 13.55h Presentation by the Gates Foundation (Samuel Thevasagayam, through online link)
- 14.20h Presentation by the Livestock Vaccines Initiative (Vincent Guyonnet, online link)

- 14.40h Presentation by the Feed the Future Innovation Lab for Livestock Systems (LSIL) at the University of Florida (Adegbola Adesogan, online link)
- 15.00h. Close.

Aim of the session

For those interested in understanding the way funding for research and international development in animal health is changing, to help improve the understanding of the drivers affecting funding decisions and directions, in the area of animal health including FMD . It is also assist the funding agencies to disseminate information of their programmes and likely future developments.

From these discussions, we hope to draw conclusions on how we can further improve the flow of information in two directions, on the needs, gaps and potential of research, and the priority setting and calls for proposals by the funding agencies.

UK EXPERIENCE OF MODELLING IN SUPPORT OF FMD CONTROL, APPLYING NEW APPROACHES TO KNOWLEDGE TRANSFER, AND TACKLING THE CHALLENGE OF MAINTAINING AND MAKING BEST USE OF GLOBAL FUNDING IN SUPPORT OF RESEARCH AND INNOVATION

N. Gibbens. Chief Veterinary Officer - UK

How the UK's approach to the use of modelling for FMD has evolved, from the experience gained from the major epidemic in 2001 to the present day, highlighting the main lessons learned and giving examples of where we see modelling as adding most value and where we see limitations. Looking at the challenges of maintaining skills in our veterinary and other responders as we move from a position of a majority with personal experience to a field force that relies on training and exercising to establish and maintain expertise, focusing on the practical application of modern teaching methods. Conclusion: Looking at how the UK has deployed science funding to deliver globally relevant research and maintain cutting edge disease response laboratory capability, how that is challenged at a time of austerity, and the need for international coordination to ensure that research and surveillance capability is maintained.

BIOSAFETY AND BIOSECURITY OF FOOT AND MOUTH DISEASE IN AZERBAIJAN

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Introduction

FMD is so important because it is highly infectious, spreads rapidly throughout animal populations and over long distances and hence it is difficult and costly to control. Basic biosafety and biosecurity measures are very necessary in helping to minimize the spread of disease, and this becomes critical when there is a high risk of infection from a FMD outbreak.[http://www.thepigsite.com/pighealth/article/448/footandmouth-disease-fmd/]

Materials and Methods

In order not to spread of the FMD to the territory of the Azerbaijan Republic, from the neighboring countries that are not safe for the disease, in our country we use all available anti-epidemic methods and techniques, as well as methods of biosafety and biosecurity.

Results

Results of studies showed that FMD can spread quickly on the wind and is therefore that much more difficult to keep out, however the biosafety and biosecurity measures could help to reduce the risk of spread. It is important to standardize animal movements and keep to an absolute minimum; do not forget that people and vehicles are a potential source of contamination; allow only to essential visitors to the farm and provide your own Personal Protective Equipment at the entrance; must use an approved disinfectant and so on.

During 2015-2016 years we together with the staff of our institute have conducted seminars on "Biosafety and Biosecurity" on FMD for veterinarians, farmers and pastoralists in the several districts of Azerbaijan (such as Astara, Gakh, Guba, Ismayilli, Masalli, Shamakhi). Audiences finds this activity very useful and therefore seminars will be held in other regions of the country.

Discussion

Vaccination and other necessary measures, which have been taken to prevent FMD in the pre-epidemic period, and strict adherence to the rules of biosafety and biosecurity - the most effective and economical way to protect herds from the disease.

MOLECULAR CHARACTERIZATION OF ISOLATED FOOT-AND-MOUTH DISEASE VIRUSES IN TANZANIA

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Introduction

Phylogenetic techniques are used to visualize genetic relationships, including their interpretation in terms of epidemiological clustering and/or geographical/ecological source.nFoot and Mouth Disease (FMD) is endemic in Tanzania and serotypes SAT1, SAT2, A and O have been identified since 1954. This project aims to assess the topotypic distribution of FMDV strains in Tanzania.

Materials and Methods

356 FMDV isolates were obtained from outbreaks in various parts of Tanzania between 2008 and 2013. The single-plex real-time RT-PCR (qRT-PCR) with appropriate primers was used for FMDV pan-type detection and serotype specific diagnosis. One-Step, serotype specific RT-PCR was carried out using VP1 primers followed by sequencing of post PCR products. Phylogenetic analysis was by assembling of sequences using SeqMan II (DNAStar Lasergene 8.0). Midpoint-rooted neighbour-joining (NJ) trees were constructed using the Kimura 2-parameter (MEGA 5.0).

Results

Findings indicated that 53% of samples (n = 176) were positive for FMDV genome by qRT-PCR with Ct values ranging from 14 to 32. VP1 sequences from 52 samples representing the four serotypes were compared with previously obtained sequences from the Great Lakes countries.

Discussion

The VP1 sequence data revealed that serotype A topotypes clustered into the Africa G1 topotype, those of serotype O into the East Africa 2 (EA-2) topotype, those of SAT1 into the NWZ topotype and the SAT2 isolates into I topotype. In this study, no single topotype was found to be peculiar to Tanzania. The findings of this study suggest that FMDV strains currently circulating in Tanzania probably do not differ genetically from the pre-2009 previously studied by Kasanga et al., (2013). The genetic features of these strains could be influenced by geographical, epidemiological, ecological and animal movement patterns shared with neighbouring countries.

Keywords; Serotypes, phylogeography, phylogeny, VP1 sequence, topotypes/genotypes, Tanzania

FOOT AND MOUTH DISEASE (FMD) IN JORDAN, AND THE EFFECT OF THE MIDDLE EAST CRISIS ON THE LIVESTOCK

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The virology unit, is the central lab for viral diseases diagnosis in Jordan. It works in accordance to the (Oie manual of diagnostic tests and vaccines for terrestrial animals), with regards to PCR and antibodies (ELISA) detection of FMD virus.

Introduction
After the Iraqi/Syrian crisis, large numbers (over 75K) of livestock (Sheep, Goat and Cattle) entered the Jordanian borders illegally, and merged with the local live stock as a result of Jordan's confined area. As a consequence, an active sero- surveillance was carried out in cooperation with Food and Agriculture Organization (FAO) for the detection of tans boundary diseases; especially FMD.

Materials and Methods
12 749 blood samples were collected from the 12 Jordan governorates by veterinary services, which were transported to the Virology unit for testing.

Spp.	*Number of blood samples*
Sheep	*4900*
Goat	*4900*
Cattle	*2949*

SVANOVIR FMDV 3ABC Ab –ruminant kits used.

Results
The primary results showed that the percentage of sero-positive samples for FMD was between 7-10%

Discussion
In the future the AWS in Jordan needs a strict strategy to control infectious diseases especially FMD for Jordan is considered the middle of the Middle East Region. FMD in Jordan is a real danger for that region because it may spread to other surrounded countries such as Saudi Arabia, Egypt .

THE ROLE OF EARLY RESPONSE SYSTEM TO CONTROL SPREAD OF FMDV NEW STRAIN IN ARMENIA

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Introduction

The main objective of the single integrated system of FMD measures in Armenia was to create buffer zones to prevent spreading of exotic FMD viral types coming into the country from Turkey and Iran. Implementation of systematic mass vaccination of susceptible animals utilizing a polyvalent vaccine with a high protective activity helped to stabilize the situation. Despite significant control efforts, FMD persists in region and new strains of FMD are periodically reported into the neighbor countries of Armenia.

Materials and methods

Regularly EUFMD sent the information regarding the situation in the region. All veterinarians of the buffer zones were informed the new strain circulation in the Turkey and Iran. The first notification of FMD cases was 23.12.2015.The preliminary diagnosis was done in the laboratory of RA, FMDV type A was detected by ELISA. The pathological materials were sent to "ARRIAH" and 15.01.2016 was received confirming the diagnosis FMD type A, genetic line A/G-VII.

Results

The outbreak was in the Armavir marz, Arazap community near the borders with Turkey, which shares the river Araks. The epidemic units was 1 farm, the event happened mainly in a completely vaccinated cattle population in this year, so the Veterinary service decided to stamping out the animals with clinical signs of FMD and organize the quarantine with continuously supervisory activities, implementation sanitary measures, before having the confirmation diagnoses.

Discussion

Through early response and excellent collaboration with international organizations, timely diagnosis and the measures taken, FMD outbreak has been localized and eliminated within the short period of time. The new vaccine which is produced in "ARRIAH" from A Iran 05, A G-VII, O PanAsia1, Asia1 Sindh08 strain of FMDV is an effective measure for susceptible animals, but there are need to organize the further serosurvey for assessment real FMD epidemic situation in the Armenia.

MOLECULAR BIOLOGICAL ANALYSIS OF THE FMD VIRUS IN THE KYRGYZ REPUBLIC

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Introduction

FMD is one of the most dangerous infectious diseases that can spread rapidly to large areas, causing significant economic losses to livestock. At the outbreak of FMD in dairy and meat cattle breeding

productivity may be reduced to 35-40%, the death of young animals causes significant damage.

Material and methods

We took the blood serum, pathological material from sick animalsfor the research, which was selected in the farms unfavorable for FMD. The epizootological, classical virological and immunobiological methods were used. the results of serological monitoring used. To confirm these results held molecular biological analysis of different methods of PCR, sequencing.

Results

The last five years for FMD epizootic situation in Kyrgyzstan remains tense. The 71 unfavorable point for FMDhave been identified in the region of Republic during this years, along with this diseased recorded not only in livestock (cattle, sheeps and goats, pigs), but also in wild animals

In 2013, in the Chui region were observed disease cases among vaccinated animals. The investigation were identified the type of virus FMD from aphthous and serum test animals. Sequencing of amplicons and conducted phylogenetic analysis of the nucleotide sequences set showed that the virus that caused the outbreak of foot and mouth disease, a member of the genetic line of type A Iran-05 FMD virus type A and Group-2 PanAziya FMD virus type O.

Discussion

According to phylogenetic analysis revealed that the vaccine, which was used previously from other strains of the genetic line, could not provide sufficient immunity in animals because it differed significantly in their immunogenic properties and may not be suitable for the preventive vaccination of susceptible animals. Therefore, it is necessary to produce a vaccine based on direct local circulating strains for the high efficiency of preventive measures.

Using ELISA method we revealed the presence of non-structural proteins of the FMD virus in vaccinated and unvaccinated cattle yaks and sheeps. It speaks of virus in animals of different status epizootic. Consequently such animals are the reservoir of FMD virus

A VACCINE MATCHING STUDY FOR FOOT AND MOUTH DISEASE VIRUS SEROTYPE A IN TURKEY

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Introduction

Foot and mouth disease (FMD) is a highly transmissible vesicular disease of cloven-hoofed animals with a high morbidity rate and causes production losses in adult livestock. To date, three of the seven

serotypes have been found in circulation (A, O, Asia1) and A serotype being responsible for most of the outbreaks in domestic animals in Turkey. This disease is present in much of Turkey and its control is mainly on the basis of vaccination. The effect of vaccination largely rely on the quality of the selected vaccine. To detect the suitability of a vaccine strain, antigenic matching is usually studied by in vitro analysis.

Materials and methods

The study was conducted from January 2014 to January 2015 in Turkey. Serotype A FMDV isolated strains within this study were matched with some of reference vaccine strains of serotype A FMDV isolated from archived in the βAP Institute (FMDV Institute) to choose an appropriate vaccine strains to control the disease.. For the matching test, this board of sera is tested for its skill to react with the homologous FMD vaccine strain and the FMDV field isolate to be matched using VNT. All sera were tested three times by neutralization tests using BHK-21cells.

Results

SN results of the sera representing parallel vaccine status to the field viruses. The r1 values of field virus strains (N1 and N2) are calculated as 0,5 and 0,6 respectively.

Discussion

Two serotype A viruses (N1 and N2 strains) strains were used for vaccine matching study and at the end of the results, βap Institute Vaccine Strain (ATUR11) estimated to protect against to FMDV field strains.

BELARUS AND FMD: COUNTRY'S PREPAREDNESS; EARLY DETECTION AND RESPONSE SYSTEM

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Introduction

Regular risk assessment and disease monitoring, frequent trainings of national experts and performance of simulation exercises on FMD take place in the Republic of Belarus and play the important role to keep the country in FMD free status without vaccination. In case of possible outbreaks it will let to early detection and fast eradication measures making less economic consequences.

Materials and methods

Repeated observation of the national and international legislation on FMD, reviewing and collecting of

new scientific data, regular amendment of national regulations and its proper implementation in real life, carrying out of national seminars for all relevant stakeholders, participation in the on-line trainings conducted by EUFMD, real time simulation exercises on FMD, development of National contingency plan, improvement of early detection and fast response measures system.

Results

Creation of the Customs Union increased probability of FMD outbreaks in former free territories and led to the reconceptualization of risks in disease introduction. Last simulation exercises in Belarus on FMD took place in 2011 and it revealed gaps in theoretical and practical knowledge on FMD epidemiology, disease communication and management and control measures. It led to formation of group of experts to amend FMD national legislation. As a result the new veterinary-sanitary rules were accepted since 2013. Further participation of Belarus national experts in on-line courses conducted by EUFMD in 2015 – 2016 revealed new gaps in knowledge and skills.

Discussion

Long absence of the FMD virus in the country makes spread of knowledge on FMD among Belarus scientists, epidemiologists, veterinarians and farmers more significant. Collaboration of Belarus scientists, state veterinary service, field veterinarians and laboratory staff with the international experts have to be continued and intensified to keep us up to date and at high level of competency.

THE ROLE OF UGANDA AS A RESERVOIR FOR FMD VIRUS AND POSSIBLE EMERGENCE OF NEW SEROTYPES IN THE REGION

Rekuma Erechu Sam Richard

Background and Justification

FMD is endemic to sub-Saharan Africa. The virus is highly contagious and economically devastating to cloven footed domestic and wild life. Uganda experiences over 100 outbreaks yearly and some of these outbreaks when reported by field veterinary epidemiologists are not responded to because of lack of financial resources to maintain a functional veterinary service for FMD surveillance, prevention and control. The sample collection, packaging and submission to the World Reference FMD Laboratory from these outbreaks are a problem due to lack of resources to carry out this program. There is therefore need to respond to these outbreaks, notify OIE and submit samples to world reference FMD laboratory for sequencing to monitor the antigenic drift in the region.

Overall Objective

The overall objective is to monitor the emergence of new FMD serotypes in circulation and identify

isolates for use as candidate strains for FMD vaccine production.

Materials and Methods

The country will be stratified into four regions for the ease classification of the FMD viruses in circulation. Epithelial tissues, probang and vesicular fluids will be collected from FMD-suspected cases from both domestic and wild animals throughout the four regions of Uganda for submission to the National reference veterinary diagnostic laboratory at Entebbe. At the National reference laboratory viruses will be isolated and serotypes identified and virus RNA extracted and submitted to the world FMD reference Laboratory for genotyping. In over 50 % total outbreaks each year, the samples will be submitted to world reference laboratory at Pirbright.

Expected Benefits

- 50 % of the total livestock population vaccinated against circulating FMD viruses
- All FMD outbreaks reported to OIE
- Genetic relatedness and antigenic drift determined
- Suitable FMD strains for vaccine candidates determined
- FMD risk maps drowned
- FMD awareness created

Timeframe and Estimated Cost

This project will be implemented in a period of 2 year, and will cost approximately US$ 150,000.

PROOF-OF-CONCEPT EFFICACY OF AN ADENOVIRUS-VECTORED FMD CATTLE VACCINE

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Merial, Athens GA USA1, Department of Homeland Security Science and Technology Directorate, Plum Island, NY and Washington, DC USA2

Introduction

Merial is the leading producer of high-quality vaccines for use in FMD control programs. Inactivated strain-specific vaccines are typically formulated using combinations of several serotypes and topotypes to meet prevailing protection needs. Conventional vaccine technology has decades of field proven effectiveness in FMD control and eradication programs in many countries and regions. Exploring new relevant recombinant technologies applied to FMDV give an opportunity to optimize several vaccine characteristics; in particular, culture of FMD virus requires dedicated, highly contained production units. Other improvements such as Differentiating Infected from Vaccinated Animals (DIVA) diagnostic

testing and parameters of vaccination cost-effectiveness are also desirable.

Results

Merial is working with the U.S. Department of Homeland Security Science and Technology Directorate to develop a "next-generation" recombinant adenovirus-vectored vaccine platform that would address some of the current vaccine limitations. In support of this platform, a U.S. Department of Agriculture product-conditional license for the 1st serotype/subtype was issued in 2012. Several proof-of-concept cattle efficacy trials have been conducted by DHS S&T, which results are summarized, have indicated similar level of performance as conventional vaccines against a number of strains. The broader applicability of the technology to all FMD strains, and the ease with which a vaccine against a new FMDV variant can be generated is still to be explored.

Conclusion

It is recognized that delivery of a product that reaches the same level of performance as conventional, high-quality vaccines is an ambitious challenge, however, initial data presented here indicates that the adenovirus-vectored technology could be a safe, efficacious and industrially viable platform

AN OVERVIEW INTO THE CURRENT SITUATION OF FMD IN AFRICA

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The epidemiology of foot-and-mouth disease (FMD) in Africa is unique in the sense that six of the seven serotypes of FMDV (Southern African Territories [SAT] 1, SAT2, SAT3, A, O, and C), with the exception of Asia-1, have occurred in the last decade. The epidemiology is further complicated by the fact that SAT1, SAT2, and SAT3 viruses are maintained and spread by wildlife, persistently infected African buffalo (Sincerus caffer) in particular. Although the precise mechanism of transmission of FMD from buffalo to cattle is not well understood, it is facilitated by direct contact between these two species. Once cattle are infected they may maintain SAT infections without the further involvement of buffalo. Due to underreporting of FMD, the current strains circulating throughout sub-Saharan Africa are in many cases unknown. For SAT1, SAT2, and serotype A viruses, the genetic diversity is reflected in antigenic variation, and indications are that vaccine strains may be needed for each topotype. This has serious implications for control using vaccines and for choice of strains to include in regional antigen banks. No single strategy for control of FMD in Africa is applicable. Decision on the most effective regional control strategy should focus on an ecosystem approach, identification of primary endemic areas, animal husbandry practices, climate, and animal movement. Within each ecosystem, human behaviour could be integrated in disease control planning. Different regions in sub-Saharan Africa are at different

developmental stages and are thus facing unique challenges and priorities in terms of veterinary disease control. Many science-based options targeting improved vaccinology, diagnostics, and other control measures have been described, but not necessary implemented. This review aims to identify the current limitations that are experienced in the control of FMD in endemic settings in Africa caused by gaps in knowledge of epidemiology, transmission, vaccinology, and diagnostics.

EVALUATION OF A MONOCLONAL ANTIBODY-BASED ASSAY FOR IMPROVED DETECTION OF FOOT-AND-MOUTH DISEASE

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Introduction

Currently, the World Reference Laboratory (WRL) for Foot-and-Mouth Disease (FMD) uses a polyclonal antibody-based indirect sandwich ELISA for serotyping of FMDV diagnostic submissions. Polyclonal antibodies detect multiple epitopes on a target protein, which can result in cross reactivity and high background signal due to non-specific binding. Improvements include evaluation of monoclonal antibodies which have high specificity for more conserved epitopes.

Materials and methods

In this study, fourteen different serotype-specific monoclonal antibodies (MAbs) produced by the National Institute of Animal Health (NIAH), Japan were assessed. The panel of MAbs evaluated aimed to detect all seven serotypes of FMDV: O (n=1), A (n=4), C (n=1), SAT 1 (n=2), SAT 2 (n=2), SAT 3 (n=2), ASIA 1 (n=1) and pan-serotypic (n=1). These MAbs were tested via a direct sandwich ELISA (Morioka et al., EuFMD 2016) using characterised FMDV isolates, which included all seven serotypes and various topotypes.

Results

All MAbs tested in the direct ELISA successfully serotyped all samples and limited cross reactivity was observed. Serotype O-specific MAb (70C4) failed to detect recent Cathay isolates tested. Pan-serotypic MAb (1H5) detected all samples with the exception of a few Southern African Territories (SAT) isolates. The MAbs were not cross-reactive to Seneca Valley Virus (SVV) or Swine Vesicular Disease Virus (SVDV).

Discussion

Overall, the MAbs evaluated appear to be promising candidates for FMDV diagnostics. These MAbs

were tested using elements of a validation panel (Morris et al., EuFMD 2016), however further validation should be carried out including recent strains of concern. Further research is also required to identify a MAb for the detection of O Cathay topotype.

OCCURRENCE OF FOOT-AND-MOUTH DISEASE (FMD) SEROTYPES IN TANZANIA: A RETROSPECTIVE STUDY OF TONGUE EPITHELIAL TISSUE SAMPLES

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Introduction

Foot-and-mouth disease(FMD) caused by a variety of FMD virus serotype (strain) is the second most important transboundary animal disease in cattle after Contagious bovine pleura pneumonia in Tanzania. The disease is characterized by vesicles, oral, feet, and teat lesions, low mortality (1-2%) in high susceptible herds and low productivity. Unpublished annual health reports from seven zonal located veterinary investigation centers, (VIC) compiled at the Epidemiology Unit indicate that forty-five outbreaks of FMD were reported in 29 out of 120 districts in Tanzania mainland during the year 2002. Of the 2491 individual animal cases recorded during the same year, 54 animals were reported to have died of FMD.

Materials and methods

Suspected FMD samples, collected from 1997 to 2004, were derived from cattle (n =142) and wildebeest (n =8) that suffered from oral and foot lesions. Epithelial tissue and vesicular lesions of the tongue were taken on glycerol buffer saline for serotyping of FMD virus. Antigens of FMD disease virus detected by indirect-sandwich enzyme-linked immunosorbent assay.

Results:

Indirect-sandwich ELISA results indicated that serotype O, SAT 1 and SAT 2 viruses had being circulating in Tanzania. Serotyping of the 65(43.3%) sero-positive samples indicated serotypes O (41.5%), SAT 1 (32.3%) and SAT 2 (26.2%). No serotype A was recovered from animal samples screened. No serotypes were recovered from Central and Western zone regions.

Discussion:

The geographical distribution of the seropositive cases suggested that, SAT 1 exposure was widespread and particularly high in Southern and Eastern zone regions whereas serotype SAT 2 and O was patchy

and more concentrated in the Northern and Southern highland zone. There is a need therefore, to undertake a systematic study targeting a wider scope of livestock specie, areas, and seasonality in order to come up with a wider informed status of the disease in Tanzania.

MOLECULAR DYNAMICS OF FOOT AND MOUTH DISEASE VIRUS SEROTYPES IN PAKISTAN

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Introduction

Foot and mouth disease (FMD) is a highly infectious disease of cloven hoofed animals and a major transport barrier for animal trade. FMDV has seven serotypes while Serotype O, A and Asia-1 are prevalent in Pakistan. Prevalence of serotype O is higher in comparison with other two serotypes of FMDV.

Materials and Methods

Phylogenetic studies of FMDV lead to detection of different types of lineage and sub-lineage of serotypes that has caused major restrictions in controlling the FMD in the country. We sequenced and analyzed about 25 recent FMD Isolates for all three prevalent serotypes O, A and Asia-1. We also compared these recent sequences with the already published sequences and compared the results.

Results

Phylogenetic analysis of genome regions encoding for structural proteins of FMDV A/IRN/2005 sub-lineage displayed distinct serotype-specific clustering and an evolutionary linkage with the A22 sub-lineage. Serotype A isolated and identified from samples was found similar to already circulating in Pakistan and Iran.

Phylogenetic analysis of FMDV serotype Asia-1 showed that three different groups of this serotype are circulating in Pakistan since 1998 and these groups are named as Group-II, Group-VI and Group-VII.

FMDV serotypes O detected in Pakistan belonged to Pak-98, Iran-2001, Pan-Asia or Pan-Asia-II 2006 lineages while FMDV serotype Pan-Asia II lineage was discovered circulating in most of the time during last five years.

Discussion

The information gathered here is useful to understand the genetics of FMDV serotypes as well as it may help to design a national vaccination program for FMD control in Pakistan. It would also be

helpful in developing quality vaccine for FMD at country level which will ultimately affect economics of the country.

Keywords: History; dynamics; FMDV serotype; vaccination and control

GENETIC AND ANTIGENIC CHARACTERISTICS OF FOOT AND MOUTH DISEASE VIRUS STRAINS ISOLATED IN 2011 AND 2015 IN NORTHERN BOTSWANA

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Introduction

Phylogenetic, genetic and antigenic studies of Southern African Territories (SAT) serotypes of foot-and-mouth disease virus prevalent in sub-Saharan Africa have shown a high level of antigenic variability (Maree, et al. 2011). In the present study we analyzed the genetic and antigenic characteristics of SAT2 viruses from two outbreaks which occurred in 2011 and 2015 in Botswana in order to determine any intra- and inter-outbreak mutational changes of the viruses.

Material and methods

The field samples were subjected to sequencing of the VP1 gene followed by phylogenetic analysis. Vaccine matching was determined by two dimensional virus neutralization test using vaccine strains SAT251 and SAT2035.

Results

There was 100% amino acid sequence similarity between the two outbreaks. When compared to the more recent SAT 2 vaccine strain (SAT2035), approximately 5% amino acid positions contained residues that had different physicochemical properties with majority of these occurring in the G-H loop as compared to 11.6% variation against SAT251 vaccine strain (older vaccine strain). SAT2035 differed by 17% from the older vaccine strain. The relationship coefficient calculated ranged between 0.51 and 0.87 against outbreak strains against SAT2035 vaccine strains and in the range of 0.36 and 0.55 against SAT251.

Discussion

All of the variations occurred in regions that are of known antigenic sites (Maree et al., 2011). The

outbreak samples and SAT2035 vaccine strain clustered on the phylogenetic tree with reference samples belonging to SAT 2 topotype III but SAT251 vaccine was determined to be of topotype II (Vosloo et al., 1995). These findings are evidence that the vaccines provide satisfactory immunity to the field isolates representing FMDV strains currently circulating in the field (Samuel et al., 1990; Rweyemamu, 1984; Paton et al., 2005). The r1 value results show that the vaccine strain currently in use in Ngamiland is still relevant to confer protection against circulating field strains. The findings of this study are showing that the vaccine strains are genetically and antigenically related to the circulating field virus strains and that minimal mutation occurred intra- and inter-outbreaks.

A POSITIVELY CHARGED RESIDUE AT ANTIGENIC SITE 4 OF FOOT-AND-MOUTH DISEASE VIRUS SEROTYPE O CONFER COMPLETE RESISTANCE TO NEUTRALIZATION

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Introduction

Routine genetic and antigenic characterization of three serotype O field isolates collected from a village of Odisha from a natural field outbreak during the year 2011 revealed that two isolates (PD351/2011 and PD352/2011) showed r1-value of > 0.3 and one isolate (PD353/2011) reacted poorly to BVS against the vaccine strain. The capsid coding region sequence of the three isolates was compared and reverse genetic approach was used to identify a residue responsible for antigenic variability.

Materials and Methods

Two dimensional micro-neutralization test (2D-MNT) was carried out as described earlier (Rweyemamu et al., 1978) using bovine vaccinate serum (BVS) against the currently used vaccine strain (INDR2/1975). RNA extraction, Reverse transcription and PCR amplification of P1 region was carried essentially as described earlier (Subramaniam et al., 2015). The nucleotide sequences were aligned and compared using Megalign module. A previously described megaprimer-mediated capsid swapping protocol (Biswal et al., 2015) was followed to swap the capsid coding region of naturally variant isolate PD353/2011 into the donor plasmid pOR2/1975. An inverse PCR-mediated site-directed mutagenesis experiment was conducted on the chimeric full-length cDNA clone (pO353/11 –O) to introduce nucleotide substitution

Result

Substitutions were observed in two antigenically critical positions; at position VP1-144 that defines antigenic site 1 in serotype O, all the three isolates showed substitution (IβV) and similar observation was also made earlier in other antigenically homologous serotype O field isolates. The

other substitution was found at position VP3-58 that defines antigenic site 4 in serotype O. The non-conservative EβK at substitution at position VP3-58 was found only in PD353/2011. In other two isolates (PD351/2011 and PD353/2011) and vaccine strain, the site was occupied by E. In order to further confirm, this position was modulated using the reverse genetic approach. The isolate engineered to carry the mutation EβK at VP3-58 showed less antigenic match with the vaccine strain. This altogether confirms the role of charge shift at VP3-58 in changing the antigenic behaviour of the virus.

Discussion

Though correlating sequence changes and antigenic diversity was not always successful, there are few studies in which antigenic diversity was explained from genetic changes (Asfor et al., 2014). In the present analysis, a positively charged residue at VP3-58 is shown to have profound effect on the antigenic behaviour of the virus. The emergence of antigenically variant viruses during a field outbreak is a regular phenomenon due to volatile nature of the FMDV genome (Domingo et al., 1980). Such antigenically variant strains are always not successful in establishing itself in the nature.

IMPROVEMENT OF A MONOCLONAL ANTIBODY-BASED SANDWICH DIRECT ELISA TO DETECT THE SEVEN SEROTYPES OF FOOT-AND-MOUTH DISEASE VIRUS

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Introduction

In a previous study, we developed a monoclonal antibody (MAb)-based sandwich direct ELISA (MSD-ELISA) to detect all seven serotypes of foot-and-mouth disease virus (FMDV) and obtain typing information for four FMDV serotypes (O, A, C and Asia1) (Morioka et al., 2009, 2014). In this study, we employed a multi-serotype reactive MAb, and serotype-specific reactive MAbs for SAT1, SAT2 and SAT3, in order to improve the MSD-ELISA to detect and type antigens for all seven serotypes.

Materials and methods

The MAbs were generated using a conventional hybridoma-fusion method, and affinities for FMDV isolates were compared by indirect ELISA. The multi-serotype reactive Mab was used as antigen trapping antibody. The multi-serotype reactive MAb and each serotype-specific reactive MAbs were used as peroxidase-labeled MAbs detecting antibodies. Sixteen FMDVs, representing all seven serotypes, were used to evaluate the assay.

Results

The multi-serotype reactive MAb (16D6) was able to detect all 16 FMDVs tested. The use of 16D6 in the MSD-ELISA provided analytical higher sensitivity for some strains tested than the previous MSD-ELISA. Moreover, the newly established serotype-specific MAbs for SAT1, SAT2 and SAT3 were able to detect each serotype with greater than ten times higher sensitivity compared to the results of multi-serotype MAb.

Discussion

In this study, a newly established multi-serotype reactive MAb (16D6) improved the sensitivity of multi-serotype antigen detection, and serotype-specific MAbs for SAT1, SAT2 and SAT3 enabled serotyping of all seven serotypes. According to the partial validation exercise of these MAbs (Thapa et al. EU-FMD 2016), the serotype-specific MAbs for SAT1, SAT2 and SAT3 were able to detect wide range of SAT1, SAT2 and SAT3 isolates, respectively. In the future, MAb 16D6 will be validated using isolates from around the world, and the serotype-specific MAbs will be incorporated in a lateral-flow system for typing all seven serotypes of FMDV.

SAFETY OF INACTIVATED AFTOVAXPUR DOE VACCINE AGAINST FOOT-AND-MOUTH DISEASE IN 2 WEEK OLD CATTLE, SHEEP AND PIG

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Introduction

In case of an outbreak of Foot-and-Mouth Disease (FMD) in an FMD-free country, an early vaccination of all age classes of livestock is a prerequisite for an efficient control of the disease. The present work was designed to assess the safety of an inactivated AFTOVAXPUR DOE vaccine under GLP guidelines following administration of repeated doses to very young animals of 3 major target species.

Materials and methods

An overformulated vaccine (2 to 5 times more antigens than the commercial product) was administered twice 21 days apart, at a dose volume of 2 ml, to groups of 2 week old calves (n=9, SC), lambs (n=10, SC) or pigs (n=10, IM). Control groups (9 calves, 9 lambs, 10 pigs respectively), were administered physiological saline at the same volume, route and regimen.

All animals were monitored for 42 days for local reactions, rectal temperatures and body weights. At the end of the study, all surviving animals were necropsied and injection sites were inspected.

Results

A limited (about 1°C) and transitory (1 day) mean increase of rectal temperature was observed in all species. Vaccinations were mostly followed by moderate, transient swelling (11 cm diameter in cattle, 7 cm in sheep and 4 cm in pig). At necropsy, granulomatous inflammation of the injection sites was observed in all vaccinated groups. There was no statistical difference in body growth between the vaccinated and the control groups in any of the species.

Discussion

The vaccine was well tolerated in all species and had no impact on weight gain. The reactions produced in very young animals were typical for this type of oily-adjuvanted inactivated vaccine and similar to those seen in older animals. AFTOVAXPUR DOE vaccine can thus be safely administrated at a minimum age of 2 week old in these 3 target species.

MOLECULAR CHARACTERIZATION OF FMD VIRUS SEROTYPE O FROM DOMESTIC PIGS: IMPLICATIONS FOR MULTI-SPECIES DISEASE CONTROL IN UGANDA

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Introduction

Despite the control strategies used in Uganda such as ring vaccinations and quarantines, FMD outbreaks are still rampant, causing grave economic consequences to individual farmers and the country as a whole. Constant phylogenetic studies and inclusion of other potential FMD hosts in research and FMD control activities are paramount in designing effective FMD control strategies. In this study, molecular characteristics of the foot-andmouth disease virus (FMDV) isolated from domestic pigs in western Uganda are investigated.

Materials and Methods

In 2010, twelve (12) lesion swabs were collected from individual domestic pigs from Rakai district that showed clinical signs of FMD. The samples were subjected to RNA extraction, cDNA synthesis and conventional PCR. Partial VPI capsid protein coding sequences for positive samples were amplified and later sequenced using the automated DNA sequencer (ABI Prism® 3700). Individual sequences were analysed using CLC DNA work bench 5.6.1. The test sequences and other FMDV related sequences from the GenBank were analysed using MEGA5 to establish sequence divergences. A phylogenetic tree was drawn to infer evolutionary history and to elucidate the relationships between the sequences.

Results

Eight partial VP1 sequences were successfully obtained and were confirmed as being 100% identical and belonging to serotype O. Phylogenetic analysis of the test sequences with other Ugandan FMDV sequences, showed a close relatedness (average of 3.77% pair-wise distance) to viruses isolated from central and western Uganda in the years 2005 and 2006 from cattle, thus belonged to the same strain.

Discussion

These results show that domestic pigs had been infected with an FMD strain that had been in circulation in cattle in 2005/2006. These results highlight the implications for FMD control in other livestock species that are potential FMD hosts and emphasised the inclusion of these other livestock (domestic pigs and shoats) during FMD prevention and control drives.

THE SITUATION OF FOOT AND MOUTH DISEASE IN ETHIOPIA 2013 TO 2016

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Abstract

The Seroprevalence of FMD in Benshangul Gumz was 28.57% in bovine and 4.64% in sheep and goats while in Somali region 23.75% in bovine and 6.6% in sheep and goats. The overall prevalence of FMD in bovine, sheep and goats was 13.93%. A total 21408 samples tested for certification 11.40% were positive for FMD virus antibody in cattle prevalence ranges from 13.5 to 55.23% while in sheep and goat 4.5 to 7.4%. Outbreak investigation showed that 45.2% of 372 samples were positive for FMD virus antibody and of 263 (tissues, swabs and oro- pharyngeal fluids) tested by FMD antigen detection ELISA 53.6 % were positive for FMD virus. Serotype O, serotype A, serotype SAT2, and serotype SAT1 are FMD serotypes that were detected in outbreaks. Neighbor–joining trees VP1 coding sequence of serotype A, serotype O and SAT2 FMD virus at WRLFMD showed that similarity of virus with the previous isolates of Ethiopia. Some serotype O closely related to Yemen isolates of 2006/08/09. Some serotype of SAT2 was also related to isolate of Oman in the same year. FMD serotype A isolate in Ethiopia during 2015 was more closely related to FMD serotype A of Sudan isolate in 2011. Occurrence of multiple FMD serotypes (O, A, and SAT2) which also circulates across the borders of neighboring countries make complex epidemiology of FMD. The FMD isolates of O/ETH/3/2015 and O/ETH/1/2016 were antigenically matched with O 3039 and O/TUR/5/2009 and unlikely match with O Manisa vaccines strain. The FMD SAT2 isolates were antigenically matched with SAT ERI than that of SAT2 ZIM vaccine strain. The FMD isolate of serotype A had poor antigenic matching with vaccine strain. Prophylactic vaccination which protect against all serotypes and animal movement control may contribute to control of FMD

in Ethiopia.

Key words: FMD, bovine, sheep and goats, Ethiopia

MANAGEMENT AND INNOVATIONS IN VACCINES & DIAGNOSTICS IN GLOBAL IMMUNIZATION FOR FOOT & MOUTH DISEASE CONTROL

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Foot and Mouth Disease (FMD) is the most economically important disease which made more than INR 25000 crore (5 Billion USD) economic loss to the Indian GDP. The prevalence of FMD in India is major trade barrier in global economy participation of India and Asia.

Vaccine development, Vaccinalogy and immunotherapy in the emergence of providing solution to infectious diseases in man and animals generated visible interest in 20th century. The term vaccine and vaccination started the concept back to the time of Edward Jenner (1749-1823) as a father of Vaccinalogy. vaccinology developed as a science of "vaccines" from bench to bush and lab to field. In veterinary science provided platform for animal vaccine development, first virus identified as Foot and Mouth disease virus (FMD) by Loffler in Germany. Thus veterinary vaccines and diagnostics emerged as a solution to control infectious diseases.

Foot and mouth disease vaccine is being produced in India as a trivalent vaccine comprising of Type O (IND R2/75), Type A (IND 40/2000) and Type Asia 1 (IND 63/72) tissue cultured inactivated oil and gel vaccine. There is requirement of almost 300 million doses of vaccine requirement in India. Lack of early warning of the emergence of new antigen types of FMD virus, regional and national vaccine banks, monovalent, bivalent vaccine banks. The diagnosis of the virus types/subtypes/ availability of reagents on time. Biosecurity and quarantine regulations are the major important factors need serious improvement in quality, delivery, vaccination strategy on scientific sero monitoring Visa vis antigenic mass for vaccinating dose are the major important factors needs serious attention in management of FMD control. Needs application of IoT, E diagnosis on movement, temp and physical movement in the herd. Disorder functioning of heat regulatory centre which leads to panting which one of clue of E diagnosis to be implemented in Indian village level. Therefore the economic losses due the livestock industry attributed to the FMD are the highest as per OIE, FAO, APHCA. Man plays a massive significance to control and eradicate FMD from India, in order to enhance productivity, and economic rehabilitation through livestock development in rural sector.

Management of innovation edge technology of DIVA due to NSP antibody response induced after multiple administration of inactivated vaccine preparation ia the major hurdle on the way to diffentiate / identify infected animals in the village environment.

VOTE !

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