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UK & International Veterinary Vaccinology Network Conference 2019

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Welcome

Dear delegates,

It is a pleasure to welcome you all to London for the Veterinary Vaccinology Network (VVN) and International Veterinary Vaccinology Network (IVVN) joint annual conference. This is the fifth and final annual meeting of the VVN and we hope to give it a send-off that is worthy of all that this Network has achieved. Although the VVN is coming to an end, its journey is being continued by the IVVN which has taken on the core ethos of the VVN and extends it to all our colleagues from across the globe - we are delighted to see so many of you here for this meeting. The VVN established a unique forum for anyone with interest in the many disciplines that contribute to vaccine development to come together to share ideas, expertise and experience. The IVVN has the ambition to adopt a similar approach to accelerate the development of vaccines that are needed to improve animal health and 'one-health' issues that are of particular relevance to low-and-middle income countries (LMICs).

We hope that by bringing a broad cross-section of the vaccinology community together the VVN/IVVN meetings enable researchers to establish new and innovative collaborations and through funding from the UK government's Global Challenges Research Fund (GCRF) we aim to support the best ideas through provision of catalyst funding. So, during the next couple of days please discard your inhibitions, talk enthusiastically to all of the participants and identify your future collaborators that will help you achieve your scientific aims. Equally important is that you let us know what the VVN/IVVN are doing right and what your ideas are for how we could do things better - please find us and let us know your ideas. The Networks are here to support you so take this opportunity to talk to us face-to-face, we are delighted to hear what you have to say.

We look forward to talking to you all over the next two days, and wish you all an enjoyable and productive meeting.

The VVN and IVVN teams

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Led by The Royal Veterinary College in partnership with the London School of Economics and Political Science, the London School of Hygiene and Tropical Medicine, and SOAS, University of London, the programme focuses on the development of low-cost, portable diagnostic tools and vaccines to counter infectious diseases and increasing resistance to antimicrobials. The Bloomsbury SET ('Science, Economics, Technology') aims to connect place, people, businesses, ideas and infrastructures in pursuit of innovative scientific / technical solutions (tools, vaccines, models) that will help safeguard human health. At the same time, it will use the collaboration's convening power to test whether proposed public health interventions are acceptable socially, economically and politically - the factors which determine their success in the real world. This will facilitate innovation and productivity within UK and other partner businesses, whilst also helping to shape public health policies and practices.

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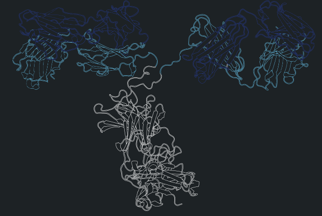

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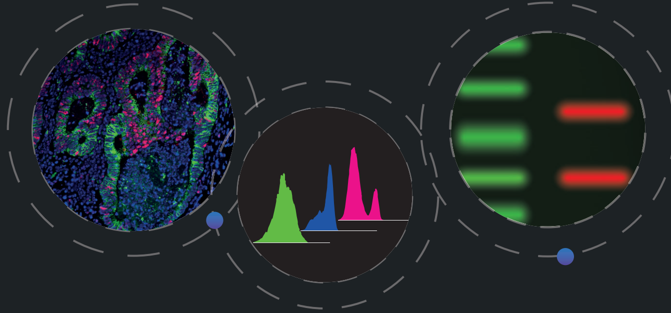

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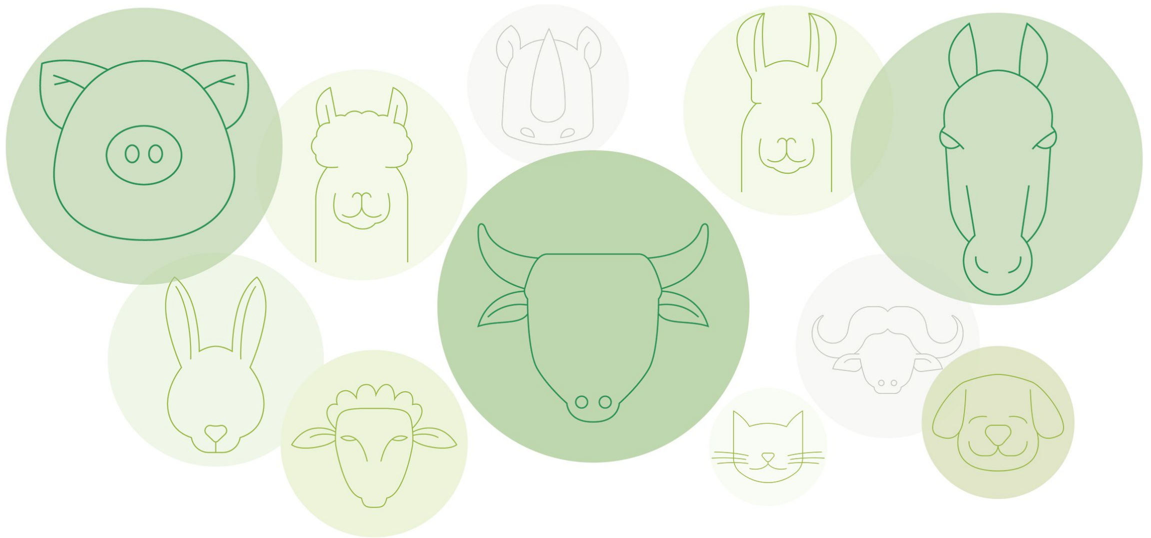

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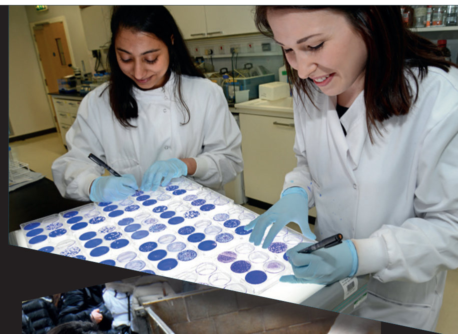

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Agenda

Day 1 – 9th January 2019

Time	Session
0830 - 0930	**Registration**
0930 - 0940	**Welcome & Introduction** Prof. Bryan Charleston (The Pirbright Institute, UK)
0940 - 0950	**UK Veterinary Vaccinology Network** Madeleine Clark (The Pirbright Institute, UK)
0950 - 1000	**International Veterinary Vaccinology Network** Dr. Tim Connelley (The Roslin Institute, UK)
	Theme 1: Vaccines for Ectoparasites **Chair: Professor Christine Maritz-Olivier (University of Pretoria, South Africa)**
1000 - 1030	**Targeting host-vector-pathogen interactions to reduce the global burden of tick-borne diseases** Professor Jose de la Fuente (Instituto de Investigación en Recursos Cinegéticos, Spain)
1030 - 1100	**The potential for vaccination to control poultry red mite** Dr. Alasdair Nisbet (Moredun Research Institute, UK)
1100 - 1130	Tea & Coffee
1130 - 1200	**Sea lice vaccine development** Professor Frank Nilson (University of Bergen, Norway)
1200 - 1230	**SophisTICKated anti-tick vaccines – cattle tick and Australian paralysis tick** Professor Ala Tabor (University of Queensland, Australia)
1230 - 1250	**A decavalent vaccine based on recombinant tick salivary proteins decreases successive infestations with Rhipicephalus microplus in cattle** Professor Isabel Kinney Ferreira de Miranda Santos (University of Sao Paulo, Brazil)
1250 - 1305	**A dual mixture of recombinant tick antigens decrease fecundity in Rhipicephalus appendiculatus under laboratory conditions** Irene Kiio (International Livestock Research Institute, Kenya)
1305 - 1315	Group Photo
1315 - 1430	Lunch & Networking
	Theme 2: Vaccine Commercialisation **Chair: Dr. Jeremy Salt (GALVmed, UK)**
1430 - 1500	**Factors that Influence the Success and Speed in the Development of Vaccines** Dr. Mahesh Kumar (Zoetis, USA)
1500 - 1530	**Towards sustainable supply of quality registered veterinary vaccines: the East Africa Community's Mutual Recognition Procedure** Dr Lois Muraguri (GALVmed, UK)
1530 - 1600	Tea & Coffee
1600 - 1630	**Technology Licensing: Art or Science?** Dr. Peter Jeffries (Business Development Adviser and Chief Executive of GALVmed)
1630 - 1645	**Catalysing demand for livestock vaccines: Gender and youth-specific considerations in adoption of thermostable Newcastle disease vaccine in Eastern Kenya** Tabby Karanja-Lumumba, International Development Research Centre (IDRC), Kenya
1645 - 1700	**Elimination of Taenia solium transmission by pigs in a field trial undertaken in Nepal using Cysvax, a commercially manufactured TSOL18 vaccine** Professor Marshall Lightowlers (The University of Melbourne, Australia)
1700 - 1800	**Networking Activity**
1800 - 1900	**Drinks Reception, Poster Session & Networking**
1930	**Conference Dinner**

Day 2 – 10th January 2019

	Theme 3: Antigen Discovery Chair: Dr. Vish Nene (International Livestock Research Institute, Kenya)
0900 - 0930	**Analyses of the intracellular Proteome of African swine fever virus** Dr. Axel Karger (Friedrich-Loeffler-Instituts, Germany)
0930 - 1000	**Development of a vaccine for contagious bovine pleuropneumonia** Dr. Volker Gerdts (VIDO-InterVac, Canada)
1000 - 1030	Tea & Coffee
1030 - 1100	**T cell antigen discovery for new vaccination approaches to East Coast Fever** Dr. Nicola Ternette (University of Oxford, UK**)**
1100 - 1130	**Programmable Animal Vaccines: The Modified Dendrimer-mRNA Platform** Dr. Omar Khan (Tiba Biotech, USA)
1130 - 1145	**Multiple bacterial veterinary pathogens contain phase-variable regulons; phasevarions** Dr. John Atack (Griffith University, Australia)
1145 - 1200	**Exploring the cattle MHCII ligands** Andressa Fisch (University of Sao Paulo, Brazil)
1200 - 1215	**Sequencing and characterization of a novel micro exon gene (Tb-MEG1) in a myxozoan parasite: its utility as a vaccine candidate and as a biomarker of proliferative kidney disease (PKD) in rainbow trout** Marc Faber (University of Aberdeen, UK)
1215 - 1315	Lunch & Networking
	Theme 4: Controlling AMR with Vaccination Chair: Professor Peter Borriello (Veterinary Medicines Directorate, UK)
1315 - 1345	**Vaccines: safe, cheap, effective: but will livestock keepers use them?** Dr. Delia Grace (International Livestock Research Institute, Kenya)
1345 - 1415	**Prioritization of animal diseases for which vaccines could reduce antimicrobial use** Dr. Vish Nene (International Livestock Research Institute, Kenya)
1415 - 1445	**Could and should vaccination be used to control antimicrobial use or antimicrobial resistance in animal populations?** Professor Ruth Zadoks (University of Glasgow, UK)
1445 - 1515	Tea & Coffee
1515 - 1545	**InnoVet-AMR** Dr. Shahida Syed (Global AMR Innovation Fund (GAMRIF), UK Department of Health and Social Care (DHSC), UK)
1545 - 1600	**Dedicated adjuvants for bacterial autogenous vaccines** Dr. BingLing XU (SEPPIC, France)
1600 - 1700	**Keynote presentation: The factors affecting the livelihood of small holder farmers in LMICs** Dr. Nicoline de Haan (International Livestock Research Institute, Kenya)
1700 - 1715	**Concluding comments** Professor Gary Entrican (Moredun Research Institute, UK)

Speaker Abstracts

Theme 1: Vaccines for Ectoparasites

Targeting host-vector-pathogen interactions to reduce the global burden of tick-borne diseases

Professor José de la Fuente, SaBio. Instituto de Investigación en Recursos Cinegéticos IREC (CSIC-UCLM-JCCM), Spain

Ticks are blood feeding arthropod ectoparasites that transmit pathogens causing diseases in humans and animals worldwide. Tick-borne diseases (TBDs) represent a growing burden for human and animal health worldwide. Several approaches including the use of chemicals with repellency and parasiticidal activity, habitat management, genetic selection of hosts with higher resistance to ticks, and vaccines have been implemented for reducing the risk of TBDs. The complex molecular interactions between ticks, hosts and pathogens are analyzed by a systems biology approach that allow the integrated analysis of metabolomics, transcriptomics, proteomics and other omics datasets for discovery of key pathways and molecules that mediate tick-host-pathogen interactions. A vaccinomics approach could then be used to identify and fully characterize candidate protective antigens and validate vaccine formulations, including development of effective screening platforms and algorithms for discovery and validation of candidate protective antigens. The application of latest gene editing technologies in combination with vaccines likely combining tick and pathogen derived antigens and other control measures would result in the development of effective, safe, and environmentally sound integrated control programs for the prevention and control of TBDs and other infectious diseases.

The potential for vaccination to control poultry red mite

Dr. Alasdair Nisbet, Moredun Research Institute, UK

In recent years, several vaccine candidates have been identified in Dermanyssus gallinae by employing native protein fractionation and testing and/or by selecting antigens by their inferred orthology with protective antigens from other species. Many of the recombinant D. gallinae antigens or native extracts previously tested for vaccine efficacy using an in vitro feeding device demonstrated increased D. gallinae mortality after mites had fed on blood from immunised hens. However, translation of this efficacy into sustainable control in field tests has had variable results. For example, an extract of D. gallinae (termed “SME”) which induced 24% mortality in mites feeding in vitro on blood from hens which had been immunised with SME, also resulted in 75% reductions in D. gallinae populations when used as a prototype vaccine in a large field trial. In contrast, immunisation of hens with recombinant versions of 3 key immunogenic proteins from SME failed to give any protection in field trials, in spite of results from in vitro feeding assays which demonstrated that mites feeding on blood from hens immunised with each of the recombinant proteins were 1.7-2.8 times more likely to die than mites feeding on blood from control hens.

Sea lice vaccine development

Professor Frank Nilson, University of Bergen, Norway

Sea lice represent one of the largest costs for the salmon farming industry worldwide. Traditionally the main approach for controlling these ectoparasites is through medical treatment. However, during the last decade resistance towards one or several of the available medicines have been detected and characterized. This has resulted in the development of non-medical treatment approaches but these methods involve far more handling of the fish and, hence the fish welfare has been compromised. An anti-sea lice vaccine would be a very useful tool for combating sea lice. Research towards ectoparasite vaccines has been ongoing for decades but there is only one commercial available vaccine against cattle tick. Identifying protective antigens is regarded as the main challenge largely due to the complexity of these parasites. A few groups have been working on sea lice vaccines but so far no commercial available vaccine is available. There are a few reports describing significant protection in small scale lab-experiments. The present presentation will give an overview of some of the experiences with sea lice vaccine work and point to some of the current challenges in relation to antigen discovery and experiment design in clinical trials of test vaccines.

SophisTICKated anti-tick vaccines – cattle tick and Australian paralysis tick

Professor Ala Tabor, University of Queensland, Australia

The cattle tick Rhipicephalus microplus or Rhipicephalus australis co-evolved with Asian bovines (zebu breeds) and due to the global migration of Bos taurus taurus European breeds for dairy production during the 18th-19th centuries, this tick spread across tropical and sub-tropical regions of the world. The world-wide annual economic burdens for cattle industry has been calculated at $US22-30b with the application of chemical acaricides as the main control treatment. The eastern paralysis tick, Ixodes holocyclus, is indigenous to Australian wildlife and incidentally affects livestock, domestic pets and also humans with approximately 100,000 animals affected each year. Anti-tick vaccines need to be tailored to address the behaviour and/or niche of the particular tick species in association with the affected host (bovine – cattle tick) and hosts (multiple hosts – paralysis tick). The approach to develop anti-tick vaccines needs to be tailored to address the feeding habits of the particular tick species and should also focus upon producing a protective host immune response to ticks. The concept of concealed antigens developed with the discovery of Bm86 in the tick gut of R. microplus. However due to the multiple boosting required from Bm86 based vaccines, exposed proteins have been exploited to attempt to boost antigenicity during natural tick challenge. Other vaccine approaches have been to target a protein shown critical for tick survival following RNA interference knockdown of the corresponding mRNA. The latter relies upon the ingestion of corresponding host antibodies which can perturb the tick vaccine target to also disrupt the tick life cycle. This approach has varied as some targets exhibiting high RNAi knockdown effects are intracellular proteins which cannot be targeted by host antibodies. Very little focus has been on immunogenic traits of vaccine antigens. For example Bm86 has predicted B cell binding epitopes but has no predicted MHCII epitopes. We developed a reverse vaccinology approach identifying several cattle tick vaccine candidates following 12 years of research (antigen discovery, bioinformatics, in vitro immune screening, and in vitro antibody tick feeding) and seven "proof of concept" cattle tick challenge trials. For the Australian paralysis tick, vaccine candidates were identified from transcriptome reads (Illumina HiSeq) prepared from the salivary glands and viscera of semi-engorged I. holocyclus female adult ticks collected from paralysed pets. This led to the characterisation of a large family of neurotoxins (holocyclotoxins/HT) which are responsible for host paralysis symptoms when adult female ticks engorge for 3-5 days. A cocktail HT vaccine has protected dogs from I. holocyclus induced paralysis symptoms. Both vaccines are now under commercial development phases. Funding: Cooperative Research Centre for Beef Genetic Technologies, Queensland State Government's National and International Research Alliances Program, Meat & Livestock Australia, Australian Research Council Linkage Project (LP120200836) and Elanco.

A decavalent vaccine based on recombinant tick salivary proteins decreases successive infestations with Rhipicephalus microplus in cattle

Professor Isabel Kinney Ferreira de Miranda Santos, University of Sao Paulo, Brazil

Poor immune memory limits usefulness of tick vaccines based on “hidden” antigens, argued to be efficient because they do not mediate escape mechanisms. However, tick saliva contains “exposed” key mediators of parasitism, which can be neutralized by antibodies. Evidence for this is provided by genetically tick-resistant breeds of cattle that produce many more specificities of anti-saliva antibodies than tick-susceptible breeds. We profiled global gene expression in salivary glands from R. microplus feeding on resistant and susceptible bovines. Candidate antigens were chosen among annotated CDS based on gene expression patterns suggestive of reduced amounts of protein in ticks feeding on resistant hosts, putative functions and, within large protein families, degree of similarity with members. Nine salivary protein sequences were produced in Escherichia coli as recombinant proteins and used to immunize Holstein calves (n = 6/group; three doses of each antigen in alum were administered every four weeks; controls received PBS in alum); four and fifteen weeks after the third immunization, animals were successively challenged with 15,000 and 5,000 R. microplus larvae, respectively. Engorged female ticks were counted, weighed and assessed for fertility. Levels of antigen-specific total IgG were assessed by ELISA in serially collected sera. Compared to the control group, in vaccinated cattle the number of engorged female ticks was reduced by 62% and 71% after the first and second challenge infestations, respectively; reduction in weight and fertility of eggs compared to the control group resulted in overall efficacy of the multicomponent vaccine of 67.6% and 77.7%, respectively. Immunized animals seroconverted for total IgG antibodies against all antigens ($p<0.05$, Student t test); total IgG antibody responses for five and two of the antigens were boosted after the first and second challenge infestations, respectively. Hierarchical clustering of animals according to intensity of antibody responses to individual antigens indicated that tick loads were inversely correlated with the intensity and breadth of antibody responses. Funding: FAPESP; Bayer Animal Health

A dual mixture of recombinant tick antigens decrease fecundity in Rhipicephalus appendiculatus under laboratory conditions

Kiio I. K[1,2], Kanduma E. G[2], Kamau L.M[3], Muge E.K[2], Owido G.M[1], Parizi L. F[4], Nene V[1], Githaka N. W[1].

[1] International Livestock Research Institute (ILRI) Nairobi, Kenya.
[2] Department of Biochemistry, University of Nairobi, Kenya.
[3] Department of Zoological Sciences, Kenyatta University, Kenya.
[4] Centro de Biotecnologia and Faculdade de Veterinária, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil

Background
Tick vaccines are considered a critical component of an integrated tick control strategy.
Methods: Recombinant Rhipicephalus appendiculatus antigens; rRa05 and rRafer2 were over expressed in Escherichia coli and purified. Naïve rabbits were randomly grouped into experimental groups of three animals each. Group 1 and 2 animals were subcutaneously vaccinated with three 100μg doses of rRafer 2 and rRa05 adjuvanted in Incomplete Freunds' Adjuvant (IFA) at two-week intervals respectively. Dual mixtures at 50 μg and 100μg of each antigen were similarly administered to group 3 and 4 respectively. Phosphate buffered saline in IFA was administered to the control group. A homologous tick challenge was carried out with 30 pairs of adult and 200 nymphs of R. appendiculatus (Muguga strain). Tick engorgement weight, egg mass and hatchability were determined.

Results
A 72 % reduction in hatchability in eggs from ticks infested on dual mixture group at 100μg antigen dose was significantly different from that of the control group (P=0.0081). However, there were no significant differences in tick engorgement weight, egg yield and hatchability in experimental groups vaccinated with rRa05, rRafer 2 and the dual mixture of 50μg of each antigen and control group. Both the individual and combined antigen formulations did not show any effect on nymphal engorgement and moulting.

Conclusion
The dual mixture is a promising vaccine candidate against R. appendiculatus.

Theme 2: Vaccine Commercialization

Factors that Influence the Success and Speed in the Development of Vaccines

Dr. Mahesh Kumar, Zoetis, USA

There is never a shortage of opportunities for vaccines R&D. Interest in the development of vaccines, from academic institutions, research institutions and industry needs constantly drive us to innovate. Research into vaccines can be for improving existing vaccines, be it for safety, efficacy or duration of immunity and other innovations to better the vaccines in use. While a large portion of R&D goes into this space, newer diseases are another significant area of investment. Here, diligence in choosing the programs to invest in and ones to pass are important. Many diseases and outbreaks while important, are not always a commercial success. Many times, the outbreak is contained through a program of culling and eradication, and vaccines are seldom used. The presentation will provide an overview on some of the elements that aid us in the selection of candidates, speed to which we can manage and the eventual success commercially.

Towards sustainable supply of quality registered veterinary vaccines: the East Africa Community's Mutual Recognition Procedure

Dr Lois Muraguri, GALVmed, UK

Obtaining approval to place veterinary medicines on the market requires a marketing authorisation (licence) from the National Regulatory Authority in each country where the product is to be sold. In the six countries making up the East African Community (EAC), this involved applying for a licence separately in each country – until now. The EAC's newly launched Mutual Recognition Procedure (MRP) overcomes this lengthy, resource-intensive and often unpredictable process. MRP was preceded by the harmonisation of the registration requirements for immunologicals under a project initiated in 2011 supported by the Global Alliance for Livestock Veterinary Medicines (GALVmed) with funding from the Bill and Melinda Gates Foundation and UK Aid.

Through a partnership between EAC, and HealthforAnimals, EAC has implemented an initiative to harmonise the registration requirements and application procedure for veterinary immunologicals across all EAC countries leading to mutual recognition. MRP allows applicants to apply simultaneously for licences in multiple countries. This saves time and allows countries and applicants to use their resources more efficiently. MRP increases the likelihood for the sustainable supply of quality-registered vaccines in the region. The first licences for a veterinary vaccine submitted for registration under the EAC MRP were issued in July and October 2018. Two other products are in the process of registration.

Technology Licensing: Art or Science?

Dr. Peter Jeffries, Business Development Adviser, UK

Drawing on his business development experience in multi-national companies and numerous licensing negotiations, Dr Jeffries will explore some of the ways companies assess technology opportunities they are considering licensing or acquiring from universities and research institutes, as well as the challenges companies often face in completing licensing agreements. He will discuss the importance of effective contracts, ensuring that value is fairly distributed, the types of agreements that may be put in place and what to do when things go wrong.

Catalysing demand for livestock vaccines: Gender and youth-specific considerations in adoption of thermostable Newcastle disease vaccine in Eastern Kenya

Tabby Karanja-Lumumba, Research Award Recipient, Livestock Vaccines Innovation Fund (LVIF), International Development Research Centre (IDRC), Kenya

It is widely recognized that there are gender disparities in adoption of agricultural technologies. However, a few studies have shown that these disparities are not necessarily systematic. This paper uses sex- and age-disaggregated cross-sectional data collected from 512 poultry enterprises to test gender disparities in adoption of thermostable Newcastle vaccine. The study analyses adoption decisions by female adults (>35 years), male adults (>35 years), female youth (18-35 years) and male youth (18-35 years). Jointly-owned poultry enterprises were also included in the study. A chi-square test to examine the relation between gender and the rate of adoption revealed that no systematic gender disparities exist in adoption patterns of thermostable Newcastle vaccine. The highest adoption rates (46.3%) were observed in jointly-owned poultry enterprises. Enterprises owned by female adults, female youth, male youth and male adults had significantly low vaccination rates at 38.5%, 36.3%, 35.4% and 31.3% respectively. Qualitative information collected through focus group discussions revealed differences in gender and youth-specific considerations made in adoption of the vaccine. Male adults were more likely to adopt the vaccine if the vaccine information was delivered via their trusted messengers who comprise of local leaders and public extension personnel. Female adults were more likely to vaccinate if they were trained on how to vaccinate and given vaccination schedules on a vaccination pamphlet/card. Female youth were more likely to vaccinate if they were assured of a ready market for their poultry. The paper makes important policy recommendations with a potential to catalyse commercialization through enhancing demand for livestock vaccines.

Elimination of Taenia *solium* transmission by pigs in a field trial undertaken in Nepal using Cysvax, a commercially manufactured TSOL18 vaccine

Professor Marshall Lightowlers, The University of Melbourne, Australia

Taenia solium is a zoonotic cestode parasite which causes human neurocysticercosis. Pigs transmit the parasite by acting as the intermediate host. An intervention was implemented in pigs to control transmission of T. solium in Dalit communities of Banke District, Nepal. Every 3 months, pigs were vaccinated with the TSOL18 recombinant vaccine recently registered as Cysvax by Indian Immunologicals Limited and, at the same time, given an oral treatment with 30mg/kg oxfendazole (Paranthic 10% MCI, Morocco). At the start of the intervention the prevalence of porcine cysticercosis was 23.6% and 34.5% in control and intervention areas, respectively. Following the intervention, the prevalence of cysticercosis in pigs from the control area was 16.7% (no significant change), whereas no infection was detected after complete slicing of all muscle tissue and brain in animals from the intervention area (P=0.004). A three-monthly vaccination and drug treatment intervention in pigs is an effective and practical method for reducing T. solium transmission, thereby reducing the incidence of human neurocysticercosis.

Theme 3: Antigen Discovery

Analyses of the intracellular Proteome of African swine fever virus

Dr. Axel Karger, Friedrich-Loeffler-Instituts, Germany

African swine fever (ASF) is a viral disease that affects members of the Suidae family such as African bush pigs, warthogs, but also domestic pigs, and wild boar. Transmission can occur by contact of naïve with infected pigs but also by Ornithodoros ticks. After an introduction into Georgia in 2007, the African swine fever virus (ASFV) has now spread into Eastern and Central European countries. Very recently, cases in Belgium and in China have been reported. As currently no efficient vaccine is available, ASFV is a severe threat to the pig industry worldwide. ASFV is a large enveloped ds DNA-virus encoding at least 150 open reading frames. Many of the deduced gene products have not been described, less functionally characterized. In order to identify potential targets for a vaccine and to improve our understanding of the ASFV replication cycle, we have conducted a mass-spectrometric study to analyze ASFV OURT88/3 protein expression in three susceptible mammalian cell lines from susceptible (wild boar) and non-susceptible species (human and green monkey). Total amounts of ASFV protein were high reaching 17 mole % of the cell protein content in the wild boar cell line. Overall, we could identify 94 ASFV proteins in the late phase of infection, 23 of them are so far uncharacterized. Expression levels of several newly identified ASFV proteins were remarkably high indicating importance for the viral replication cycle. Protein expression profiles of ASFV proteins in the three cell lines differed markedly, indicating cell-specific requirements for the maintenance of the ASFV infection in cell culture. Proteins corresponding to six of the 32 multi-gene-family members were identified, three of them were expressed in all three cell lines. For four MGF 110 proteins the predicted cleavage of a signal peptide was experimentally confirmed.

Development of a Subunit Vaccine for Contagious Bovine Pleuropneumonia

Dr. Volker Gerdts, Vaccine and Infectious Disease Organization-International Vaccine Centre, Canada

Contagious Bovine Pleuropneumonia (CBPP) is a respiratory disease of cattle caused by infection with Mycoplasma mycoides subsp. mycoides (Mmm). The disease is characterized by severe fibrinous bronchopneumonia, breathing difficulties and high fever. The disease is found in many Sub-Saharan countries and responsible for significant economic losses. Vaccines are available, however, they are only moderately effective and often responsible for severe adverse events following immunization. We used a reverse vaccinology approach to develop a novel subunit vaccine for CBPP that is safe, effective and DIVA compatible. Using a combination of bioinformatics and proteomics, >65 different antigens were expressed and subsequently screened in Boran and Zebu cattle for their ability to protect against infection with Mmm. Based on these trials, a combination of four antigens was selected and further optimized through use of potent adjuvants. When benchmarked with a live attenuated T1/44 vaccine in a challenge trial in Zebu cattle, only 1/8 vaccinated animals showed small lung lesions, while in the T1/44 group 5/8 animals displayed lesions in their lungs. Current work is focused on establishing scale-up manufacturing and field-testing of the vaccine in several Kenyan counties.

T cell antigen discovery for new vaccination approaches to East Coast Fever

Dr. Nicola Ternette, University of Oxford, UK

My talk will be focussing about our approach to try and identify parasite-derived antigens presented by BoLA molecules on Theileria parva infected cells. Here, we used specific immunoprecipitation of BoLA molecules, to enrich for BoLA-bound peptides, and analysed the obtained pools using liquid chromatography tandem mass spectrometry technology. With this approach, we could identify many previously unknown T.parva antigens and could further utilize the comprehensive datasets as training sets for NetMHCpan, to globally improve binding prediction of BoLA ligands.

Programmable Animal Vaccines: The Modified Dendrimer-mRNA Platform

Dr. Omar F. Khan, Tiba Biotech, USA

To combat orphaned indications, sudden outbreaks, evolving pathogens and agriculture security threats, Tiba Biotech has developed a fully synthetic cross-species replicon RNA platform for the rapid design, screening and scalable manufacture of vaccines that reproducibly generate protective cellular (T cell) and humoral (antibody) responses. Antigens are encoded in mRNA replicons, which induce potent interferon responses upon controlled, finite intracellular replication. The mRNA is delivered via a chemically-defined modified dendrimer system. Using this platform, experimental vaccines were shown to generate protective immunity against a broad spectrum of lethal pathogens in animal challenge models, including H1N1 influenza, Toxoplasma gondii, Ebola virus, Venezuelan Equine Encephalitis, and HPV-induced cancer. Our delivery system is immunosilent and does not lead to local dose-limiting toxic effects or reactogenicity. Furthermore, a straightforward self-assembly process reproducibly yields synthetic nanoparticles of uniform size and shape enabling rapid drug product formulation. The modified dendrimer delivery system features a large payload capacity for multiplexing (the co-delivery of multiple large nucleic acid molecules in a single nanoparticle), which enables the simultaneous transport of complex or multiple subunit antigens and potentially the induction of cross-protective immunity to multiple strain sequences. Beyond multivalent protection, multiplexing is also advantageous for higher-throughput in vivo antigen discovery applications.

Multiple bacterial veterinary pathogens contain phase-variable regulons; phasevarions

John M. Atack[1], Patrick J Blackall[2] & Michael P. Jennings[1]

[1]Institute for Glycomics, Griffith University, Gold Coast, Queensland 4222, Australia
[2] QAAFI, The University of Queensland, St Lucia Queensland 4067, Australia

Many bacterial pathogens contain randomly-switching methyltransferases that control phase-variable regulons – phasevarions. All current examples control expression of genes involved in pathogenesis and host-adaptation, and many regulate putative and current vaccine candidates. Effective vaccines require stably expressed targets; individual phase-variable genes can be identified in silico as they contain easily recognised features, but genes controlled by phasevarions do not, complicating the rational design of vaccines. We have identified and begun to study phasevarions controlled by the switching of both Type I and Type III methyltransferases in several important bacterial veterinary pathogens: Streptococcus suis and Actinobacillus pleuropneumoniae are major swine pathogens, with S. suis also a major cause of bacterial meningitis in humans, particularly in S.E. Asia; Mannheimia haemolytica is a major bovine pathogen; multiple species of the Mycoplasmataceae, obligate intracellular pathogens, cause disease in a range of livestock. All these organisms contain both Type I and Type III methyltransferases that are able to phase-vary, a phenomenon never before observed in individual species.

Pacific Biosciences SMRT sequencing and methylome analysis of the methyltransferases from these organisms has deciphered their specificity, and demonstrated that different genes/alleles methylate different target sequences, therefore controlling different phasevarions. Analysis of the protein profiles of strains containing phase-variable methyltransferases shows protein expression differences correlating with methyltransferase switching.

Our analysis shows that phasevarions are present in diverse veterinary pathogens, and need to be characterised in order to identify the stably expressed protein repertoire of these organisms. This work will provide a framework for the rational design of vaccines and treatments against these bacteria

Exploring the cattle MHCII ligands

Andressa Fisch[1,6], Birkir Reynisson[2], Lindert Benedictus[3], Nicola Ternette[4], Morten Nielsen[2,5], Beatriz Rossetti Ferreira[1], Isabel K. F. M. Santos[6], Timothy Connelley[3]

[1] Ribeirao Preto College of Nursing, University of Sao Paulo, Ribeirao Preto, Brazil.
[2] Department of Bio and Health Informatics, Technical University of Denmark, Kongens Lyngby, Denmark.
[3] The Roslin Institute, Royal (Dick) School of Veterinary Studies, University of Edinburgh, UK
[4] Jenner Institute, University of Oxford, Oxford, UK.
[5] Instituto de Investigaciones Biotecnológicas, Universidad Nacional de San Martín, Buenos Aires, Argentina.
[6] Ribeirao Preto Medical School, University of Sao Paulo, Ribeirao Preto, Brazil.

CD4 T cell activation is necessary to the development of immune responses mediated by CD8 T cells and B cells after immunization with protein antigens, and occurs when peptides presented through MHC II molecules are recognized by the cognate TCR. Thus, the identification of MHC II ligands is a useful strategy for CD4 T cell epitope discovery. Aiming the characterization of peptide ligand motifs of bovine DRB3 molecules, lysed Theileria annulata infected bovine cells homozygous for DRB3 alleles *1101 and *1001 were submitted to immunochromatography with anti-bovine DR antibody (ILA21) immobilized in protein-A resin. The MHC II:peptides complexes recovered after acidic elution were submitted to HPLC to peptide isolation. Peptides were characterized by LC/MS2 and sequence interpretations were performed using 23970 bovine entries available at UniProt through PEAKS 8.5 software. We identified 1985 peptides for sample DRB3*1101, and 6992 peptides for sample DRB3*1001. Length distribution of the peptides identified the presence of peptides between 10 to 21-mer (MHC II ligands), and the extensive presence of 9-mer peptides, indicating MHCI contamination of samples. Peptides containing between 8 and 21 mer were clustered using GibbsCluster software for discovery of ligand motifs. For both samples, three clusters were identified, being one correspondent to a classic MHC II ligand motif, with conserved amino acids at anchor positions, and the other two representing already described MHC I ligand motifs. The workflow presented here was successful to identify peptides bound to bovine DR molecules and define the ligand motifs of each allele tested, and can be applied to the characterization of DRB3 ligand motifs aiming the development of BoLA-II ligand prediction tools for optimized CD4 epitope discovery to be applied in vaccine development.

Sequencing and characterization of a novel micro exon gene (Tb-MEG1) in a myxozoan parasite: its utility as a vaccine candidate and as a biomarker of proliferative kidney disease (PKD) in rainbow trout

Marc Faber[5], C Tafalla[1], G Wiens[2], B Okamura[3], H Hartikainen[4], T Wang[5], Jason Holland[5], C J Secombes[5]

1 Centro de Investigación en Sanidad Animal, Madrid, Spain
[2] National Center for Cool and Cold Water Aquaculture, ARS-USDA, USA
[3] Department of Life Sciences, Natural History Museum, London, UK
[4] Institute of Aquatic Ecology, Switzerland
[5] University of Aberdeen, UK

PKD is one of the most serious diseases affecting trout aquaculture in the UK. Caused by the myxozoan parasite, *Tetracapsuloides bryosalmonae*, PKD is elicited by the temperature-dependent development of parasite spore sacs in colonial bryozoans. Our investigations have focused on *putative T. bryosalmonae* virulence factors in order to unravel host immune evasion mechanisms exploited by the parasite, whilst shortlisting candidates for vaccine studies.

Recently we uncovered an unknown gene which appears to exhibit a mechanism of antigenic variability previously thought to be unique to helminth parasites, particularly in schistosomes parasites. These so called micro-exon genes (MEGs) are intrinsically disordered secreted proteins some of which have been shown to interfere with host immunity. Over 75% of the coding region of MEGs consists of micro exons (<36 bp) which drive antigenic variability through alternative splicing. Splice variants are thought to enable greater plasticity in host protein targets to subvert immunity over the course of infection. Here we report the sequencing and characterization of the first non-helminth MEG gene from different *T. bryosalmonae* populations. The 264 amino acid open reading frame of the full length molecule is encoded by 65 exons, with only 5 exons > 30 bp. The protein is predicted to consist of an intrinsically disordered loop containing a tandem repeat region flanked by a conserved signal peptide at the N-terminus and a C-terminal domain with a strongly predicted nuclear localization signal. Using a validated anti-MEG MoAb, we have demonstrated the protein is endogenously expressed in and on the surface of parasites and a subset of host immune cells within the kidneys of infected fish. We have also demonstrated a potent Tb-MEG1-specific IgM antibody response in sera from parasite-infected farmed rainbow in three different countries. In addition, this antigen has been tested in combination with other antigens in vaccine trials and was shown to partially reduce the gross kidney pathology associated with PKD.

Overall, the discovery and characterisation of Tb-MEG1 may provide insights into host immune evasion mechanisms exploited by myxozoan parasites whilst having major implications concerning the evolution of antigenic variability in metazoan parasites.

Theme 4: Controlling Antimicrobial Resistance (AMR) with Vaccination

Vaccines: safe, cheap, effective: but will livestock keepers use them?

Dr. Delia Grace, International Livestock Research Institute (ILRI), Kenya

Vaccines are a highly attractive way of preventing disease and as such could have an important role in tackling antimicrobial resistance. Vaccines against bacterial infections will directly reduce the use of antimicrobials. Viral diseases may lead to immune suppression or otherwise pre-dispose to bacterial infections and vaccines against viral diseases can indirectly reduce antimicrobial use. Commercial farmers in developed and developing countries have been quick to adopt vaccines but less is known about uptake by the nearly one billion poor livestock keepers.

We present evidence on: a) limited use of veterinary vaccines among poor livestock keepers; b) reasons for limited use; c) interventions to increase vaccine use. We illustrate and seek to understand farmer behaviour with examples from ILRI research on prevention of Newcastle disease, cysticercosis, East coast fever and trypanosomosis. We then discuss the implications of low vaccine adoption for antimicrobial use and antimicrobial resistance and make recommendations for maximising the benefits of vaccines.

Prioritization of animal diseases for which vaccines could reduce antimicrobial use

Dr. Vish Nene, International Livestock Research Institute (ILRI), Kenya

Antimicrobial resistance (AMR) is recognized as a global threat and has resulted in public health challenges in the treatment of several diseases, especially as the development of new antibiotics has stagnated. The mis-use of antibiotics is viewed as one factor that contributes to the development and spread of AMR. Vaccination has proved highly efficacious in the prevention of disease. Hence, vaccines could be used to reduce the use of antibiotics and the AMR threat posed by animal agriculture. In an attempt to prioritize diseases for which vaccines could reduce antimicrobial use in animals the OIE convened two ad hoc groups to assess and rank poultry, fish, swine and ruminant diseases. This process and the results from the group discussion will be presented. The pathogen and disease lists should serve to inform funders of research and the research community in the fight against AMR.

InnoVet-AMR

Renée Larocque[1], Armando Heriazon[1], Kevin Tiessen[1], Santiago Alba Corral[1], Shahida Syed[2], Erica Westwood[2], Louise Norton-Smith[2]

[1] International Research Development Centre (IDRC), 150 Kent St, Ottawa, ON K1P 0B2, Canada
[2] Global AMR Innovation Fund (GAMRIF), UK Department of Health and Social Care (DHSC), 39 Victoria Street, London, SW1H 0EU, UK

In April 2018, the International Development Research Centre (IDRC) in Canada and the UK Government's Global AMR Innovation Fund (GAMRIF) – managed by the UK Department of Health and Social Care (DHSC) – announced a new four-year, £17 million partnership to fund research on Innovative Veterinary Solutions for Antimicrobial Resistance (InnoVet-AMR). InnoVet-AMR will provide research funding to develop new animal vaccines and other alternative innovations to fight antimicrobial resistance (AMR) in livestock and aquaculture in low- and middle-income countries (LMICs). This initiative responds to a need identified by the international

scientific and development communities and is supported with several high-level policy processes—including the UN political declaration on AMR (2016), G7/G20 ministerial statements, Global Health Security Agenda and Action Plan, as well as Global Action Plans on AMR of the World Health Organisation (WHO) and the World Organisation for Animal Health (OIE). The partnership builds on DHSC's expertise championing innovation by supporting research and technology to improve lives and reduce poverty, and draws on IDRC's history as a development research funder with decades of experience building knowledge-focused, cross-sector partnerships. While supporting research, InnoVet-AMR also aims to build effective partnerships to better coordinate discovery, development and sustainable delivery of affordable innovative veterinary solutions to reduce the use of antibiotics in livestock and aquaculture in LMICs.

IDRC is a Canadian Crown corporation that funds research in developing countries to create lasting change on a large scale. Canada's IDRC supports research that generates local solutions, bringing choice and change to those who need it most in the developing world. We achieve this by investing in knowledge and innovation, supporting the leaders of the future, and by being a partner of choice for the public and private sectors.

GAMRIF was established to support early-stage, innovative research and development, specifically targeting neglected and underinvested areas in the field of antimicrobial resistance (AMR). GAMRIF is a £50m Official Development Assistance investment, which means all projects funded must support research primarily and directly for the benefit of people living in developing countries. The Fund takes a 'One Health' approach, seeking to invest in potential solutions to reduce the threat of AMR in humans, animals, aquaculture and the environment.

Dedicated adjuvants for bacterial autogenous vaccines

Ghislaine Ionkoff [1], Héloïse Imbault [1], BingLing Xu [1], Nicolas Versillé [1], François Bertrand[1]

[1] SEPPIC, 22 Terrasse Bellini, 92806 Puteaux Cedex, France

Bacterial autogenous vaccines are more and more used, especially to follow the European plans of antibiotic reduction. Autogenous vaccines are inactivated vaccines, and adjuvants are necessary to increase the duration and efficacy of vaccine-induced immune responses. Adjuvants play other roles such as enhancing the overall stability of the vaccine formulations. Oil emulsion is commonly used as adjuvant formulation in veterinary vaccines. Destabilization of vaccine emulsions can be observed during storage when high concentration of enzymes is present in antigenic media such as bacterial media. Resistant formulations are needed to ensure stability of vaccines. SEPPIC have developed adjuvants for autogenous vaccines, resistant to destabilizing antigenic media, for both avian species and swine. Oil emulsions have different preferences based on the target species, its sensitivity and immune responsiveness towards a particular type of emulsion in a vaccine formulation. Water in oil (W/O) emulsion is preferable for avian species whereas swine will usually require well tolerated adjuvant like oil in water (O/W) emulsion. In this study, oil adjuvants designed for destabilizing bacterial antigen media were evaluated for their emulsion stability, safety, and efficacy in avian and swine.

W/O and O/W vaccines based on destabilizing model antigenic medium were prepared by using commonly used adjuvants and resistant adjuvants. The formulation were compared for emulsion stability over time. The resisting adjuvants were assessed in the field and target animals. In a first trial, safety and efficacy of the W/O resistant adjuvant, Montanide™ ISA 71 R VG (ISA 71R), were tested in Riemerella anatipestifer vaccine for geese. In a second trial, safety and efficacy of O/W resistant adjuvant, Montanide™ ISA 28 R VG (ISA 28R), were tested in swine vaccine against Actinobacillus pleuropneumoniae. ISA 71R and ISA 28 R allowed the formulation of stable vaccines under severe stress conditions. In each trial, formulations based on those two adjuvants showed acceptable safety levels and efficacy profiles in target species.

These results demonstrate that Montanide™ ISA 71 R VG and Montanide™ ISA 28 R VG are safe and efficient adjuvants to be used in bacterial autogenous vaccines for avian species and swine.

Keynote Presentation

Why is understanding the factors of livelihoods important for vaccine development?

Dr. Nicoline de Haan, International Livestock Research Institute, Kenya

One of IVVN's aims is to identify novel approaches "to effectively address critical 'bottle-necks' in vaccine development for LMIC-relevant pathogens". This paper posits that one of these novel approaches is developing a second generation of research on the users of the vaccines in LMIC. To date most of the attention has been on developing the vaccine, but limited attention has been paid to who the user is – mainly small holders and the growing entrepreneurs in these countries. With globalization, and consequential rural transformation, the profile of this person and the institutional environment is changing. The paper will touch on this change but will also look at issues of access, acceptability, and adaptability of producers within the systems. It will examine the institutional and livelihood context of the user and how this contributes to the present vaccine landscape in Africa and Asia. It will show how factors outside of animal health can have an impact on the decision making around animal health care, and what the implication of this will be. It hopes to develop a framework to support the next generation social and economic research to address the critical bottle neck of vaccine uptake and use to safeguard and protect an important asset in the livelihoods of a majority of livestock keepers.

Poster Abstracts

The protection of highly potent inactivated Foot & Mouth Disease virus vaccine against induced repeated infection using different serotypes of Foot & Mouth Disease Virus type O

M. S. Abousenna[1], D. M. Darwish[1], M. A. Saad[2];

[1] CLEVB, Cairo, Egypt,
[2] VSVRI, Cairo, Egypt.

Background
Foot and mouth disease (FMD) is a highly infectious disease in cloven- hoofed animals. The regular vaccination is widely used to control and prevent FMD infection.

Methods
Detection the protective level of vaccinated calves with highly potent inactivated FMD vaccine against FMDV Vaccinal strain type O (O/EGY/4/2012) and different circulating FMDV field isolates type O (O/EGY/6/2011 and O/EGY/23/2014) in Egypt using challenge test with consideration for the SNT titre screening through different time intervals (28 dpv(days post vaccination), 60dpv, and 120 dpv). Sixteen calves were used in this experiment and allotted for 10 vaccinated calves and 6 calves as control positive for challenge test (2 calves for each challenge test). The vaccinal strain and different circulation FMDV types O were supplied and adjusted for challenge dose by CLEVB.

Results
it was found that the protection level of the vaccine in vaccinated calves using challenge test against O/EGY/4/2012 (vaccinal strain), O/EGY/6/2011 (field isolate) , and O/EGY/23/2014 (field isolate) viruses at the 28th day, 60th day and 120th day respectively showed that the protection against O/EGY/4/2012 and O/EGY/6/2011 was100% while the protection against O/EGY/23/2014 was 80%, with consideration to antibody screening against FMDV type O using SNT at the 28th day, 60th day and 120th day were 1.98, 2.64 and 2.13 log10 TCID50 respectively.

Conclusions
All these results revealed the efficacy and potency of high potent inactivated FMD vaccine against repeated infection thus afford the protection for vaccinated animals against current different circulating FMDV types O in Egypt.

Identification and Characterization of Antigenic Proteins of Amphistomes (Trematoda: Paramphistomidae) in Buffaloes, Pakistan

Kiran Afshan[1], Rubab Ali[1], Muddassar Nazar[1]

[1] Department of Animal Sciences, Faculty of Biological Sciences, Quaid-i-Azam University Islamabad, 45320, Pakistan

Mixed infection with digenetic trematode of the superfamily Paramphistomoidea seems common in buffaloes of Pakistan, which contributes heavy economic losses to livestock industry in terms of reduced fertility, milk and meat production. The present study was aimed to characterize the diagnostic antigens in buffaloes with mixed amphistomiasis. The somatic and excretory/secretory (ES) antigens of Gastrothylax crumenifer and Gigantocotyle explanatum were identified. Adult flukes (n= 500) were collected from the rumen and bile duct of naturally infected buffaloes. After their homogenization and centrifugation, somatic antigens were prepared and ES separated after incubating the worms in PBS and analyzed by SDS-PAGE. The immunogenicity of antigens was determined by Western blot (WB). Indirect ELISA analysis was performed on sera from buffaloes naturally infected with amphistomes along with control sera Fasciola spp., Cotylophoron spp. and Paramphistomum spp. The SDS-PAGE results of somatic and ES products of G. crumenifer identified proteins of size between 10-123 kDa, showing maximum abundance of 10, 15, 25- 28, 36, 38-72, 95-123 kDa proteins. The ES product showed ≥95, 72, 55 and 40 kDa proteins were more abundant. The somatic and ES polypeptides of G. explanatum ranged 5-105 kDa. Polypeptides ranged 5-25kDa and 86-105kDa showed high occurrence in adult worm extracts. The antigenic analysis of these proteins on WB revealed a polypeptide of 55-70 kDa in somatic extract of G. crumenifer and 38-72 kDa of G. explanatum were antigenic, while metabolic extracts did not show any antigenicity when reacted with sera obtained from infected buffaloes. The sensitivity and specificity of ELISA test for 38-72 kDa somatic antigens of G. crumenifer was 85.71%, 89.74% and G. explanatum was 95.45%, 87.1% respectively. Kappa value for both somatic antigens tests revealed that the strength of agreement is considered to be 'good'. The cross reactivity of the assay with other trematodes was recorded 10-20%. Antibodies were tested against 38-72 kDa somatic antigen of G. crumenifer 19.69% (39/198) and G. explanatum 21% (42/198) buffaloes were found positive, while 12.1% (24/198) infection with fecal/postmortem examination. The study confirmed that ELISA established for 38-72 kDa somatic antigen of G. crumenifer and G. explanatum had good value for serodiagnosis of mixed amphistome infections. These polypeptides could be potential candidates for further immunodiagnostic and vaccine studies.

Identification of Epitopes from Putative Salivary Proteins of Rhipicephalus Microplus Tick for The Development of a Multicomponent Vaccine

Almeida, L.G.N.[1]; Fisch, A.[1]; Daher, I.P.[1,2]; Moraes, A.[1]; Peña, M.S.[2]; Pupin, M.A.F.[2]; Nascimento, M. O.[1]; Ferreira, B.R.[2]; Santos, I.K.F.M.[1]

[1] Ribeirão Preto Medical School, FMRP/USP, Ribeirão Preto, Brazil
[2] Ribeirão Preto College Of Nursing - EERP/USP, Ribeirão Preto - SP – Brazil

Background
Ticks are obligate hematophagous arthropods and one of the most important vectors in disease transmission. Currently, several vaccines are under development, in addition to the use of in silico techniques that aim to shorten the path in the search for new antigens.

Objective
We aim to combine in silico and in vitro tools to predict and to map epitopes of proteins present in Rhipicephalus microplus tick saliva for later development of a multicomponent vaccine.

Methods and Results
From transcriptome analysis, we selected nine putative proteins present in the tick saliva and performed a heterologous expression in Escherichia coli. These proteins were used in the immunization of Holstein cattle and evaluated for induction of seroconversion. The immunization process had three doses, spaced within a 28-day interval, and each application was composed of 50 µg of individual recombinant protein in aluminum salt as adjuvant. We analyzed the serum of the immunized animals by ELISA technique and it was possible to detect seroconversion of total IgG for every antigen. Meanwhile, it was performed in silico predictions for linear and discontinuous B-cell epitopes by Bepipred and Epitopia, respectively. The sequence of the proteins were submitted to Bepipred under a threshold of 0.35. The percentage of epitopes in each sequence ranged from 11% up to 56%. For discontinuous epitope prediction, after protein modelling by Robetta platform, 3D structures were submitted to Epitopia and results ranged from 26% up to 72% of immunogenic regions in the vaccine candidates.

Conclusion
The confirmation of seroconversion by ELISA allows the realization of in vitro epitope mapping by phage display technique. The data generated in silico will be compared with those generated in vitro, resulting in an enhanced mapping of the immunogenic epitopes. Financial Support: FAPESP (2017/14297-6, 2015/09683-9); CAPES; CNPq; Bayer S. A. Animal Health.

Using reverse vaccinology for identifying novel vaccine candidates against animal African trypanosomiasis

Delphine Autheman and Gavin J. Wright

Cell surface Signalling laboratory
Wellcome Trust Sanger Institute
Wellcome Trust Genome Campus
Cambridge CB10 1SA

Animal African trypanosomiasis (AAT) is a major livestock disease in sub-Saharan Africa that affects many important farm animals. AAT-induced production loss directly impacts livelihoods of millions of people living in endemic regions and represents a major barrier for the socioeconomic advancement of many African countries. The disease is mainly caused by two species of trypanosome, T. congolense and T. vivax which are primarily transmitted through the bite of an infected tsetse fly. Infection of wild animals constitutes an important limitation of the disease control as livestock has to be constantly monitored and treated against trypanosome infections. Vaccination against AAT remains the ideal solution to achieve eradication of the disease. However, vaccine development has been hampered because trypanosomes use antigenic variation which prevents the host from acquiring protective antibodies. The aim of our study is to identify invariant proteins on the trypanosome cell surfaces which are susceptible vaccine targets.

We have created a library of forty surface-associated proteins of the bloodstream forms for each parasite. To increase the chance for these recombinant proteins to be correctly folded and thus to ensure that vaccine-elicited antibodies are raised against native parasite surface epitopes, we have expressed them in a mammalian expression system. To see whether they can confer protection, we have used AAT infection models where mice have been systematically vaccinated with individual proteins and then challenged with the parasites. The parasite load has been quantified during the infection course as readout for protection. From our initial screen, vaccination with five T. vivax surface-associated proteins have shown to confer different extent of protection, including one which achieve sterile protection.

Modified chromatographic strip test for Foot-and-Mouth Disease virus antibody screening

Jong Chul Choi, Yeong Lim Kang, Ji Yun Jeong, Hwi Yeon Choi, Sang Won Lee, In Soo Choi, Chang Seon Song, Seung Yong Park and Joong Bok Lee

Laboratory of Veterinary Infectious Disease, College of Veterinary Medicine, Konkuk University, 120 Neungdong-ro Gwangjin-gu, 05029, Seoul, Korea

There are three methods in OIE Terrestrial Manual for Foot-and-mouth disease(FMD) serological tests, which are virus neutralizing test(VNT), solid-phase competition ELISA(SPCE), liquid-phase blocking ELISA(LPBE). The VNT requires cell culture technique, live FMD virus and takes 1–2 weeks to get results. ELISA methods are high throughput and provide relatively accurate results. Among two ELISAs, the outcomes of LPBE present strong correlation with those of VNT. In previous studies, we applied the immunochromatographic strip test instead of ELISA to modify LPBE suitable for field surveillance. And we screened vaccinated pigs and cattle serum collected in the commercial farms with the LPB-chromatographic strips test and compared the results of the strip tests with that of SPCE and LPBE. In this study, we introduced mutations into the nucleotide sequence of the FMD antigen and adjusted concentration of the antigen to overcome some mismatches between the results of immunological tests. As a result, the correlation between the tests was improved and some non-specific reaction was resolved. In consequence, modified chromatographic strip test could be a serological tool for surveillance and quarantine after several confirmational tests.

Anti-vector immunity against a simian adenovirus vector and its influence on vaccine immunogenicity in livestock

Madeleine H.A. Clark[1,2], Nick J. Edwards[2], Danny Wright[2], Caitlin L. Blundell[3], Susannah R. Blundell[3], Anna Stedman[1], Bryan Charleston[1], Katie J. Ewer[2], George M. Warimwe[4,5]

[1] Transmission Biology Group, The Pirbright Institute, Pirbright, Woking, United Kingdom
[2] The Jenner Institute, Nuffield Department of Medicine, University of Oxford, Oxford, United Kingdom
[3] Department of Biochemistry, University of Oxford, United Kingdom
[4] Biosciences Department, KEMRI-Wellcome Trust Research Programme, Kilifi, Kenya
[5] Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, United Kingdom

Background
Adenoviruses have successfully been adapted for use as vaccine vectors and are in development for a wide range of human disease indications. Simian adenoviruses, in particular, are among the most promising platforms owing to their excellent safety profile, immunogenicity and low prevalence of anti-vector immunity (i.e. naturally acquired immune responses to the adenovirus type from which the vector was derived). Anti-vector immunity is thought to be a key factor influencing performance of adenovirus-vectored vaccines in humans but is yet to be studied in livestock. To address this, we here measured anti-vector humoral and cellular immune responses in sheep, goats, cattle and dromedary camels before and after immunisation with a simian adenovirus vectored Rift Valley Fever vaccine (ChAdOx1 RVF) and related these to vaccine immunogenicity.

Using an established adenovirus neutralising antibody assay we have detected varying levels of antibodies against the simian adenovirus vector (ChAdOx1) in all four livestock species. We have found no correlation between this anti-vector response and vaccine induced antibody responses. Further analysis is ongoing, including measurement of cellular immune responses in animals receiving escalating doses of ChAdOx1 RVF.

Results of these studies will be presented at the meeting.

Novel Vaccine Development and Virus Challenge Models at the Agri-Food and Biosciences Institute

K. Lemon[1], C. Duffy[1], V. Smyth[1], M. McMenamy[1], P.J. Collins[1], P. Savage[1], U.F Power[2], S.L. Cosby[1,2]

[1] Virology Branch, Veterinary Sciences Division, Agri-Food and Biosciences Institute, Belfast
[2] Centre for Experimental Medicine, School of Medicine, Dentistry and Biomedical Sciences, Queen's University Belfast

The Virology Branch at the Veterinary Sciences Division (VSD), Agri-Food and Biosciences Institute (AFBI) has a history of highly successful vaccine development and commercialisation. Inactivated vaccines for both porcine circovirus 2 and salmon pancreas disease, produced at AFBI, have been on the market for a number of years and are widely used internationally. We are moving forward into a new era of vaccine design and delivery. In addition, a number of animal challenge models have been developed to test our own, commercial vaccines as well as those of collaborators. Two approaches to vaccine design are being taken (i) novel delivery methods for inactivated vaccines and (ii) recombinant replication competent and replication incompetent vaccines which have inbuilt safety strategies.

Vaccine candidate development

Reverse genetic platforms for a range of animal RNA viruses including swine influenza virus, Newcastle disease virus, chicken astrovirus and fish Rhabdoviruses are currently under development. Rational attenuation strategies including gene deletion/truncation, cold-adaptation and codon-deoptimisation are being used. Recombinant vectored vaccines against, bovine respiratory syncytial virus, and Nipah virus are being produced in collaboration with Queen's University Belfast. Nanoparticle formulated vaccines against bovine parainfluenza virus type 3 and salmon pancreas disease virus are currently under development in collaboration with SiSaf Ltd.

Animal models of disease for vaccine trials

We have established animal challenge models in cattle, sheep, pigs, poultry and fish. Examples are: bovine respiratory syncytial virus and bovine parainfluenza virus type 3 (latter in cattle and sheep); Challenge models for a range of avian viruses, particularly for hatchery diseases of chickens including runting stunting syndrome and white chick disease; In pigs PCV-2, rota virus and swine influenza models (including colostrum derived); Salmon pancreas disease virus and other virus challenge models have been developed in fish.

Facilities

AFBI VSD has a range of animal and laboratory facilities including an onsite experimental farm, fish tanks, high containment large animal facilities up to BCL 3 plus state of the art laboratory facilities.

Applying the phage display method as a strategy for the development of a multi-antigenic epitope-based vaccine against Rhipicephalus sanguineus ticks

Isabela Daher[1,2], Andressa Fisch[1,2], Luiz G. N. Almeida[2], Mariana Nascimento[1,2], Alexsander De Moraes[1,2], Maria A. F. Pupin[1], Mauricio Peña[1], Isabel K. F. M. Santos[2], Beatriz R. Ferreira[1]

[1] Ribeirão Preto College of Nursing, EERP/USP, Ribeirão Preto, Brazil
[2] Ribeirão Preto Medical School, FMRP/USP, Ribeirão Preto, Brazil

Ticks are hematophagous arthropods that parasite vertebrate hosts and transmit diseases to humans and animals. Currently available anti-tick vaccines are based in unique antigens and present limited efficacy. Due to the complexity of this parasite, development of multi-target vaccines based on protective epitopes could be a useful strategy for tick control. In this context, we aim to develop a protective multi-antigenic epitope-based vaccine against R.sanguineus ticks. For this, we immunized dogs with nine recombinant proteins produced in E. coli, antigens identified in sialotranscriptomes of R.microplus ticks (50 µg each protein + 150 µg (AlOH)3, 4 times, each 28 days). Data showed that the immunization promoted 36% of cross protection against R.sanguineus infestation. All vaccinated animals presented positive IgG seroconversion to all antigens after the 4rd dose. To identify the conformational B cell epitopes of the protective formulation, we applied the phage display method, using antigen-specific IgY (hens immunized with individual recombinant antigens + Freund's adjuvant, 3 times each 30 days) as capture antibody to select reactive phages from a 12-mer peptides random phage library. The phages bound to antigen-specific IgY were recovered after competitive elution and were sequenced by Sanger method. An average of 25 different reactive peptides were identified for each protein, showing that a high number of conformational epitopes are present in the candidate antigens. Next, we plan to validate the reactivity of the eluted phages with sera from the immunized and control dogs by ELISA. Finally, we will immunize animals with the positive phages to generate hiperimmune sera that will be used to feed R.sanguineus tick through in vitro feeding system, where the protective effects of the antibodies on tick development can be evaluated. The peptide sequences of the protective phages can then be used as part of a multi-antigenic synthetic anti-tick vaccine. Financial support: FAPESP (2015/09683-9, 2017/26759-4, 2018/18397-8), CAPES, CNPq, Bayer S.A.

Designing and evaluation of Variant 2 (IS-1494 /GI-23) Genotype of Avian Infectious Bronchitis Inactivated Vaccine: Higher protection in comparison with commercial vaccine

Arash Ghalyanchilangeroudi[1], Ahmad Erfanmanesh[2], Donya Nikaein[2], Seyed Ali Ghafouri[3], Hossein Hosseini[4], Mohammad Hossein Fallah Mehrabadi[5]

[1] Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
[2] The Academic Center for Education, Culture and Research (ACECR), Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran.
[3] Iranian Veterinary Organization, Tehran, Iran.
[4] PCR lab, Tehran, Iran.
[5] Department of Poultry Diseases, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Tehran, Iran.

Infectious bronchitis virus (IBV) is the cause of avian infectious bronchitis (IB). IB is one of the most highly contagious diseases with many economic losses in the poultry industry worldwide. According to the nature of this virus, new genotypes are continuously emerging and the use of proper vaccination is the most suitable way of fighting against this disease. One of the novel genotypes of IBV that has been circulated in the Middle Eastern countries and problematic in the poultry industry is the variant 2 (IS-1494/GI-23) genotype. This study aims to design and produce autogenous variant 2 vaccine, evaluate the immunity of the vaccine and compare it with available commercial vaccines in Iran. After isolatation and characterization of the Iranian variant 2 IBV, the inactivated vaccine was formulated and evaluated for clinical efficacy based on OIE guidelines in different aspects (purity, titration, inactivation, immunization). The designed vaccine passed all of OIE-approved quality control standards for the inactivated vaccines. In assessing the function of these vaccines, cross-protection in the groups receiving the variant 2 and commercial vaccines, was 67% and 60%, respectively. Although the differences were not significant, it provided better protection, and the viral load in feces and kidney of the group receiving the autogenous variant 2 vaccine was lower than that of the commercial vaccine. It is suggested that this strain should be added as one of the local strain to commercial inactivated vaccines in areas affected by this genotype. The use of this vaccine in layer and breeder flocks can help to protect them against the variant 2 during production period. In addition, transfer of maternal antibodies to offspring can provide a strain specific immunity for one-day old chicks.

Comparison of Autogenous and commercial H9N2 Avian Influenza Vaccines in a Challenge with Recent Dominant virus

Arash Ghalyanchilangeroudi[1],Hossein Hosseini[2], Mohammad Hossein Fallah Mehrabadi[3], Seyed Ali Ghafouri[4]

[1] Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran.
[2] PCR lab, Tehran, Iran.
[3] Department of Poultry Diseases, Razi Vaccine and Serum Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Tehran, Iran.
[4] Iranian Veterinary Organization, Tehran, Iran.

Avian Influenza subtype H9N2 is a prevalent viral disease with enormous economic losses in poultry farms of many countries including Iran. The degree of protection obtained from a vaccine strongly depends on the level of antigenic similarity between challenge and vaccine virus. Phylogenetic studies indicate continuous antigenic drift in Iranian circulating viruses since 1998. In the present study, we tried to evaluate effects of these antigenic changes on the ability of two commercial vaccines with an autogenous vaccine. These two commercial vaccines use two different vaccine seed that isolated from earlier outbreaks. qRT-PCR show that there is no significant difference on H9N2 viral load in the trachea, within vaccinated groups on 5 DPC, but on 15 DPC, the autogenous vaccine significantly lowered viral load compared to commercial vaccines ($p \leq 0.05$). In reviewing the results of the viral load in the fecal swabs, there were no significant differences between autogenous and commercial vaccine A, and both of them significantly inhibited viral load compared to no vaccinated group ($p \leq 0.05$). In addition, the highest HI titer obtained from the autogenous vaccine. Regarding these results, inactivated vaccines that used isolates from previous outbreaks, no longer able to create proper immunity against H9N2 challenge and it is time to change vaccine strain of used commercial vaccines to more recently isolates to have more antigenic similarity with current circulating H9N2 viruses in the region.

Cost-effective soluble expression of Bacillus anthracis protective antigen in Escherichia coli and evaluation of its biological activity

S Jauro[1,4], C. Ellis[5], A. Buys[5], OC Ndumnego[2], W Beyer[3], H van Heerden[1]

[1] Department of Veterinary Tropical Diseases, University of Pretoria, Onderstepoort, 0110, Pretoria, South Africa
[2] Africa Health Research Institute, Durban 4013, South Africa
[3] Department of Livestock Infectiology and Environmental Hygiene, University of Hohenheim, Stuttgart, Germany
[4] Department of Veterinary Microbiology, University of Maiduguri, Maiduguri, Nigeria
[5] Design Biologixcc P.O.Box 75803, Lynnwood Ridge 0042, Building 43b CSIR, Pretoria.

Bacillus anthracis the causative agent of anthrax disease, secretes protective antigen (PA) major component of the tripartite proteins. PA regulates the formation of anthrax toxins, PA plays a pivotal role in anthrax vaccine development as well as in serological and molecular diagnosis. Therefore, soluble expression of recombinant PA (rPA) is paramount. In this study we expressed rPA in pStaby2.1 vector transformed to E. coli S1 strain. The expression conditions were optimized to expressed soluble rPA at high yield (30.3 mg/L). The expression of soluble rPA was upscale to larger volume and investigating alternative purification methods to cut production costs. Modified lysis buffer and sonication was used instead of using conventional lysis buffer. Nickel column was used for purification. The yield was compared with conventional lysis buffer and no significant difference between rPA yield using conventional and modified lysis buffer and sonication twice. Sonification was significantly increase when used with modified lysis buffer. The biological activity of rPA was confirmed using indirect ELISA which demonstrated that the antibody epitopes of the rPA are active and not affected by the sonication. This was further verified by cytotoxicity assay on J774.1A cell indicating the functionality of rPA by its ability form lethal toxin. This study featured cost-effective soluble expression of biologically active rPA which can be used for recombinant vaccine development and anthrax diagnosis.

Immunogenicity of Virosome vaccine prepared from mesogenic strain against Newcastle Disease

T. R. Kannaki, E. Priyanka and Santosh Haunshi

Avian Health Lab, Directorate of Poultry Research, Rajendranagar, Hyderabad-30, India

Immunogenic potential of virosomes prepared from mesogenic Newcastle disease virus (NDV) was evaluated in chicken for protection against Newcastle disease (ND). Mesogenic NDV strain –Komarov virus stock having 210 HA titre was bulk propagated in embryonated eggs and the allantoic fluid was harvested, purified and concentrated by density gradient ultra-centrifugation. Virosome preparation was done by Triton X-100 treatment and SM 2 bio-beads method. A total of 144 Vanaraja chicks were used in immunization trial. First group was immunized with virosome vaccine (20µg/chick) through S/C route on 5th day; Second group was primed with same dose followed by booster of virosomes (20µg/chick) on 14th day. Third group was immunized with LaSota on 5th and 14th day and fourth group was kept as unimmunized control. Cell mediated immune response was analysed on 4th and 10th week of age by lymphocyte transformation test (LTT). Virosomes vaccine (two doses) group induced equivalent HI titre response to Lasota vaccine during first and second week of immunization (HI titres 3.67± 0.39; 3.40±0.02 respectively). However, during third, fourth week Lasota vaccine induced higher antibody titres (5.16±0.20; 4.20±0.31). On 9th and 10th week again virosome vaccine could induce equivalent antibody response (4.75 ±0.28; 3.08±0.31). No significant differences between the three groups in stimulation indices on 4th and 10th week. Prime immunization with virosome vaccine induces antibody titres equivalent to currently used multiple doses of lentogenic live vaccine.

Outer Membrane Vesicles vaccine based: a model for oral vaccination against Aeromonas salmonicida in Rainbow trout and characterization of the immune response assembled

Ruth Montero[1], Lara Munkler[1,2], Sven Ostermann[1], Bernd Köllner[1]

[1] Friedrich-Loeffler-Institute, Institute of Immunology, Greifswald-Insel Riems, Germany.
[2] Hochschule Esslingen, Department of Applied Natural Sciences, Esslingen am Neckar, Germany.

Infectious diseases are one of the main risks even in modern aquaculture, which can cause serious economic losses. Several vaccines were developed, however they are not effective enough and the application route (intraperitoneal, intramuscular) stress the fish. And despite the remarkable progress in the characterization of fish immune mechanisms, vaccines are still empirically tested, thus a rational design and evaluation needs to be developed and established.

It is known Gram-negative bacteria produce Outer membrane vesicles (OMVs), non-replicating and highly immunogenic particles that could serve as a platform to develop a vaccination strategy for fish. Hence, the present research is focused on developing a modular oral vaccine based in OMVs of the fish pathogenic bacteria Aeromonas salmonicida, and the evaluation of the immune response in the aquaculture specie Rainbow trout.

To validate the oral stimulation, fish were injected intra-peritoneally or feed with vaccine pellets. The distribution of B and T-cell populations were analyzed in gut, peritoneum, spleen and head kidney using monoclonal antibodies by flow cytometry. Additionally, cell populations were sorted for gene characterization of membrane markers, expressed cytokines and transcription factors.

The immune response was characterized by an early proliferation of intraperitoneal B and T-cells (24-48h post stimulation). Comparing the kinetics of the cell populations observed in the peritoneum to the gut as well as the recruitment of cells from spleen or head kidney will be further analyze. Moreover, the upcoming trial will be done with the OMVs from A. salmonicida to further analysis.

Accelerating cattle antibody discovery through single B cell sequencing

James Nyagwange [1, 2], William Mwangi [1], George Warimwe [2] and John Hammond[1]

[1] The Pirbright Institute, Woking, Surrey, GU24 0NF, UK
[2] KEMRI-Wellcome Trust Research Programme CGMRC, PO Box 230-80108, Kilifi, Kenya

High-resolution studies of the antigen specific polyclonal antibody response will reveal the required breadth required for protection and promises to identify conserved pathogen epitopes. In combination with broader measurements of the antibody response, single cell sorting of B cells provides the resolution to identify natural heavy and light chain pairs. This is essential to examine antibody specificity, avidity and to identify epitopes. We have developed a protocol to stain subsets of B cells from cattle PBMCs, including antibody-secreting plasma cells, which can then be targeted and single cell sorted. This approach relies on staining the enlarged endoplasmic reticulum (due to commitment to secrete antibodies) and surface immunoglobulin. After cell lysis, a multiplex primer reverse-transcription step is followed by a limited-cycle nested PCR that amplifies either the IgG or IgM heavy chain (depending on the antibody being expressed) and the light chain from the one cell. Currently, we are able to recover paired heavy and light chains from approximately 65% of sorted cells. Using this method we have sorted over 100 single cells and determined their natural heavy (IgH) and light chain (IgL) pairs. We have also analysed the variability and distribution of CDR3 lengths which range from 5 to 32 and 6 to 12 amino acids for the IgH and IgL respectively. The most frequent length is 23 amino acids for IgH and 10 amino acids for IgL. We have also observed clustering of highly similar IgL CDR3 in terms of variability and length. This pipeline is now being refined to include antigen specific staining prior to single cell sorting. This is being applied to existing samples from foot and mouth disease virus vaccinated cattle which developed a cross serotype reactive antibody response.

Immune response of Calves and Adult Cattle to Brucella abortus Strain 19 Vaccine administered by Conjunctival Route

Reuben A. Ocholi, Wilson J. Bertu and Amahyel M. Gusi

Brucella Research Unit, National Veterinary Research Institute, Plateau State, Vom, Nigeria

Brucellosis is an infectious disease of animals that is caused by a number of host-adapted species of the Gram-negative intracellular bacteria of the genus Brucella. The disease is characterized by abortion, retained placenta, orchitis and epididymitis. Currently, the prevention of bovine brucellosis in Nigeria is by the use of B. abortus S19 administered subcutaneously. Although S19 is of low virulence for cattle and vaccination of cattle gives good protection, it also has some disadvantages. Vaccination of pregnant cows can result in abortions, it induces persistent antibody response that confuses the serological diagnosis and is excreted in milk which may induce brucellosis in humans. To diminish these undesirable effects, conjunctiva vaccination of calves and adult animals with S19, have been suggested. Groups of 10 calves and 10 adult naïve female cattle were vaccinated with Brucella abortus Strain 19 at 78.9 x 109 colony forming units (CFU) per dose by conjunctival route. Blood samples were collected through veni-puncture from all vaccinated animals on days 15, 30, 60, 90, 120, 150, and 180 and sero-conversion monitored post-vaccination. Vaccinated animals had detectable antibodies from two weeks to two months after vaccination. All animals became negative to detectable antibodies at three months. The conjunctival route which is safer and easier to administer elicit immune response comparable to that of the subcutaneous route, and antibodies does not persist in vaccinated animals and such does not interfere with serological diagnosis of brucellosis.

Vaccination of calves with Bovine Respiratory Syncytial Virus (BRSV) as a model to understand the complications with HRSV in humans

Mustapha Oumouna[1], Sylvia Van Den Hurk[2]

[1] Faculté des Sciences, Université Dr Yahia Farès Médéa, Algeria
[2] Vaccine and Infectious Disease Organization, University of Saskatchewan, Canada.

Respiratory syncytial virus (RSV) is an important infectious agent and the leading cause of viral lower respiratory tract infection in young children worldwide. Clinical manifestations range from asymptomatic infection to bronchopneumonia, bronchiolitis, and pneumonia. Like human RSV (HRSV), bovine RSV (BRSV) is a negative-stranded RNA. It has been recognized as an important pathogen for cattle for 30 years, and it affects primarily young calves. Infection is characterized by pyrexia, coughing, and dyspnea, pneumonia, and sometimes death. The pathological lesions caused by HRSV and BRSV are very similar.

Vaccination of calves with formalin-inactivated bovine respiratory syncytial virus (FI-BRSV) induces low levels of cellular immunity that may not be protective. Since inactivated and subunit vaccines formulated with CpG oligodeoxynucleotides (ODNs) have been shown to induce cellular immune responses, we studied the ability of a FI-BRSV vaccine formulated with CpG ODN to elicit cellular immunity against BRSV. Neonatal calves were immunized with FI-BRSV, FI-BRSV formulated with CpG ODN or medium and challenged with BRSV after two immunizations. Exacerbation of disease, characterized by increases in clinical signs of infection and BRSV-specific serum IgE and decreases in IFN-γ production, has been demonstrated in calves infected with BRSV following vaccination with FI-BRSV. It is thus hypothesized that BRSV-specific cellular immune responses, characterized by interferon-γ (IFN-γ) production and BRSV-specific IgG2, could be protective against subsequent infections.

Calves vaccinated with FI-BRSV formulated with CpG ODN developed increased numbers of IFN-γ secreting cells in the peripheral blood and broncho-tracheal lymph nodes and enhanced BRSV-specific serum IgG2 in comparison to FI-BRSV immunized animals. Calves that received the FI-BRSV vaccine formulated with CpG ODN also experienced a reduction in the amount of BRSV in the lung tissue. Based on these observations, CpG ODN appears to be a suitable candidate adjuvant for inactivated BRSV vaccines.

Exploring sand fly salivary proteins to design multi-epitope subunit vaccine to fight against visceral leishmaniasis

Rajan Kumar Pandey, Vijay Kumar Prajapati

Department of Biochemistry, School of Life Sciences, Central University of Rajasthan, Bandarsindri, Kishangarh, Ajmer, 305817, Rajasthan India

Visceral leishmaniasis (VL) is caused by the parasites of Leishmania donovani complex, leads to the death of 20,000-40,000 people from 56 affected countries, worldwide. Till date, there is not a single available vaccine candidate to prevent the visceral leishmaniasis infection, and treatment only relies upon expensive and toxic chemotherapeutic options. Consequently, immunoinformatics approach was applied to design a multi-epitope based subunit vaccine to enhance the humoral as well as cell mediated immunity. Constructed vaccine candidate was further subjected to evaluation on allergenicity and antigenicity and physiochemical parameters. Later on, di-sulfide engineering was performed to increase the stability of vaccine construct. Also, molecular docking and molecular dynamics simulation study were performed to check the binding affinity and stability of TLR-4 to vaccine construct complex. Finally, codon optimization and in silico cloning were performed to ensure the expression of proposed vaccine construct in a microbial expression system.

Potential of Immunogenetics to Enhance Vaccine Efficacy

Mohammed A. Rohaim[1,2], Diwakar Santhakumar[2], Rania F El Naggar3, Muhammad Munir2

[1] Department of Virology, Faculty of Veterinary Medicine, Cairo University, Giza, 12211, Egypt
[2] Division of Biomedical and Life Sciences, Faculty of Health and Medicine, Lancaster University, Lancaster LA1 4YG, UK
[3] Department of Virology, Faculty of Veterinary Medicine, University of Sadat City, Sadat, Egypt

Innate antiviral immunity establishes first line of defense against invading pathogens through sensing their molecular structures such as viral RNA. This antiviral potential of innate immunity is mainly attributed to a myriad of IFN-stimulated genes (ISGs). Here, we generated transgenic chickens using avian sarcoma-leukosis virus (RCAS)-based gene transfer system that constitutively and stably express chIFIT5. The transgenic chickens infected with clinical dose (EID50 104 for HPAIV and 105 EID50 for vNDV) of high pathogenicity avian influenza virus (HPAIV; H5N1) or velogenic strain of Newcastle disease virus (vNDV; Genotype VII) showed marked resistance against infections. While transgenic chickens failed to sustain a lethal dose of these viruses (EID50 105 for HPAIV and 106 EID50 for vNDV), a delayed and lower level of clinical disease and mortality, reduced virus shedding and tissue damage was observed compared to non-transgenic control chickens. These observations suggest that stable expression of chIFIT5 alone is potentially insufficient in providing sterile protection against these highly virulent viruses; however, it is sufficient to ameliorate the clinical outcome of these RNA viruses. These findings propose the potential of innate immune genes in conferring genetic resistance in chickens against highly pathogenic and zoonotic viral pathogens causing sever disease in both animals and humans

In-silico design for multi-epitope DNA vaccine expressing influenza virus and infectious bronchitis virus epitopes in a multi-pass protein manner

Mahmoud Samir[1], Abdullah Selim[1], Mahmoud Bayoumi[2], Mahmoud elgamal[2], Ausama A Yousif[2], Ahmed A El-Sanousi[2]

[1] Reference Laboratory for Veterinary Quality Control on Poultry Production, Animal Health Research Institute, Dokki, Giza, Egypt
[2] Department of Virology, Faculty of veterinary medicine, Cairo University, Giza, Egypt

Background

Multiple avian influenza virus (AIV) subtypes and several infectious bronchitis virus (IBV) variant and classical strains continue to circulate and cause significant economic losses in the Egyptian poultry populations. This situation indicates that conventional vaccines require an upgrade to better cope with these viruses in the complex socioeconomic and environmental conditions. Multi-epitope (ME) DNA vaccines are increasingly viewed as possible solutions for current vaccine shortcomings through increased flexibility, antigen minimization and antigen focusing.

Methods

In this study, we utilized cryptic and linear epitopes selected from relatively more conserved regions of the target pathogen. In addition, Toll-like receptor-4 agonist was added as immunostimulatory sequence that would trigger the innate immunity. Multiple copies of each epitope were engineered in the construct in tandem as an epitope cluster. Each epitope cluster was designed for optimum physical accessibility and ubiquitination through the use of flanking motifs especially designed for these purposes. Epitope clusters were mirrored intracytosolic and intraluminal in the endoplasmic reticulum (ER) and Golgi vesicles to facilitate access for multiple processing and presentation pathways. The novel molecule was evaluated using bioinformatics tools for the assessment of structure quality, immunological potential and expected intracellular events post translation.

Results

The novel poly-protein structure showed initial promising results on the level of epitopes orientation, protein quality, construct stability, and docking potential toward Toll-like receptor-4. Furthermore, the novel context showed enhancement for immunological potential of B-cell epitopes. The expressed construct was predicted to localize in the plasma membrane in a sewing manner where epitopes are exposed to both extracellular and cytoplasmic sides.

Conclusion

Efficient epitopes expression within this context may allow several probable pathways including extraction of tethered epitopes by B-cells or intra-membrane proteolysis with liberation of epitope domains to outside and inside the cell. Both probabilities would suggest an enhanced antibody production toward conserved viral epitope regions without neglecting the cell mediated immunity. Ultimately, success of this approach may pave the way for developing universal vaccines against pathogens characterized by a high degree of antigenic diversity.

Development of a recombinant subunit Vaccine against African Trypanosomiasis

Anika Silva[1]; Eko Francis [2];Eghianruwa Kingsley [3]; Asuzu Isaac [1] and Ozumba Benjamin [1]

[1] University of Nigeria, Nsukka, Nigeria
[2] Morehouse School of Medicine, Atlanta, USA
[3] University of Ibadan, Nigeria

African Trypanosomiasis is a neglected but major parasitic disease, which affects both humans and animals in Sub-Saharian Africa and for which adequate control is yet to be achieved. Efforts made to improve the treatment protocols have failed to alleviate the effects of the disease. The strategic introduction of an effective vaccine remains a viable option that will not only control the disease but also open up for utilization the vast areas of the African Continent largely devoid of livestock because of Trypanosomiasis.

However, the development of a vaccines have been hampered by the unique antigenic variation of the parasite surface coat. Microtubules, which are especially abundant and conserved in the Trypanosomatidae, are composed of tubulin heterodimers and microtubule – associated proteins (MAPs) that contribute to the unique organization of the subpellicular microtubules. Recent reports indicate that the trypanosomal microtubule components, β-tubulin and the MAP p15 have been shown to be effective as vaccines to protect against trypanosome infections. A recombinant Vibrio cholera ghost (rVCG) platform has been designed which is capable of simultaneously delivering multiple antigens to the immune system. VCGs are bacterial cell envelopes derived from and similar to Vibrio cholerae cells in structure and morphology but non-replicating and non-toxigenic. They have been shown to be effective in inducing mucosal and systemic immunity to co-delivered antigens. We hypothesize that simultaneous delivery of MAP p15 and β-tubulin antigens by VCG will enhance trypanosomal immunity and provide significant protection against challenge infection. The ultimate goal of the project is to utilize an rVCG-based multisubunit vaccine candidate co-expressing trypanosomal MAP p15 and β-tubulin antigens to establish protection against T.brucei infection in ruminants.

Immunological Toolbox: expanding the portfolio of livestock specific immunological reagents

Lindsey A. Waddell, Anna Raper, Zhiguang Wu and Jayne C. Hope

The Roslin Institute, Easter Bush Campus, Roslin, EH25 9RG

The study of livestock (large mammal and avian) immunology is currently limited by the availability of specific and reliable reagents against key molecules which define immune cells, and allow analysis of their phenotypes and functions. The Roslin Institute Immunological Toolbox is a BBSRC core strategic funded facility which aims to expand the available portfolio through the production and characterisation of novel immunological reagents. This initiative focuses on the development of new recombinant proteins, monoclonal antibodies, assays and tools which will allow the advancement of understanding in the field of veterinary immunology; broadening the potential for research projects that are currently restricted by the lack of available reagents. The Immunological Toolbox at The Roslin Institute is closely linked with related activity at the Pirbright Institute.

At The Roslin Institute, through the Immunological Toolbox we have already produced a number of novel monoclonal antibodies and recombinant proteins which we aim to commercialise and make available to the wider community. Examples of projects successfully completed include development of a monoclonal antibody recognising ADGRE1 (F4/80) on porcine macrophages (Waddell et al., 2018) and an ELISA for chicken IL-10 (Wu et al., 2016).

The Immunological Toolbox welcomes enquires and project proposals for the development of new reagents and assays. The expertise within the facility allows projects to be individually tailored according to requirements, with advice on protocols and procedures also available. Project proposals are reviewed by a steering committee consisting of experts in the field of veterinary immunology who prioritise project proposals, taking into account the nature of the tool(s) requested, their utility, community requirements and accessibility.
Email: Roslin.Toolbox@roslin.ed.ac.uk
Website: www.ed.ac.uk/roslin/facilities-resources/immunological-toolbox

Waddell, L. A., Lefevre, L., Bush, S. J., Raper, A., Young, R., Lisowski, Z. M., Mcculloch, M. E. B., Muriuki, C., Sauter, K. A., Clark, E. L., Irvine, K. M., Pridans, C., Hope, J. C. & Hume, D. A. 2018. Adgre1 (EMR1, F4/80) Is a Rapidly-Evolving Gene Expressed in Mammalian Monocyte-Macrophages. Frontiers in Immunology, 9.

Wu, Z., Hu, T., Rothwell, L., Vervelde, L., Kaiser, P., Boulton, K., Nolan, M. J., Tomley, F. M., Blake, D. P. & Hume, D. A. 2016. Analysis of the function of IL-10 in chickens using specific neutralising antibodies and a sensitive capture ELISA. Dev Comp Immunol, 63, 206-1

Effect of adjuvant on immune responses to an experimental subunit vaccine antigen in sheep

Sean Wattegedera[1], Kelly Stronach[2], Elisa Rampacci[3], Noive Arteche Villasol[4], Riccardo Tassi[1], Jackie Thomson[1], Mara Rocchi[1], Kevin Aitchison[1], Morag Livingstone[1], David Longbottom[1] and Gary Entrican[1]

[1] Moredun Research Institute, Penicuik (near Edinburgh), Scotland, UK
[2] School of Biological Sciences, University of Edinburgh, UK
[3] Dipartimento di Medicina Veterinaria, Università degli Studi di Perugia, Italy;
[4] Department of Animal Health, Universidad de León, Spain

Introduction

The desired goal of vaccines to protect against intracellular bacterial infections is usually the induction of cellular T-helper (Th)-1 type immunity, characterised by the production of interferon (IFN)-gamma. This has been particularly challenging for subunit vaccine development in livestock. We have characterised cellular immune responses in sheep to an experimental chlamydial subunit vaccine antigen delivered in three adjuvants.

Materials and Methods

Groups of 35 sheep were immunised with a single inoculation of the experimental vaccine antigen formulated in two water-in-oil adjuvants (Montanide ISA 70 VG, Montanide ISA 61 VG) or saponin-derived QuilA. Peripheral blood mononuclear cells (PBMC) were isolated pre- and post-immunisation and re-stimulated in vitro with both the vaccine antigen and whole killed chlamydial elementary bodies (EBs). Recall responses were measured by the presence of cytokines in the PBMC culture supernates, with IFN-gamma as an indicator of Th1-type responses and interleukin (IL)-4 as an indicator of Th2-type responses.

Results & Conclusions

All three adjuvants induced antigen-specific immune responses that could be detected in recall assays to both the experimental vaccine antigen and whole chlamydial EBs. In each case, IFN-gamma was the dominant cytokine in the post-immunisation antigen-specific recall responses, with almost no antigen-specific IL-4 being detected. Mitogen-induced IFN-gamma and IL-4 was consistent pre- and post-immunisation. Of the three adjuvants, Montanide ISA 61 VG induced slightly higher levels of IFN-gamma.

Classical Th1-type responses can be elicited in sheep to a subunit antigen delivered in different adjuvants. The relative efficacy of these adjuvants needs to be determined using infection challenge models.

Expression of West Nile Virus prM-E polyprotein in tobacco as a candidate vaccine

Jennifer Wayland[1], Edward. P. Rybicki[1,2] and Ann. E. Meyers[1]

[1] Biopharming Research Unit, University of Cape Town, Cape Town, South Africa.
[2] Institute of Infectious Disease and Molecular Medicine, University of Cape Town, Cape Town, South Africa.

West Nile virus (WNV) is a widely disseminated flavivirus, with a geographic range that now includes Africa, North America, Europe, the Middle East and West Asia. The virus is vectored by Culex mosquitoes and is maintained in a bird-mosquito transmission cycle, with approximately 326 bird species of the Passeriformes order acting as reservoir hosts. In horses, approximately 20% of infections are symptomatic, of which cases 90% involve neurological disease, with 30-40% fatality rates.

The availability of several commercially produced West Nile vaccines is not beneficial to developing countries due to the high cost of importation, high cost of vaccines, and the need for annual vaccination. Mammalian expression systems are the gold standard for the production of these vaccines; however, these can be costly on a variety of levels. Transient plant-based expression systems have proven to be a very cost-effective means of making complex proteins. Plants have the ability to process proteins similarly to mammalian cells, and production does not require sterile conditions or specialised facilities. We propose that plants could be a viable means of making feasible, low-cost reagents for WNV for use as diagnostics, and virus-like particles (VLPs) for use as vaccines in South Africa and other developing countries.

The aim of this project is to use the envelope (E) and pre-membrane (prM) proteins of WNV to make non-infectious VLPs as a candidate vaccine, in tobacco plants. The E and prM genes were cloned into plant expression vectors, shuttled into Agrobacterium tumefaciens and infiltrated into Nicotiana benthamiana. The optimal OD600 for infiltration and sampling point for maximum protein yield were determined and the use of co-expressed human derived chaperone proteins on viral protein expression was investigated. We report on the successful co-expression of prM-E in tobacco plants, presenting the potential of plants as biofactories.

Accelerated development of a safe and easily manufactured Q fever vaccine

Sarah E Williams-Macdonald[1], Mairi Mitchell[1], David Frew[1], Bill Golde[1], David Longbottom[1], Alasdair J Nisbet[1], Søren Buus[2], Hendrik-Jan Roest[3], AD Koets[3], Tom N McNeily[1]

[1] Moredun Research Institute, Edinburgh, EH26 0PZ, UK
[2] Department of Immunology and Microbiology, University of Copenhagen, Denmark
[3] Central Veterinary Institute, Wageningen University & Research, Wageningen, Netherlands

Q fever is a highly contagious zoonosis of worldwide importance caused by the intracellular Gram-negative bacterium, *Coxiella burnetii*. Domestic ruminants, notably sheep and goats, are the primary reservoir of human infection, as the bacterium is excreted at high loads during parturition. Human infection occurs via inhalation of as few as 1-10 aerosolized bacteria and can result in both acute and chronic forms of disease. Generally, infection of humans is asymptomatic, however more serious complications can arise in the elderly, immunocompromised or pregnant women. In livestock, particularly sheep and goats, infection can cause abortion, stillbirth and delivery of weak offspring, resulting in substantial economic losses. Vaccination of ruminants against *C. burnetii* is important for reduction of infections in both human and livestock populations.

Vaccines based on formalin-inactivated *C. burnetii* organisms, of both phase I and phase II, are commercially available for use in both ruminants and humans, however issues relating to both their manufacture and vaccine side effects have limited their use. Furthermore, the use of whole inactivated organisms suppresses development of a diagnostic to differentiate infected from vaccinated animals (DIVA).

This project aims to develop a safe and effective subunit Q-fever vaccine for use in small ruminants. Peptide chip microarrays representing the entire *C. burnetii* proteome will be utilized to identify putative protective antigenic epitopes. Comparison of antibodies detected following immunization with the commercially available but unsafe "protective" vaccine (based on phase I *C. burnetii*), with those induced following immunization with a "non-protective" phase II *C. burnetii*-based vaccine, will identify antibody targets which are associated with protection in the phase I vaccine. Potential protective antigens will be incorporated into experimental subunit vaccines and delivered to sheep as *E. coli* recombinant proteins together with a commercially acceptable adjuvant. Antigens will be identified for the development of a DIVA antibody based diagnostic.

Vaccination in cattle against Babesia bovis combining a modified vaccinia Ankara vector and protein adjuvant formulation based on a recombinant multi – antigen

José Manuel Jaramillo Ortiz [1,3]; María José Gravisaco [1]; Ignacio Echaide [2]; Martina Paoletta [1]; Valeria Montenegro [1,3]; Sofía de la Fourniere [1,3]; Ludmila Lopez Aria[1,3]; Magalí¬ Valenzano [1]; Eliana Guillemi [1]; Marisa Farber [1,3]; Silvina Wilkowsky [1,3],*

[1] Instituto de Biotecnología, Centro de Investigaciones en Ciencias Veterinarias y Agronómicas, Instituto Nacional de Tecnología Agropecuaria, De Los Reseros y Dr. Nicolás Repetto s/N, P.O. Box 25 (B1712WAA), Castelar, Buenos Aires, Argentina
[2] Laboratorio de Inmunología y Parasitología Veterinaria. EEA INTA Rafaela. Ruta 34 Km 227, (2300), Rafaela, Santa Fe, Argentina
[3] National Research Council (CONICET), Argentina.

(*) corresponding author: wilkowsky.silvina@inta.gob.ar

The immune control against the intraerythrocytic parasite Babesia bovis requires both cellular and humoral immune responses. Therefore, combinations of immunogens targeted at both arms of the immune system are required to pursue sterilizing immunity. In this study, 13 – 15 month - old and highly susceptible male Holstein steers (n=5 per group) were immunized with a subcutaneous dose (sc) of the currently live attenuated vaccine used in Argentina (R1A) or with a subunit vaccine as a prime (sc) and an intramuscular dose (im) of a modified vaccinia Ankara vector (MVA) as a boost, both expressing a multi-antigen (rMABbo – rMVA) of B. bovis. This chimeric protein includes the immunodominant B and T cell epitopes of three B. bovis proteins: Merozoite Surface Antigen – 2c (MSA-2c), Rhoptry Associated Protein – 1 (RAP-1) and Heat Shock Protein 20 (HSP20). A prime of a heterologous recombinant protein and a boost of wild type MVA group was used as control. Eleven weeks after the first immunization, all animals were challenged (sc) with an injection of parasite-infected erythrocytes containing 107 virulent B. bovis merozoites. After challenge, all groups were monitored daily for fever and reduction of packed cell volume. Both the rMABbo – rMVA and R1A vaccinated animals showed an antigen - specific T cellular response and high titers of IgG antibodies, although the latter were not neutralizing. However, all rMABbo – rMVA cattle shown clinical symptoms of disease upon challenge, although no treatment was required for any of them.

All together, these findings show that although the novel recombinant vaccine rMABbo - rMVA exhibited a strong humoral and cellular response compared to the control groups, these responses did not correlate with protection. A detailed immune characterization of the protective response obtained by the attenuated R1A strain would be of great importance to understand the biological traits involved in the high level of efficacy of this vaccine.

Major Histocompatibity Complex (Mhc) Gene Diversity in Cattle Breeds Indigenous to Uganda: A Case Study of Nkedi

Amanyire Wilson[1], Timothy Connelley[2], Dennis Muhanguzi[1], Ewan MacLeod[3]

[1] Makerere University, Kampala, Uganda
[2] The Roslin Institute, UK
[3] University of Edinburgh, UK

The major histocompatibility complex (MHC) gene- encoded molecules play a critical role of modulating adaptive and innate immune responses. However, there is limited animal MHC diversity information particularly for African breeds. This study aimed at characterising the MHC diversity of Nkedi cattle that are native to Uganda to provide insight into a range of its applications such as identification of relevant antigens as potential vaccine candidates. The MHCI and MHCII DRB3 repertoire of Nkedi breed were characterised for the first time using MiSeq based sequencing. A total of 68 MHCI haplotypes and 34 DRB3 genes were identified. Thirty novel and 38 already existing MHC1 haplotypes were identified in the study. Twelve distinct MHCII DRB3 genes were identified. Phylogenetic analysis showed close relationship of the Nkedi with European and African breeds. The MHC information generated in the study will help accelerate antigen identification studies aimed at vaccine development of various animal diseases affecting the Uganda cattle population.

Contact us

Dr. Carly Hamilton
Network Manager

email: IVVN@roslin.ed.ac.uk
web: www.intvetvaccnet.co.uk
blog: intvetvaccnet.wordpress.com
tweet: @IntVetVaccNet