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swine fever. In this study, nest with soil and litter of seabirds were collected, to investigate Ornithodoros species from 8 uninhabited islands, Nan-do, Chilsan-do, Chilbal-do, Sogukhol-do, Googul-do, Gaerin-do, Sasu-do and Hong-do (Hallyeohaesang) located western and southern part of the Korea from July, 2017 to June in 2018. The islands are known for breeding places of migratory and resident birds. Ten nests with soil and litter of seabirds were collected from one uninhabited island for the conservation of the islands environment. Ticks were collected from nest with soil and litter of seabirds using Tullgren funnel. In total, 59 *Ornithodoros* spp. ticks from 200 seabird's (black-tailed gull, *Larus crassirotris*; streaked shearwater, *Calonectris leucomelas* and Swinhoe's storm petrel, *Oceanodroma monorhis*) nesting soil with litter in 7 islands (Nan-do, Chilsan-do, Chilbal-do, Sogukhol-do, Gugul-do, Gaerin-do and Hong-do) were collected. To identify the species of *Ornithodoros* spp. soft ticks, the sequence of *Ornithodoros* spp. showed 95% identity to *Ornithodoros sawaii* (KT372790) and *Ornithodoros capensis* (AB076080) based on 16S rRNA and 99% identity to *O. capensis* (KR907243) based on 18S rRNA. In this study, 34 *O. capensis* were collected from Chilsan-do, Chilbal-do and Hong-do, and 25 *O. sawaii* were collected from Chilbal-do, Sogukhol-do, Gugul-do and Gaerin-do. Both *O. capensis* and *O. sawaii* species were collected only in Chilab-do. The Chilbal-do is located between Chilsan-do and Gugul-do (group of island with Sogukhol-do and Gaerin-do). In conclusion, we have discovered that *O. sawaii* are habitat in west and southern part of uninhabited islands (Chilbal-do, Sogukhol-do, Gugul-do and Gaerin-do) related to breeding place of black-tailed gull and streaked shearwater. Acknowledgement: This research was supported by a fund (no. Z-1543085-2017-18-01) from Research of Animal and Plant Quarantine Agency, the Republic of Korea

DE-5. Epidemiology of ovine toxoplasmosis and neosporosis in rams from Rio Grande do Sul, Brazil.

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Although the State of Rio Grande do Sul is one of the principal sheep rearing regions in Brazil, the prevalence of *Toxoplasma gondii* and *Neospora caninum* is unknown in rams. The objective of this study was to determine the prevalence of ovine toxoplasmosis and neosporosis and the risk factors associated with the development of these diseases in rams used exclusively for breeding. Serum samples (n=1,800) from rams maintained on 705 sheep farms from the seven mesoregions of the State of Rio Grande do Sul were used during this study. Serological analyses were performed to detect anti-IgG of *T. gondii* by indirect ELISA and anti-IgG of *N. caninum* by the indirect immunofluorescence assay (IFA). The cutoff point used in IFA for positive samples was 50. All statistical data were analyzed using the multivariable logistic regression model. The prevalence of *T. gondii* was 33.05% (595/1,800), while seropositivity to *N. caninum* was 18.44% (332/1,800). Additionally, there was simultaneous seropositivity to *N. caninum* and *T. gondii* in 8.94% (161/1800) of the sera evaluated. The variables stock size (< 500ha) (Odds Ratio, OR=1.56); breeding system (semi-intensive/intensive) (OR=1.42); and natural mounting without control (OR=1.87) were considered as risk factors for the occurrence of *T. gondii*. Size of the property (< 500ha) (OR=1.58) and natural mounting without control (OR=2.62) were risk factors associated with the prevalence of *N. caninum* in rams. Additionally, separation of ewes prior to parturition was considered as a protective factor for the occurrence of *T. gondii* (OR=0.73) and *N. caninum* (OR=0.69). These results demonstrate that these two parasitic disease argents are endemic in rams throughout all regions of RS. Although this study was done exclusively in rams, the results suggest deficiencies in reproductive management systems, sharing of pasture land, and the type of economic activity at each sheep farm. Moreover, the zoonotic potential of *T. gondii* cannot be overlooked, principally for those involved in the production chain associated with sheep rearing as well as rural and urban consumers of mutton. Additionally, these results can serve as inputs for the implementation of governmental policies such as control and prophylactic measures associated with sheep rearing and health education strategies aimed at populations with the State of Rio Grande do Sul, considering that toxoplasmosis is a public health issue.

DE-6. The role of African green monkeys (*Chlorecebusa ethiops sabaeus*) in the epidemiology of chikungunya, dengue and Zika on St Kitts, West Indies.

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Large outbreaks of human febrile disease in densely populated tropical regions are often caused by chikungunya, dengue and Zika viruses circulating in an urban transmission cycle between humans and *Aedes aegypti* and *Aedes albopictus* mosquitoes. However, these viruses were originally transmitted in a sylvatic transmission cycle between monkeys and forest (sylvan) mosquitoes. Sylvatic cycles persist in Africa and Asia but it remains unclear how these contribute to the epidemiology of human febrile disease outbreaks. The Caribbean island of St. Kitts has a large African green monkey (*Chlorocebus aethiops sabaeus*) population and is ideally suited to investigate sylvatic transmission cycles by detection of virus-specific antibodies in the monkeys and a survey of mosquito populations and virus presence across five different ecosytems. In the first 6 months of the project, we have identified 9/14 possible mosquito species present on the island including all known medically important species (*Aedes aegypti*n=18,*Aedes taeniorhynchus* n=449*, Anopheles albimanus* n=2 and *Culex quinquefasciatus* n=384). Of the African green monkeys (*Chlorocebus aethiops sabaeus*), 1.01% (4/393) are positive for IgG to chikungunya virus and 5.34% (21/393) are positive for IgG to dengue virus by ELISA. The ongoing project is funded by a National Institute of Allergy And Infectious Diseases Exploratory Development Grant, National Institute of Health (USA).

DE-7. Mapping the occurrence and population structure of the invasive tick species *Rhipicephalus microplus* in Cameroon: perspectives for regional tick control program.

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Rhipicephalus microplus is the world´s most economically important tick species. It is an efficient vector of *Babesia bovis*, *Babesia begimena* and *Anaplasma* spp. This tick was relatively rare in the African continent but it has spread rapidly across West Africa following introduction in Ivory Coast through the import of infested cattle. The economic magnitude of this invasion is still unclear. Cameroon is a theatre of uncontrolled cross-border animal movements that render the country epidemiologically connected to non-neighbouring West and East African countries and increase the risk of introduction of this dreaded tick. Recent reports revealed an increased use of acaricides and tick burden. There is therefore urgent need to review the identity of ticks occurring on cattle from Cameroon to underpin successful tick control strategies. The present study aimed to investigate the presence and distribution of *R. microplus* and to define its population genetic structure. A countrywide cross-sectional survey was conducted to investigate the presence of *R. microplus*. Ticks were collected from cattle in 54 sites across the five AEZs. Sex and species were assigned using taxonomic keys. Species identity was confirmed through sequencing of mitochondrial COI and 16S