Keldur

Vísindadagur

19. apríl 2023

Dagskrá Vísindadags Keldna
19. apríl 2023

09:00-09:05	Setning Vísindadags Keldna 2023 Sigurður Ingvarsson
09:05-09:15	Ávarp ráðherra Áslaug Arna Sigurbjörnsdóttir
09:15-10:00	*One Health and Iceland's unique situation* Karl G. Kristinsson
10:00-10:45	Kaffihlé og veggspjaldasýning
10:45-11:30	*Viral threats to Icelandic salmon production* Kristrún Helga Kristþórsdóttir
11:30-12:15	*Scrapie in Iceland and recent findings of potentially protective genotypes* Stefanía Þorgeirsdóttir
12:15-13:20	Hádegishlé
13:20-14:20	*Climate change may alter the geographical distribution of animal infectious diseases* Ann Albihn
14:20-14:50	*Identification of mysterious structures brought to Keldur in past decades* Karl Skírnisson
15:00	Vísindadegi slitið og léttar veitingar

Inngangur

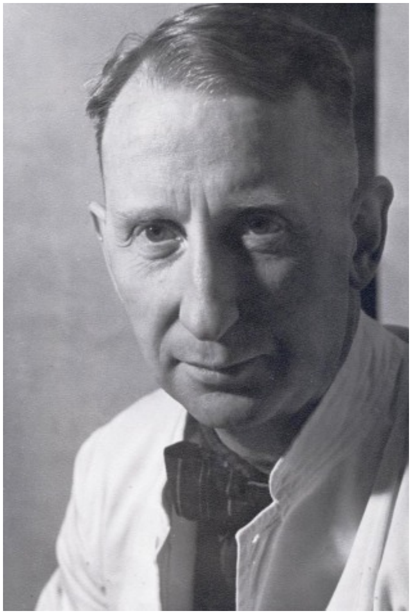
Sigurður Ingvarsson
forstöðumaður Keldna

Tilraunastöð Háskóla Íslands í meinafræði að Keldum fagnar sjötíu og fimm ára starfsafmæli í ár. Af því tilefni er ráðstefna/vísindadagur sem fer fram 19. apríl 2023 á bókasafni Tilraunastöðvarinnar. Tilraunastöðin starfar fyrst og fremst sem rannsóknastofa á háskólastigi og er eini vettvangurinn í landinu þar sem rannsóknir, skimunarverkefni og greiningar fara fram á dýrasjúkdómum á mörgum fræðasviðum. Rannsakaðir eru sjúkdómar og smitefni í flestum spendýrategundum Íslands og allmörgum fugla-, fisk- og lindýrategundum. Tilraunastöðin er í nánu samstarfi við atvinnulífið, má þar nefna landbúnað, fiskeldi, matvælaframleiðslu og líftækniiðnað. Starfið er rótgróið og gott dæmi um samlegðaráhrif vísindastarfs og atvinnulífs. Vel hefur gengið að vinna með þær sérstöku aðstæður sem eru á Íslandi varðandi dýrasjúkdóma og greiningar á þeim.

Vísindadagurinn hefur fest sig í sessi sem vettvangur fyrir kynningu á starfsemi og fræðasviðum Keldna. Ráðstefnan er allan daginn og aðgangur er öllum heimill að kostnaðarlausu. Nú er vísindadagurinn með almennara sniði en oft áður og er m.a. ætlaður sem samráðsvettvangur hagaðila sem starfa í lífvísinda- og dýraheilbrigðisfræðum. Þeir fyrirlesarar sem sjá um fræðsluna eru sérfræðingar á Keldum og aðrir sérfræðingar frá háskólum og vísindastofnunum innanlands og erlendis. Einnig verða kynnt veggspjöld sem greina frá ýmsum verkefnum á Keldum. Anna Karen Sigurðardóttir, Ásthildur Erlingsdóttir og Birkir Þór Bragason eru í vísindanefnd sem sér um undirbúning og skipulag. Ég færi þeim mínar bestu þakkir fyrir spennandi og fjölbreytta dagsskrá.

Mínar bestu árnaðaróskir til núverandi og fyrrverandi Keldnastarfsmanna og hamingjuóskir með árangur síðastliðna áratugi. Framlag þeirra hefur gert Keldur að þeirri framsýnu rannsóknastofnun dýrasjúkdóma sem hún er í dag. Á Keldum er fagleg forysta á ýmsum fræðasviðum og mikil þekking og reynsla. Ég óska Tilraunastöðinni og starfsmönnum hennar áframhaldandi velgengni og velfarnaðar í framtíðinni.









Ann Albihn, DVM
Associate professor
National Veterinary
Institute, Sweden

Climate change may alter the geographical distribution of animal infectious diseases

Climate change is getting more and more evident, and the highest temperature increase is seen in the north. The ecosystem changes as follows are directly affecting the circulation of pathogens, as well as the presence of reservoir animals and vectors. Consequently, we see changed distribution and epidemiology of climate sensitive infections (CSI) of relevance for domestic animals, wildlife, humans and the society. In a project studying CSI in the Nordic countries and Russia CSI was defined as; infections affected by climate-induced changes in the environment, prone to change epidemiology, geographical distribution, or persistence over time. Some opportunistic infections caused by climate-induced physical stress e.g., heat-stress are also considered as potential CSI.

Disease dynamics following CC may be hard to understand and predict. The unawareness of clinical symptoms from CSI in new areas may lead to delayed therapies and protection of a population. Also, species that are immunologically naïve to a new infection may be severely affected. Surveillance of vectors, reservoir animals or CSI may consume considerable resources. Examples of some surveillance studies will be presented; a citizen science-based tick-collection, sampling of farm-based milk containers to detect tick-borne encephalitis respective midges-borne Bluetongue virus, retrospective studies of laboratory diagnoses of Anaplasmosis and Babesiosis to follow distribution and from viral sequencing (NGS) of reindeer. Also, some examples of CSI and their ways of transmission will be considered.

For efficient adaptation strategies increased knowledge of CSI is essential, therefore developed surveillance, prevention and control measures are needed, preferable based on a One Health perspective.

Karl G. Kristinsson
Professor
Landspítali - The
National University
Hospital of Iceland

One Health and Iceland's unique situation

Iceland remained relatively isolated from the rest of the world until the middle of the 20th century. Endemic infectious diseases are therefore much fewer among Icelandic livestock than livestock on mainland Europe, and is one of the reasons why antimicrobial use and antimicrobial resistance (AMR) in agriculture is less than in most other countries. It is important to preserve this unique situation. Rapidly growing tourism and importation of food from all parts of the world is a threat.

AMR is the main threat to animal and human health today. If nothing is done, it is estimated that in the year 2050 human mortality due to antimicrobial resistance will be greater than to cancer and diabetes combined. Urban informal settlements or slums may be unique hotspots for environmental AMR transmission, due to density of humans and livestock, antibiotic misuse, insufficient drinking water, drainage and sanitation infrastructure. There is an urgent need to disrupt transission of AMR in and from such areas.

The most critical AMR pathogens are Gram negative bacilli such as E. coli and Klebsiella, that are members of the normal enteric flora of humans and animals. Lack of rapid and cheap methods to detect these organisms on humans, animals and food make it difficult to prevent their transmission. Interventions are needed and must be based on sound risk assessments.

Kristrún Helga
Kristþórsdóttir
Veterinarian
VETAQ

Viral threats to Icelandic salmon production

Viral diseases in salmon production are a constant threat to fish health and welfare. Although viral diseases have not been very prevalent in Icelandic salmon production so far, the threat of pathogen introduction is constant. Migration of wild salmon as well as transport of boats and equipment from abroad challenge the biosecurity of Icelandic salmon production. This lecture will shed a light on which viral diseases we should be aware of when producing salmon in Iceland, whether it is in sea or on land, and how we can recognize the clinical signs of these diseases.

Karl Skírnisson
Parasitologist
Keldur

Identification of mysterious structures sent to Keldur in past decades

Since 1971, zoologists working at Keldur have regularly been asked to identify the origin of some mysterious samples or structures that private persons or companies have sent in or brought to Keldur for examination. Often these structures have been found in food. As an example dark, elongate structures detected by a customer in a loaf of bread have been suspected to represent excrements of rodents; small bones found in meat dishes in restaurants (abroad) were believed to be rat-bones; thread-like structures found in human faeces or in nappies were thought to represent a helminth parasite; an actively moving rainworm in a toilet bowls was believed to represent a human parasite and structures found on the skin, in clothes or in beds of humans, were believed to represent a blood sucking ectoparasite. In recent decades these samples have usually been photographed in order to convince the customer about the identification. Some selected examples are presented in the lecture.

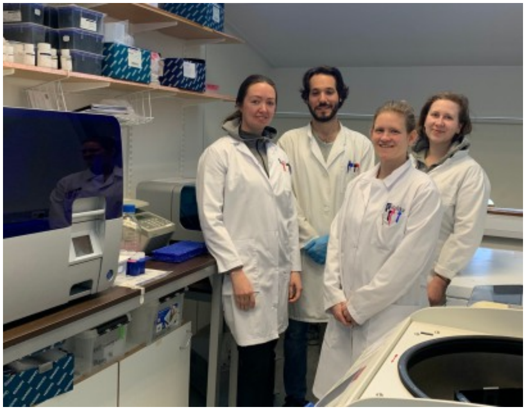
Stefanía Þorgeirsdóttir
Biologist
Keldur

Scrapie in Iceland and recent findings of potentially protective genotypes

Scrapie was apparently brought to Northern Iceland in 1878 and later spread to other parts of the country. In 1978 an eradication plan was established with movement restriction zones and stamping out of scrapie flocks, but later enhanced with disinfection of pens, two-three sheep-free years and restocking from scrapie-free areas. Despite rigorous methods to fight the disease, it remains endemic in the North, but yearly incidence has gone down to a very few cases.

The scrapie infectious agent is a misfolded protein and disease susceptibility is affected by polymorphism found within the prion gene. Although used widely in Europe, breeding for scrapie resistance in Iceland has not been a real option, since ARR, the main protective allele combination, has in the past not been found in the Icelandic sheep breed. VRQ was determined to be associated with increased risk and has since 2008 not been available in the artificial insemination centres.

A recent widespread search for scrapie protective prion protein variants in Iceland resulted in the first finding of an Icelandic sheep carrying ARR. Furthermore, a potentially protective polymorphism, T137, was found on eight farms. Although almost 30.000 samples, originating from more than one third of all sheep farms in Iceland, have been tested, the ARR allele has still only been detected on one farm in the East. A breeding program using sheep carrying these alleles is already in use and in due time will hopefully help with the eradication of this uncurable disease from the country.

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Prion genotypes in Icelandic scrapie flocks: The effect of removing rams with a VRQ allele from Icelandic breeding stations

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Classical scrapie (CS) is a contagious, fatal neurodegenerative disease, caused by a pathological form (PrPSc) of the cellular prion protein, which is expressed by the *PRNP* gene. Infectivity of PrPSc is influenced by *PRNP* genotypes of the host, as they convey different susceptibility to CS. Since 2008 no ram carrying the risk allele, VRQ, has been available in Iceland's sheep breeding stations. This study assessed the effect of removing VRQ-allele-carrying rams from Icelandic sheep breeding stations on the distribution of *PRNP* genotypes in CS flocks and their clinical suspect index samples (CSIS), as well as the age of CSIS. CS flocks, and their CSIS, from the years 2010-2019 ($n = 1450$ and 10, respectively) were compared to 1998-2007 ($n = 1081$ and 32, respectively). Samples were genotyped by DNA isolation, PCR, RFLP and electrophoresis. The age of CSIS was obtained from their ear tags. A significant difference was detected in the frequency of the corresponding amino acids at codons 136 and 154 ($p < 0.0001$ for both) in the CS flocks. However, there was no difference when comparing codon 136 in CSIS ($p = 0.9784$), and no polymorphism was found at codon 154. There was no difference in the age of CSIS ($p = 0.2808$). The results imply that the removal of VRQ-allele-carrying rams from the breeding stations has brought about a change in the genetic variance of PRNP, as there has been a decrease in the frequency of the risk genotypes that contain VRQ alleles, in CS flocks.

Strongyloides stercoralis: 10 years of colonisation attempts through imported dogs in Iceland (2012-2022)

Guðný Rut Pálsdóttir[1], Kristbjörg Sara Thorarensen, Björn C. Schäffner, and Karl Skírnisson.
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Iceland is an island in the N-Atlantic Ocean. With no bordering countries, strict conditions apply regarding importation of live animals to protect the local animal population from introduced pathogens. Since 1989, importation of dogs was permitted with a strict quarantine where faecal samples were primarily checked for helminth eggs and protozoans. In 2012, the Baermann technique was included in the routine parasitological diagnosis to test for nematode larvae such as those of *Strongyloides stercoralis.* This parasitic roundworm (Nematoda) has a complex life cycle that can alternate between free-living and parasitic cycles and involves autoinfection. It is a well-known parasite in humans, other primates, and dogs with a zoonotic potential, especially in tropical and subtropical regions. During 2012 and 2022, 2,608 dogs from 61 countries were imported to Iceland. Of those, 41 dogs (2%) were S. stercoralis positive. The breeds most frequently affected were French bulldogs (n=12) followed by Pomeranians (n=7) and Havanese (n=5). The areas where most of the positive dogs were imported from were Eastern Europe (n=19) and Scandinavia/Baltics (n=16). Although French bulldogs only represented 4% of imported dogs in this period, they amount to 30% of all S. stercoralis positive dogs. The data raises a series of questions regarding the emergence of this parasite in different countries, circumstances in kennels and a potentially higher susceptibility of certain breeds to infection or whether this nematode simply remained neglected.

HAFRANNSÓKNASTOFNUN

Rannsókna- og ráðgjafarstofnun hafs og vatna

Piridium sociabile - the inconspicuous commonplace parasite

Ásthildur Erlingsdóttir[1], Nóa Sólrún Guðjónsdóttir, and Árni Kristmundsson K.
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Piridium sociabile (*P. soc*) is an evolutionary unique marine parasite, found in the foot of the common whelk (*Buccinum undatum*). *P. soc.* was described by Ruth Patten (1936) and originally thought to be an apicomplexan parasite, but has recently been demonstrated to be an ancestor of all Apicomplexa and most closely related to the photosynthetic free-living chromerids, which are associated with coral reefs. Little has been done to gain further insight into the biology of *P. soc.* prior to this project. The aim of the project was to determine the geographical distribution of *P. soc.* around Iceland and detect other potential host species.

575 common whelks were collected around Iceland along with 258 individuals of 25 mollusc species. Samples were dissected and analyzed using a stereoscope, microscope and histology.

The results showed a great abundance and high prevailance of *P. soc.* around Iceland along with a surprising number of other host species, which are parasitized by *P. soc.* related organisms. This indicates that *P. sociabile* is a prevalent parasite of the common whelk and has a relatively wide distribution. Also, as an ancient or ancestral parasitic form, it has likely parasitized common ancestors of gastropod species and co-evolved with these hosts during speciation events.

Assessment of the parasite fauna of batoid rays in Iceland: new approaches and future implications

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Fifteen species of batoid rays occur in Icelandic waters. However, little is known about their parasites. A total of 28 parasite species were recorded from merely three species of skates, corresponding to almost 70 % of the known parasite fauna of Icelandic cartilaginous fishes. Given that only 20 % of skate species have been observed for parasites, a vast majority of parasites remains to be discovered. Investigations on the parasite fauna of the remaining batoid rays are required to rectify the sparse records, build on existing host-parasite data and contribute to the current knowledge of Icelandic marine biodiversity. Samples from a broad array of batoid species will be obtained during the Marine and Freshwater Research Institute´s spring and autumn groundfish surveys. The parasite diversity (blood-, ecto-, endoparasites) will be assessed using integrative taxonomy approaches (morphology, molecular systematics, biogeography, ecology). This project will positively contribute to efforts on the Icelandic biodiversity assessment by increasing the number of known species. The data will reveal insights on host-parasite relationships, processes of diversification, faunal differences and the biogeographical dispersal of hosts and parasites in distinct marine ecoregions in the northern Atlantic Ocean. This project will also enhance our knowledge on the history of co-evolution of marine apex predators and associated parasites in Iceland. The scientific program will provide the baseline for future transnational research collaborations, leading to new foundations in interconnected disciplines and paving the way for future scientific discovery in Iceland and beyond.

The ‘hidden’ parasite diversity of lamniform and carcharhiniform sharks in KwaZulu-Natal, South Africa

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South Africa´s bather protection program was implemented to reduce the risks of unprovoked shark attacks. The KwaZulu-Natal Sharks Board (KZNSB) currently deploys safety gear (gill-nets, baited drumlines) at 37 beaches, thereby trying to minimise environmental impacts. Apart from invaluable biological data on captured marine animals, parasite samples are obtained from a wide array of cartilaginous fishes. Given the paucity of parasitological information available, the aim of this project is to gather parasite data from marine apex predators in South Africa. The safety gear of the KZNSB is primarily aimed at large mackerel (Lamniformes) and ground sharks (Carcharhiniformes). For parasitological studies, specimens are obtained from internal organs and body surfaces and fixed for subsequent morphological and molecular methods. Apart from parasitic copepods with almost 100 reported species, information on other dominant parasite groups (i.e. endoparasitic platyhelminths) infecting cartilaginous fishes in South Africa is sparse. The large-scale, collaborative research project will assess the full spectrum of parasitic organisms and reveal the ‘hidden’ parasite fauna of lamniform and carcharhinid sharks in eastern South Africa. Future studies on this neglected faunal aspect will not only increase and build upon the largely incomplete knowledge of marine parasites but also expand the number of known species, many of which still awaiting scientific discovery.

Widespread search for potentially protective prion protein variants in the Icelandic sheep population delivers promising results

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The aim of this research project was to search for potential scrapie protective prion protein variants in a large group of Icelandic sheep originating from different regions of the country, with a specific attention to areas which had not been affected by large scale culling of sheep as part of an eradication program in the past.

Ear tag or brain samples were collected from 27.959 sheep (project on-going, numbers from July 2022), DNA isolated and the full coding region of the prion protein gene (*PRNP*) sequenced, or genotyped at codons 136, 137, 138, 151, 154, 171 by pyrosequencing.

Unexpectedly, 14 sheep (0.05%), carrying ARR (R171), were found at one farm in the far eastern part of Iceland. This is the first report of ARR in Icelandic sheep. In addition, a potentially protective polymorphism at codon 137 (T137), was found in 41 adult sheep (0.15%) from a total of eight farms located in different regions of the country.

Although found at a very low frequency, the presence of ARR and T137 offer the possibility of a careful breeding program for scrapie resistance in the Icelandic sheep breed, the best by including deep pedigree and genomic data in order not to decrease the diversity of the population. Especially, the use of sheep with T137 is promising, because in contrast to ARR, they are not all from one ancestry. An ongoing project should prove the protective effect of the identified variants against the Icelandic scrapie strains, e.g. with the PCMA and RT-QuIC tests.

Structure of the host E3 Ubiquitin ligase complex recruited by the maedi-visna virus Vif protein

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Through evolution organisms have come up with multiple ways to evade lentiviral infections. Among these host proteins is the mammalian apolipoprotein B mRNA-editing enzyme catalytic polypeptide-like 3 (APOBEC3 or A3) family of cytidine deaminases that restricts viral infections by mutating viral DNA and impeding reverse transcription. To overcome this antiviral activity, most lentiviruses express a viral accessory protein called Vif, which mediates the ubiquitylation and subsequent proteasomal degradation of A3 proteins. Different lentiviral Vif proteins have evolved to employ the same canonical E3 ubiquitin ligase complexes, along with different non-canonical host co-factors for their activities. Unlike primate lentiviral Vif which recruits CBF-beta as the non-canonical co-factor, non-primate lentiviral Vif proteins have developed differential co-factor recruitment mechanisms. Maedi-visna virus (MVV) sequesters Cyclophilin A (CypA) as the non-canonical co-factor for the Vif-mediated ubiquitination of ovine APOBEC3 proteins. Here we report a cryo-EM structure of MVV Vif in complex with CypA and E3 ligase components. Our work reveals conserved and novel structural features of MVV Vif, and the molecular mechanism by which it interacts with the E3 ligase components and CypA. The results highlight the important similarities and differences between MVV and primate lentiviral Vif proteins, advancing our understanding of the molecular determinants that help drive the evolution of lentiviral Vif proteins to capture their cognate host co-factors to evade APOBEC3 restrictions.

Ecology And Effects Of Digenean Infections In The Common Whelk Buccinum Undatum – A Case Study From Breiðafjörður, Iceland

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Parasite community composition and prevalence in the host is determined to a great extent by the population connectivity and life-history strategies of the host species. In the bay of Breiðafjörður, West Iceland, *Buccinum undatum*, the type species of the Buccinum genus (superfamily Buccinoidea) serves as an ecologically important predator, prey and parasite host in this biodiverse area. The complexity of food webs in the bay, as well as the topography of the habitat, creates an intricate system of drivers of local adaptation and polymorphism in *B. undatum*, a species typified by variable life-history traits and morphology across the North Atlantic.

In the current study, *B. undatum* in Breiðafjörður was used as a model system for the relationship of digenean prevalence to buccinid host life-history traits, body condition, shell morphology and population genetics, as well as environmental variables in the bay. The study was based on two datasets collected by 1) monthly sampling of whelk in 5 areas in a N-S transect of Breiðafjörður for a 1 ½ year in 2007-2008 with N ≈ 10,000 individuals; 2) a single sampling effort at 59 sites along the coastline of Breiðafjörður in 2007. Parasite prevalence was determined based on gross clinical signs. Environmental variables considered were latitude, longitude, depth and substrate type. Host life-history traits taken into account were sex, sexual maturity, shell height and age. Shell morphology was based on traditional morphometrics of shell and aperture, and population genetic information consisted of data on microsatellite, mtDNA and SNP variation. Body condition was estimated based on the ratio of digestive gland weight to eviscerated weight of the snail. Results from the study will be discussed in the context of how digeneans in *B. undatum* affect the host species and to what extent the fine-scaled population ecology of the gastropod host is reflected in the geographic prevalence of digenean infections in the area.

The first confirmed case of the blood sucking fowl mite Ornithonyssus sylviarum infesting a wild bird in Iceland

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[2]Suðurnes Science and Learning Center, Sandgerði, Iceland

In February, 2023 a sick juvenile merlin female *Falco columbarius* was captured in Sandgerði, SW Iceland. The lean bird was unable to fly and died after a day in captivity. By handling and examining the bird for injuries thousands of fast moving mites started crawling around on the hands of the person holding the bird, thousands of mites accumulated in the tray where the bird had been kept prior to the examination. The inspection revealed thick and crusty skin, severe scabbing and soiled feathers. Dozens of mites were sampled, fixed in 70% EtOH and brought to Keldur for identification. Specimens were mounted in a drop of Hoyer's medium under a cover slip on a microscopical slide and kept by 60°C over night prior to the microscopical examination. The species was the blood sucking fowl mite *Ornithonyssus sylviarum* (Canestrini & Fanzago, 1877). Morphological characters were photographed. This mite has not previously been identified or reported from wild birds in Iceland. As infestations by this mite are usually prominent, and easily detectable, we believe that the mite was recently introduced to Iceland. This suggestion is also supported by the fact that *O. sylviarum* was not detected in a recent survey on poultry parasites in Iceland. In that survey, however, the morphologically similar species, the red poultry mite *Dermanyssus gallinae*, was detected. *D. gallinae* has been known to infest poultry in Iceland for decades. The infested bird was obviously overwintering in Iceland. Most members of the merlin population, however, leave the island in the autumn and overwinter abroad.