

Non-invasive methods for monitoring parasite infections in free-range livestock

CPH cattle seminar 2022

Amalie Camilla Pedersen

PhD student,

Veterinary Parasitology

IVH, KU-SUND

acp@sund.ku.dk

KØBENHAVNS UNIVERSITET



Background

Nature preservation with livestock (rewilding)

- Parasites are a common problem

Large pasturelands

- Mustering and sampling are difficult or impossible

Certain interventions may be regulated

- Use of supplementary feed and use of anti-parasitic drugs may be restricted

Objective

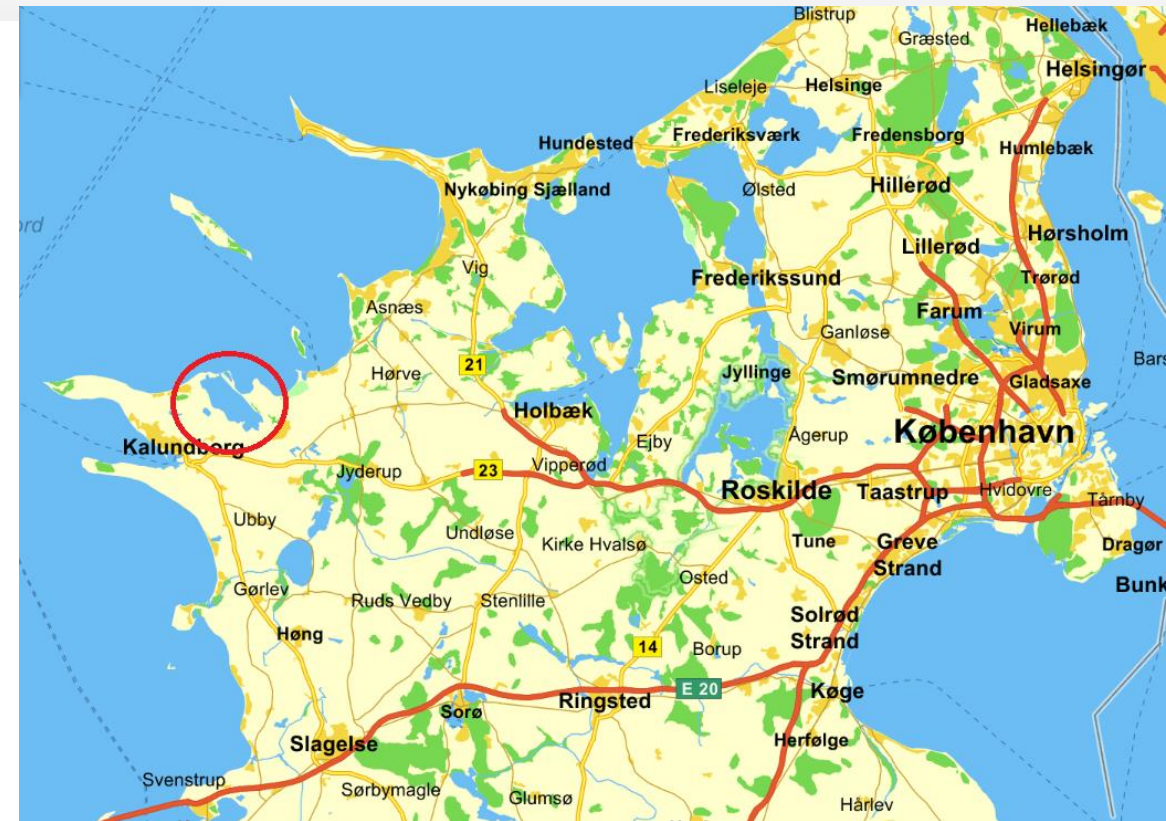
- To develop methods of monitoring parasite infections in livestock in large pasturelands, in a non-invasive manner
- And at same time, to diagnose individual infections in order to treat potential parasitic problems



Saltbæk Vig – field study

Protected nature area

- 1200 ha land (plus 1400 ha lake)
- Grazed by beef cattle (Red Angus)
 - Approx. 90 cows,
 - 115 heifers, some calves and bulls.
 - Housed during winter, grazing May-November
 - Calves born outside on pasture during late spring
 - Daily supervision of the cattle
 - Low stocking density
- 1.2 m below sea level
- Low pasture quality
- Large population of red deer, rare birds and plants



Grazing cattle = Parasites (Nematodes)

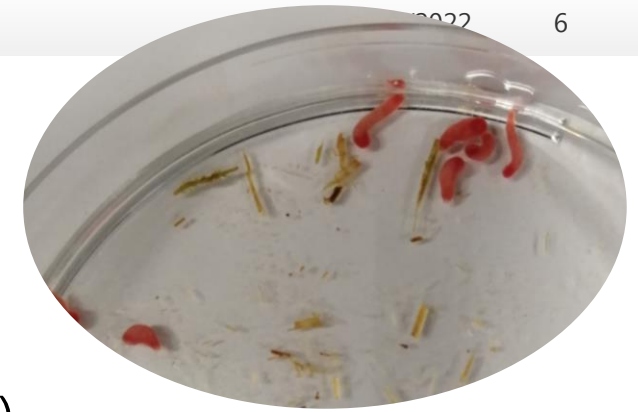
Gastrointestinal nematodes (GIN)

- *Ostertagia ostertagi* (abomasum) and *Cooperia oncophora* (small intestine)
 - Clinical and subclinical disease (reduced productivity)

Lungworm (*Dictyocaulus viviparus*)

- Adult stages localized in bronchi of the cattle
 - Coughing

Grazing cattle = Parasites (Flukes)



- Liver flukes (*Fasciola hepatica*):
 - Intermediate host – mud snail (“lille pytsnegl”)(*Galba truncatula*)
 - Adult flukes localized in bile ducts → eggs excreted with faeces of the host.
- Rumen flukes (probably *Calicophoron daubneyi*)
 - Juvenile flukes excyst and feed in the duodenum until migration into the rumen and reticulum, where the adult flukes are localized
 - Same intermediate host
 - Impact: debated

Diagnostics:

- Faecal egg count by sedimentation
 - Liver flukes: yellow eggs
 - Rumen flukes: grey or colourless eggs



What we have done so far (2022) ...

Monitoring of infections:

Two groups of animals:

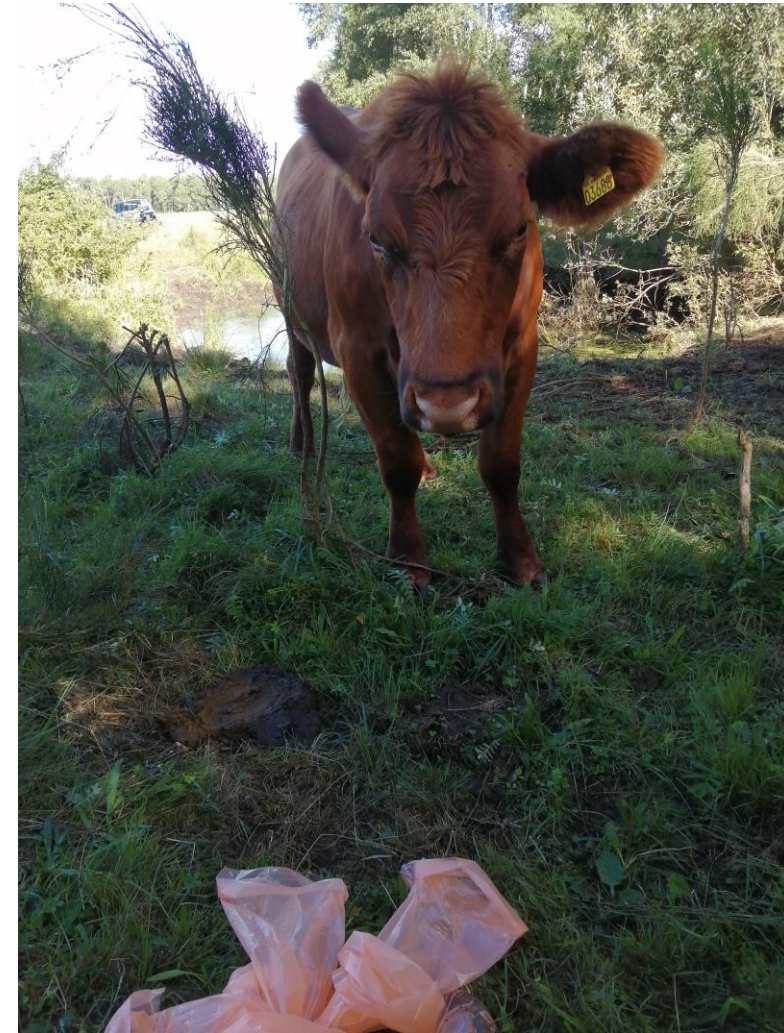
- 2nd year heifers from summer 2020
- 1st year heifers from summer 2021

1st sampling: 12.05.2022 (INVASIVE) – at turn out

- Blood and rectal faecal samples
- 45x 1st year, 14x 2nd year

Monthly sampling after turnout

- Faecal samples collected from ground
- 20x 1st year, 20x 2nd year
- Fresh faeces = warm, moist



Methods

- Blood (only 1st sampling)
 - Diagnostic of *Babesia* (blood smear, PCR)
- Faeces
 - McMaster (GIN)
 - Baerman (lungworm)
 - Sedimentation (flukes)
 - Stored for Nemabiome (larvae culture) and barcoding (fresh faeces at -80°C)



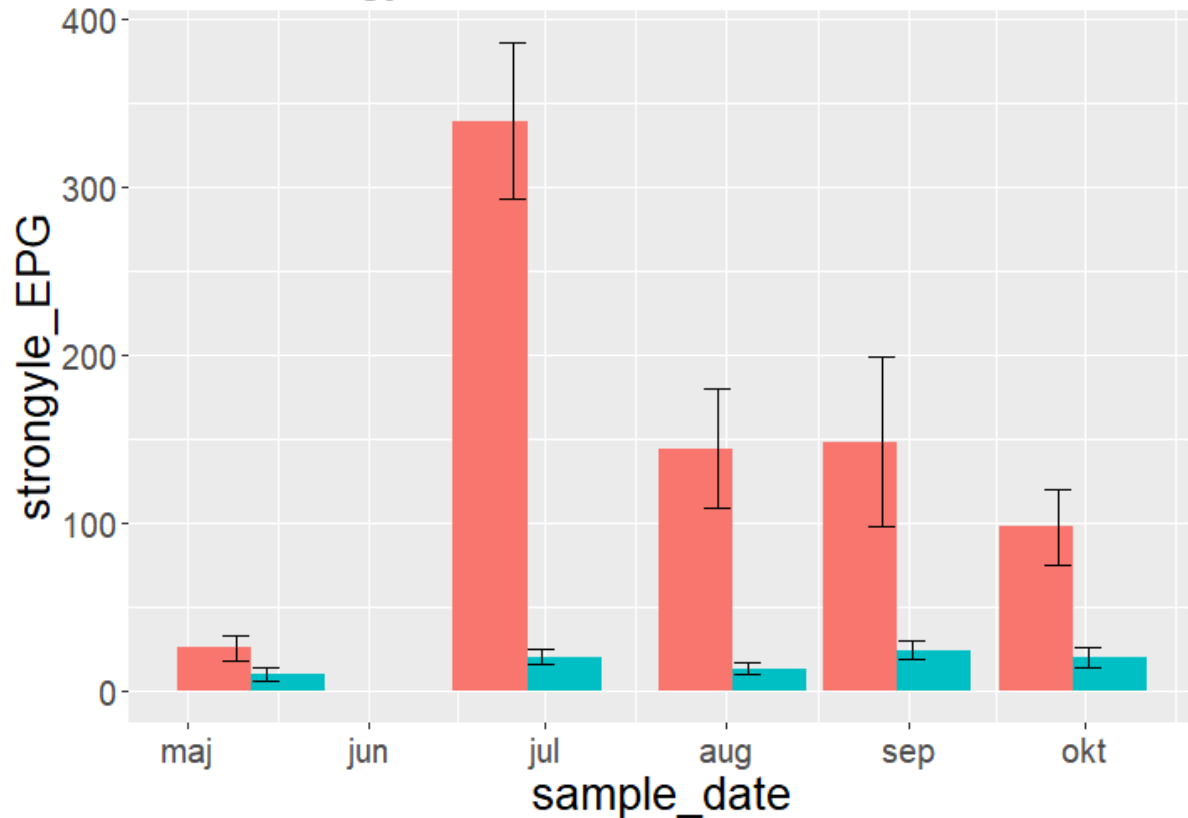
Challenges in non-invasive sampling:

- Diagnostic of individual – which sample is from which animal
- Contamination – soil nematodes
- Not always fresh samples – hatched eggs

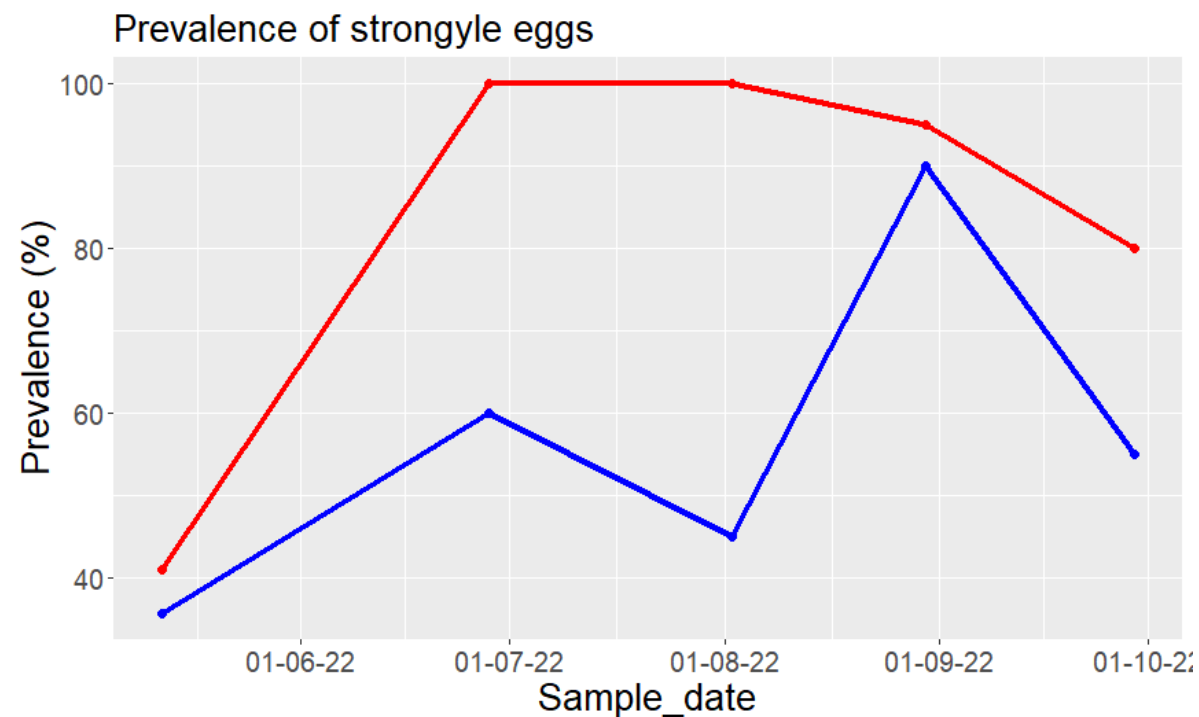


Preliminary results

Mean strongyle EPG



year_age
■ first
■ second

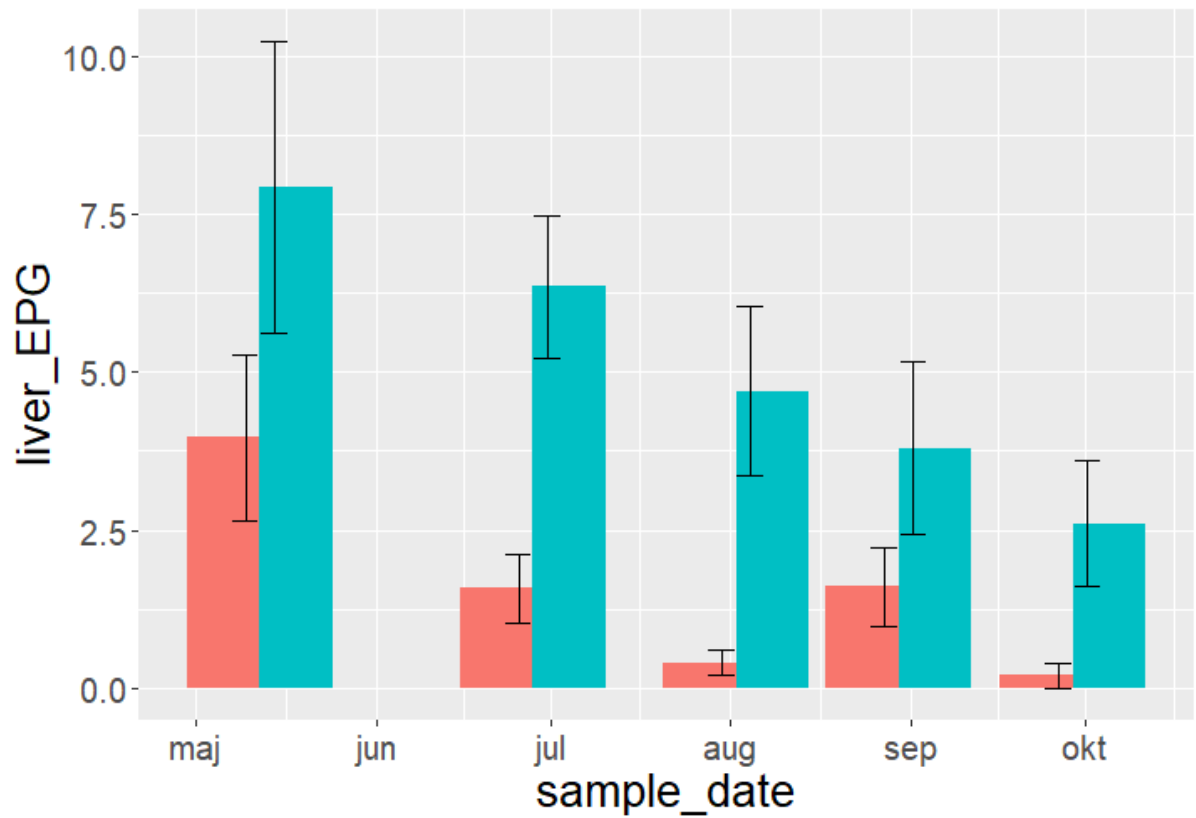


GIN count:

- 1st year: development of immunity
- 2nd year: resistant towards reinfection

Preliminary results

Mean liver fluke egg count



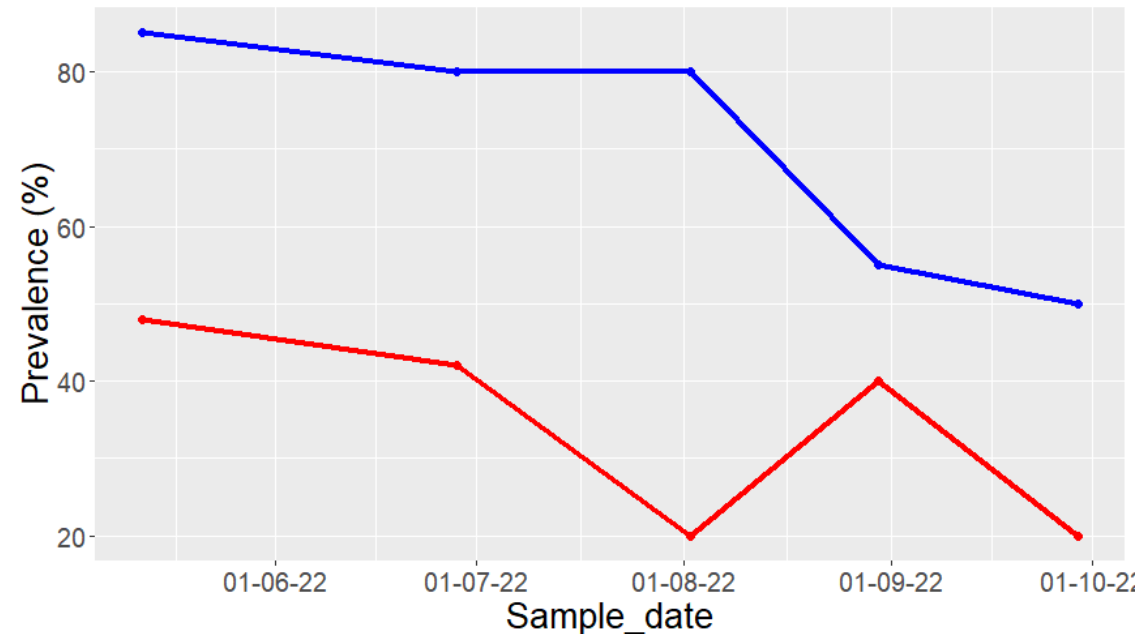
Liver fluke egg count:

- Levels decreasing throughout the season
- 2nd year: higher levels

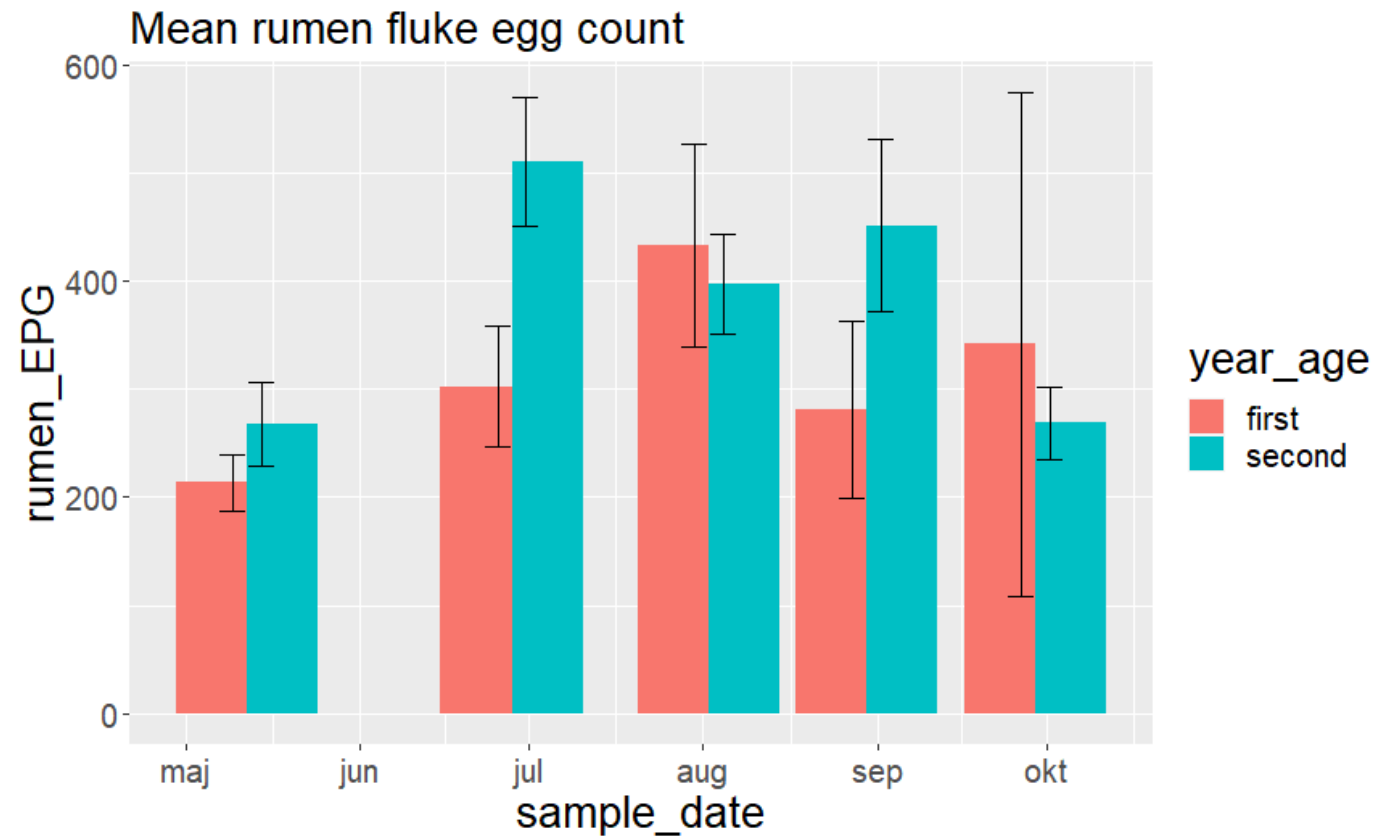
year_age



Prevalence of liver fluke eggs



Preliminary results



Rumen fluke egg count:

- Similar between age groups
- Prevalence of 100%

Conclusions

- We have described the parasite occurrence and dynamic of one grazing season in the area
 - Development of resistance toward GIN infection
 - Decreasing levels of liver fluke egg counts
 - High prevalence of rumen fluke and a need to look more into this infection

What is the further plan

Non-invasive sampling

- Nemabiome – which GIN are found in the samples
 - Deep amplicon sequencing (or metabarcoding), targeting the internal transcribed spacer 2 (ITS-2) rDNA locus, for describing the exact composition of the nematode population (<https://www.nemabiome.ca/>, Avramenko et al., 2015, Avramenko et al., 2017).
- Barcoding
 - Are the samples from different animals
 - Which sample is from which animal
 - Which individual have the highest egg excretion
 - Which individuals have the highest level of infection
 - How to: DNA database of all animals in the group
 - Each faecal sample contains DNA → match in database

What is the further plan

- Environmental monitoring of flukes (eDNA on water or snails)
- *Babesia* – infections
- Rumen flukes and their impact

- Sampling plan for next season
 - Should we proceed with only one group
 - Then which age group



Questions (or Suggestions) ?
acp@sund.ku.dk