Workshop on poultry red mite genomics

April 26th-27th 2018 Oslo Norway

Report on Workshop

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Purpose of the workshop

The overall objective of COREMI is to consolidate existing expertise and knowledge to gain a better understanding of poultry red mites and the economic and societal impacts of this pest, using this information to implement more efficient and sustainable control methods. COREMI COST Action is divided into four working groups; three dedicated to integrating scientific and technical knowledge from various disciplines while the 4th aims towards end-user stakeholders involvement. In COREMI's working group 3, ***Genetic structure in a changing world (lead Roy, co-lead Øines)*,** advances are encouraged for the characterization of the genetic structure of the poultry red mite in the current context of a world dominated by long-distance trade and the heavy use of acaricides for treatments. In order to ensure progress in the field of PRM research, we have identified a need to consolidate PRM genetic resources available through COST partners, as research activities can be dependent on the availability of genetic PRM databases, annotated PRM genomes, bioinformatics resources and analysis pipelines and technologies to ensure further PRM research.

This workshop was planned, to help identify genetic resources on PRM, discuss any planned, ongoing or finished projects from COREMI members that are relevant to red mite genomics. We seek to collate the information to help highlight and identify data resources and analysis platforms, which could be useful for research colleagues in the COST-action member research-groups.

Control Red Mite COREMI

Veterinærinstituttet
Norwegian Veterinary Institute

Agenda 26/4-27/4

Day 1 -

0900-0920: Introduction & Welcome -why are we here…? – Oivind will try to address this

0920-1000: Overview of existing genomic/transcriptomic resources for *D. gallinae* – Stewart Burgess

1000-1015: Coffee

1015-1100: The MRI *D. gallinae* genome project – an introduction – Stewart Burgess

1100-1200: *De novo* gene prediction and annotation pipelines at the University of Gent – Stephane Rombauts

1200-1245: Lunch & Networking

1300-1400: An overview of the Online Resource for Community Annotation of Eukaryotes (ORCAE) – Stephane Rombauts

1400-1500: Live Demo (Part I) – ORCAE gene curation for *D. gallinae*– Stephane Rombauts

1500-1530: Coffee & Networking

1530-1700: Live Demo (Part II) – ORCAE gene curation for *D. gallinae* – Stephane Rombauts

1900-ish: Social/Group dinner – Mahayanas

Day 2

0830-0915: Review of Day 1 and introduction to Day 2 – Øivind Øines

0915-0945: ONT minION sequencing technologies for PRM research –Stewart Burgess and Øivind Øines

0945-1025: Olfactory systems in mites: what is known and what knowledge is lacking about chemical interactions between PRM and its environment including hen host? -Lise Roy

1030-1100 Norway research group on Cod genomics –Ole Kristian Tørresen, University of Oslo

1100-1130 Lessons from the Salmon genome –Bjørn Høyheim Norwegian University of Life Sciences

1130-1155: TBC: Sequencing technologies and bioinformatics available in Oslo -Arvind Sundaram Norwegian Veterinary Institute/Norwegian Sequencing Centre

1200-1300: Lunch & Networking

1315-1345: Red mite transcriptomes to identify SNPs as genetic markers -Eleanor Karp-Tatham RVC

1345-1415: Wrapping up and future directions –where to now..?

1400: Return Flights

Introduction and overview

COREMI COST actions overall aim is to *Improve current understanding and research for sustainable control of the poultry red mite Dermanyssus gallinae* – to better understand and research the poultry red mite, in order to find a sustainable method of control. Poultry red mites are the most significant pest in egg-laying poultry in Europe and current norms for poultry red mite infection in commercial housing cannot be considered acceptable and must be reduced. COREMI seek to advance and disseminate Integrated Pest Management for poultry red mites by collating knowledge of mite biology, mite-host relationship and novel control measures, and coordinate further research work in the area. This information will be used to produce industry 'Gold Standards' for poultry red mite prevention and control, tailored to individual countries and their production systems. A more complete research-based understanding of poultry red mite impact to poultry and other sectors, including public health, will be initiated through the Action. The scientific topics covered in COREMI partners concentrates on different but interrelated areas relating to multiple aspects of poultry red mites. The four working-groups align with the scientific programme:

- WG 1: Developing alternative control measures
- WG 2: End users (One Health)-interdisciplinary approach
- WG 3: Genetic structure in a changing world
- WG 4: Epidemiology, pathology, geographical mapping and surveillance tools
  One important aspect of this is research targeting parts the parasite genomes and molecular interactions.

Aspects of PRM genomics cover activities from all working groups, and in many ways give the foundations for applied research in various PRM fields. PRM genomics would be applicable to vaccine research, epidemiology, vector potential, host infection and parasite biology as well as diagnostics. This meeting was organised in Norway, at the Norwegian Veterinary Institute. We were restricted to a maximum of 5000 euro towards this meeting, which limited the amount of paid seats to ca. 10. We were therefore a little bit restricted in the total amount of people that were allowed to be invited, although the possibility of extra seats was kept open for any self-paid participants, should there be more people interested. In total we were 11 COST member participants, representing research groups in Belgium, UK, France, Macedonia and Norway. The participants included one representative from the core group, three representatives from the COREMI management group, two inclusiveness target country researchers (ITC), and two early career investigators (ECI). We also included three external researchers from different research arenas in Oslo, representing two researchers from groups on core expertise on *de novo* genome assembly-research from the marine environment. We also invited one researcher from NorSeq, a sequence facility representative, giving information on the different instruments, and the potential for sequence tasks being out-sourced through their non-profit activities.

Technologies and methodological approaches

A number of platforms is currently in use through partners in the network, both for sequence generation, but also for bioinformatics, analysis platforms and competence. From many of the external talks, as well as some of the talks from the participants, new sequence technologies and methods useful for genomic research were presented. In particular, various sequence platforms, including low-cost systems such as nanopore sequencing, and long DNA molecule visualisation such as BioNano technologies were examples of systems brought forward.

Bioinformatics, databases and data exchange (rules?)

We wanted to highlight some of the solutions in place through the ongoing collaboration MRI has with VIB-UGhent, and Stephane Rombauts contributed by demonstrating bioinformatic platforms available through their network, with demonstrations from relevant research projects on various mite species. Going through practical annotation and retrieval of genes and gene information through their network was a useful demonstration in the workshop. During and following the workshop, several of the participants have exchanged data and information that will increase the availability of PRM genomic resources for future research projects. Some round table discussion on rules of use and how this should be regulated (IPR) between partners.

The workshop fitted in to the plan of the ITC institution (Macedonia) to establish an NGS platform soon. The presentations, discussions and networking will help to choose an appropriate technology and customize it according to the own diagnostic and research needs with the aim to strengthen the capacity of the institution.

Summary of talks and discussions

On the first day, the workshop started with a short round table presentation of all participants to allow everyone an insight of their affiliation, current research focus, and a brief comment why PRM genomics is relevant to their research activities. Stewart Burgess presented the current status of the PRM genome and their PRM transcriptome work, presenting data on genome size and scaffolds in the current version. Stephane Rombauts further expanded on these PRM data, and related it with other mite genome projects, in particular spider mite and scabies mite. The web interface for genome searches and annotations, were demonstrated by Stephane Rombauts, and all participants were able to try this themselves later that day, by logging into the ORCAE (Online Resource for Community Annotation of Eukaryotes) gene curation system available through VIB-UGhent, and performing gene prediction, annotations and corrections on the *Sarcoptes scabiei* genome. Genomeview and Jalview were demonstrated. Online community driven curation was encouraged to be the way forward with this PRM genomic work, as it was said it would be a good approach to make the work more efficient and with a sufficient level of quality control, even if no SOP or detailed protocol for how this should be carried out is currently available. The day ended after a nice social dinner at a restaurant in the city.

The second day Øivind Øines introduced Nanopore as a sequencing platform, and showed some preliminary results from metagenomics and pathogen screening on PRM/sheep using this technology. Data analysis pipelines were also presented. Stewart Burgess further expanded on this technology, and their use in the future. Lise Roy showed some interesting research on olfactory studies in mite, and why available genomic resources could add to practical behavioural and biological experiments in PRM. Following this session, external researcher Ole Kristian Tørresen (UiO) presented his work with the cod genome project at the university and the development of technologies and pipelines relevant also to us, and showed how the cod genome needs revision and improvement. Then professor Bjørn Høyheim (NMBU) presented his historical perspective on his involvement with several genome projects relevant to veterinary research and highlighted potential pitfalls, and possible solutions to this from his point of view. Arvind Sundaram closed this session with a brief presentation and information on sequence technologies, and how they can provide a variety of such services through the NorSeq consortium. At the end of the workshop, Eleanor Karp-Tatham (RVC) presented her PRM-PhD project, where much of the above technologies and analysis pipelines could be relevant. Following a brief discussion on her preliminary data, the workshop was closed with a brief discussion on the way ahead and possible exchange of data which may be relevant for further improving on the soon to be publicly available PRM.

Suggested outputs

From our workshop we suggest to further expand on the use of ORCAE and to collate relevant data with this database to further improve as a community driven collection of PRM genomic resource, when becoming available. Data related to PRM that was identified in the group, and that will be made available in the near future, besides the genome with its annotation, includes Illumina and 454 RNAseq and resequencing data for another PRM population. More open networking by sharing data and technologies between the participants could also allow more projects to be initiated between the cost action participants. A brief discussion on potential collaboration with other mite research communities making benefit of knowledge and skills from both agronomy and livestock fields (-a possible future COST-action perhaps…?) was brought up.

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