



MASTS-SFC Saltire Emerging Researcher Scheme (MASTS-SERS)

Final Report

MASTS in association with the Scottish Funding Council supported the Saltire Emerging Researcher Scheme, which represented an important and exciting opportunity for Post Graduate Researchers (PGR) and Early Career Researchers (ECR) to engage in substantive collaboration with colleagues from Europe (EA, EEA and EFTA countries).

The scheme aimed to promote mobility between Scotland and European research partners with the aim of strengthening existing, and seeding future, research relationships. Participants are expected to demonstrate the impact of their exchange through the publication of novel research work, the formation of new collaborations and project/ funding submissions, and the dissemination of their results.

As your exchange has now come to a close, we ask that you reflect on the exchanges and provide a report by filling in the form below. The reports will need to demonstrate the potential benefits of the grant for both the recipient and their collaborators. Please return this within four weeks of completing your exchanges to masts@st-andrews.ac.uk. When you do so, you are agreeing that your answers may be used to promote the activities of MASTS, including being used on the website and social media channels.

Please note that MASTS may also contact you, the participants, and/or your supervisors to gather additional post-exchange impact information. This information must be provided on request.

Contact information

| | |
|---|---|
| Participant name(s) | 1. Dr. Alexander Innes Thomson 2. Alexandre Detain |
| University & Department | 1. Scottish Association for Marine Science - University of the Highlands and Islands 2. Nord University - Faculty of Biosciences and Aquaculture |
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| Host name(s) | 1. Dr. Christopher J. Hulatt 2. Dr. Thomas Leya 3. Dr. Matthew Davey |
| University or Institution & Department | 1. Nord University - Faculty of Biosciences and Aquaculture 2. Fraunhofer Institute for Cell Therapy and Immunology IZI-BB - CCCryo Culture Collection of Cryophilic Algae 3. Scottish Association for Marine Science - University of the Highlands and Islands |
| Email address | 1. christopher.j.hulatt@nord.no 2. thomas.leya@izi-bb.fraunhofer.de 3. matt.davey@sams.ac.uk |

Exchange overview

| | |
|--------------------------------------|--|
| Title | Enhancing genomics and metabolomics capabilities for cryophilic algae |
| Start date | 01/03/2022 |
| End date | 06/08/2022 |
| Project location(s)/exchanges | 1. Alex Detain to the Scottish Association for Marine Science (SAMS), University of the Highlands (UHI) and Islands – 27 th June to 15 th July 2022 2. Alex Thomson to Nord University, Bodo, Norway – 23 rd July to 6 th August 2022 3. Alex Thomson to IZI-BB CCCryo, Potsdam, Germany – Planned 17 th to 23 rd April – cancelled (Covid) – re-organised 5 th to 11 th June – cancelled (injury/illness) |

Abstract (max 300 words)

Provide a brief summary of the exchange using language accessible to a non-specialist. Describe what the exchange objectives were, the activities that were carried out, and the subsequent outcomes. This may be published on the MASTS website.

Snow algae have adapted to some of the most extreme conditions on the planet. Not only are they able to survive the deep polar winter, they are also able to photosynthesize and bloom in the snow itself once summer arrives.

This exchange programme aimed to enhance the genomic and metabolomic capabilities available to analyse snow algae at a molecular level. The exchange focussed on three key areas of snow algal research: 1) the molecular identity of algal species within snow algae blooms using eDNA approaches; 2) characterizing the products of snow algal cells, including fats, proteins, and amino acids; and 3) the sequencing, assembly, and gene annotation of the genomes of two selected algal strains.

The first part of the exchange involved Alexandre Detain, a PhD student at Nord University, visiting SAMS-UHI, Oban, to gain experience in analysing the products of photosynthesis and cellular processes in snow algae using HP-LC and GC-MS analysis techniques, with help from Dr Matt Davey.

Dr Alex Thomson then visited Nord University to assemble and annotate the genomes of two Antarctic algal strains, under the guidance of Dr Chris Hulatt. The annotation was undertaken using a predictive approach based on known protein coding pathways in related algal species. The identification of one of the strains was supported by online discussions and the sharing of algal material with Dr Thomas Leya, from the CCCryo, Potsdam. The investigation will be followed up by sequencing the RNA transcriptome of each strain to provide direct evidence of gene structures across the genome.

Species identity within snow algae communities was investigated using eDNA (metabarcoding) approaches, whereby the whole community is characterised at a molecular barcode level. Field community samples from Norway and Scotland were prepared for Nanopore sequencing at SAMS. This represented the first Scottish snow algae survey since 1968.

Impact (max 600 words)

Please demonstrate the impact of your exchange from your perspective, and that of your exchange partner. Describe what the wider benefits of the exchange were to you as participant, your own and host institutions, and the wider community.

The exchange has had major impacts on the work within my research group at SAMS UHI, that of Dr Chris Hulatt's group at Nord University, and future investigations and collaborations between Dr Hulatt's group, Dr Leya's laboratory, and SAMS UHI. In addition, the exchange programme has had a significant effect on my own professional development as a post-doctoral researcher, widening my network of colleagues and collaborators, and encouraging my own independent investigation, supported by my PI, Dr Matt Davey.

Part of the work undertaken during the exchange followed on from existing investigations at SAMS, lead by Dr Davey. These included the sequencing of the whole genomes of two microalgal isolates, sampled from Antarctic by Dr Davey in 2019, as well as the development of the Nanopore community metabarcode sequencing approach. The Saltire programme provided the additional stimulus and funding to expand these investigations and increase the scope and impact of the work produced.

The genome investigation expanded on an existing project which had sequenced the nuclear genomes of two Antarctic snow algal isolates. The exchange programme supported the next steps in the process of assembling and annotating those genomes. Dr Hulatt had previously published the detailed genome annotation of another polar cryophilic algae, *Diacronema lutheri*. The Saltire programme allowed me to reach out and build ties with Dr Hulatt in a structured and supported manner. The knowledge and expertise gained from Dr Hulatt was invaluable in advancing the investigation beyond basic assembly steps to a full, publishable annotation. The improved annotation will be of benefit in future applications of the genome within our own research, for instance in targeted investigations of pigment production pathways, as well as in acting as more reliable resource for the wider snow algae and algal genomic research communities. The knowledge gained from Dr Hulatt in how to approach the annotation of algal genomes will also be invaluable in enhancing in-house genomic capabilities within our own research group, as well as within other research groups in SAMS and UHI. An informal seminar, to share the knowledge gained from my time with Dr Hulatt, is planned for next month at SAMS.

The programme also supported the continued development of an Oxford Nanopore Technology (ONT) based metabarcoding approach to investigate community composition in snow algal blooms. ONT metabarcoding approaches are much less established than Illumina sequencing-based alternatives, yet offer a number of potential advantages for metabarcoding studies, primarily from the longer read-length offered by ONT sequencing. Once again, the Saltire programme provided the stimulus to develop this approach fully, using field material from both Scotland and Norway as a showcase of how the approach can be applied. The analysis is ongoing, but if the approach proves successful, the results will provide high-accuracy species-resolution identification of community members in snow algae blooms, as well as offering novel comparative phylogenetic perspectives on algal communities from metabarcode data. The findings will represent the first comprehensive community analysis of snow algae in the Norwegian coastal range, and the first reporting and analysis of snow algae in the UK since 1968. The results will contribute to our wider understanding of biodiversity and ecology in the mountain environment in the UK and Norway and will act as a baseline of snow microbial community composition in the face of a changing climate.

Outputs (max 300 words)

Has this exchange resulted in clear outputs, such as the generation of a proposal, research results, or publication? Please provide brief details here. Do any of these outputs have relevance to larger programmes such as the UN SDGs, Blue Economy Action Plan etc?¹

The draft genome annotations represented one of the major outputs from the programme. The genomes were assembled using multiple approaches and curated to provide the best quality assemblies for annotation. Genome annotation was undertaken using a predictive approach based on known gene structures and protein coding pathways in well-studied close-relative species. This will be improved further using direct transcriptomic evidence from both isolates as part of the ongoing investigation. The completed genome annotations will be the focus of two separate publications. The publications of the two annotated genomes will be followed up by a comparative genome study of 4 related Chlamydomonad algae.

One of the strains sequenced was also identified as a possible novel species. Online discussions and collaboration with Dr Leya have been instrumental in resolving the taxonomy and establishing a novel species description of that strain, which will be included in the genome publication.

Alex Detain's exchange led to the preparation of a metabarcode library from samples collected from the Nord region during summer 2022. The analysis will be the focus of a publication on community composition in maritime Norwegian snow algae communities. The Scottish snow algae samples will similarly be processed and prepared. The published results will provide the first molecular investigation into UK snow algae. The surveying of snow algae in the Scottish mountains during the exchange will represent the first documentation of snow algae in the UK since 1968.

The pigment and metabolite analysis undertaken by Alex Detain during his stay at SAMS provided important pilot information for future experimental designs and thesis work. Alex plans to return to SAMS in 2023 to follow up the trial study. The results will contribute to Alex's thesis, as well as a planned publication on the effects of light stress on photosynthetic physiology in the species of interest.

¹ All successful applicants will be expected to represent, promote and formally acknowledge the sponsors (MASTS, SFC & Scottish Government) during the course of their project and in any subsequent related outputs. All research outputs and any material used publicly must carry the funders' logos. The following acknowledgement should be used in all publications resulting from this funding. ["This work received funding from the Scottish Funding Council Saltire Emerging Researcher Scheme and the MASTS pooling initiative (The Marine Alliance for Science and Technology for Scotland) and their support is gratefully acknowledged. MASTS is funded by the Scottish Funding Council (grant reference HR09011) and contributing institutions"]

The Future (max 300 words)

How do you plan to ensure a sustainable collaboration in the longer-term and maximise opportunities and impact in the future? How will you carry forward the benefits now the exchange has been completed? Please outline five concrete plans for future collaboration as a result of your exchange.

The planned publications from the work undertaken during the exchange provide a strong incentive for continued collaboration between the exchange partners. At least 5 publications are expected from the work undertaken during the exchange, along with a further 2 potential follow up publications. The continued discussion of the publications will provide a strong stimulus for further idea development and collaboration. Beyond this, the friendships and understanding developed during the exchanges have provided a strong connection that will encourage future collaboration, knowledge exchange, and idea development. All partners involved have stated an interest in pursuing future proposal opportunities should the right funding call come up. In particular, Dr Hulatt, and his colleague Hirono Suzuki, are keen to develop ideas, and possible proposals, around community characterisation, isolation and cultivation, and genome sequencing of cryophilic algae.

More immediately, I am due to visit Dr Leya in Potsdam in November for an in-person discussion on the identity of one of the genome sequenced strains, as well as on a paper describing a potentially new/unresolved genus of Chlamydomonaceae. Alex Detain and I aim to present the findings from the Norwegian and Scottish metabarcoding work at the 2022 Snow Algae Meeting (SAM), in Prague this November. I will also be delivering an informal seminar on algal genome annotation at SAMS in October to share this knowledge with other interested research groups at SAMS. I am also planning to deliver a seminar on the findings from the exchange, as well as my broader work, at Nord University as part of their research seminar series. Alex Detain and Hirono Suzuki both plan to make visits to SAMS in 2023/24, Alex as part of his ongoing thesis experiments, and Hirono as part of a knowledge exchange, potentially as part of a CCAP workshop on algal isolation at SAMS.

Any further comments (max 500 words)

Please use this space to provide any additional comments. These may include, but are not limited to; what you would do differently if you could take the exchange again; what contingency measures you had to use (if any); details of any unexpected benefits or problems; any significant variations in costs;

One of the biggest setbacks during the exchange was the twice-cancelled exchange trip to Potsdam to visit Dr Leya at the CCCryo. The first trip was cancelled after both myself and Dr Leya caught covid within a few weeks of the planned trip. The re-organised trip was again cancelled due to health issues. Despite these setbacks, Dr Leya and myself were able to have numerous constructive discussions online. In addition, Dr Leya kindly sent material for analysis from Potsdam to SAMS, and has invited me to CCCryo for 3 days of discussion and lab-work in November as a follow up to the exchange work.

One unexpected cost came in the form of RNASeq transcriptomic sequencing to support the genome annotation work. The RNASeq work arose from discussions and recommendations from Dr Hulatt following the initial ab-initio annotations of the two isolate genomes. Dr Hulatt felt that, considering the unusual levels of repetition observed in the two genomes, and the non-model nature of the two species, a direct evidence based approach to gene prediction using transcriptome data would provide the greatest accuracy for the final genome annotations. After consulting with MASTS, the decision was made to redirect some of the exchange funds to cover the costs of this sequencing.

I am extremely grateful to the MASTS Saltire programme for giving me the opportunity to undertake this exchange and for supporting my work and the work of my collaborators going forward. The experience and knowledge gained from the exchanges has been invaluable and will be of huge help in my current and future research. The partnerships and relationships built have also been hugely beneficial and a great source of joy, and I look forward to continuing to interact with Alex Detain, Dr Hulatt, and Dr Leya as both friends and colleagues. I look forward to sharing the work produced during the exchange as part of the MASTS Seminar series, and will make sure to give full credit to MASTS Saltire in all associated outputs.

Final expense report * Please see attached project costs breakdown spreadsheet for detailed costs and expenditures

| Item Number | Description | Cost per Unit | Number of Units | Total Amount (£) |
|------------------------------|---|---------------|--|-------------------|
| 1 | Alex Thomson Travel – Oban-Bodo return | £697.22 | 1 x return flights Oban – Bodo + airport travel | £697.22 |
| 2 | Alex Thomson accommodation – Bodo x 12 nights | £1316.34 | 12 x nights | £1316.34 |
| 3 | Alex Thomson expenses – Bodo x 14 days | £338.22 | Food and bus tickets | £338.22 |
| 4 | Alex Thomson travel Oban-Potsdam - non-refunded losses | £447.41 | 1 x Return flights + 1 flight change charge | £447.41 |
| 5 | Alex Thomson accomadation Potsdam - non-refunded losses | £121.54 | 1 x night | £121.54 |
| 6 | Alex Detain Travel – Bodo-Oban return | £560.44 | 1 x return flights + 1 x return train | £560.44 |
| 7 | Alex Detain accommodation – Oban x 17 nights | £1,185.39 | 17 x nights | £1,185.39 |
| 8 | Alex Detain Food – Oban x 18 days | £232.45 | Food x 18 days | £232.45 |
| 9 | Scottish fieldwork - travel and expenses | £151.90 | Mileage + food | £151.90 |
| 10 | Lab consumables – metabolomics | £1843.48 | Lab consumables | £1843.48 |
| 11 | Lab consumables – metabarcoding (Nanopore) | £1256.95 | Lab consumables | £1256.95 |
| 12 | Lab consumables – isolate culturing | £382.30 | Lab consumables | £382.30 |
| 13 | Genomics expenses - RNAseq | £435.84 | Transcriptomic sequencing to support genome annotation | £435.84 |
| 14 | Overheads | £7.88 | | £7.88 |
| Total | | | | £8,976.73 |
| | | | | |
| In-kind contributions | Salary/project time (Dr. Matthew Davey) | £601/day | X 10 | £6,010.00 |
| | Salary/project time (Dr. Christopher Hulatt) | £500/day | X 10 | £5,000.00 |
| | Salary/project time (Dr. Alex Thomson) | £425/day | X 10 | £4,250.00 |
| | Bench fees (SAMS) | £50/day | X 10 | £500.00 |
| | In-cash contributions | | | £0.00 |
| Total | | | | £15,760.00 |
| | | | | |
| Grand Total | | | | £24,736.73 |

