# WP3 Genetics and disease (UiB, UiO, IOCAS, SAMS, Industry)

## Overview of main activity and plans:

- Samples of sugar kelp have been collected from 23 sites along the Norwegian coast including a large fjord. Population genetics will be examined by using RADseqs, and an additional study focusing on fjord populations will be carried out using microsatellites.
- The RADseq data will later be compared with data collected in Scotland.
- The study will show potential genetic groupings, and barriers for gene flow.

**Upstart 2018:**

- In the continuance, isolated cultures of sugar kelp from different latitudinal origin (South-West, Mid-, and North-Norway) will be grown in three separate common garden experiments, exposed to different nutrient, temperature and light conditions, and the expressed genes profile of the different cultures will be compared.
- Their RNA transcriptome libraries will be scanned to find possible local to regional-specific differences in functional genes, for cultivar purposes.

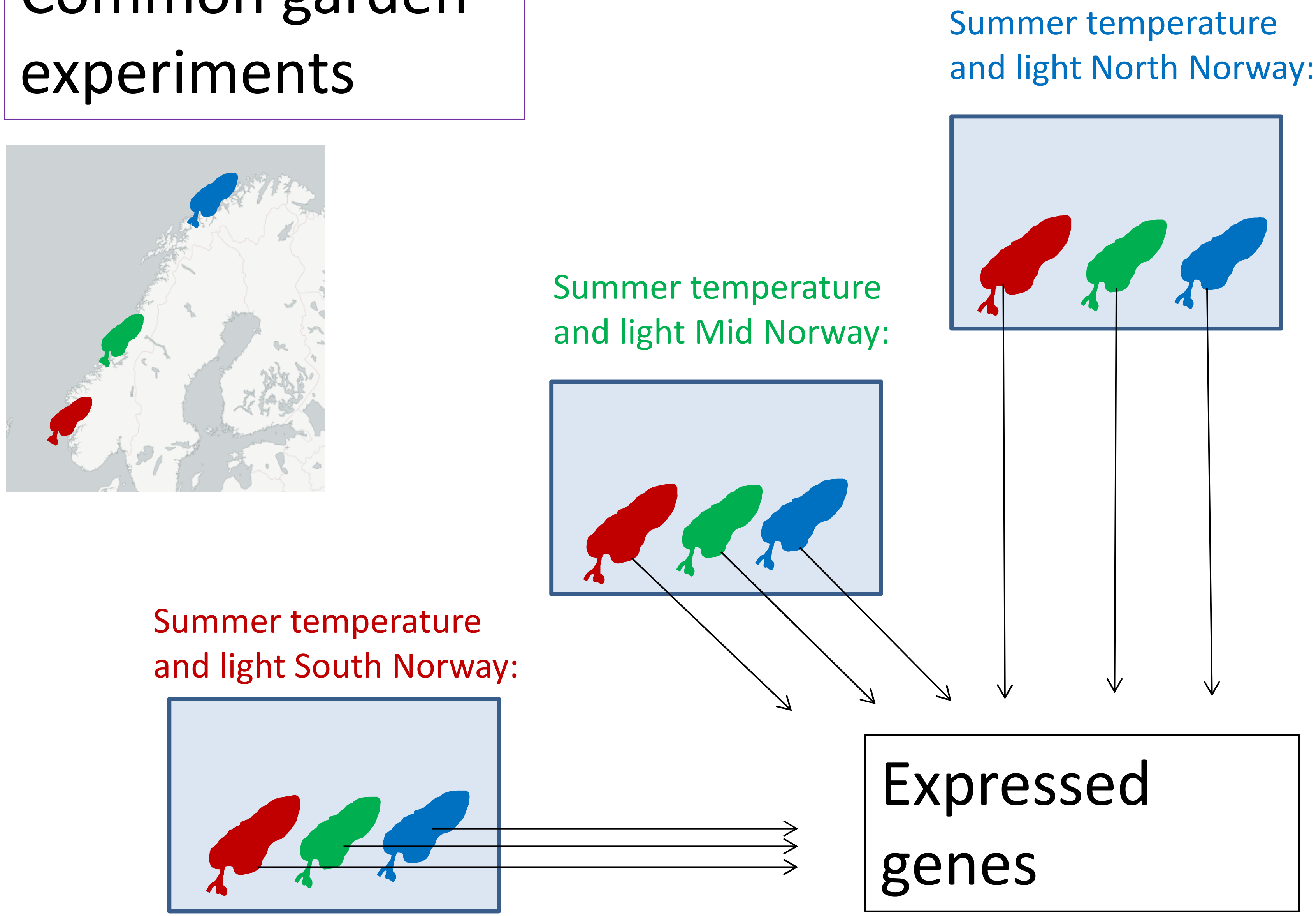
- Gene expression in cultivated sugar kelp at different depths and after depth change (experiment by Silje Forbod, Mid-Norway)

**Tasks:**

***T3.1:*** *Develop quality indicators (genetic markers) for cultivated macroalgae (linked to WP1 and WP2).*

This part is connected to scanning RNA libraries of **expressed genes** of *Saccharina latissima* cultivar strains from different latitudinal origins (South-West, Mid-, and North-Norway), and will be carried out by joint activity of WP1 and WP3. **Common garden experiments on juvenile crops from the cultivar strains** will be performed in climate rooms. The different cultivar strains will be exposed together to different environmental conditions, and the expressed gene profiles compared.

# Common garden experiments



Summer temperature and light North Norway:

Summer temperature and light Mid Norway:

Summer temperature and light South Norway:

Expressed genes

**Planned for spring 2018, using the lab facilities in Bergen**

***T3.2:*** *Determine the genetic diversity of target species at different spatial scales.*

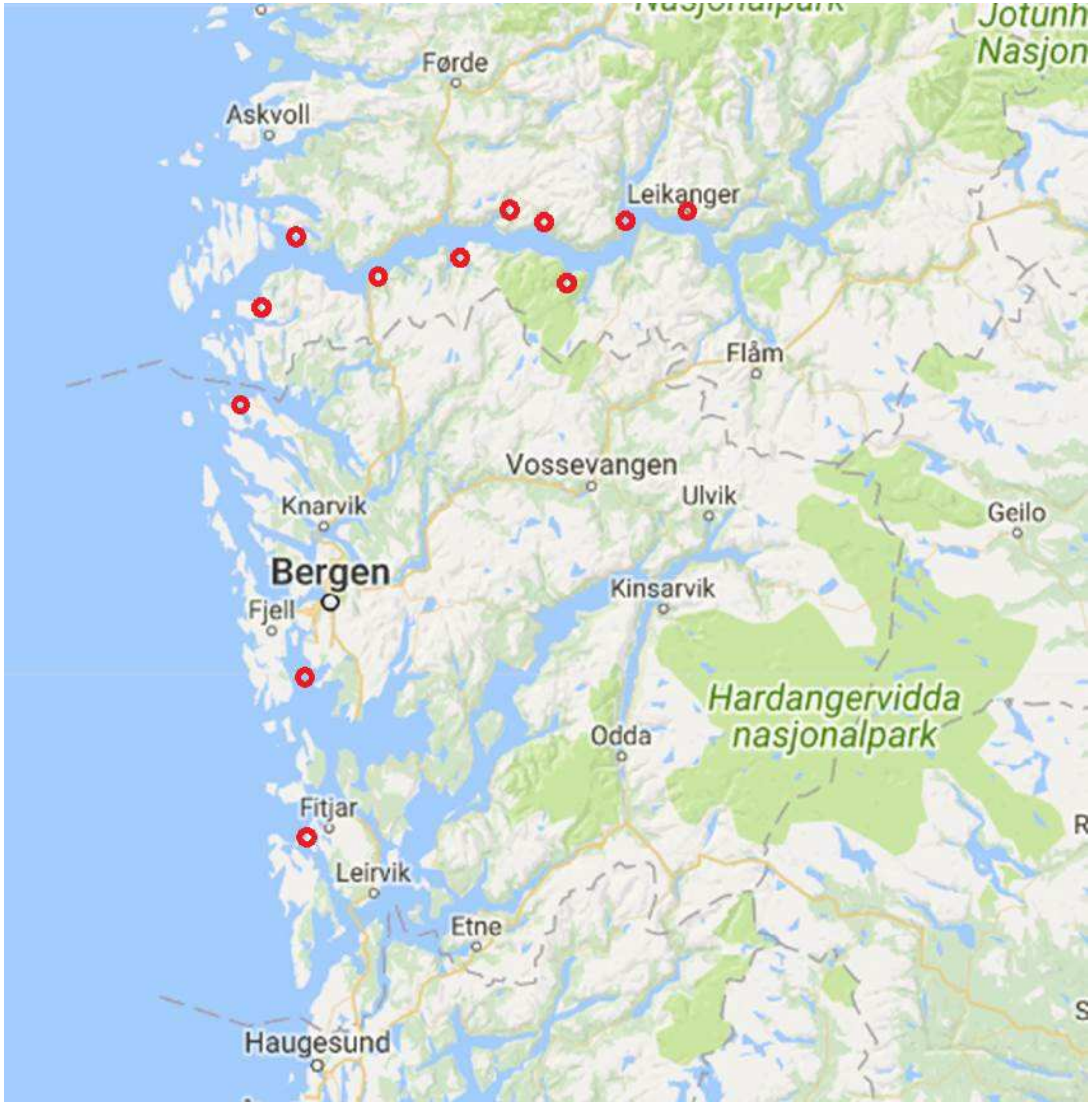
- We will use RADseq techniques to find **SNP markers** for sugar kelp. Samples from 11 sites along the Norwegian coast and 7 sites from a local sampling (Sognefjorden and area outside) are now under processing (up to 10 individuals per site)

- **Microsatellite** analysis (10 microsatellites) of sugar kelp from a number of fjord sites (20-30 individuals per site) and selected additional sites from the regional sampling, will be carried out by a master student next year (Tonje Næss, UiB)

SNP = Single-nucleotide polymorphism; variation in a single nucleotide that occurs at a specific position in the genome.

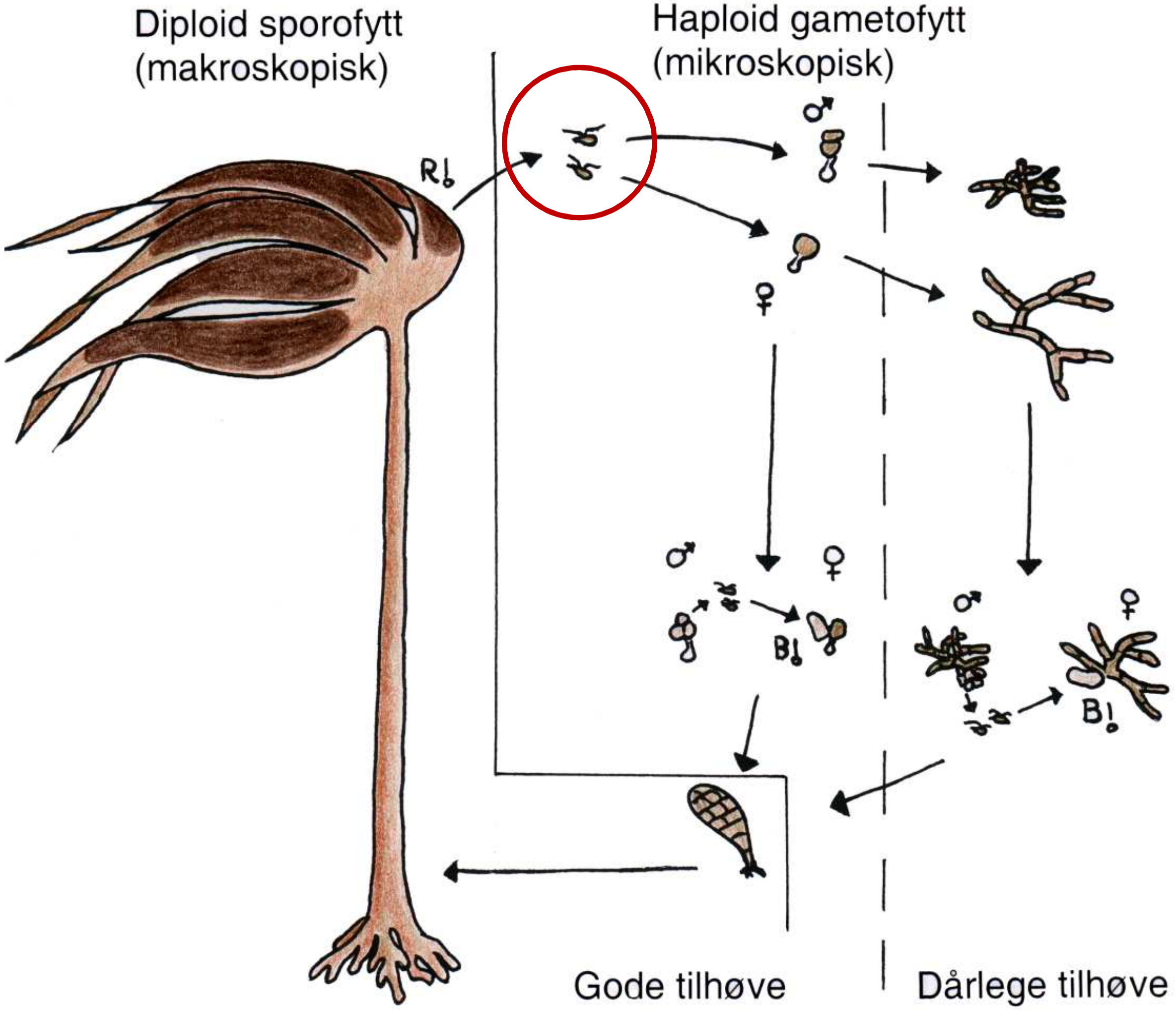
# Regional sample sites from cultivation companies and collaborators

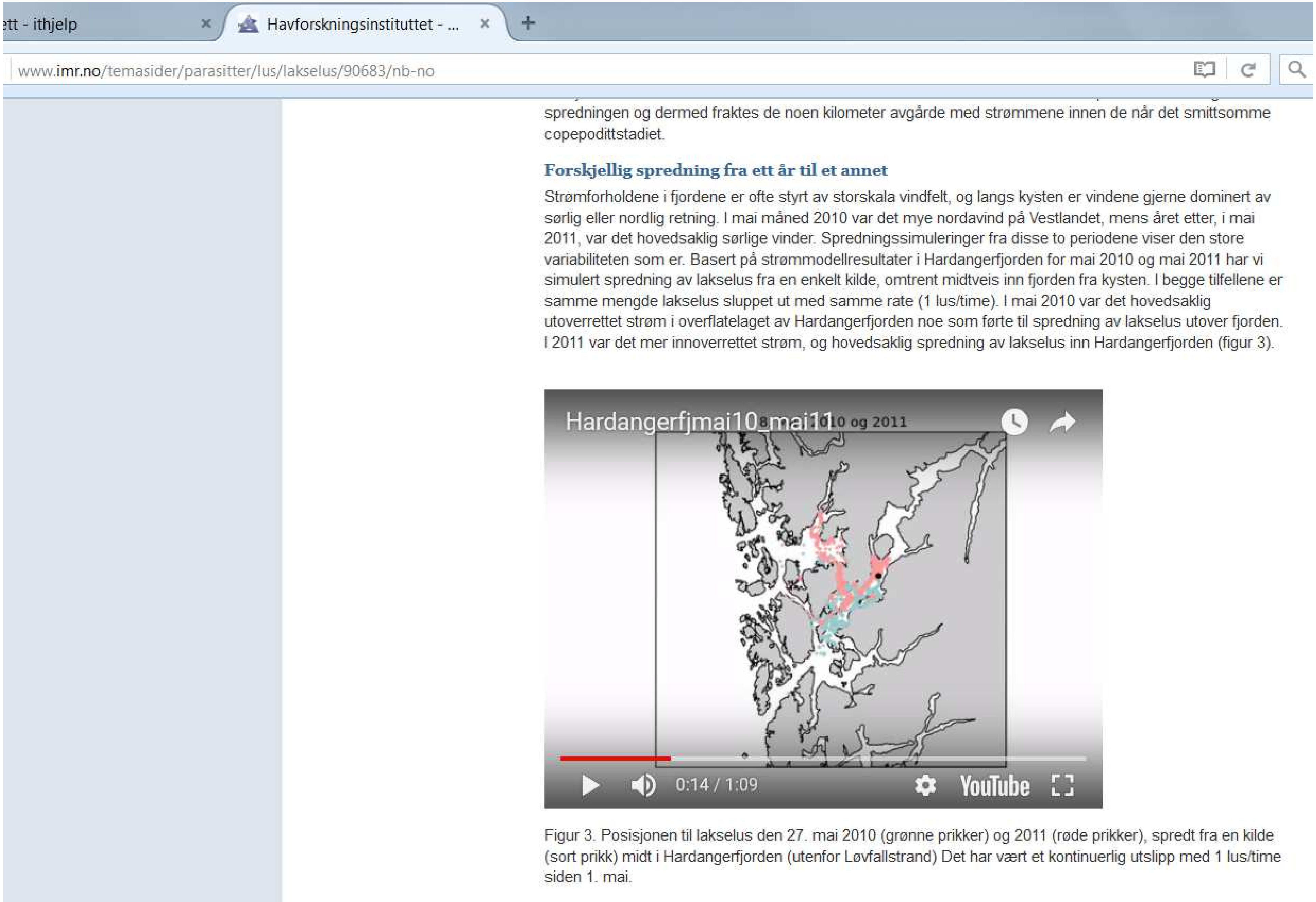
# Grid of fjord stations for microsatellite analysis



# Life cycle of kelp – dispersal by zoospores

*Laminaria hyperborea* (Gunnerus) Foslie - Stortare





spredningen og dermed fraktes de noen kilometer avgårde med strømmene innen de når det smittsomme copepodittstadiet.

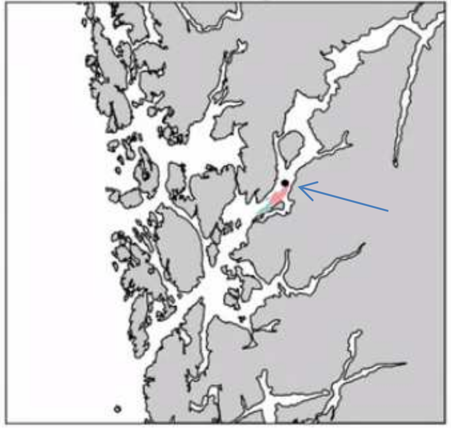
### Forskjellig spredning fra ett år til et annet

Strømforholdene i fjordene er ofte styrt av storskala vindfelt, og langs kysten er vindene gjerne dominert av sørlig eller nordlig retning. I mai måned 2010 var det mye nordavind på Vestlandet, mens året etter, i mai 2011, var det hovedsaklig sørlige vinder. Spredningssimuleringer fra disse to periodene viser den store variabiliteten som er. Basert på strømmodellresultater i Hardangerfjorden for mai 2010 og mai 2011 har vi simulert spredning av lakselus fra en enkelt kilde, omtrent midtveis inn fjorden fra kysten. I begge tilfellene er samme mengde lakselus sluppet ut med samme rate (1 lus/time). I mai 2010 var det hovedsaklig utoverrettet strøm i overflatelaget av Hardangerfjorden noe som førte til spredning av lakselus utover fjorden. I 2011 var det mer innoverrettet strøm, og hovedsaklig spredning av lakselus inn Hardangerfjorden (figur 3).

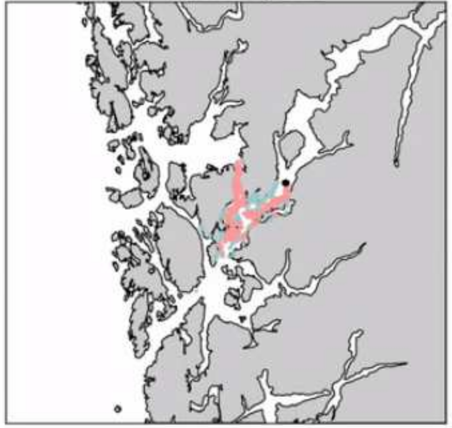
Figur 3. Posisjonen til lakselus den 27. mai 2010 (grønne prikker) og 2011 (røde prikker), spredt fra en kilde (sort prikk) midt i Hardangerfjorden (utenfor Løvfallstrand) Det har vært et kontinuerlig utslipp med 1 lus/time siden 1. mai.

# Model for spreading, one month (May) during 2010 (green dots) and 2011 (red dots)

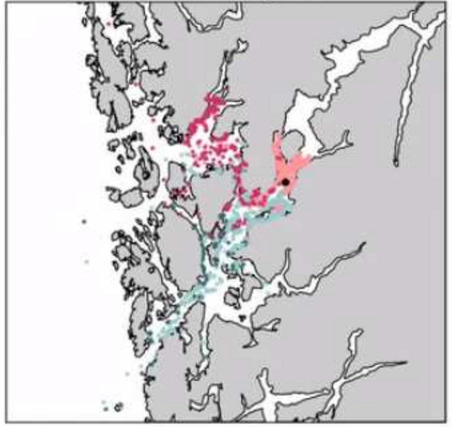
2. Mai, 2010 og 2011



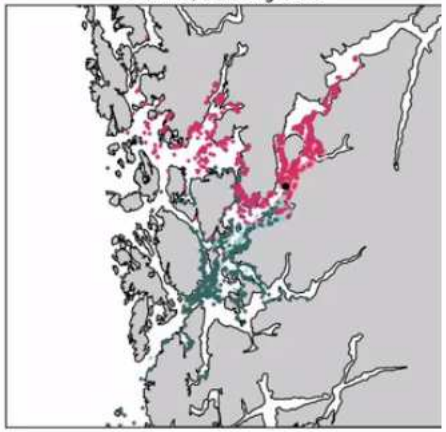
5. Mai, 2010 og 2011



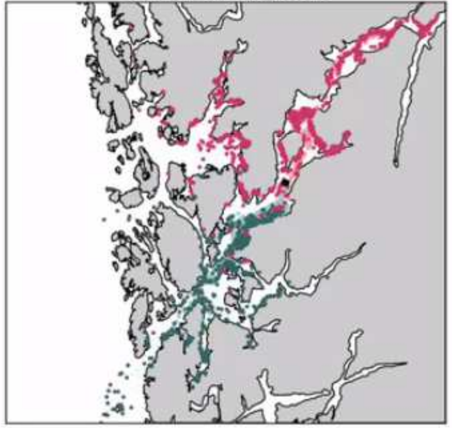
10. Mai, 2010 og 2011



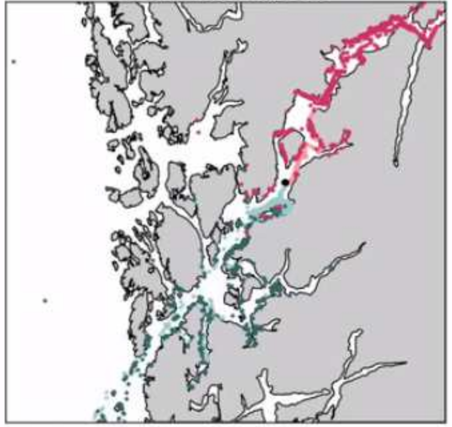
15. Mai, 2010 og 2011



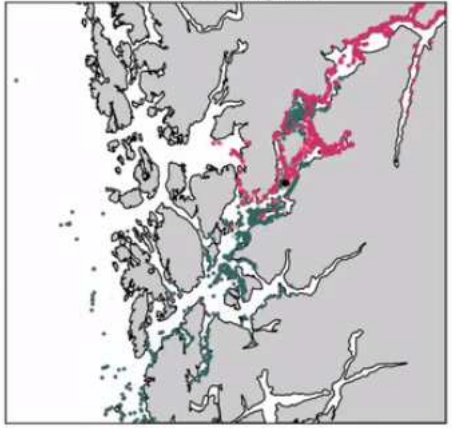
20. Mai, 2010 og 2011



25. Mai, 2010 og 2011



30. Mai, 2010 og 2011



***T3.3:*** *Draw up a strategy for domestication of selected species.*

This will be developed in cooperation with other partners (Professor Shaojun Pang, IOCAS, and Dr. Mei-Lie Tan and Hortimare). Outcrossing tests and the possibility of forming sterile crops of cultivar strains with favorable traits in cultivation will be looked into.

Professor  Pang has provided a short essay to introduce what they think would be a good strategy for the Macrosea project to perform domestication of, for selected species in European waters.

Professor Shaojun Pang, IOCAS:

In European waters, two critical points should be given special attention:
1) Choice of parental plants
2) Timing of harvest

For choice of parental plants, consecutive long-term targeted selection will lead to population with specialized agronomical features (both genetic and morphological). Once such a cultivar is put into use, the danger of release of its offspring into the surrounding environment will always exist. This strategy does not fit the current law and policy in your countries.

Search of natural population of which the offspring possess mostly the features that are pursued (morphology, chemical contents etc.) and use of the individuals from such a population as parental plants for generating offspring should be an ideal solution. To avoid the effect of selection, each year, the population of parental plants could be renewed such that the selection effect is minimized.

For timing of harvest, it would be always good to harvest the plants before they produces sorus. The danger of “contaminating” the natural population is minimized too.

***T3.4:*** *Identifying genes related to susceptibility pathogen defense.*

This task will be performed in close cooperation with Michele Stanley, SAMS, and involve a PhD student from SAMS.

OPEN

The ISME Journal (2017), 1–5
www.nature.com/ismej

## SHORT COMMUNICATION

# Phaeoviruses discovered in kelp (Laminariales)

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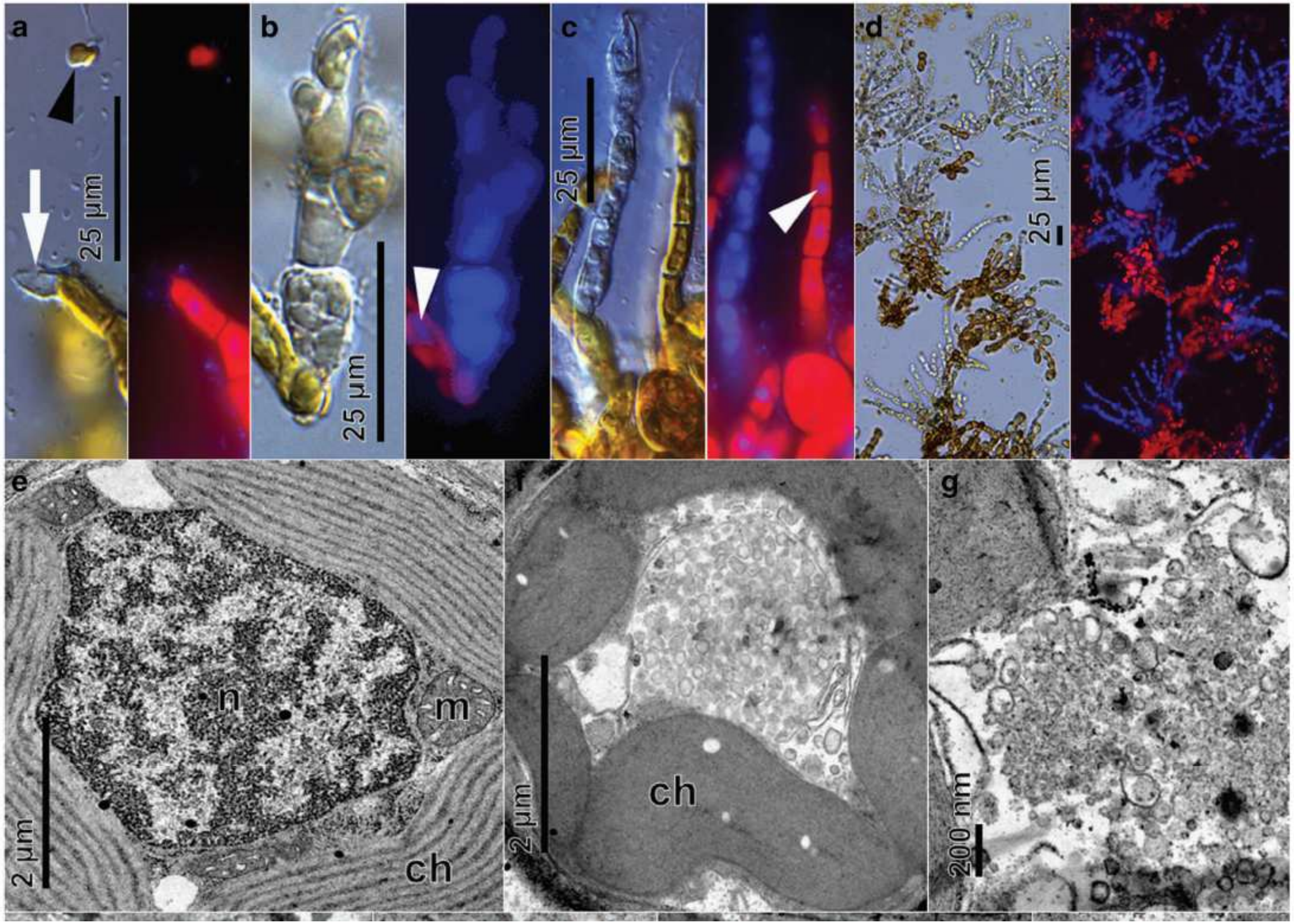
**Phaeoviruses are latent double-stranded DNA viruses that insert their genomes into those of their brown algal (Phaeophyceae) hosts. So far these viruses are known only from members of the Ectocarpales, which are small and short-lived macroalgae. Here we report molecular and morphological evidence for a new *Phaeovirus* cluster, referred to as sub-group C, infecting kelps (Laminariales) of the genera *Laminaria* and *Saccharina*, which are ecologically and commercially important seaweeds. Epifluorescence and TEM observations indicate that the *Laminaria digitata* Virus (LdigV), the type species of sub-group C, targets the host nucleus for its genome replication, followed by gradual degradation of the chloroplast and assembly of virions in the cytoplasm of both vegetative and reproductive cells. This study is the first to describe phaeoviruses in kelp. In the field, these viruses infected two thirds of their host populations; however, their biological impact remains unknown.**

*The ISME Journal* advance online publication, 25 July 2017; doi:10.1038/ismej.2017.130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