Single-cell population genomics of an invasive microeukaryote LIND RAPHAEL GOLLNISCH, DAG AHRÉN, KARIN RENGEFORS | LUND UNIVERSITY (SWEDEN), DEPARTMENT OF BIOLOGY UNIVERSITY

Single-cell approach to explore dispersal patterns of the invasive microalga Gonyostomum semen, and to discover the genetic basis of differentiation among populations in Europe and N. America.

Main objectives for single-cell population genomics:

• Bypass cultivation of clonal isolates through whole genome amplification



- Direct genotyping of a large number of SNPs de novo
- Optimize for large genome sizes (G. semen: approx. 100 Gb)

RADseq on single-cell amplified genomes

Producing reduced representation libraries of single-cell amplified genomes (SAGs) by combining Multiple Displacement Amplification (MDA) and RADseq (Restriction site Associated **DNA sequencing)** - Figure 1

The Challenge: random bias in MDA leads to non-uniform amplification and high allelic dropout

(1) **MDA**: Whole genome amplification with polymerase φ 29 and random primers; Alkaline lysis and DNA denaturation improve amplification efficiency (Figure 2)



<u>Figure 1:</u> MDA + RADseq for population genomics on SAGs

2 RADseq: Sample SNPs across the whole genome by sequencing DNA fragments flanking restriction sites (reduced complexity)

- Applicable for large-scale **population structure** analysis
- Large number of SNPs to analyse demography of populations

Improved MDA increases number of shared loci among SAGs compared to original amplification protocol (Figure 4).



<u>Figure 2:</u> MDA of single-cell genomes compared to extracted DNA (pos. control); neg. control without template

Population structure and dispersal direction

RADseq on DNA extracted from clonal cultures of dam G. semen revealed new patterns in the population structure and migration direction of the expanding population in Fenno-Scandinavia (Figure 5)

Gonyostomum semen



Blooms of *G. semen* (Raphidophyceae) disrupt lake food webs, decrease the recreational value and affect drinking water quality. A recent rapid spread across Europe is not observed to the same extent in North America. Its large genome size hypothetically promotes adaptation during invasion events.

Figure 5: Structure and directional migration pattern of G. semen populations in Fenno-Scandinavia (plot modified from divMlgrate)

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