**AB332/832 curriculum 2019** - final

**Introduction to molecular tools (Anna)**

# Kress WJ, Garcia-Robledo C, Uriarte M and Erickson DL (2015). DNA barcodes for ecology, evolution, and conservation. Trends in Ecology and Evolution 30: 25-35.

# Creer A, Deiner K, Frey S, Porazinska D, Taberlet P, Thomas WK, Potter C, Bik HM (2016). The ecologist’s field guide to sequence-based identification of biodiversity. Methods in Ecology and Evolution 7:1008-1018.

Joli N, Monier A, Logares R, Lovejoy C (2017). Seasonal patterns in Arctic prasinophytes and inferred ecology of *Bathycoccus* unveiled in an Arctic winter metagenome. ISME J 11: 1372-1385.

**Population genetics (Kim)**

Andrews AJ, Christiansen JS, Bha, S, Lynghammar A, Westgaard J-I, Pampoulie C, Præbel K (2019). Boreal marine fauna from the Barents Sea disperse to Arctic Northeast Greenland. Scientific Reports 9: 5799.

Madsen ML, Nelson JR, Fevolden S-E, Christiansen JS, Præbel K (2016). Population genetic analysis of Euro-Arctic polar cod *Boreogadus saida* suggests fjord and oceanic structuring. Polar Biology 39: 969-980.

Selkoe KA, D’Aloia C, Crandall ED, Iacchei M, Liggins L, Puritz JB, Heyden S, Toonen RJ (2016). A decade of seascape genetics: contributions to basic and applied marine connectivity. Mar Ecol Prog Series 554: 1-19.

**RNA (Anna)**

Caron DA, Alexander H, Allen AE, Archibald JM, Armbrust EV *et al* (2016). Probing the evolution, ecology and physiology of marine protists using transcriptomics. Nature Reviews Microbiology 15: 6-20.

Meshram AR, Vader A, Kristiansen S, Gabrielsen TM (2017). Microbial eukaryotes in an Arctic under-ice spring bloom north of Svalbard. Frontiers in Microbiology 8: 1099.

Nguyen D, Maranger R, Balague V, Coll-Llado M, Lovejoy C, Pedros-Alio C (2015). Winter diversity and expression of proteorhodopsin genes in a polar ocean. ISME J 9: 1835-1845.

Vader A, Laughinghouse D, Griffiths C, Jakobsen KS, Gabrielsen TM. Expression of proton-pumping rhodopsins by microbial eukaryotes in a high-Arctic fjord (2018). Env Microbiol 20:90-902.

**Molecular tools in prey detection seminar (Tove)**

King RA, Read DS, Traugott M, Symondson WOC (2008). Molecular analysis of predation: a review of best practice for DNA-based approaches. Molecular Ecology 17: 947–963.

Pompanon F, Deagle BE, Symondson WOC, Brown DS, Jarman SN, Taberlet P (2012). Who is eating what: diet assessment using next generation sequencing. Molecular Ecology 21: 1931-1950.

Tverin M, Esparza-Salas R, Stromberg A, Tang P, Kokkonen I, Herrero A et al (2019). Complementary methods assessing short and long-term prey of a marine top predator–Application to the grey seal-fishery conflict in the Baltic Sea. PLoSONE 14: e0208694.

**Molecular phylogenetics (Tove)**

San Mauro D and Agorreta A (2010). Molecular systematics: a synthesis of the common

methods and the state of knowledge. Cellular and Molecular Biology Letters 15:

311-341.

Pyron RA (2015). Post-molecular systematics and the structure of phylogenetics. TREE 30: 384-389.

Yang Z and Rannala B (2012). Molecular phylogenetics: principles and practice. Nature reviews, genetics 13:303-314.

**NGS analyses (Magda, Ramiro)**

Bik HM, Porazinska DL, Creer S, Caporaso JG, Knight R, Thomas WK (2012). Sequencing our way towards understanding global eukaryotic biodiversity. Trends in Ecology and Evolution. 27: 233–243.

Pedros-Alio C, Acinas SG, Logares R, Massana R (2018). Marine microbial diversity as seen by high-throughput sequencing. In *Microbial Ecology of the Oceans*. Third edition 2: 47-97. Gasol JM, Kirchman DL (eds). John Wiley & Sons Inc.

**Further reading (background or in depth information):**

*Lab project related*

Chambouvet A, Morin P, Marie D and Guillou L (2008). Control of toxic marine dinoflagellate

blooms by serial parasitic killers. Science 322: 1254-1257.

Paulsen ML, Dore H, Garczarek L, Seuthe L, Muller O, Sandaa R-A, Bratbak G and Larsen A (2016). *Synechococcus* in the Atlantic Gateway to the Arctic Ocean. Frontiers in Marine Science 3:191.

*Relevant online resources (labprotocols and applications):*

<https://www.qiagen.com/no/resources/molecular-biology-methods/ngs/>

<https://www.qiagen.com/no/resources/molecular-biology-methods/dna/>

<https://www.qiagen.com/no/resources/molecular-biology-methods/pcr/>

<https://www.qiagen.com/no/resources/molecular-biology-methods/rna/>

*Relevant online resources (RNA):*

http://en.wikipedia.org/wiki/RNA

http://en.wikipedia.org/wiki/Messenger\_RNA

<http://en.wikipedia.org/wiki/Ribosomal_RNA>

*Relevant online resources (NGS):*

http://assets.geneious.com/documentation/geneious/GeneiousManual.pdf

http://qiime.org/

<http://www.mothur.org/wiki/Main_Page>

*The Arctic marine ecosystem*

Sakshaug et al (2009). Ecosystem Barents Sea. Tapir forlag, Norge.

Hop H et al (2002). The marine ecosystem of Kongsfjorden, Svalbard. Polar Research 21: 167-208.

Lovejoy C (2014). Changing views of Arctic protists (marine microbial eukaryotes) in a changing Arctic. Acta protozoologica 53: 91-100.

Berge J et al (2015). In the dark: A review of ecosystem processes during the Arctic polar night. Progress in oceanography 139: 258-271.

# *Barcoding*

Bucklin A, Steinke D, Blanco-Bercial L (2011). DNA barcoding of marine metazoa. Ann Rev Mar Sci 471-508.

# Cristescu ME (2014). From barcoding single individuals to metabarcoding biological communities: towards an integrative approach to the study of global biodiversity. Trends in Ecology and Evolution. Vol. 29 No. 10.

*NGS*

Buermans HPJ, den Dunnen JT (2014). Next generation sequencing technology: advances and applications. Biochimica et Biophysica Acta 1842: 1932-1941.

Comeau AM, Li WKW, Tremblay J-E, Carmack EC, Lovejoy C (2011). Arctic Ocean microbial community structure before and after the 2007 record sea ice minimum. PLOS One 6: e27492.

*qPCR*

Bustin et al (2009). The MIQE Guidelines: Minimum information for publication of quantitative real time PCR experiments. Clinical Chemistry 55:4.

*RNA*

Stoeck, T, Zuendorf A, Breiner H-W, Behnke A (2007). A molecular approach to identify active microbes in environmental eukaryote clone libraries. Microbial Ecology 53: 328-339.

Lin S, Zhang H, Zhuang Y, Tran B, John Gill J (2010). Spliced leader–based metatranscriptomic analyses lead to recognition of hidden genomic features in dinoflagellates. PNAS 107: 20033–20038.