# ECOGEN - Ecosystem change and species persistence over time: a genome-based approach

**Main goal**
Develop high taxonomic resolution ancient environmental DNA methods in order to evaluate how drivers of change (human, climate, biota) affect species persistence and ecosystem tipping points in arctic-alpine biomes

**Subgoals**
1) Improve methods for full genome analyses of environmental DNA
2) Compile palaeo data to plan a balanced design of climatic and human impacts
3) Do full genome analyses of lake cores to obtain information on past presence and abundance of vascular plant species and key herbivores
4) Identify biotic drivers and disentangle their effects from human land use and climate change on ecosystem resilience and ecosystem services
5) Estimate species persistence across periods of changes and identify factors causing extinction
6) Provide methods and knowledge to inform species conservation and ecosystem management

**Summary – see announcement**

**Project tasks**
We are seeking a research fellow that will join a cross-disciplinary team (ecology, palaeoecology, genetics, archaeology, geology, niche modelling) working in two geographical regions (Norway and the Alps). We will expand our knowledge on past vascular plant and animal diversity and abundance at a taxonomic depth that has not been possible until now due to methodological limitations. We expect to disentangle the effects of past human land-use (hunting, husbandry, burning, agriculture), climate change, and biota on species and ecosystem changes and thereby be able to answer questions central to our understanding of our biological resources, such as the level of persistence of species and resilience of ecosystems to environmental drivers, the extinction risk of species, and the capacity of mountain landscape to buffer against these changes. By identifying drivers of shifts in ecosystem services through time, we may inform future management.

The successful candidate will work on development of improved technology. The most recent applications of ancient plant DNA analyses are largely developed by our team (Taberlet *et al.* 2007, Sønstebø *et al.* 2010, Yoccoz *et al.* 2012, Willerslev *et al.* 2014). For vascular plants, the 50-100 base pair long P6 loop region of the chloroplast trnL (UAA) intron is used in a PCR based method (Taberlet *et al.* 2007), which allows identification of all plant families, most genera (>75%), and one third of the species (Sønstebø *et al.* 2010). When applied to modern lake sediments, half of the species present within 2 m of lakes were detected (Alsos *et al.* In prep.). Our recent study of an 8500 year old core from Svalbard show that the method detect all except two genera identified in a macrofossil study from the same lake (Alsos *et al.* 2015). Overall, 1.2 times more taxa of vascular plants were identified with ancient DNA than macrofossils, and the number of taxa identified per sample was 2.7 times higher for the former. Thus, DNA analyses of Holocene lake sediment can reveal the presence of rare taxa and thereby allow for a better estimation of species persistence (Fig. 1). Further, the method is now resource-efficient and repeatable, and it can be extended to any group of organisms, given that a DNA reference library and adequate primers are developed . It also allows for semi-quantitative interpretations based on the number of PCR repeats where taxa are identified (Pansu *et al.* 2015). We will do minor optimization of these applications and analyse all samples for vascular plants and key herbivores.

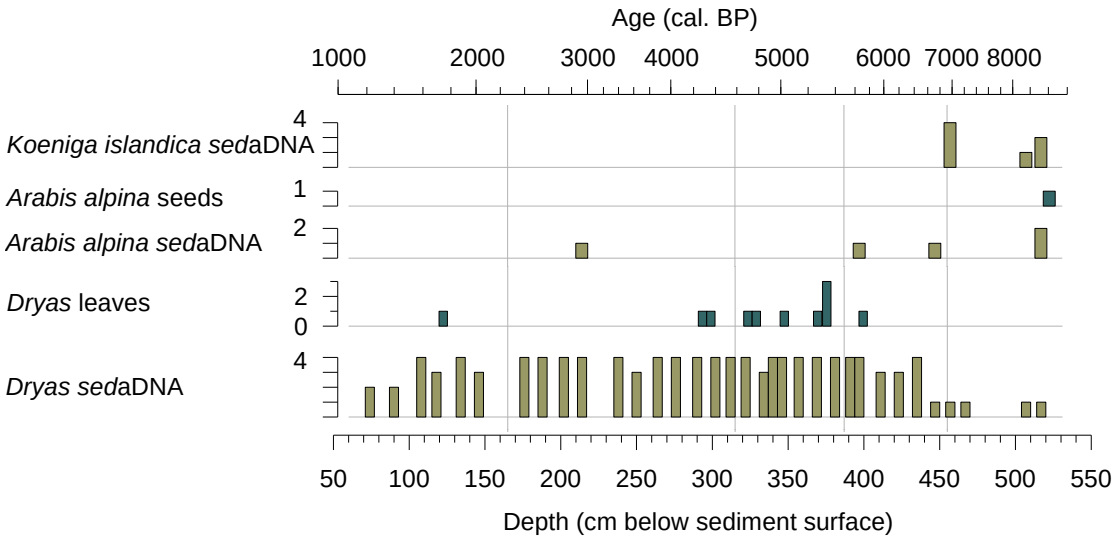


Fig. 2. Taxa detected by macrofossil (numbers of fragments) and ancient sedimentary DNA (number of PCR repeats where taxa were discovered). *Koenigia islandica* was only detected by sediment ancient DNA (sedaDNA), whereas *Arabis alpina* and *Dryas octopetala*, were detected more frequent in sedaDNA. Note that while macrofossil indicate scattered occurrence of species through time, ancient DNA shows more clearly that they actually did persist (Alsos *et al.* 2015 ).

The short fragments of the P6 loop do however limit the taxonomic information. In addition, as many sequence errors generally are produced during PCR, it is necessary to use very stringent filtering conditions reducing the amount of usable data (Coissac *et al.* 2012). To overcome these problems, we will do shotgun sequencing of the DNA extracts from lake sediments and thus avoiding specific PCR. After being corrected for deamination biases (Jónsson *et al.* 2013), the resulting sequences will be mapped against the new taxonomic reference library composed of whole plastid genomes and nuclear ribosomal DNA (see details in Taberlet *et al.* 2012). A whole genome reference library is currently being built using a shotgun approach for the alpine flora of the Alps (PhyloAlps, 1500 species) and Norway (NorBOL, 2000 species http://www.norbol.org/). The new reference libraries will give low coverage for single copy nuclear genes but sufficient coverage for plastid and rDNA which are present in many copies per cell. The new genomic reference library will thus also include the classic barcoding markers (CBOL *et al.* 2009) and the P6 loop. Thus, while identification of taxa in the only attempt of shotgun analyses of ancient sediment samples so far was strongly limited by data available in reference libraries (Smith *et al.* 2015), our complete reference libraries may allow 100% resolution at species level for vascular plants and key herbivores. In addition, our new shotgun applications will also improve the quantitative interpretation of past flora and fauna as it avoids the PCR step.

## References


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