Workshop - Incorporating adaptation and genomic studies in ITEX
9am-10:30am April 10th

In attendance: Cassandra Elphinstone, Loren Rieseberg, Marco Todesco, Ned Fletcher, Liz Stunz, Anne Bjorkman, Robert Hollister, Kai Sattler, Karin, Matteo, Teagan Maclachlan

Rough meeting notes:

Metabarcoding mosses

Hypothesis: Bud development the year before in species with larger genomes/ploidy
- Pollen size, cell size, petal size

GWAS - Correlating genomes size, repeat content, ploidy

Common gardens maintaining DNA methylation

Isolation by distance with elevation

Warming to control comparisons with north south patterns

Phenology - transcriptome - Michael Moody

mRNA methylation - anyone doing this?

Plasticity in Arctic plants - evolve reproductive isolation quickly also some converting to dioecious (Silene)

Ancient Variation - selfers/inversions might be less important - ages of the haplotypes used to colonize the Arctic

Come up with a list of where samples are
- Gothenburg maybe
- List can be used for future funding

Long term pressure vs extreme events- plastic vs slow change

GEA analyses - genetic architecture of adaptation without needing the phenotypes

To do
List of all Arctic alpine species with reference genomes

Compile list on ongoing Arctic genomics studies

Slack channel - ongoing conversation to continue thinking of questions and discuss new and ongoing projects

Funding - Marco and Loren have 100k matching funding on a national grant opportunity

Canadian Biogenomes project - ask Marco about asking ITEX