

GCTAC Minutes November 30th, 2007

GCTAC Members Attending: Sally Aitken, Brian Barber, Dave Kolotelo, Tongli Wang, Jack Woods, Alvin Yanchuk

GCTAC Regrets: Andreas Hamann, Scott Green, Greg O'Neill, Alex Woods

Guests: Christine Chourmouzis, Sierra Curtis-McLane; Amanda de la Torre; Diane Douglas, Karolyn Keir, John King, Don Pigott, Pia Smets

Sally introduced Amanda de la Torre who is a new graduate student at the Centre for Forest Conservation Genetics <http://www.genetics.forestry.ubc.ca/cfcg/>. More information on Amanda's project will be forthcoming.

GCTAC Plan

A brief overview of the last FGC meeting and their acceptance of the GCTAC plan was presented. The only outstanding issue was the location for the recommended FTE. Brian outlined discussions between himself and Alvin (as the Ministry representatives to resolve the "stalemate") and their ultimate decision for the position to be located within Research Branch. This recommendation will then go to FGC which will forward it to Jim Snetsinger for his endorsement.

The Research Branch position will be a Genetic Conservation specialist and not a research Scientist position. This position would have a reporting relationship similar to the Pest Management research position (Ward Strong) and PMTAC. An annual workplan and budget would be produced and reviewed at GCTAC for approval.

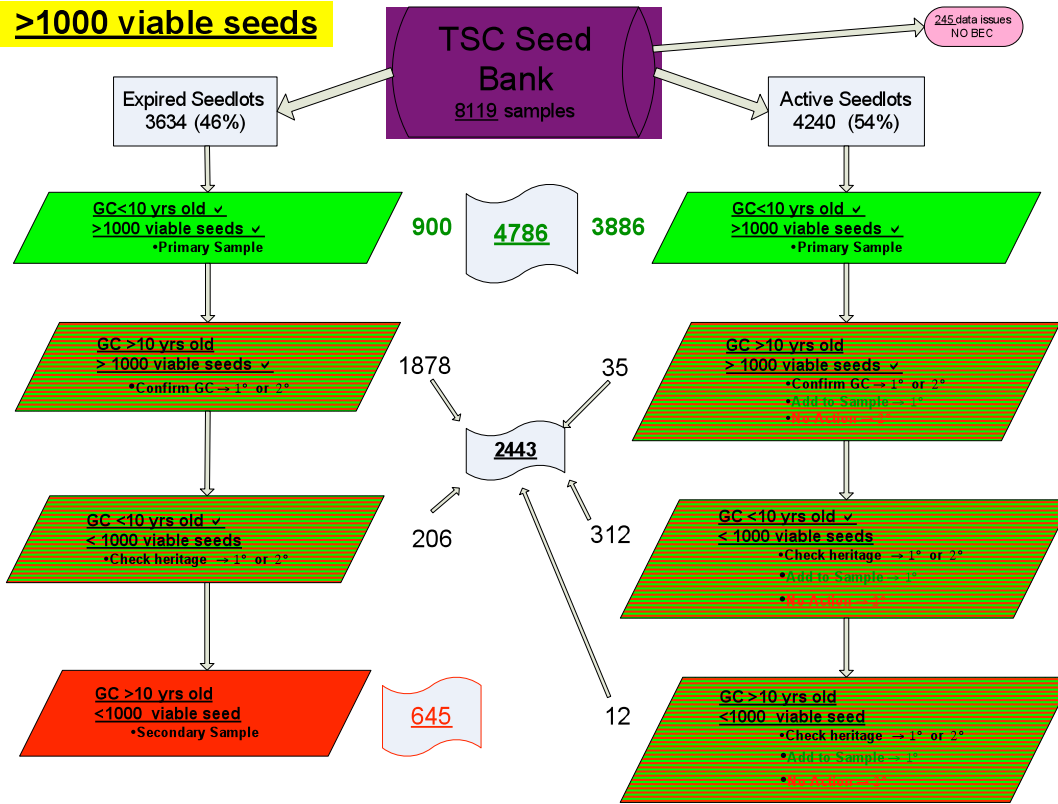
Ex-Situ Seed Bank

Dave presented an overview of the seed bank at the TSC and a rough management plan to ensure that the seed bank provides a representative sample of seed for all species * BEC combinations. In the past and in Andreas' initial analysis, the seed bank was thought to have value only when there were gaps for in-situ protection. With climate change, the fate of parks etc., is not certain and the seed bank should be the source of insurance (germplasm for regeneration) for all species and species subdivisions (BEC zones providing a good approximation across a common platform for all species).

An indication of number of samples per species and BEC is not sufficient and an indication of viable seeds seems to be the appropriate variable. Estimates of viable seeds are based on the product of grams of seed * seeds per gram * germinability estimate. The most uncertain element is the germinability and I have subdivided the samples based on whether there has been a germination test within the last decade. Another important management element is whether the seedlots from which samples are derived are active (have a current balance) or expired (no longer have seed in the inventory). The distinction is important as there is always the ability to augment existing samples from active seedlots, but this is no longer possible with expired seedlots.

The wealth of the seed bank was presented in terms of the number of samples with estimates of 1000 and 5000 viable seeds. There was general consensus that 1000 viable seeds was a reasonable level to move forward with for planning and that 5 samples per species*BEC zone combination is a good starting point for determining which cells are gaps. For those not at the meeting I'm enclosing a couple of images from the handouts indicating the status of the seed bank based on the 1000 viable seed threshold level. The figures are an ex-situ starting point for inclusion in the UBC cataloguing effort. There are still some data issues to resolve, but it provides a snapshot to work for moving forward. I will be producing a more formal plan for the seed bank and this will be distributed to GCTAC sometime before the end of the fiscal.

>1000 viable seeds



Sample Distribution {>1000 viable seed; GC estimate <10 years old}

	AT	BG	BWBS	CDF	CWH	ESSF	ICH	IDF	MH	MS	PP	SBS	SBPS	SWB	SUM	%Tot
Alnucri	6								3			1			10	0.2%
AT			2					2				3		1	8	0.2%
BA	1		1		71	5	5	1	22						106	2.2%
BG				3	5		5								13	0.3%
BL	8		1		1	44	39	2	5	2		23	1		126	2.6%
BN	2				3										5	0.1%
CW	2			11	140	17	92	6	9		1	2			280	5.9%
DG					1										1	0.0%
DR				2	13				2						17	0.4%
EP			2		1	1	8	3				7			22	0.5%
FDC	15			55	113	1		8	9			1			202	4.2%
FDI	2				3	33	203	156		41	8	61	11		518	10.8%
HM	1				18	5	4		8						36	0.8%
HW	6			3	174	10	47		26						266	5.6%
LT			2												2	0.0%
LW	1	1				20	73	26	1	39	1				162	3.4%
PLC	3			3	24	2	17	2				2			53	1.1%
PLI	14	1	66		9	243	245	232		229		463	74	2	1578	33.0%
PW				3	21	15	39	2	6	1			1		88	1.8%
PY	1	7					30	100		2	34				174	3.6%
SB			4									3			7	0.1%
SS	3			6	67								2		78	1.6%
SX	30	2	55		20	299	156	46	1	77	1	269	9		965	20.2%
SXS	1				22	3	16		1						43	0.9%
YC	1				13	1			11						26	0.5%
SUM	97	11	133	86	719	699	979	586	104	391	45	835	98	3	4786	100%
%TOT	2%	0%	3%	2%	15%	15%	20%	12%	2%	8%	1%	17%	2%	0%	100%	

indicates a species *BEC combination with at least 5 samples

indicates a new species or BEC by going from 5000 to 1000 viable seeds

Inter-Situ Resources

This is the third component of the UBC cataloguing project. Alvin spoke to some of the issues regarding the appropriate data and whether both provenance and progeny tests will be included within this framework. A template has been prepared by Greg, Sally and Alvin to capture the relevant data. It was agreed that the inter-situ data would be supplied by March 31, 2008 or the cataloguing report from UBC would be completed and published without the inter-situ data. The inter-situ and ex-situ data are also feeding into a national initiative called CAFGRIS that will be a geospatial catalogue of genetic conservation 'resources' across Canada.

Catalogue Overview

Currently chapter 1 dealing with all 49 (maybe 50 now with *Juniperus maritima*) BC tree species has been completed by Christine and Sally is reviewing it and it will soon be available for GCTAC comment. Chapter 2 deals with the 'commercial' species on an SPU basis and this is where the inter-situ information would be inputted. There is a need for this catalogue to be completed and reviewed to provide a framework for the genetic conservation specialist.

CONFORGEN

CONFORGEN is a pan-Canadian program for the conservation of forest genetic resources. Initiated by Judy Loo and others from the CFS in Fredericton, CONFORGEN was initially launched at a forum in Charlottetown, PEI in July of 2006. CONFORGEN is led by a Steering Committee (Jack Woods is BC's member), with support from a Technical Committee (Sally Aitken and Alvin Yanchuk participate from BC). CONFORGEN is envisioned as a collaborative and cooperative organization with federal and provincial governments, First Nations, industry, and academia represented. Objectives include:

- to promote conservation of genetic resources of native tree species
- to define pan-Canadian science-based guidelines for conservation of genetic resources of native tree species in all aspects of sustainable management
- to monitor genetic resources of native tree species and consistently report on Canada's national and international commitments
- to identify emerging issues and highlight research priorities

CONFORGEN is still in the start-up phase and has sought financial support from the Canadian Council of Forest Ministers. It is envisioned that CONFORGEN will coordinate data collection and the presentation of data through CAFGRIS, as CFS-led conservation database and system for presenting conservation information.

Blister Rust Resistance in western White pine / Whitebark pine provenance testing +

John King provided an overview of the blister rust program for western white pine and potential implications for whitebark pine (Pa). Don discussed collections available to date for provenance testing (17 + Sierras sources) as well as some potential sites that have good accessibility. There was general agreement to continue to pursue Pa cone crops to fill in existing gaps in BC, possibly trade seed with Alberta and obtain seed from the US for the provenance trial. It is expected that **at least** one more year of collecting cones is required before we can move forward with the trial. The expectation is that John and Don will put together a provenance test plan for Pa to be distributed to GCTAC for comment. It was felt that this test is in a grey area between GCTAC and genecology research within Research Branch. There was general support for Pa testing, but there was not much support for a full blown breeding or a resistance screening program.

Chairs peanut gallery comments: The question of how we move forward with whitebark is still unclear and although Whistler was a good meeting I'm not sure there is general agreement on what we do next. Here is my take to invoke further discussion:

Assumption: Moving forward aggressively with whitebark pine will reduce resources available to other programs. I'm not sure I believe this as there are lots of opportunities to obtain funding for whitebark pine outside FIA/MFR and there are some dedicated individuals interested in working on the problem (i.e Brendan Wilson who has already collected cones from putatively resistant individuals / Elizabeth Campbell FSP

proposal). I think this is a good example of the general need for genetic conservation co-ordination (i.e. new RB position) so that we keep moving forward and involve all interested parties. The first step in this process is to have a plan on the table to discuss.

CFCG Study Reports/Updates

Sierra Curtis McLane

Whitebark pine project update

Sierra Curtis-McLane's progress report detailed the status of her current project, which is to establish whitebark pine common gardens both within and northwest of the current species range in order to ground truth species distribution models that predict the need for whitebark pine (*Pinus albicaulis*) to migrate hundreds of kilometers north under climate change scenarios. In the summer and fall of 2007, cones were collected from seven populations and nine common gardens were established along a latitudinal gradient between Whistler and Tatshenshini-Alsek Provincial Park. Further planting will be done using stratified and scarified seeds in June of 2008, and monitoring for germination and survival will be performed during the summers of 2008 and 2009. Sierra will be spending the spring of 2008 continuing to analyze her lodgepole pine provenance trial tree cores, as well as studying for her comprehensive exam.

Karolyn Keir

Pacific Dogwood Project Update

To better understand how genetic variation is partitioned through the native range of Pacific dogwood, *Cornus nuttallii*, I am employing two molecular markers, microsatellites and chloroplast sequence data.

As of November 30, 2007, I have completed sampling and successfully isolated DNA from all 606 samples. I am currently in the process of genotyping these 606 individuals (30 individuals per population for 20 populations throughout the native range) with 5 microsatellite markers. Approximately 65% of all microsatellite genotyping has been done and I expect to finish by the end of January 2008.

Preliminary sequence data of 6 different chloroplast regions has shown evidence of variation at the population level. Ten individuals per population for all 20 populations will be sequenced at 5 of the 7 regions.

In addition to laboratory work, a common garden has been established. In January 2007, 5407 seeds from 11 populations were planted in the greenhouse at UBC. Despite extensive rat damage sustained while the plants were being held in the greenhouse, 940 seedlings, in 12 blocks, were out-planted in Totem field in June 2007. Data collected from this common garden will not be included with in my thesis work, but will be combined with molecular data at a later date.

Pia Smets

Population response to temperature (lodgepole pine and interior spruce).

Compared to the former (BIOCAP) experiment, this extension using more extreme climates, drought treatments, and root competition resulted in two major findings: water became the most important experimental factor, and response curves to temperature were flattened. Response of populations relative to each other was consistent with former growth chamber experiments for pine. Consistency with field response curves still needs to be evaluated, especially for interior spruce. A more thorough analysis awaits the completion of the second replication in September of 2008.

Tongli Wang

Update on Climate BC / universal response function

Tongli, Greg and Sally have developed a novel approach called "universal response function" (URF) to predict the response of populations to climate change based on lodgepole pine provenance trial data. The URF integrates both ecological and genetic effects of climate variables on the performance of populations. As the URF makes full use of provenance data, sample size could be substantially reduced without sacrificing the predictive power. This feature will make less comprehensive provenance tests in other species useful for climate change studies and make future provenance tests more affordable. Meanwhile, the URF allows us to determine and compare the climatic and genetic effects on the performance of populations. The URF can be used to predict the performance of any population growing under any climatic conditions in BC, thus can be used as a convenient tool for facilitated migration decisions in changing climate.