Роль современных популяционно-геномных и молекулярно-экологических исследований для защиты леса в условиях глобального изменения климата и для селекции устойчивых древесных пород

Konstantin Krutovsky

Department of Forest Genetics and Forest Tree Breeding

Büsgen-Institute

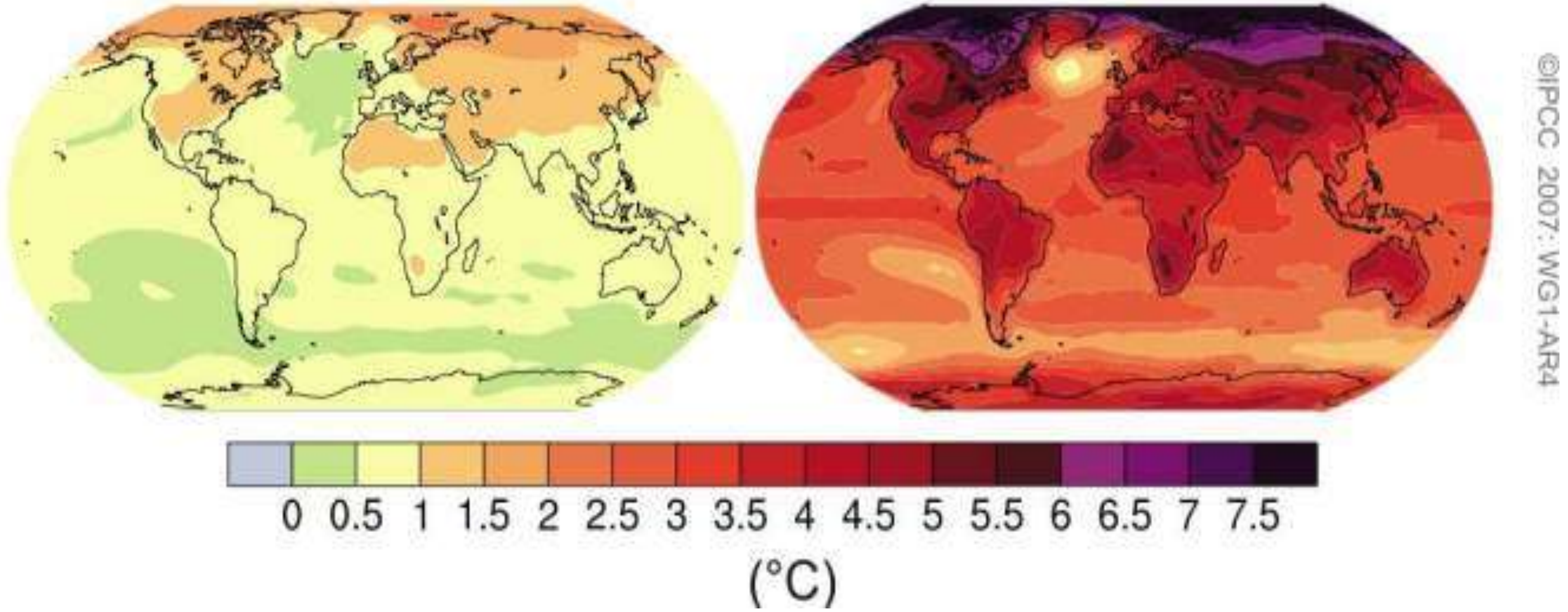
Georg-August-University of Göttingen

Germany

A warmer, future Earth

2020 - 2029

2090 - 2099



Anticipated temperature increase ranges from

2 to 11.5 °C for “full range”, or

3.1 to 7.2 °C for “best estimate” (midpoint)

(Intergovernmental Panel on Climate Change, 2007)

What did we learn from the past?

20th-Century global warming of roughly 0.6°C has been already affecting many forests and has already caused :

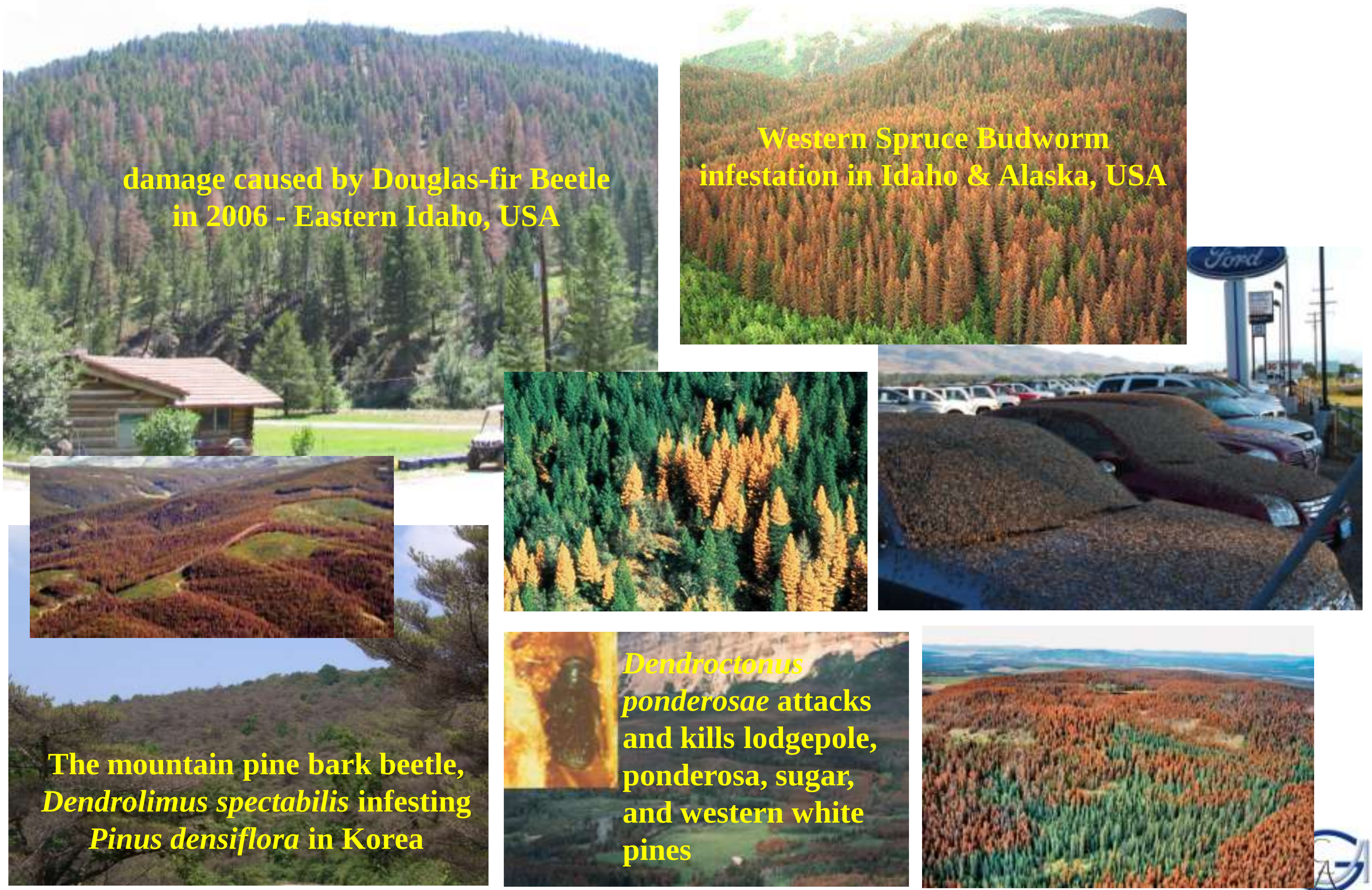
- changing phenology
- changing patterns of tree growth & mortality

- severe droughts that promoted pest and disease outbreaks
- shifts in species distributions
- shifts in forest tree ranges, particularly at higher latitudes and towards the poles
- shifts in seasonality of ecosystem processes

(e.g., Parmesan 2006 Ann Rev Eco Evo Sys 37:637)

What did we learn from the past?

Severe droughts promote pest outbreaks!



damage caused by Douglas-fir Beetle in 2006 - Eastern Idaho, USA

Western Spruce Budworm infestation in Idaho & Alaska, USA

The mountain pine bark beetle, *Dendrolimus spectabilis* infesting *Pinus densiflora* in Korea

Dendroctonus ponderosae attacks and kills lodgepole, ponderosa, sugar, and western white pines

What did we learn from the past?

Forest trees have tremendous adaptive potential!

They are sessile, long living organisms and developed unique adaptive mechanisms to survive in spatially and temporally heterogeneous environments, such as high:

- phenotypic plasticity
- genetic adaptive variation
- epigenetic memory

To unlock the adaptive potential and to be able to predict and mitigate effects of climate change and to breed resilient trees we have to understand evolutionary responses and molecular mechanisms of genetic adaptation

- **evolutionary response** is a **genetic adaptation** via genetic change that promotes adaptation of plants and animals to their natural environment, including their interactions with members of their own and other species (the biotic environment) as well as the physical environment (the abiotic environment).

- multiple genes are involved in **genetic adaptation**, so its study **requires innovative genomic methods and genome-wide approaches**

Innovative genomic methods to study genetic adaptation in forest trees

- new type of functional genomic markers of candidates genes for Quantitative Trait Locus (QTL) mapping and association studies
- use of adaptive trait related candidate genes in population studies
- association mapping with phenotypic and environmental variation using high-density genome-wide genotyping via high-throughput sequencing (NGS) in field and common garden experiments (provenance, progeny and clonal tests)
- detecting selective signatures and loci under adaptive genetic divergence in natural populations using neutrality tests and outlier-detection approaches
- genomic breeding using intense phenotyping, high-density genome-wide genotyping and regression models to predict phenotypes and breeding values in the progeny based on their genome-wide genotypes alone

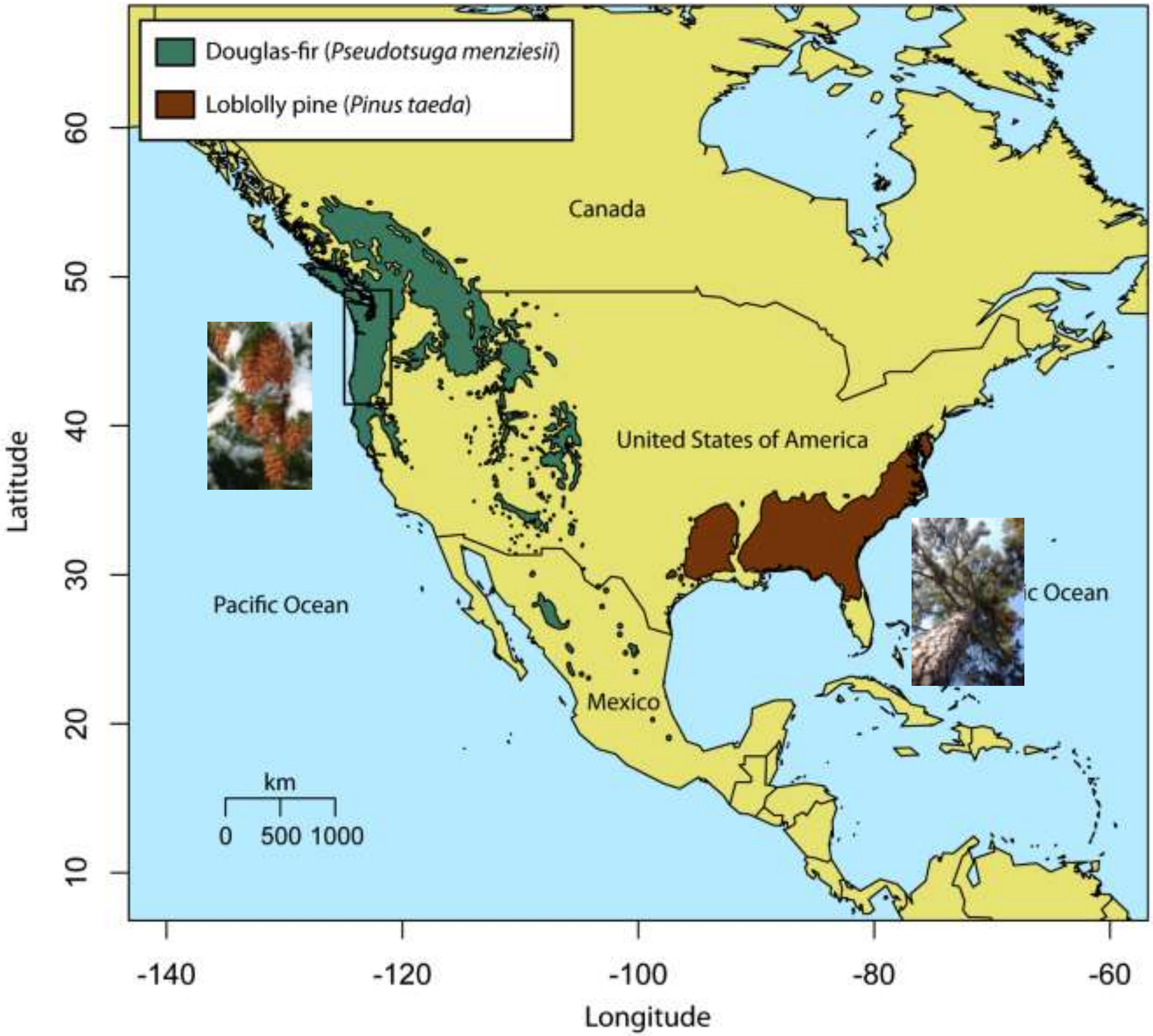
Douglas-fir and Loblolly pine case studies

- United States Department of Agriculture (USDA) National Research Initiative Competitive Grant Program (NRICGP), Plant Genome, Bioinformatics, and Genetic Resources, # 2004-35300-14670, PI: D. B. Neale, CoPIs: **K. V. Krutovsky**, Glenn T. Howe, and J. B. St. Clair, 3 years, **2004-2007**, $ 490,000, "**Association mapping of adaptive traits in Douglas-fir (*Pseudotsuga menziesii* Mirb. Franco)**".

- USDA NRICGP Plant Genome Program / National Institute of Food and Agriculture (NIFA) Agriculture and Food Research Initiative (AFRI) Competitive Grants Program, Applied Plant Genetics Coordinated Agricultural Project (CAP), #CA-D-PLS-2038-CG, Project Directors: D. B. Neale, T. D. Byram, D. E. Harry, G. T. Howe, D. A. Huber, F. Isik, **K. V. Krutovsky**, S. E. McKeand, C. D. Nelson, J. B. St. Clair, J. L. Wegrzyn, N. C. Wheeler, R. W. Whetten and others (http://dendrome.ucdavis.edu/ctgn/people/), **2004-2011**, $6,000,000; "**Conifer Translational Genomics Network**".

- USDA NIFA AFRI Competitive Grants Program, CAP, Climate Change Program 1: Regional Approaches to Climate Change, Program Area Code – A3101, #2011-68002-30185, PI: Timothy Martin, CoPIs: R. Abt, D. Adams, G. Boyd, R. Boyles, H. Burkhart, T. Byram, D. Carter, W. Cropper, F. Cubbage, J. Davis, J.-C. Domec, T. Fox, J. Gan, D. Grebner, S. Grunwald, T. Hennessey, J. Holliday, W. Hubbard, D. Huber, J. Idassi, F. Isik, K. Johnsen, E. Jokela, J. Jones, M. Kane, J. King, M. Kirst, **K. V. Krutovsky**, C. Loopstra, D. Markewitz, S. McKeand, S. McNulty, M. Megalos, M. Monroe, C. D. Nelson, A. Noormets, G. Peter, G. Powell, R. Rubilar, L. Samuelson, J. Seiler, S. Sriharan, J. Stape, B. Strahm, G. Sun, E. Taylor, R. Teskey, J. Vogel, R. Whetten, R. Will, D. Wilson, R. Wynne, 5 years, **3/1/2011-2/28/2016**, $19,976,825; "**Integrating research, education and extension for enhancing southern pine climate change mitigation and adaptation**".

Douglas-fir and Loblolly pine case studies



ADAPTIVE TRAITS IN DOUGLAS-FIR

Bud flush

Propensity to lammas flush

Length of lammas flush

Cold damage to buds, needles and stems

Bud set

Drought

Douglas-fir Genome Project (DFGP)

collaborators

David Neale

University of California, Davis
Department of Plant Sciences
One Shields Avenue
Davis, CA 95616
Phone: (530) 754-8431
Fax: (530) 754-9366
e-mail: dbneale@ucdavis.edu

Kathleen D. Jermstad

Institute of Forest Genetics
USDA Forest Service - Pacific Southwest Research Station
2480 Carson Road
Placerville, CA 95667
phone: (530) 622-1225
Fax: (530) 622-2633
e-mail: kdjermstad@ucdavis.edu

Konstantin (Kostya) V. Krutovsky

Department of Forest Science - Texas A&M University
2135 Tamu
College Station, TX 77843-2135
Phone: (979) 458-1417
Fax: (979) 458-0159
e-mail: k-krutovsky@tamu.edu

Glenn Howe

Department of Forest Science
321 Richardson Hall
Oregon State University
Corvallis, OR 97331-5752
Tel: (541) 737-9001
Fax: (541) 737-1393
e-mail: Glenn.howe@oregonstate.edu

Marilyn Cherry

Department of Forest Science
321 Richardson Hall
Oregon State University
Corvallis, OR 97331-5752
Tel: (541) 737-6579
Fax: (541) 737-1393
e-mail: Marilyn.Cherry@oregonstate.edu

Brad St Clair

USDA Forest Service - Pacific Northwest Research Station
3200 SW Jefferson Way
Corvallis, OR 97331-4401
Phone: (541) 750-7294
Fax: (541) 750-7329
e-mail: BSTCLAIR@fs.fed.us

Sally Aitken

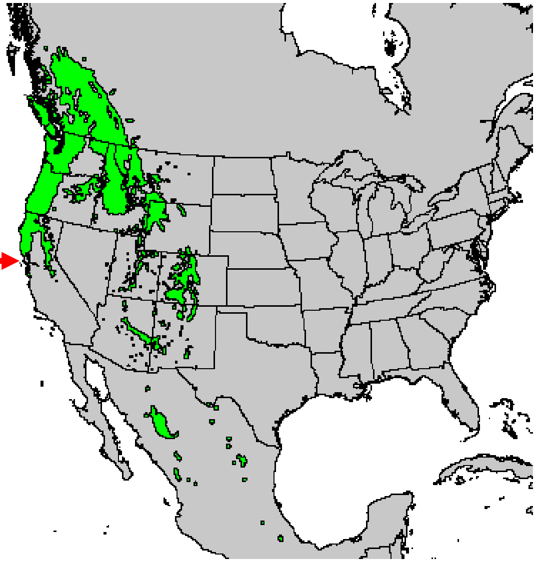
Department of Forest Sciences - Faculty of Forestry
The University of British Columbia
3rd Floor, Forest Sciences Centre #3041 - 2424 Main Mall
Vancouver, British Columbia
Canada V6T 1Z4
Tel: (604) 822-6020
Fax: (604) 822-9102
e-mail: aitken@interchg.ubc.ca

Nicholas C. Wheeler

Molecular Tree Breeding Services, LLC
21040 Flumerfelt Rd SE
Centralia, WA 98531
Phone: 360-278-3535
Fax: 360-278-3092
e-mail: nickwheeler@scattercreek.com

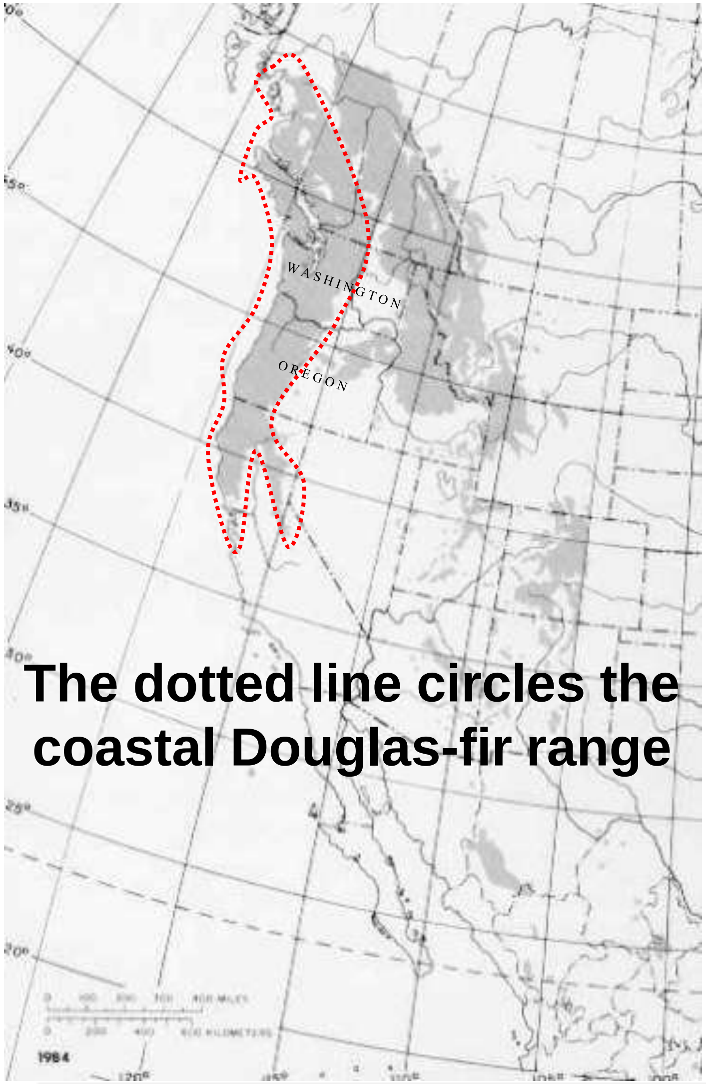
David Harry

Genetic Foundations
PO Box 1019
Philomath, OR 97370
Phone: (541) 740-7444
e-mail: deharry@peak.org
www.geneticfoundations.com



University of California, Davis

Candidate gene based association mapping in Douglas-fir

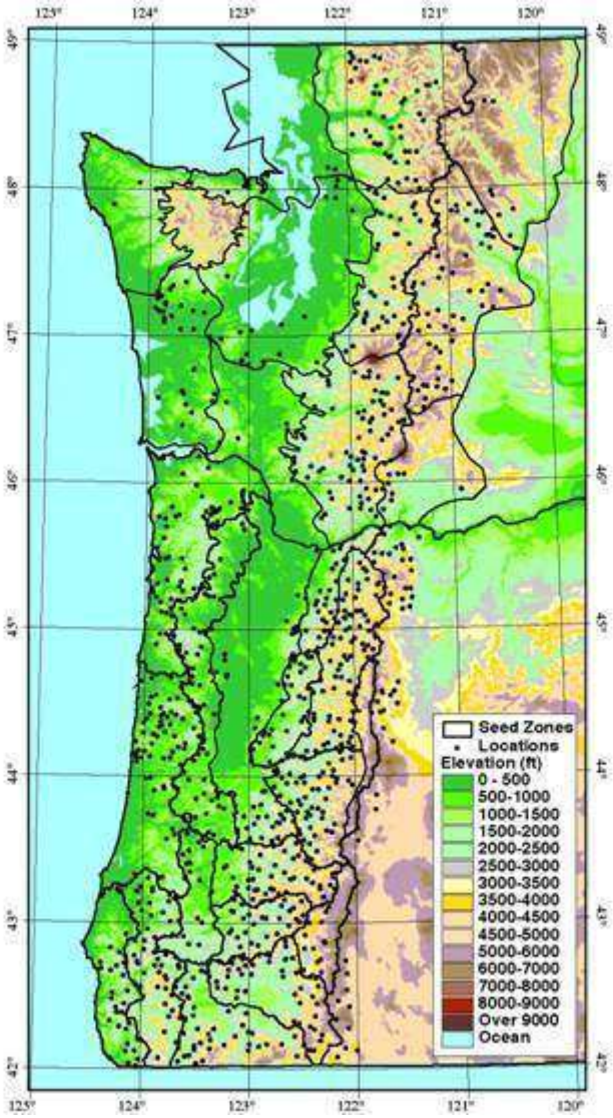


The dotted line circles the coastal Douglas-fir range

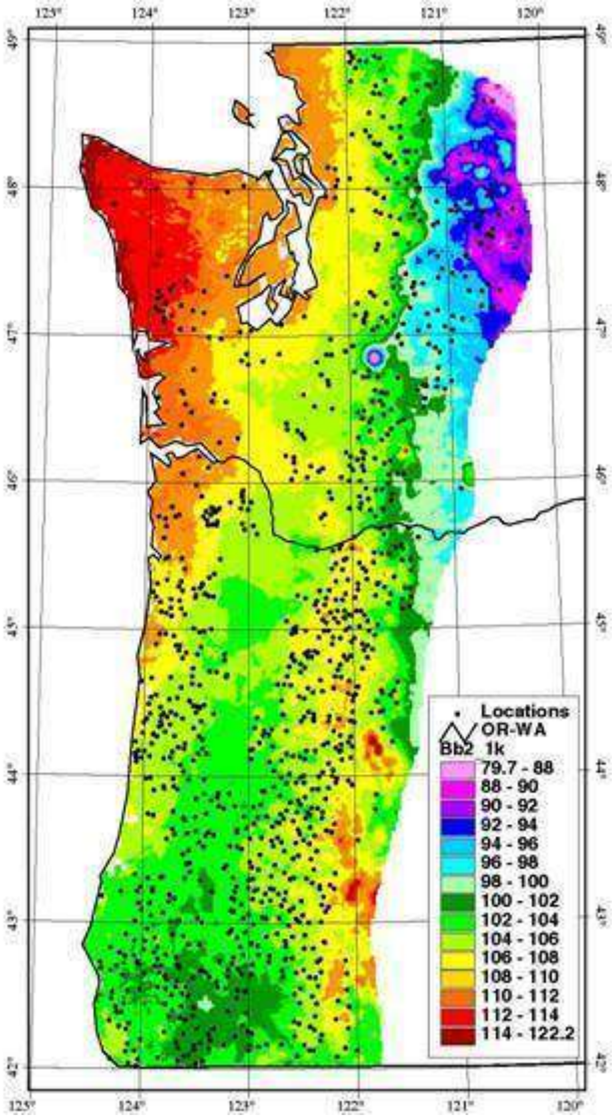
- ~**700** trees in the association mapping population representing the entire range
- phenotyped for **21** growth rhythm (bud flush, bud set) and cold-hardiness related traits
- genotyped for **384 SNPs** in **117** candidate genes using Illumina GoldenGate genotyping assay

Eckert, A.J., A.D. Bower, J.L. Wegrzyn, B. Pande, K.D. Jermstad, K.V. Krutovsky, J.B. St. Clair and D.B. Neale, 2009 Association genetics of coastal Douglas-fir (*Pseudotsuga menziesii* var. *menziesii*, Pinaceae). I. Cold-hardiness related traits. *Genetics* **182**: 1289-1302

GIS derived maps of parent trees in the common-garden population



Elevation and seed zones



Julian day for family mean bud flush

(Brad St. Clair *et al*. 2005, 2006)

Candidate gene-based association mapping in Douglas-fir

- **30** highly significant genetic associations for **12** candidate genes (*4CL*, *LEA*, *F3H2*, *MADS-box* and *MYB-like TFs*, *a-expansin*, etc.) and **10** were discovered.

- **7** markers had elevated levels of differentiation between sampling sites situated across the Cascade crest in northeastern Washington.

- Marker effects were small (**1% < r^2 < 3.6%**) and within the range of those published previously for forest trees, but **6 SNPs** explained **17%** of the phenotypic variance in cold damage to stems.

Eckert, A.J., A.D. Bower, J.L. Wegrzyn, B. Pande, K.D. Jermstad, K.V. Krutovsky, J.B. St. Clair and D.B. Neale, 2009 Association genetics of coastal Douglas-fir (*Pseudotsuga menziesii* var. *menziesii*, Pinaceae). I. Cold-hardiness related traits. *Genetics* **182**: 1289-1302

Conifer Translational Genomics Network
Coordinated Agricultural Project

CTGN CAP

Bringing Genomic Assisted Breeding
to Application in Tree Improvement

USDA United States Department of Agriculture
National Institute of Food and Agriculture

$5.9M (2007-2011)

www.pinegenome.org/ctgn

Conifer Translational Genomics Network (CTGN)

- **CTGN** is a multi-state, multi-institution **Coordinated Agricultural Project (CAP)** funded by USDA and USDA Forest Service

- **Project goal: Genomic Assisted Breeding** by linking experimental research with tree breeding

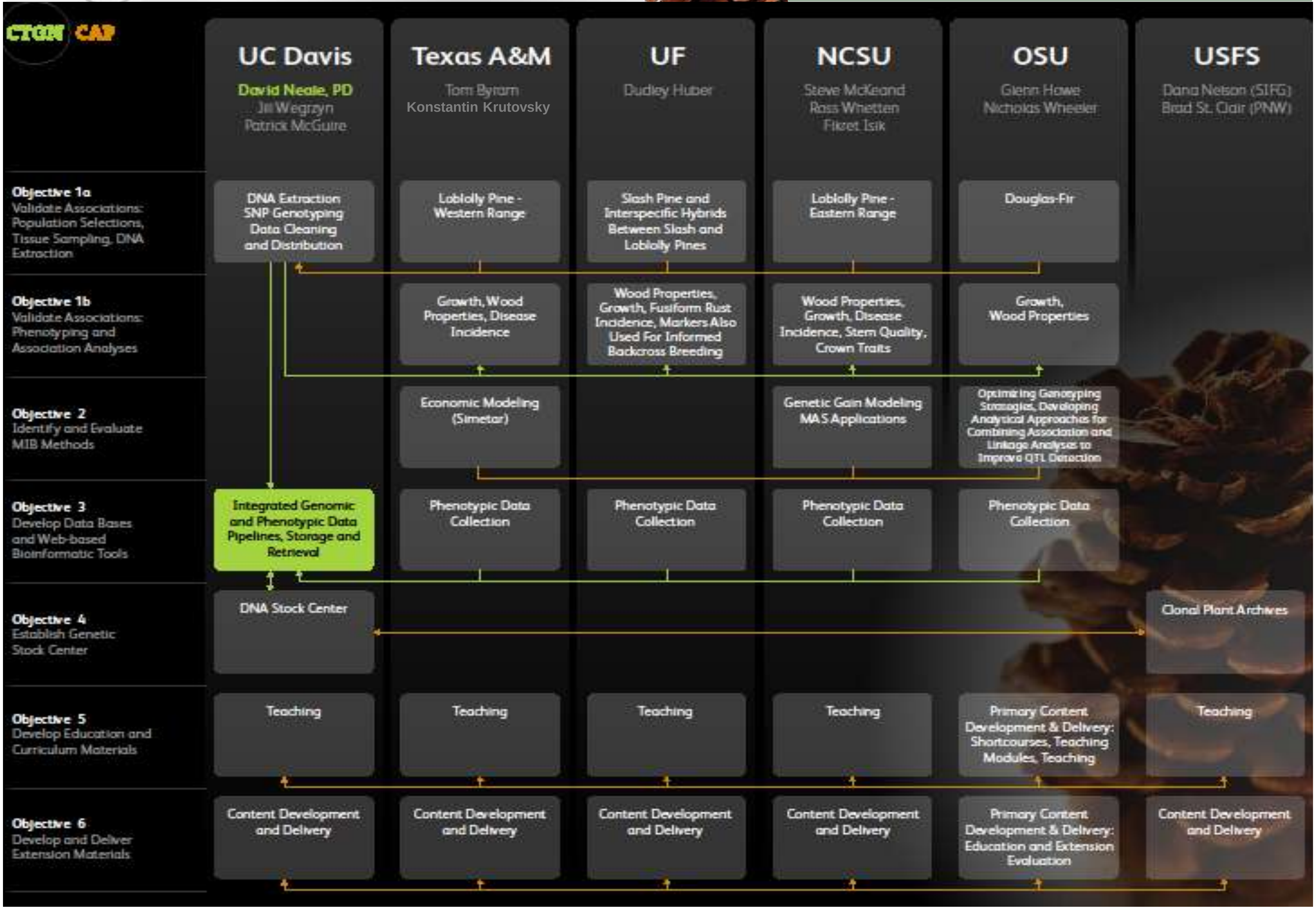
- **Project Approach**:
  - large scale genotyping in elite loblolly pine and Douglas-fir populations belonging to tree improvement cooperatives
  - validating genetic marker / phenotypic trait associations
  - modeling, outlining and implementing optimal approaches for incorporating markers in breeding programs

www.pinegenome.org/ctgn

Conifer Translational Genomics Network
Coordinated Agricultural Project

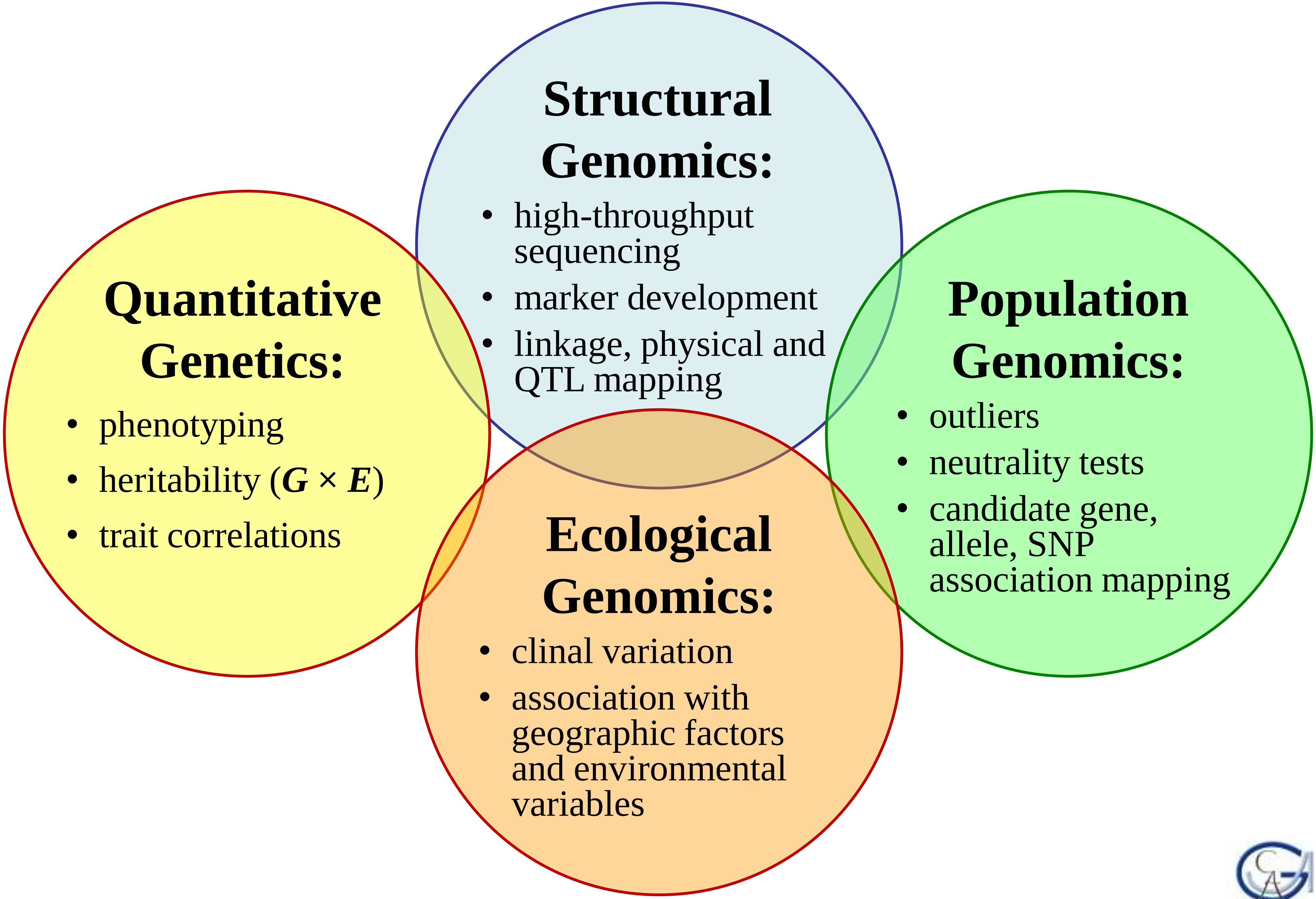
GCTGCTGNACAPTCATCCATGATTAGCTTAGCTGGACCTA

dendrome.ucdavis.edu/ctgn



CTGN CAP	UC Davis **David Neale, PD** Jill Wegrzyn Patrick McGuire	Texas A&M Tom Byram Konstantin Krutovsky	UF Dudley Huber	NCSU Steve McKeand Ross Whetten Fikret Isik	OSU Glenn Howe Nicholas Wheeler	USFS Dana Nelson (SIFG) Brad St. Clair (PNW)
Objective 1a Validate Associations: Population Selections, Tissue Sampling, DNA Extraction	DNA Extraction SNP Genotyping Data Cleaning and Distribution	Loblolly Pine - Western Range	Slash Pine and Interspecific Hybrids Between Slash and Loblolly Pines	Loblolly Pine - Eastern Range	Douglas-Fir	
Objective 1b Validate Associations: Phenotyping and Association Analyses		Growth, Wood Properties, Disease Incidence	Wood Properties, Growth, Fusiform Rust Incidence, Markers Also Used For Informed Backcross Breeding	Wood Properties, Growth, Disease Incidence, Stem Quality, Crown Traits	Growth, Wood Properties	
Objective 2 Identify and Evaluate MIB Methods		Economic Modeling (Simetar)		Genetic Gain Modeling MAS Applications	Optimizing Genotyping Strategies, Developing Analytical Approaches for Combining Association and Linkage Analyses to Improve QTL Detection	
Objective 3 Develop Data Bases and Web-based Bioinformatic Tools	Integrated Genomic and Phenotypic Data Pipelines, Storage and Retrieval	Phenotypic Data Collection	Phenotypic Data Collection	Phenotypic Data Collection	Phenotypic Data Collection	
Objective 4 Establish Genetic Stock Center	DNA Stock Center					Clonal Plant Archives
Objective 5 Develop Education and Curriculum Materials	Teaching	Teaching	Teaching	Teaching	Primary Content Development & Delivery: Shortcourses, Teaching Modules, Teaching	Teaching
Objective 6 Develop and Deliver Extension Materials	Content Development and Delivery	Content Development and Delivery	Content Development and Delivery	Content Development and Delivery	Primary Content Development & Delivery: Education and Extension Evaluation	Content Development and Delivery

CTGN: Linking Genotype to Phenotype & Environment



Structural Genomics:

- high-throughput sequencing
- marker development
- linkage, physical and QTL mapping

Quantitative Genetics:

- phenotyping
- heritability (***G*** × ***E***)
- trait correlations

Population Genomics:

- outliers
- neutrality tests
- candidate gene, allele, SNP association mapping

Ecological Genomics:

- clinal variation
- association with geographic factors and environmental variables

CTGN: Results of ecological & population genomic studies of loblolly pine (*Pinus taeda* L.)

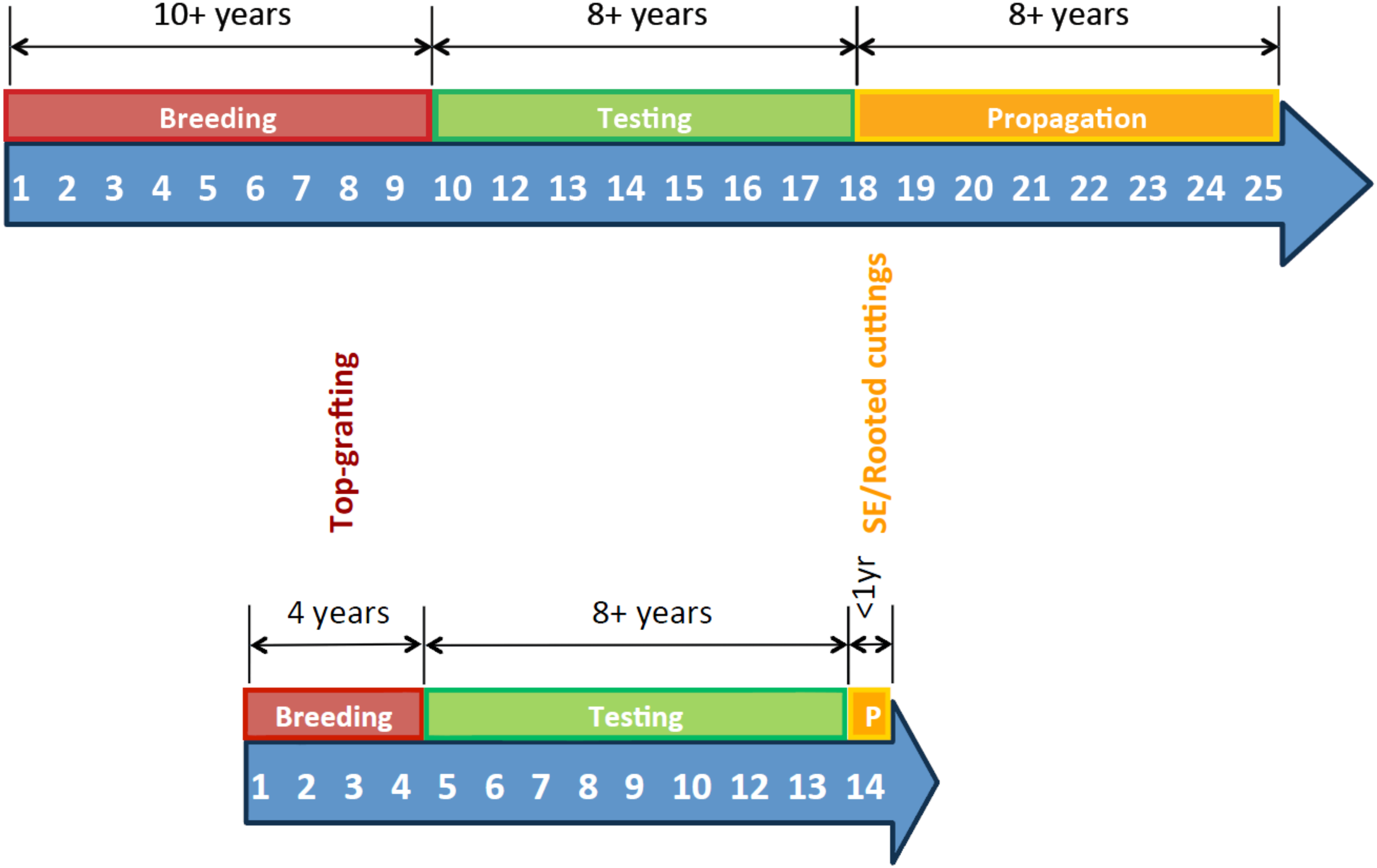
- SNPs from >4000 loci were genotyped in >4500 trees sampled from numerous natural and breeding populations covering the full-range of the species
- Significant associations were found between adaptive trait phenotypes, geographic and environmental variables (temperature, growing degree-days, precipitation and aridity) and a diverse sets of genes including abiotic stress response genes ranging from trans-membrane proteins to proteins involved in sugar metabolism and transcription factors
- Numerous genes under selection were found (outliers)
- Multiple allele candidates for local adaptation were discovered

Eckert *et al*. 2010 *Genetics* 185: 969–982;
Eckert *et al*. 2010 *Molecular Ecology* 19: 3789–3805
Chhatre *et al.* 2012 *Tree Genetics and Genomes* (submitted)

CTGN:

Genomic based selection for more resilient and better trees

Traditional pine breeding



10+ years

8+ years

8+ years

Breeding

Testing

Propagation

1 2 3 4 5 6 7 8 9 10 12 13 14 15 16 17 18 19 20 21 22 23 24 25

Top-grafting

SE/Rooted cuttings

<1yr

4 years

8+ years

Breeding

Testing

P

1 2 3 4 5 6 7 8 9 10 12 13 14

(*Adapted from Matias Kirst*)

Traditional molecular breeding and Marker-Aided Selection (MAS)

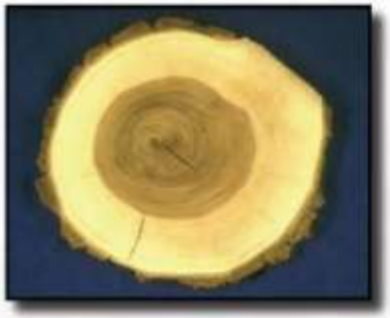
Growth

Adaptability

Straightness

Disease resistance

Insect resistance



Wood quality

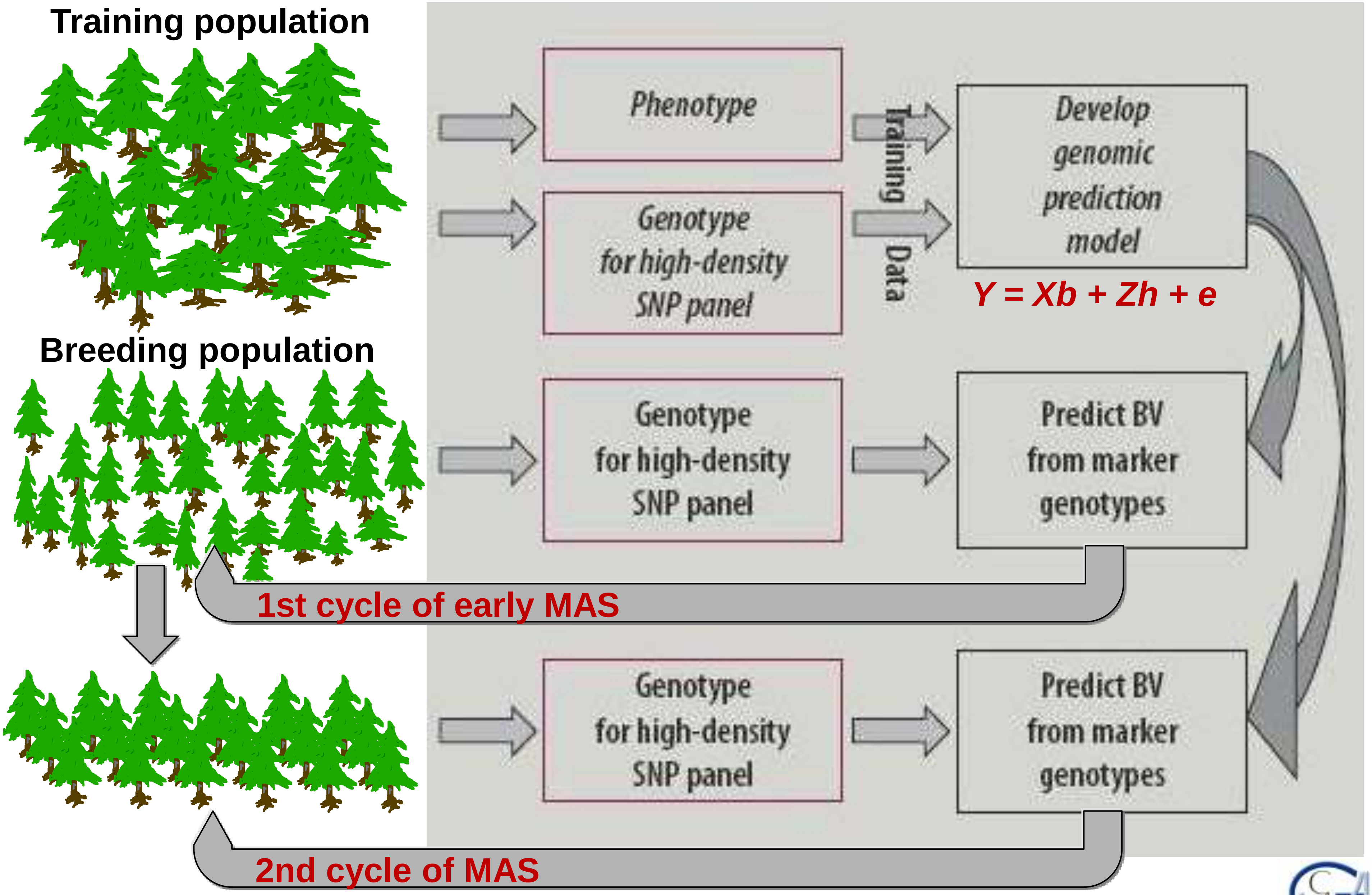
(Adapted from Dave Neale)

What we have learned from traditional forest tree breeding:

- Most breeding and adaptive traits are complex quantitative traits controlled by environment and multiple genes of small effect

- Genomic based selection is needed to accelerate breeding

Genomic selection



Training population

Phenotype

Genotype for high-density SNP panel

Training Data

Develop genomic prediction model

$Y = Xb + Zh + e$

Breeding population

Genotype for high-density SNP panel

Predict BV from marker genotypes

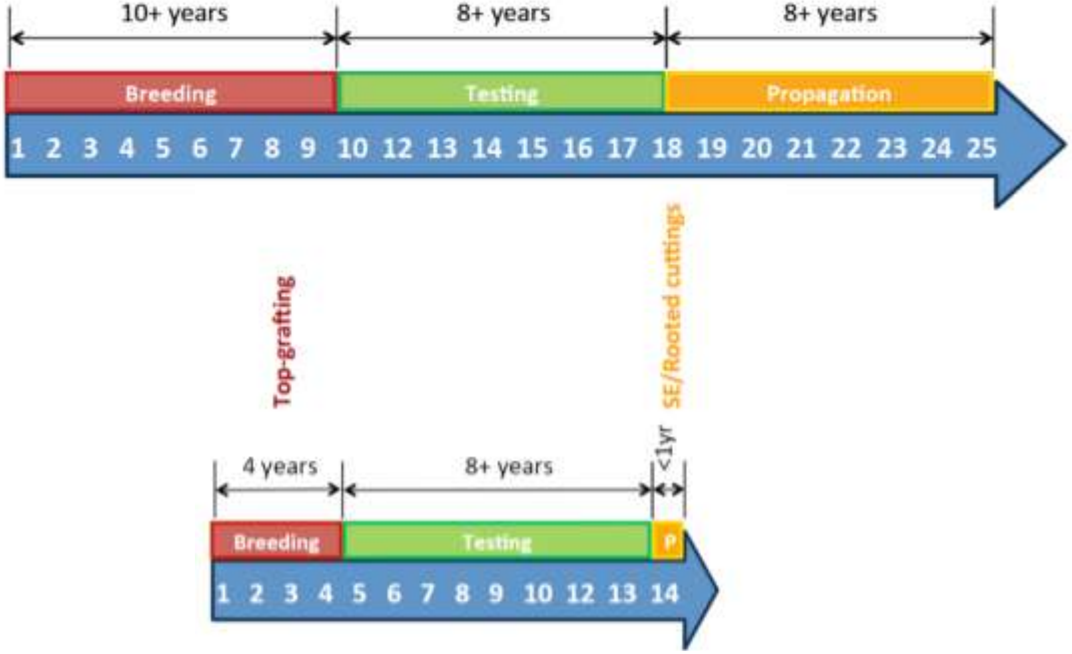
1st cycle of early MAS

Genotype for high-density SNP panel

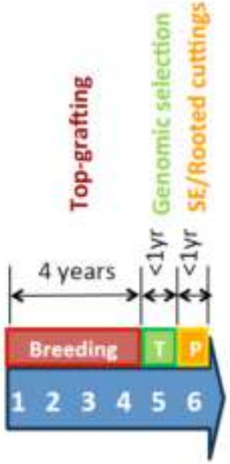
Predict BV from marker genotypes

2nd cycle of MAS

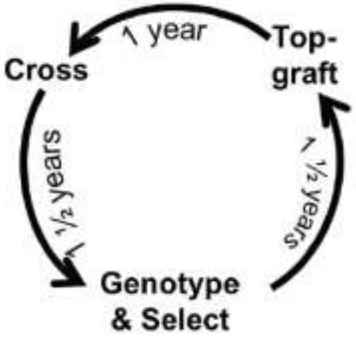
Traditional pine breeding:



Genomic selection:



Genomic Selection Guided Crosses



"Surgical" breeding

(Adapted from Matias Kirst)

Genomic selection – Conclusions

- Accuracy of predicting desirable traits and breeding values (BV) based on genome-wide genotypes will increase with:
  - more markers
  - more individuals
  - higher heritability
  - higher LD
- Genomic selection can be done, but most likely in the family based breeding

Ecosystem Science and Management

Prestigious USDA Departmental Award

Read more...

Awards & Merits

Dr. Brad Wilcox - Outstanding Contribution to Rangeland Management

The Most Prestigious USDA Departmental Award presented by the Secretary of Agriculture to the Conifer Translational Genomics Network including Dr. Tom Byram, Dr. Konstantin Krutovsky, and PhD student Vikram Chhatre.

News & Events

The Most Prestigious USDA Departmental Award presented by the Secretary of Agriculture to the Conifer Translational Genomics Network including Dr. Tom Byram, Dr. Konstantin Krutovsky, and PhD student Vikram Chhatre

Excerpt from the letter:

Congratulations!

The Conifer Translational Genomics Network Coordinated Agricultural Project has been selected to receive a 2011 U.S. Department of Agriculture (USDA) Secretary's Honor Award in the category of *Helping American promote sustainable agricultural production and biotechnology exports as America works to increase food security*. These awards are the most prestigious Departmental awards presented by the Secretary of Agriculture and recognize exceptional leadership, contributions, or public service by individuals or groups who support the mission/goals of USDA.

I am very pleased that you have been selected to receive a 2011 Secretary's Honor Award in recognition of your efforts to create the Conifer Translational Genomics Network Coordinated Agricultural Project. On September 14th, I look forward to recognizing you for your contributions.

Sincerely

Chavonda Jacobs-Young
Acting Director

The group from TAMU was part of a team comprising 30 researchers working from nine different institutions on a project coordinated by Dr. David Neale at UC Davis.

All three are from the Department of Ecosystem Science and Management, College of Agriculture and Life Sciences, Texas A&M University and Texas Forest Service.

USDA NIFA Climate Change Program 1: Regional Approaches to Climate Change

PI: Timothy Martin, 2011-2016, $19,976,825; “Integrating research, education and extension for enhancing southern pine climate change mitigation and adaptation”.

Ecosystem Science and Management

ESSM Team of Scientists

Drs. Tom Byram, Carol Loopstra and Kostya Krutovsky will be the genetics team from Texas A&M University.

Among this project's main objectives are the study of loblolly pine's genetic adaptation to potential climate change. The goal is to use this knowledge to develop a new seed deployment tool that will help mitigate the detrimental effects of warmer and drier climate in the southeastern United States. Association and population genetics analysis will be used to characterize important adaptation and mitigation traits to support future breeding efforts. The genetics program will support development of growth and yield models, stand-level biophysical carbon balance modeling, multi-scale policy and economic analysis of market and non-market forest benefits and services, and an education program to deliver state-of-the-art forest management solutions. Texas A&M will assist collaborators at sister organizations in meeting these objectives through a local genetics team.

Me

$20 million grant to study effects of climate change

Six scientists from Ecosystem Science and Management will be part of a $20 million grant to study effects of climate change on agricultural and forest production

On Friday, Feb. 18, the USDA National Institute of Food and Agriculture (NIFA) awarded three Coordinated Agriculture Projects (CAP) representing a major scientific investment in studying the effects of climate change on agriculture and forest production. NIFA Director Roger Beachy made the announcement at the annual meeting of the American Association for the Advancement of Science in Washington, D.C.

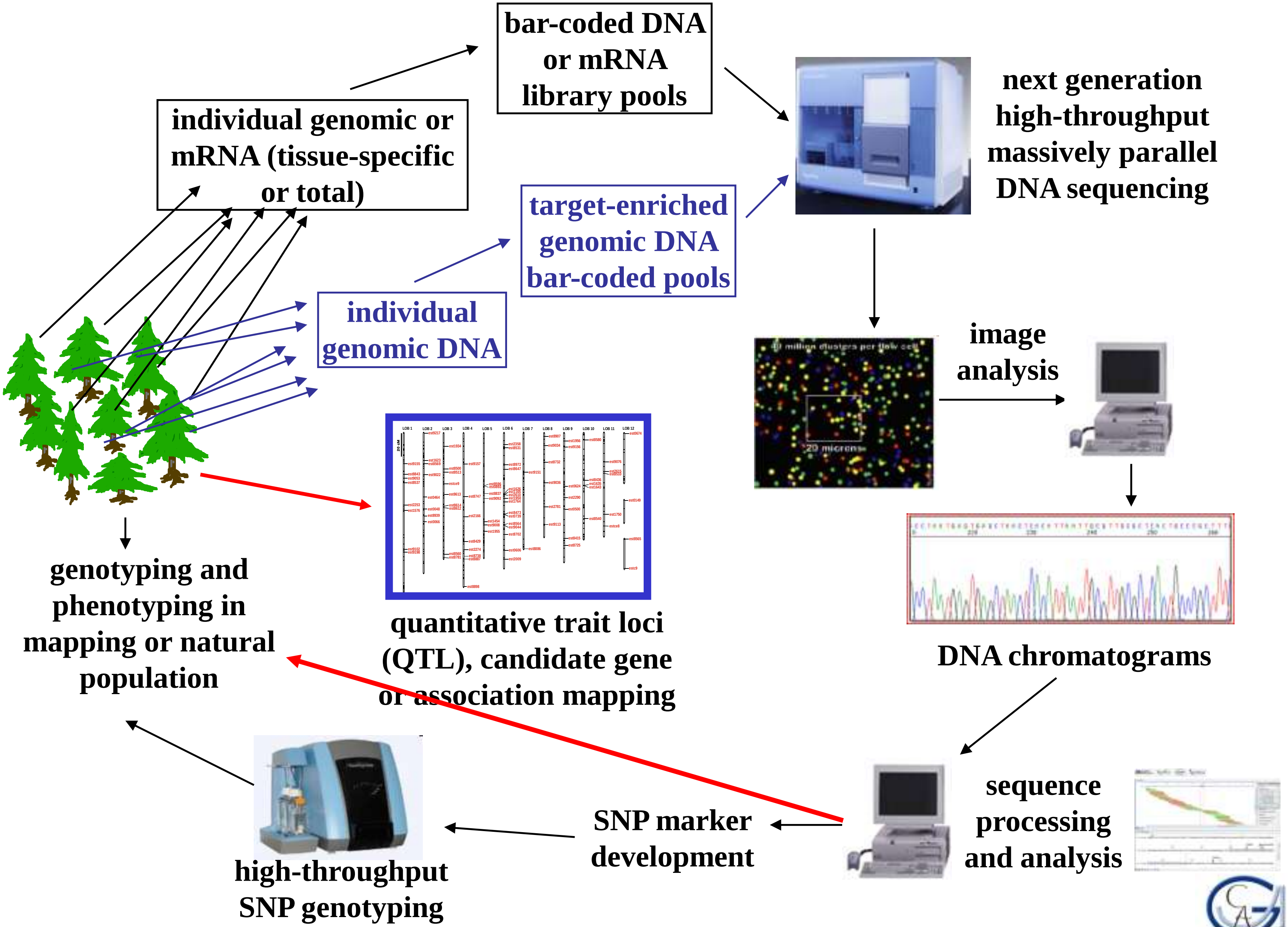
"Climate change has already had an impact on agriculture production. Going forward agriculture producers need sound scientific information to plan and make decisions to ensure their economic viability," Beachy said. "These projects ensure we have the best available tools to accurately measure the effects of climate change on agriculture, develop effective methods to sustain productivity in a changing environment and pass these resources on to the farmers and industry professionals who can put the research into practice."

Institute of Food and Agriculture announced the award of a five-year, $20 million grant, to fund research, outreach and education to develop and transfer better management methods for southern pine, notably loblolly pine. They will study climate change mitigation and adaptation as it relates to southern pines, particularly loblolly pine, which comprises 80 percent of the planted forestland in the Southeast. It's widely used for lumber, pulp and paper production, and has great potential for biofuel production.

NIFA made the awards through its Agriculture and Food Research Initiative funding opportunity. AFRI's Climate Change challenge area is focused on reducing greenhouse gas emissions and increasing carbon sequestration in agricultural and forest production systems and preparing the nation's agriculture and forests to adapt to changing climates.

Two-thirds of all the drinking water in the U.S. comes from forested watersheds.

Genomic markers development and genotyping using next generation sequencing



individual genomic or mRNA (tissue-specific or total)

bar-coded DNA or mRNA library pools

individual genomic DNA

target-enriched genomic DNA bar-coded pools

next generation high-throughput massively parallel DNA sequencing

image analysis

DNA chromatograms

sequence processing and analysis

SNP marker development

high-throughput SNP genotyping

genotyping and phenotyping in mapping or natural population

quantitative trait loci (QTL), candidate gene or association mapping

Genomic DNA target enrichment for high-throughput massively parallel sequencing using the Agilent's SureSelect Target Enrichment System

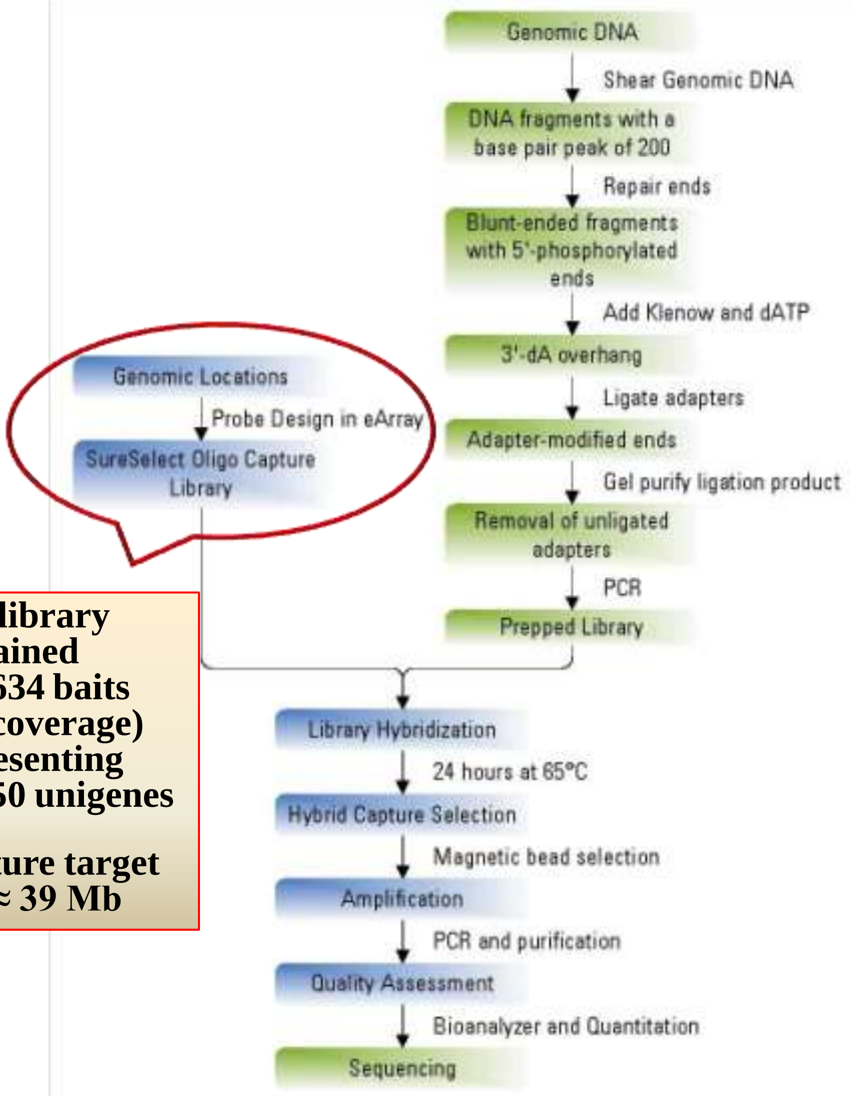


Figure 1 Overall sequencing sample preparation workflow.

- **Our library contained 647,634 baits (2X coverage) representing 35,550 unigenes**
- **Capture target size ≈ 39 Mb**

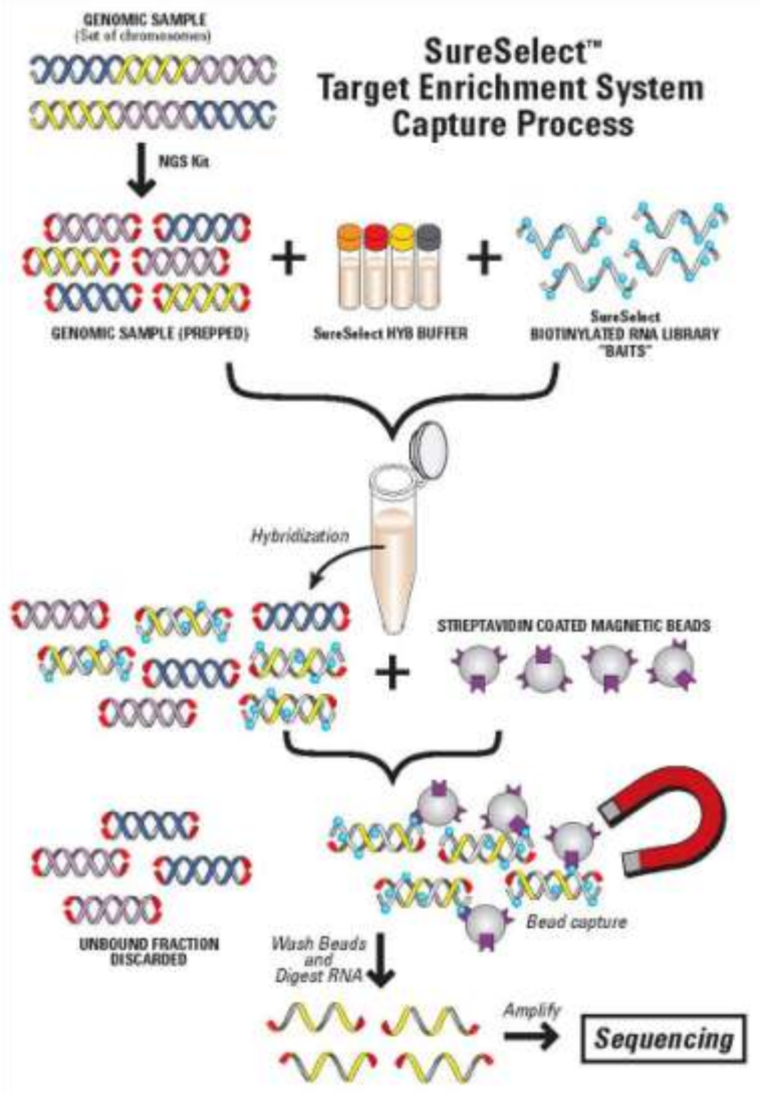
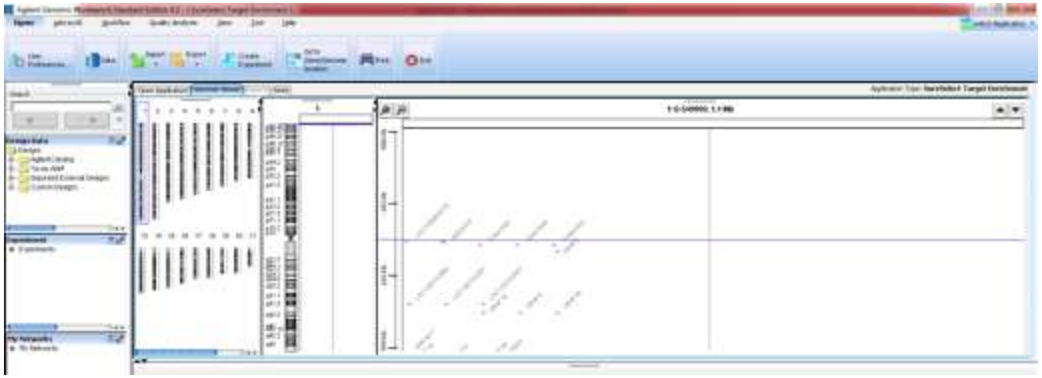


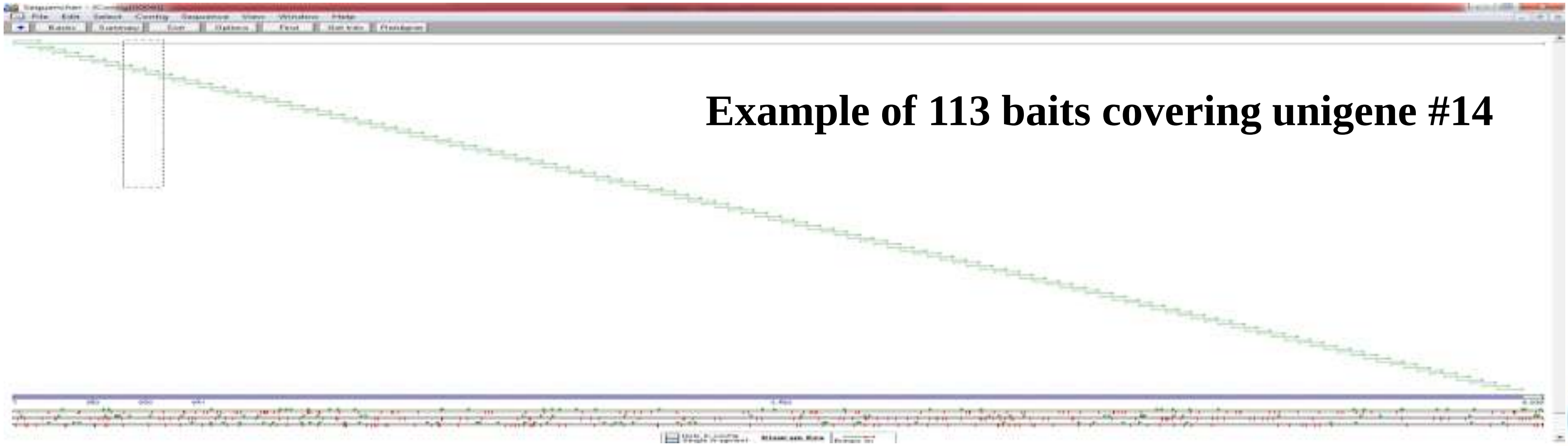
Figure 2 SureSelect Target Enrichment System Capture Process

http://www.opengenomics.com/SureSelect_Target_Enrichment_System

Genomic DNA enrichment for 35,550 genes in loblolly pine for high-throughput massively parallel sequencing using bar-coding and the Agilent's SureSelect Target Enrichment System

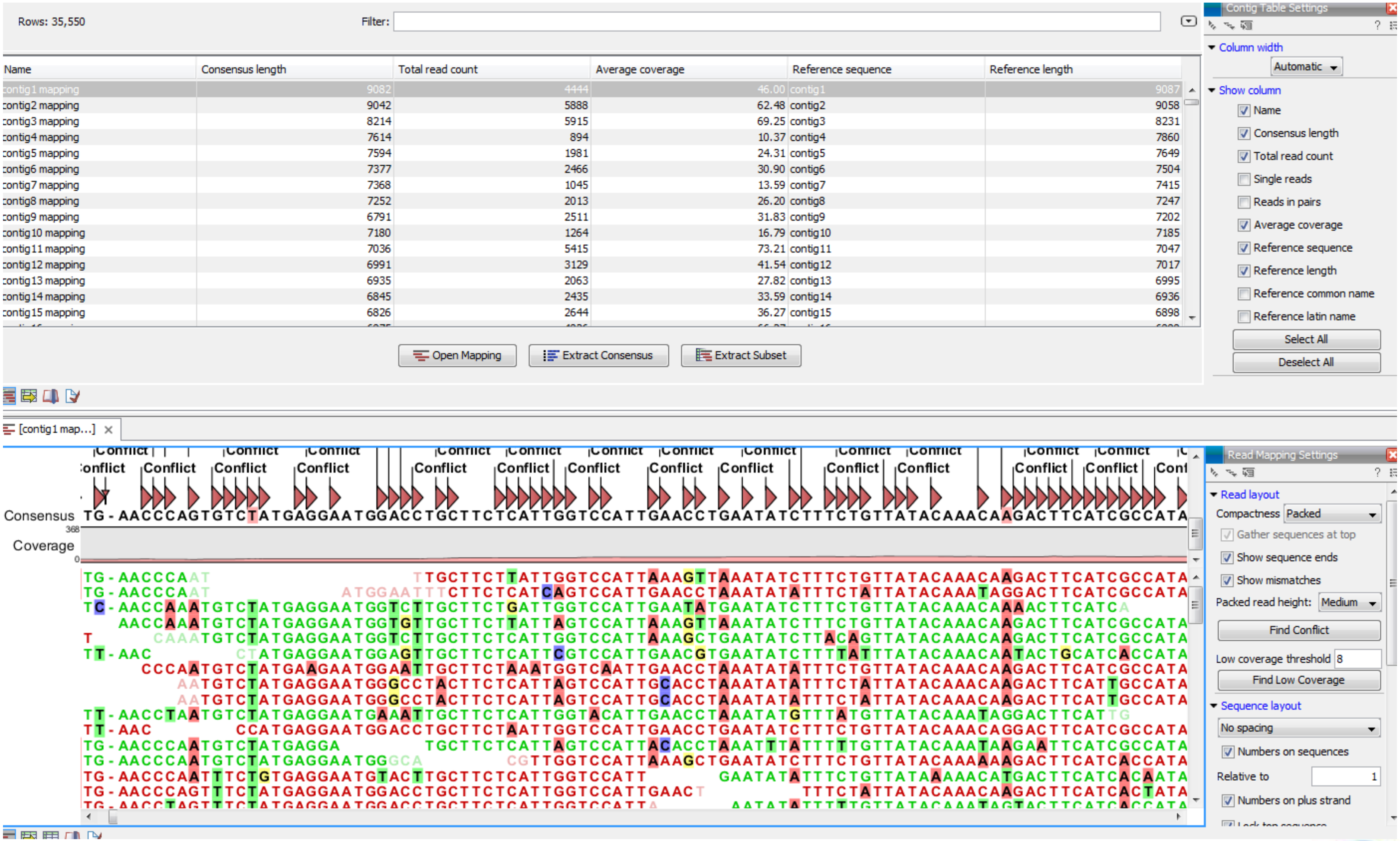


647,634 oligonucleotide hybridization 120 bp long probes (baits) based on 35,550 unigenes build by Dr. Chun Liang (Miami University) were designed to target 39 Mb of gene space using Agilent Genomic Workbench software to gene enrich DNA libraries for sequencing



Example of 113 baits covering unigene #14

Mapping short reads back to the unigenes or other reference sequences using the *CLCbio* software



Rows: 35,550

Filter:

Name	Consensus length	Total read count	Average coverage	Reference sequence	Reference length
contig1 mapping	9082	4444	46.00	contig1	9087
contig2 mapping	9042	5888	62.48	contig2	9058
contig3 mapping	8214	5915	69.25	contig3	8231
contig4 mapping	7614	894	10.37	contig4	7860
contig5 mapping	7594	1981	24.31	contig5	7649
contig6 mapping	7377	2466	30.90	contig6	7504
contig7 mapping	7368	1045	13.59	contig7	7415
contig8 mapping	7252	2013	26.20	contig8	7247
contig9 mapping	6791	2511	31.83	contig9	7202
contig10 mapping	7180	1264	16.79	contig10	7185
contig11 mapping	7036	5415	73.21	contig11	7047
contig12 mapping	6991	3129	41.54	contig12	7017
contig13 mapping	6935	2063	27.82	contig13	6995
contig14 mapping	6845	2435	33.59	contig14	6936
contig15 mapping	6826	2644	36.27	contig15	6898

Contig Table Settings

Column width: Automatic

Show column
- ☑ Name
- ☑ Consensus length
- ☑ Total read count
- ☐ Single reads
- ☐ Reads in pairs
- ☑ Average coverage
- ☑ Reference sequence
- ☑ Reference length
- ☐ Reference common name
- ☐ Reference latin name

```
Consensus  TG-AACCCAGTGTCTATGAGGAATGGACCTGCTTCTCATTGGTCCATTGAACCTGAATATCTTTCTGTTATACAAACAAGACTTCATCGCCATA
      368
Coverage
        0
           TG-AACCCAAT                 TTGCTTCTTATTGGTCCATTAAAGTTAAATATCTTTCTGTTATACAAACAAGACTTCATCGCCATA
           TG-AACCCAAT           ATGGAATTTCTTCTCATCAGTCCATTGAACCTAAATATATTTCTATTATACAAATAGGACTTCATCGCCATA
           TC-AACCAAATGTCTATGAGGAATGGTCTTGCTTCTGATTGGTCCATTGAATATGAATATCTTTCTGTTATACAAACAAAACTTCATCA
              AACCAAATGTCTATGAGGAATGGTGTTGCTTCTTATTAGTCCATTAAAGTTAAATATCTTTCTGTTATACAAACAAGACTTCATCGCCATA
           T     CAAATGTCTATGAGGAATGGTCTTGCTTCTCATTGGTCCATTAAAGCTGAATATCTTACAGTTATACAAACAAGACTTCATCGCCATA
           TT-AAC       CTATGAGGAATGGAGTTGCTTCTCATTCGTCCATTGAACGTGAATATCTTTTATTTATACAAACAATACTGCATCACCATA
                CCCAATGTCTATGAAGAATGGAATTGCTTCTAAATGGTCAATTGAACCTAAATATATTTCTGTTATACAAACAAGACTTCATCGCCATA
                   AATGTCTATGAGGAATGGGCCTACTTCTCATTAGTCCATTGCACCTAAATATATTTCTATTATACAAACAAGACTTCATTGCCATA
                   AATGTCTATGAGGAATGGGCCTACTTCTCATTAGTCCATTGCACCTAAATATATTTCTATTATACAAACAAGACTTCATTGCCATA
           TT-AACCTAATGTCTATGAGGAATGAAATTGCTTCTCATTGGTACATTGAACCTAAATATGTTTATGTTATACAAATAGGACTTCATTG
           TT-AAC       CCATGAGGAATGGACCTGCTTCTAATTGGTCCATTGAACCTGAATATCTTTCTGTTATACAAACAGGACTTCATCGCCATA
           TG-AACCCAATGTCTATGAGGA       TGCTTCTCATTAGTCCATTACACCTAAATTTATTTTTGTTATACAAATAAGAATTCATCGCCATA
           TG-AACCCAATGTCTATGAGGAATGGGCA       CGTTGGTCCATTAAAGCTGAATATCTTTCTGTTATACAAAAAAGACTTCATCACCATA
           TG-AACCCAATTTCTGTGAGGAATGTACTTGCTTCTCATTGGTCCATT      GAATATATTTCTGTTATAAAAACATGACTTCATCACAATA
           TG-AACCCAGTTTCTATGAGGAATGGACCTGCTTCTCATTGGTCCATTGAACT       TTTCTATTATACAAACAAGACTTCATCACTATA
           TG-AACCTAGTTTCTATGAGGAATGGACCTGCTTCTCATTGGTCCATTA      AATATATTTTTGTTATACAAATAGTACTTCATCACCATA
```

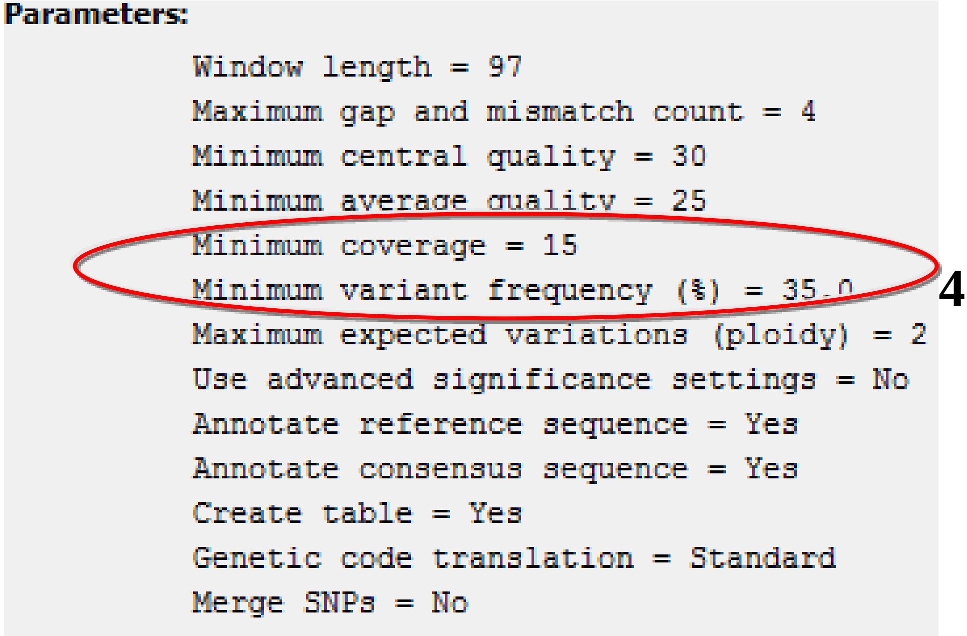
Read Mapping Settings

Read layout
- Compactness: Packed
- ☑ Gather sequences at top
- ☑ Show sequence ends
- ☑ Show mismatches
- Packed read height: Medium

Low coverage threshold: 8

Sequence layout
- No spacing
- ☑ Numbers on sequences
- Relative to: 1
- ☑ Numbers on plus strand

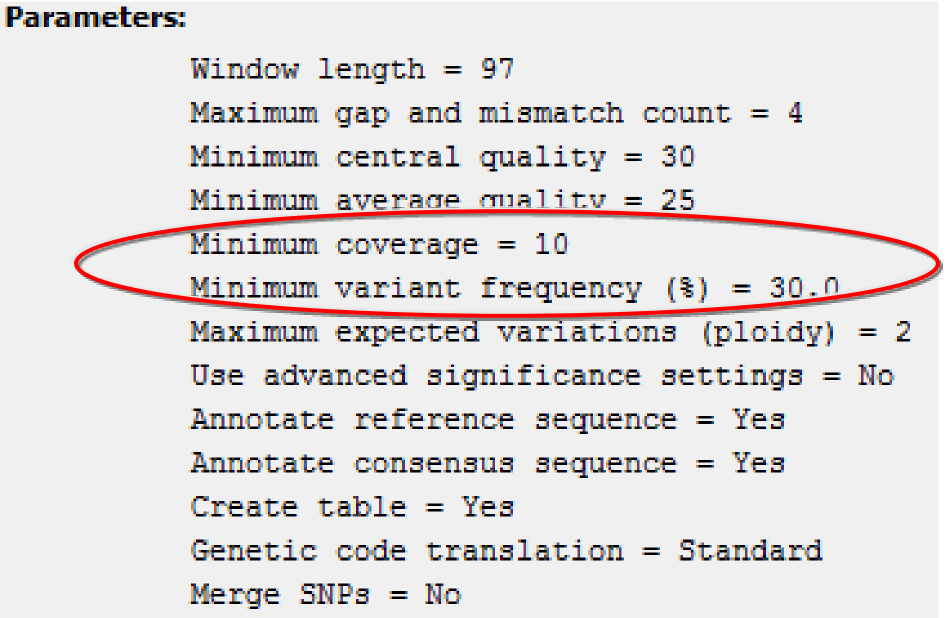
SNP detection using the *CLCbio* software



```
Parameters:
        Window length = 97
        Maximum gap and mismatch count = 4
        Minimum central quality = 30
        Minimum average quality = 25
        Minimum coverage = 15
        Minimum variant frequency (%) = 35.0
        Maximum expected variations (ploidy) = 2
        Use advanced significance settings = No
        Annotate reference sequence = Yes
        Annotate consensus sequence = Yes
        Create table = Yes
        Genetic code translation = Standard
        Merge SNPs = No
```

48,761 candidate SNPs, 1 SNP per ≈1,000 bp

(total contig length / number of SNPs)



```
Parameters:
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        Minimum central quality = 30
        Minimum average quality = 25
        Minimum coverage = 10
        Minimum variant frequency (%) = 30.0
        Maximum expected variations (ploidy) = 2
        Use advanced significance settings = No
        Annotate reference sequence = Yes
        Annotate consensus sequence = Yes
        Create table = Yes
        Genetic code translation = Standard
        Merge SNPs = No
```
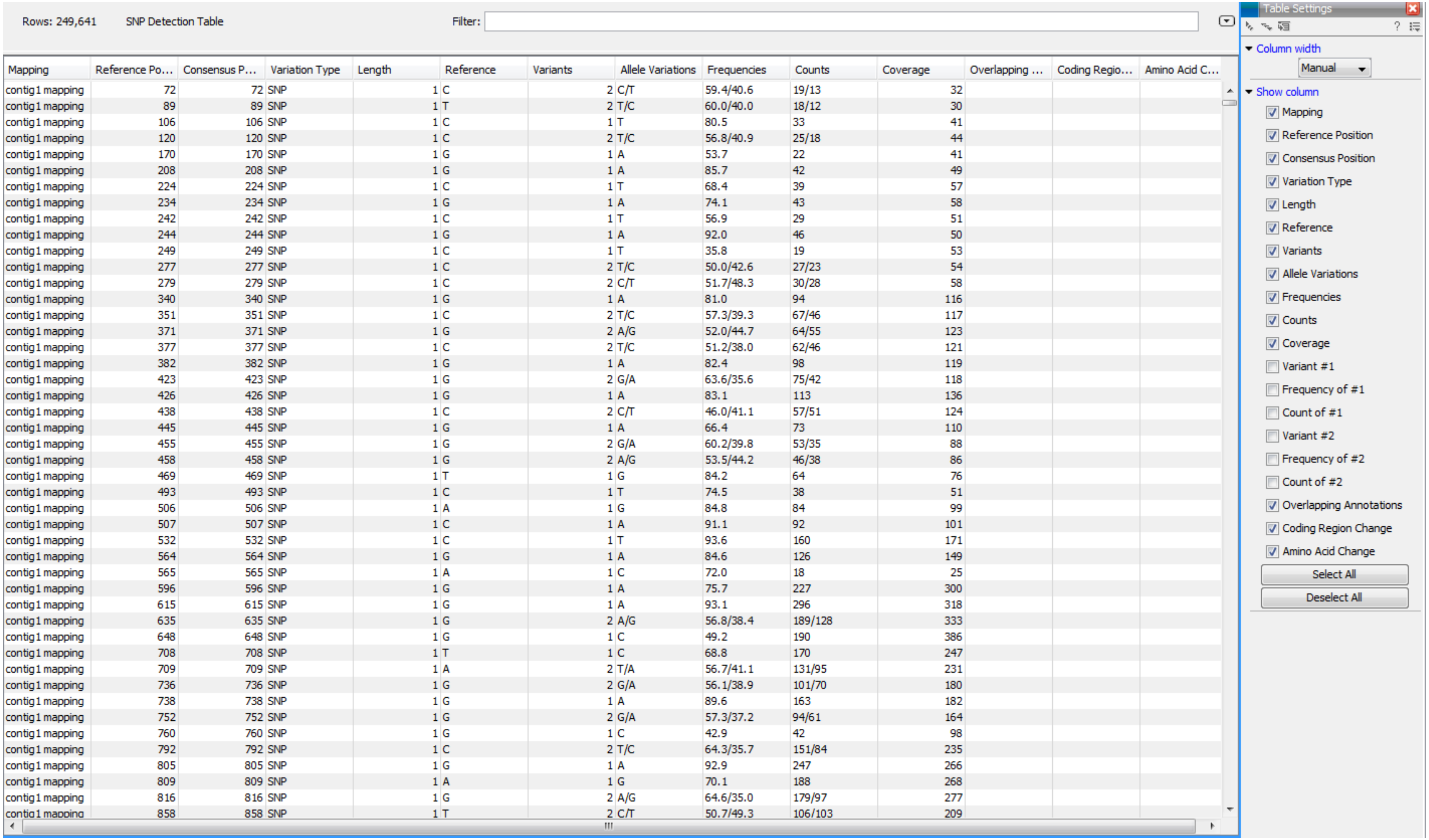

97,140 candidate SNPs, 1 SNP per ≈500 bp

SNP detection using the *CLCbio* software



Rows: 249,641   SNP Detection Table   Filter:

Mapping	Reference Po...	Consensus P...	Variation Type	Length	Reference	Variants	Allele Variations	Frequencies	Counts	Coverage	Overlapping ...	Coding Regio...	Amino Acid C...
contig1 mapping	72	72	SNP	1	C	2	C/T	59.4/40.6	19/13	32			
contig1 mapping	89	89	SNP	1	T	2	T/C	60.0/40.0	18/12	30			
contig1 mapping	106	106	SNP	1	C	1	T	80.5	33	41			
contig1 mapping	120	120	SNP	1	C	2	T/C	56.8/40.9	25/18	44			
contig1 mapping	170	170	SNP	1	G	1	A	53.7	22	41			
contig1 mapping	208	208	SNP	1	G	1	A	85.7	42	49			
contig1 mapping	224	224	SNP	1	C	1	T	68.4	39	57			
contig1 mapping	234	234	SNP	1	G	1	A	74.1	43	58			
contig1 mapping	242	242	SNP	1	C	1	T	56.9	29	51			
contig1 mapping	244	244	SNP	1	G	1	A	92.0	46	50			
contig1 mapping	249	249	SNP	1	C	1	T	35.8	19	53			
contig1 mapping	277	277	SNP	1	C	2	T/C	50.0/42.6	27/23	54			
contig1 mapping	279	279	SNP	1	C	2	C/T	51.7/48.3	30/28	58			
contig1 mapping	340	340	SNP	1	G	1	A	81.0	94	116			
contig1 mapping	351	351	SNP	1	C	2	T/C	57.3/39.3	67/46	117			
contig1 mapping	371	371	SNP	1	G	2	A/G	52.0/44.7	64/55	123			
contig1 mapping	377	377	SNP	1	C	2	T/C	51.2/38.0	62/46	121			
contig1 mapping	382	382	SNP	1	G	1	A	82.4	98	119			
contig1 mapping	423	423	SNP	1	G	2	G/A	63.6/35.6	75/42	118			
contig1 mapping	426	426	SNP	1	G	1	A	83.1	113	136			
contig1 mapping	438	438	SNP	1	C	2	C/T	46.0/41.1	57/51	124			
contig1 mapping	445	445	SNP	1	G	1	A	66.4	73	110			
contig1 mapping	455	455	SNP	1	G	2	G/A	60.2/39.8	53/35	88			
contig1 mapping	458	458	SNP	1	G	2	A/G	53.5/44.2	46/38	86			
contig1 mapping	469	469	SNP	1	T	1	G	84.2	64	76			
contig1 mapping	493	493	SNP	1	C	1	T	74.5	38	51			
contig1 mapping	506	506	SNP	1	A	1	G	84.8	84	99			
contig1 mapping	507	507	SNP	1	C	1	A	91.1	92	101			
contig1 mapping	532	532	SNP	1	C	1	T	93.6	160	171			
contig1 mapping	564	564	SNP	1	G	1	A	84.6	126	149			
contig1 mapping	565	565	SNP	1	A	1	C	72.0	18	25			
contig1 mapping	596	596	SNP	1	G	1	A	75.7	227	300			
contig1 mapping	615	615	SNP	1	G	1	A	93.1	296	318			
contig1 mapping	635	635	SNP	1	G	2	A/G	56.8/38.4	189/128	333			
contig1 mapping	648	648	SNP	1	G	1	C	49.2	190	386			
contig1 mapping	708	708	SNP	1	T	1	C	68.8	170	247			
contig1 mapping	709	709	SNP	1	A	2	T/A	56.7/41.1	131/95	231			
contig1 mapping	736	736	SNP	1	G	2	G/A	56.1/38.9	101/70	180			
contig1 mapping	738	738	SNP	1	G	1	A	89.6	163	182			
contig1 mapping	752	752	SNP	1	G	2	G/A	57.3/37.2	94/61	164			
contig1 mapping	760	760	SNP	1	G	1	C	42.9	42	98			
contig1 mapping	792	792	SNP	1	C	2	T/C	64.3/35.7	151/84	235			
contig1 mapping	805	805	SNP	1	G	1	A	92.9	247	266			
contig1 mapping	809	809	SNP	1	A	1	G	70.1	188	268			
contig1 mapping	816	816	SNP	1	G	2	A/G	64.6/35.0	179/97	277			
contig1 mapping	858	858	SNP	1	T	2	C/T	50.7/49.3	106/103	209			

Table Settings

Column width: Manual

Show column

- ☑ Mapping
- ☑ Reference Position
- ☑ Consensus Position
- ☑ Variation Type
- ☑ Length
- ☑ Reference
- ☑ Variants
- ☑ Allele Variations
- ☑ Frequencies
- ☑ Counts
- ☑ Coverage
- ☐ Variant #1
- ☐ Frequency of #1
- ☐ Count of #1
- ☐ Variant #2
- ☐ Frequency of #2
- ☐ Count of #2
- ☑ Overlapping Annotations
- ☑ Coding Region Change
- ☑ Amino Acid Change

Conclusions

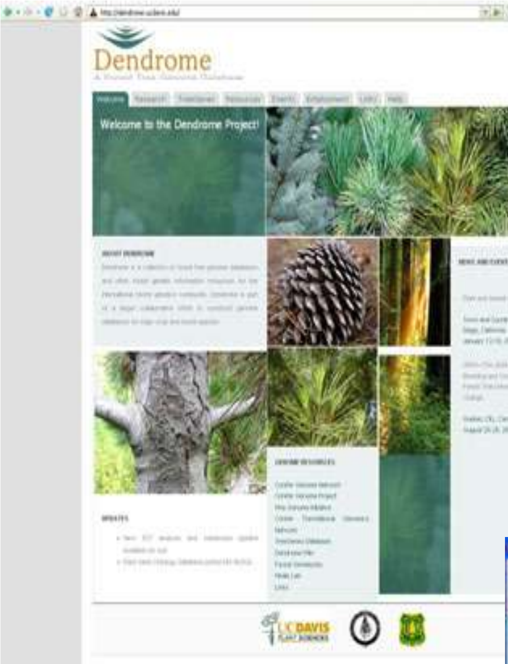
- Genome-wide association mapping help to identify genes responsible for adaptive trait variation, to study local adaptation, and to find genes and alleles under selection

- Genomic selection should help with **breeding for resilient trees**

- Technology of gene enrichment are effective for genome-wide gene genotyping via sequencing

Forest Tree Genome Databases

ForestTreeDB

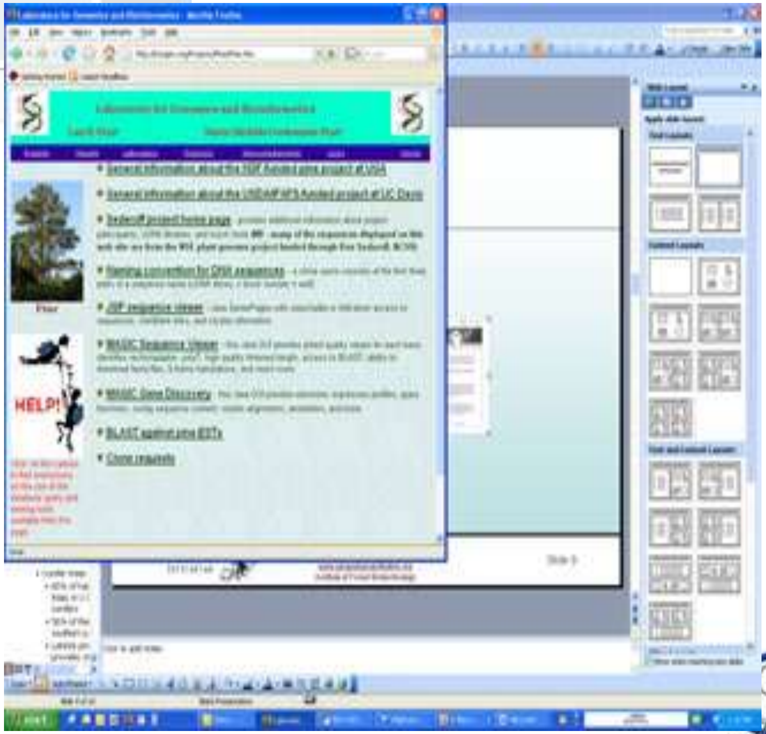


Dendrome

A Forest Tree Genome Database

Welcome to the Dendrome Project!

ConiferGDB



Welcome to Treenome.

a site for Forest Tree Population Genomics.

About Treenome

Site Under Construction

Межд. научная конф. «Защита леса – инновации во имя развития» 29-30 ноября 2012 г. ВНИИЛ, г. Пушкино, РФ

Current & Nearest Future Studies

- Discover all expressed genes in loblolly pine and provide partial to complete sequence (e.g., on-going DOE JGI sponsored projects)
- Complete genome sequence for major conifers (Douglas-fir, Norway spruce, Loblolly, Sugar, Scots and Maritime pines: (there are several projects in progress in Sweden, USA, EU and Russia)
- Landscape and ecological genomics: finding associations of SNPs, alleles, haplotypes, and genotypes with environmental factors, adaptive traits and phenotypes
- Genomic Selection (selection based on genome wide genotyping): genome wide markers are used to infer kinship relationships and to develop a regression model between markers and phenotypes in a training population and apply it to other breeding populations to predict and select the best performing individuals

Why complete genome sequence is important?

How would forest genetics and forest protection benefit from complete genome sequence for major conifers?

- identify and annotate genes, other functional elements (sRNA, transcription factors, regulatory elements, etc.) and genetic networks that control adaptation and disease resistance

- develop highly informative genetic markers that can be used in population genetic studies to create database of barcodes for individual populations to fight illegal timber harvest and trade

- develop genome-wide genetic markers for association studies for linking genetic variation (SNPs, alleles, haplotypes, and genotypes) with environmental factors, adaptive traits and phenotypes for better understanding genetic control of agronomically and economically important traits

- develop genome-wide genetic markers for genomic-assisted selection to breed for better adapted and desirable quality trees

- integrate proteomics, transcriptomics and metabolomics

- reference genome for resequencing

Current complete *de novo* conifer genome sequencing projects

Species	**Leading organization (PI, budget, start year)**
Norway spruce **(*Picea abies*)**	Umeå Plant Science Centre, Sweden (Dr. Pär Ingvarsson, $12M, 2010)
Loblolly pine **(*Pinus taeda*),** Douglas-fir **(*Pseudotsuga menziesii*),** Sugar pine **(*Pinus lambertiana*)**	University of California, Davis, USA (Dr. David Neale, $15M, 2011)
White, Sitka and Black spruce **(*Picea glauca* , *P. sitchensis* & *P. mariana*)**	Université Laval, Canada (Dr. John MacKay, $10M, 2010)
Maritime pine **(*Pinus pinaster*),** Scots pine **(*Pinus sylvestris*)**	European Union (Dr. María-Teresa Cervera, INIA CIFOR, Spain, $10M, 2011)
Siberian larch **(*Larix sibirica*),** Siberian pine **(*Pinus sibirica*)**	Siberian Federal University, Russia (Dr. Konstantin Krutovsky, $2M, 2011)

Scale of the problem: gigantic size of the genome!

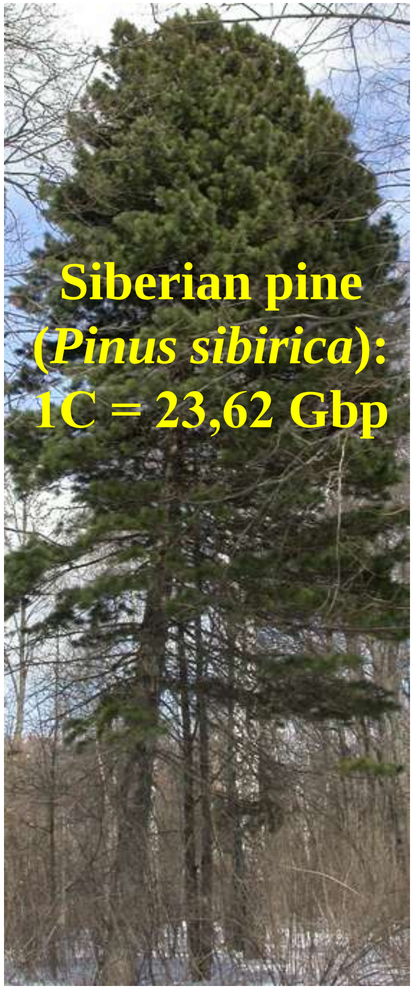
Comparative genome sizes in conifers that are objects of genome sequencing in current projects

Species [1]	DNA (1C)		Ratio to human genome
	pg	*Gbp*	
Human **(*Homo sapiens*)** [2]	**3.47**	**3.20**	**1**
Siberian larch **(*Larix sibirica*)** [3]	**12.30**	**12.03**	**4**
Douglas-fir **(*Pseudotsuga menziesii*)** [4]	**19.05**	**18.63**	**6**
Norway spruce **(*Picea abies*)** [5]	**20.01**	**19.57**	**6**
White spruce **(*Picea glauca*)** [3]	**20.20**	**19.76**	**6**
Loblolly pine **(*Pinus taeda*)** [4]	**22.10**	**21.61**	**7**
Scots pine **(*Pinus sylvestris*)** [5]	**22.98**	**22.47**	**7**
Siberian pine **(*Pinus sibirica*)** [6]	**24.15**	**23.62**	**7**
Maritime pine **(*Pinus pinaster*)** [3]	**24.35**	**23.81**	**7**
Sugar pine **(*Pinus lambertiana*)** [7]	**29.55**	**28.90**	**9**

[1] All **Pinaceae species** have 12 chromosome pairs except Douglas-fir that has 13 (http://data.kew.org/cvalues); [2] IHGSC 2004; [3] Ohri & Khoshoo 1986; [4] O'Brien *et al*. 1996; [5] Fuchs *et al*. 2008; [6] Siberian pine genome size hasn't been studied yet, and the data are given for the closest species *P. cembra* (Greilhuber 1986); [7] Wakamiya et al. 1993.

Scale of the problem: gigantic size of the genome!


Sugar pine
(*Pinus lambertiana*):
1C = 28.90 Gbp


Siberian pine
(*Pinus sibirica*):
1C = 23,62 Gbp


Norway spruce
(*Picea abies*):
1C = 19.57 Gbp


Siberian larch
(*Larix sibirica*):
1C = 12.03 Gbp

Human genome,
Homo sapiens:
1C = 3.20 Gbp

Other problems

- **highly repetitive** (75-80% of entire genome)
- **high allelic variation**
- **large gene families**

Optimization and innovative approaches are needed!

Innovative approaches

- **Combination of different size libraries: 200-800 bp paired-end tags (PET), 2-5 kb mate paired-end tags (MPET) or paired-end jumping libraries, 454 long reads, barcoded pooled fosmid libraries (30-40 Kb)**
- **Haploid tissue from single megagametophytes**
- **New assemblers (i.e., based on deBruijn graphs)**
- **Optical mapping (OpGen, Inc.; www.opgen.com)**
- **Haploid tissue culture**
- **Genome partitioning:**
  - **chromosome microdisection using laser capture microscopy (LCM) followed by**
  - **whole genome amplification (WGA)**

Acknowledgements

- United States Department of Agriculture
- National Science Foundation
- Western Gulf Forest Tree Improvement Program
- Texas Forest Service and Industry Partners
- CTGN Members & Collaborators
- Genetics Graduate Program, Texas A&M University
- Siberian Federal University
- Ministry of Science and Education, Russian Federation

TAMU Department of Ecosystem Science and Management

Laboratory of Forest Genomics

(http://treenome.tamu.edu/subpages/krut_lab.html)

Dr. Kostya Krutovsky
Associate Professor
k-krutovsky@tamu.edu
(979) 458-1417

Dr. Judy Brooks
Research Assistant
jebrooks@tamu.edu

Xixu Cai
Graduate Student
xixucai@tamu.edu

Dr. Tomasz Koralewski
Research Associate
tkoral@tamu.edu

Mengmeng Lu
Graduate Student
mira0501@tamu.edu

Vikram Chhatre
Graduate Student
crypticlineage@gmail.com

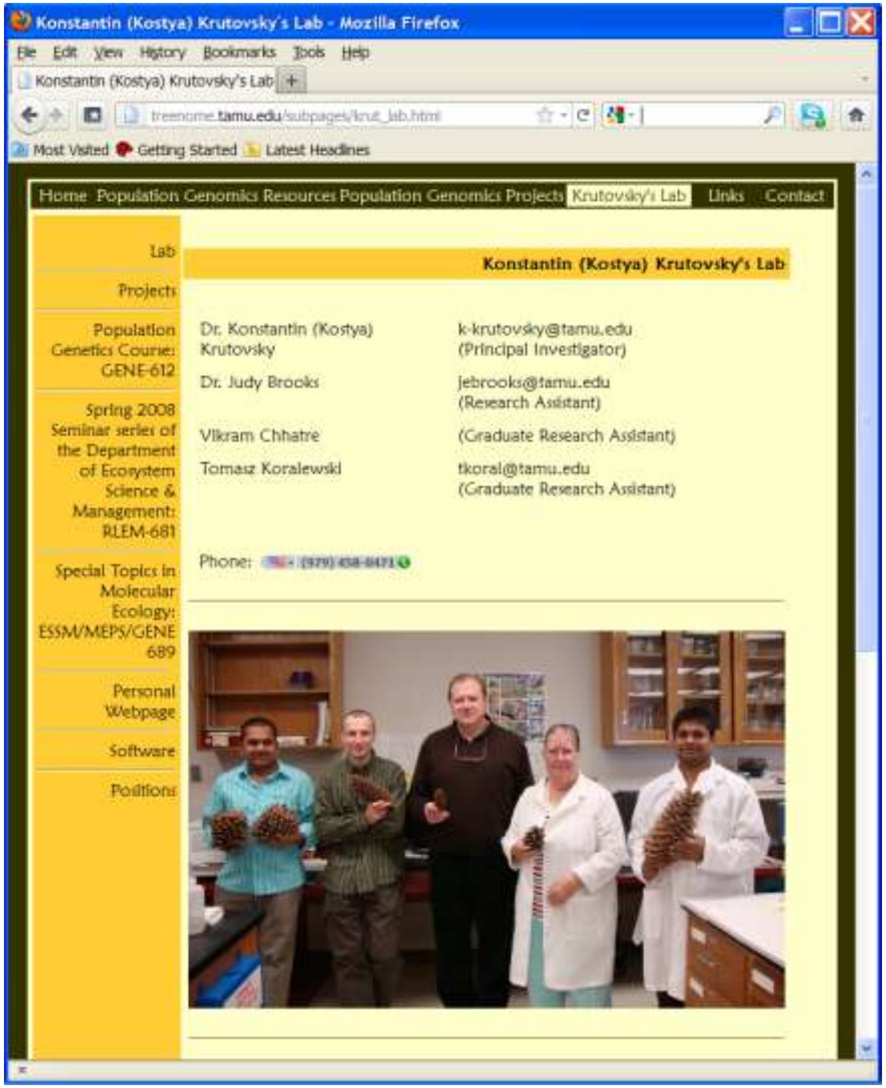
Habibul Islam
Graduate Student
milon237@tamu.edu

Acknowledgements

TAMU Department of Ecosystem Science and Management

Laboratory of Forest Genomics

(http://treenome.tamu.edu/subpages/krut_lab.html)



Konstantin (Kostya) Krutovsky's Lab

Dr. Konstantin (Kostya) Krutovsky	k-krutovsky@tamu.edu (Principal Investigator)
Dr. Judy Brooks	jebrooks@tamu.edu (Research Assistant)
Vikram Chhatre	(Graduate Research Assistant)
Tomasz Koralewski	tkoral@tamu.edu (Graduate Research Assistant)

Phone: + (979) 458-8471

Dr. Carol Loopstra
c-loopstra@tamu.edu

Texas A&M University ESSM

Dr. Tom Byram
t-byram@tamu.edu

TEXAS FOREST SERVICE
The Texas A&M University System

SIFG Southern Institute of Forest Genetics

Sedley Josserand
sjosserand@fs.fed.us

FOREST SERVICE U S DEPARTMENT OF AGRICULTURE

Ираида Николаевна Третьякова
Наталья Викторовна Орешкова

V. N. Sukachev Institute of Forest
Институт Леса им. В.Н. Сукачёва

Ирина Владимировна Чубугина

Krasnoyarsk Center for Forest Protection

Перспективы для сотрудничества

http://essm.tamu.edu/people-info/faculty/krutovsky-konstantin.aspx)

СИБИРСКИЙ ФЕДЕРАЛЬНЫЙ УНИВЕРСИТЕТ
SIBERIAN FEDERAL UNIVERSITY

Department of Ecosystem Science and Management

Dr. Konstantin "Kostya" V. Krutovsky

Title	Professor
Specialization	Forest genomics, population genetics, conservation genetics
Education	Ph.D., Population Genetics, N. I. Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow, Russia, 1984 M.Sc., Genetics, Institute of Cytology and Genetics, Russian Academy of Sciences and Department of Life Sciences, Novosibirsk State University, Novosibirsk, Russia, 1979 B.Sc., Genetics, Department of Genetics and Embryology, Samara State University, Samara, Russia, 1978 Diploma, Computer application in information and communication systems, Central Institute of Information Systems and Communication, Moscow, Russia, 1988
Office Phone	[illegible] (off.)
Office Fax	[illegible] (cell)
Email	[illegible]
Address	Department of Forest Genetics and Forest Tree Breeding Büsgen-Institute Georg-August-University of Göttingen Büsgenweg 2 D-37077 Göttingen Germany
Website	Visit Website

Research Web Site

Scientific Director, Genome Research and Education Center, Siberian Federal University

Texas A&M University
ESSM

TEXAS FOREST SERVICE
The Texas A&M University System

Forest Genetics and Forest Tree Breeding

Prof. Dr. Konstantin V. Krutovsky
Forest Genetics and Tree Breeding
Büsgen-Institut
University of Göttingen
Büsgenweg 2, D-37077 Göttingen

Prof. Dr. Konstantin "Kostya" V. Krutovsky

RESEARCH INTERESTS

- Evolutionary, population, conservation and ecologi
- Environmental stress and adaptive genes
- Comparative and population genomics
- Complete pine genome sequencing
- Genome, QTL, comparative, candidate gene and a mapping
- Genomic breeding
- Plant molecular systematics and phylogeny
- Introgressive hybridization, gene flow and mating s
- Molecular genetic marker development

EDUCATION

Ph.D. 1984 Population Genetics, Laboratory of Popu Genetics, N. I. Vavilov Institute of General Genetics, Academy of Sciences, Moscow, Russia
M.Sc. 1979 Genetics, Laboratory of Evolutionary Ger of Cytology and Genetics, Russian Academy of Scie Department of Life Sciences, Novosibirsk State Uni Novosibirsk, Russia
B.Sc. 1978 Genetics, Department of Genetics and E Samara State University, Samara, Russia
Diploma 1988 Computer application in information communication systems, Central Institute of Inform and Communication, Moscow, Russia

PROFESSIONAL EXPERIENCE

7/12 – present Professor, Department of Forest Gen Forest Tree Breeding, Büsgen-Institute, Georg-Augu Göttingen, Göttingen, Germany
9/12 – present Adjunct Professor, Department of Eco Science & Management, Texas A&M University, Colle USA
3/12 – present Scientific director, Genome Research Center, Siberian Federal University, Krasnoyarsk, Russia

Genome Research and Education Center
Siberian Federal University

Leadership

Leadership of Genome Research and Education Center

The Scientific director of the Center is Dr. **Konstantin V. Krutovsky**, Professor of Texas A&M University (USA) and the University of Göttingen (Germany).

Address: Department of Forest Genetics and Forest Tree Breeding
Büsgen-Institute
Georg-August-University of Göttingen
Büsgenweg 2
D-37077 Göttingen
Germany

Title: Professor

Specialization: Forest genomics, population genetics, conservation genetics

Education: Ph.D., Population Genetics, N. I. Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow, Russia, 1984
M.Sc., Genetics, Institute of Cytology and Genetics, Russian Academy of Sciences and Department of Life Sciences, Novosibirsk State University, Novosibirsk, Russia, 1979
B.Sc., Genetics, Department of Genetics and Embryology, Samara State University, Samara, Russia, 1978

IUFRO
The Global Network for Forest Science Cooperation

DIVISION 2 - PHYSIOLOGY AND GENETICS

2.02.00 – Conifer breeding and genetic resources

Coordinator: Konstantin (Kostya) Krutovsky, Germany
Deputies: [illegible], China

About Unit

This Research Group has the objective of genetically improving the growth and other properties of major coniferous tree species. It is also concerned with the identification and distribution of genetic variation in forest trees and with the preservation of genetic resources of conifers for the future.

Under construction

No upcoming meetings found for Unit 2.02.00.
Calendar of Meetings

Send comments to Konstantin (Kostya) Krutovsky (Coordinator)

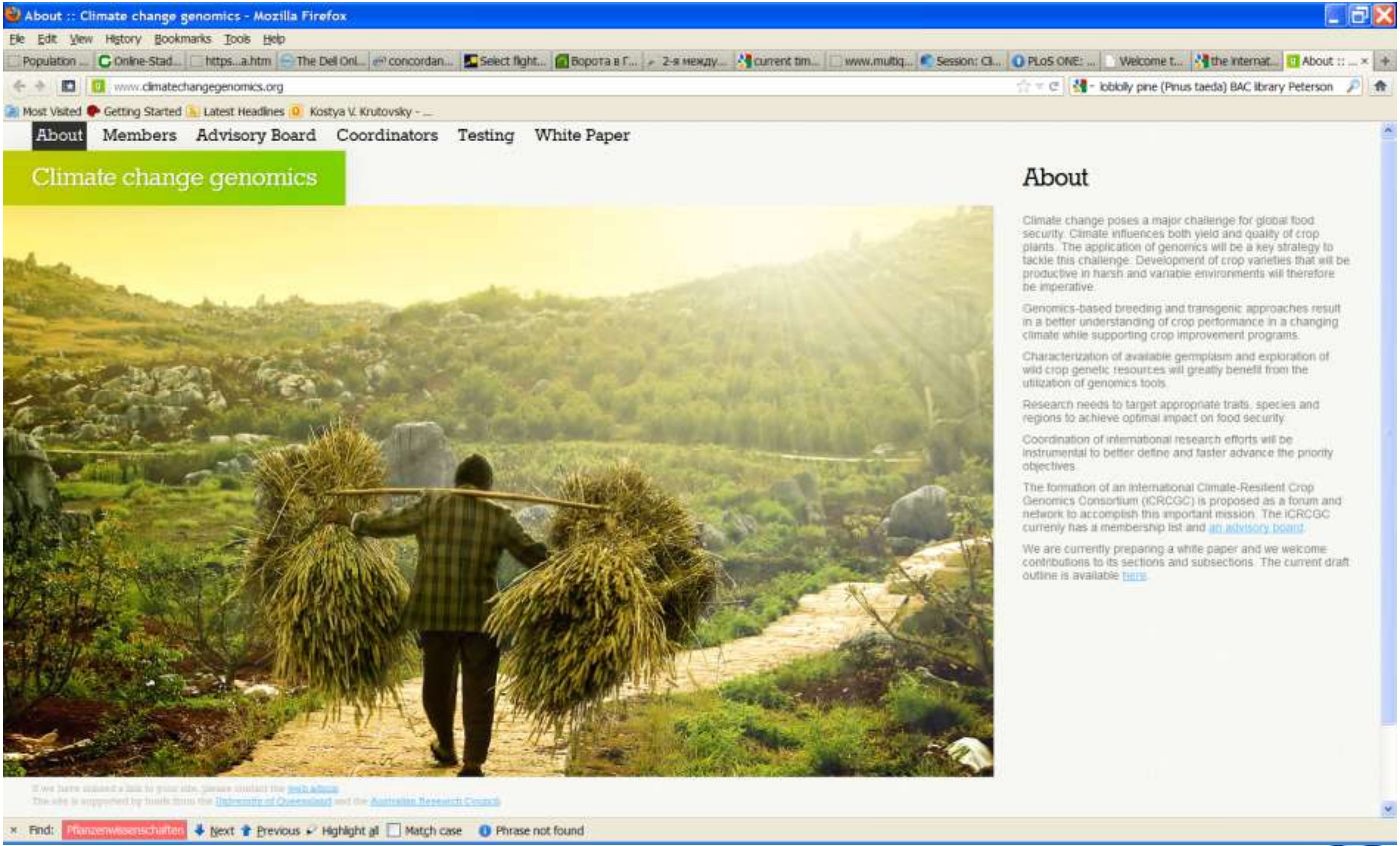
Southern Institute of Forest Genetics

FOREST SERVICE
U.S. DEPARTMENT OF AGRICULTURE

Krasnoyarsk Center for Forest Protection

V. N. Sukachev Institute of Forest
Институт Леса им. В.Н. Сукачёва

Перспективы сотрудничества: The International Climate-Resilient Crop Genomics Consortium (ICRCGC)



About

Climate change poses a major challenge for global food security. Climate influences both yield and quality of crop plants. The application of genomics will be a key strategy to tackle this challenge. Development of crop varieties that will be productive in harsh and variable environments will therefore be imperative.

Genomics-based breeding and transgenic approaches result in a better understanding of crop performance in a changing climate while supporting crop improvement programs.

Characterization of available germplasm and exploration of wild crop genetic resources will greatly benefit from the utilization of genomics tools.

Research needs to target appropriate traits, species and regions to achieve optimal impact on food security.

Coordination of international research efforts will be instrumental to better define and faster advance the priority objectives.

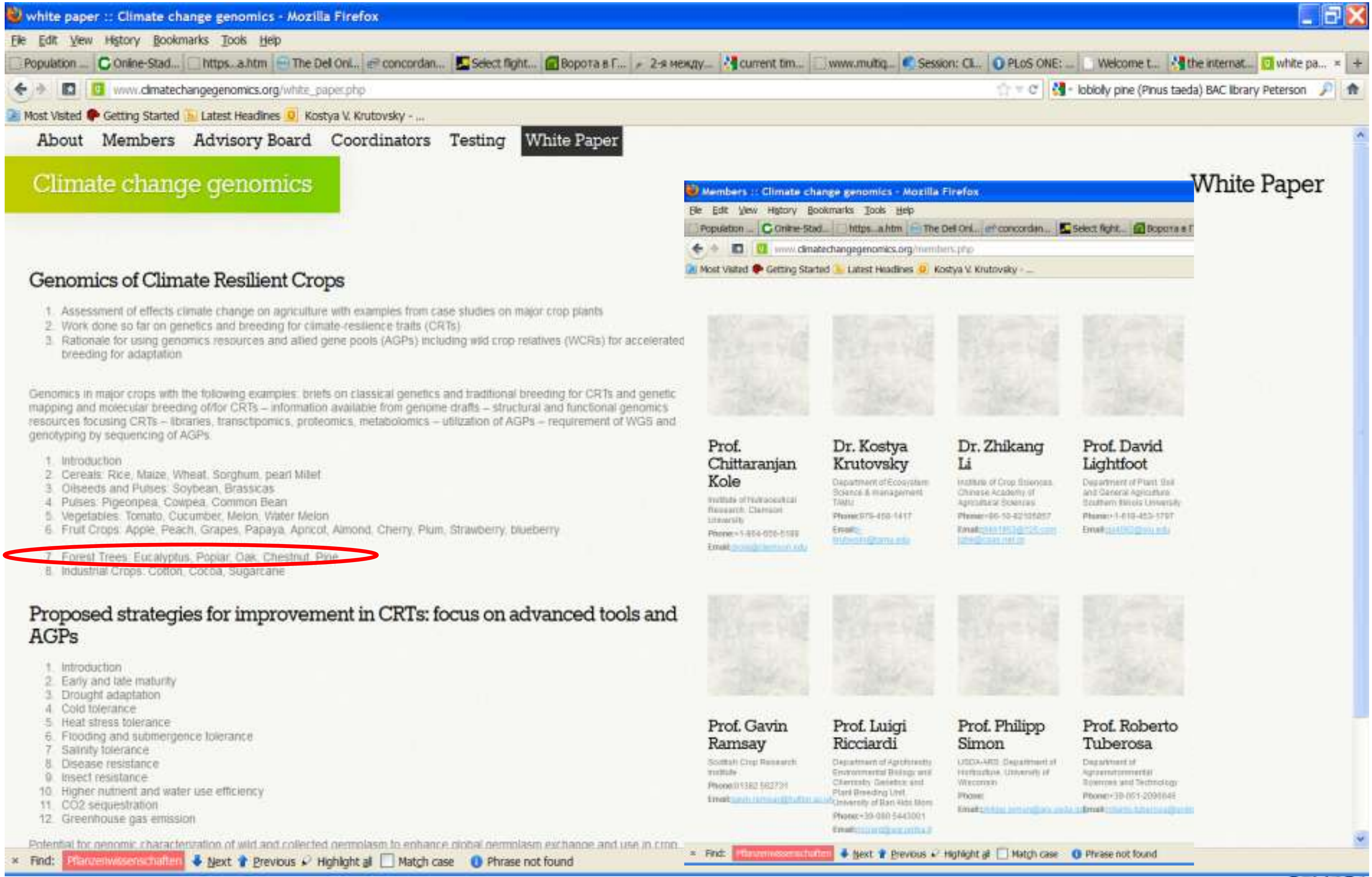
The formation of an international Climate-Resilient Crop Genomics Consortium (ICRCGC) is proposed as a forum and network to accomplish this important mission. The ICRCGC currently has a membership list and an advisory board.

We are currently preparing a white paper and we welcome contributions to its sections and subsections. The current draft outline is available here.

If we have missed a link to your site, please contact the web admin.
The site is supported by funds from the University of Queensland and the Australian Research Council

http://www.climatechangegenomics.org

Перспективы сотрудничества: The International Climate-Resilient Crop Genomics Consortium (ICRCGC)



White Paper

Genomics of Climate Resilient Crops

1. Assessment of effects climate change on agriculture with examples from case studies on major crop plants
2. Work done so far on genetics and breeding for climate-resilience traits (CRTs)
3. Rationale for using genomics resources and allied gene pools (AGPs) including wild crop relatives (WCRs) for accelerated breeding for adaptation

Genomics in major crops with the following examples: briefs on classical genetics and traditional breeding for CRTs and genetic mapping and molecular breeding of/for CRTs – information available from genome drafts – structural and functional genomics resources focusing CRTs – libraries, transctiponics, proteomics, metabolomics – utilization of AGPs – requirement of WGS and genotyping by sequencing of AGPs.

1. Introduction
2. Cereals: Rice, Maize, Wheat, Sorghum, pearl Millet
3. Oilseeds and Pulses: Soybean, Brassicas
4. Pulses: Pigeonpea, Cowpea, Common Bean
5. Vegetables: Tomato, Cucumber, Melon, Water Melon
6. Fruit Crops: Apple, Peach, Grapes, Papaya, Apricot, Almond, Cherry, Plum, Strawberry, blueberry
7. Forest Trees: Eucalyptus, Poplar, Oak, Chestnut, Pine
8. Industrial Crops: Cotton, Cocoa, Sugarcane

Proposed strategies for improvement in CRTs: focus on advanced tools and AGPs

1. Introduction
2. Early and late maturity
3. Drought adaptation
4. Cold tolerance
5. Heat stress tolerance
6. Flooding and submergence tolerance
7. Salinity tolerance
8. Disease resistance
9. Insect resistance
10. Higher nutrient and water use efficiency
11. CO2 sequestration
12. Greenhouse gas emission

Potential for genomic characterization of wild and collected germplasm to enhance global germplasm exchange and use in crop

Prof. Chittaranjan Kole
Institute of Nutraceutical Research, Clemson University

Dr. Kostya Krutovsky
Department of Ecosystem Science & Management TAMU

Dr. Zhikang Li
Institute of Crop Sciences Chinese Academy of Agricultural Sciences

Prof. David Lightfoot
Department of Plant Soil and General Agriculture Southern Illinois University

Prof. Gavin Ramsay
Scottish Crop Research Institute

Prof. Luigi Ricciardi
Department of Agroforestry, Environmental Biology and Chemistry, Genetics and Plant Breeding Unit University of Bari Aldo Moro

Prof. Philipp Simon
USDA-ARS, Department of Horticulture, University of Wisconsin

Prof. Roberto Tuberosa
Department of Agroenvironmental Sciences and Technology

Перспективы сотрудничества: Проекты в США

Научный договор с Лесной службой США, **руководитель проекта «Геномный анализ ладанной сосны - секвенирование и картирование»**, 1 год, 6/29/2012-4/30/2013, бюджет $42,491 (USDA Forest Service Coop Agreement Award #12-CA-11330126-064, PI: K. V. Krutovsky, CoPI: Nurul Islam-Faridi, 1 year, 6/29/2012-4/30/2013, $42,491, “Genomic Analysis of Loblolly Pine - Sequencing and Mapping”)

Техасский агро-механический университет, Научная инициатива по целостно-системным геномном исследованиям, **руководитель проекта «Высокопроизводительное секвенирование целых хромосом изолированных с помощью лазерной микроскопии»**, 1 год, 1 сентября 2011 г. – 31 августа 2012 г., бюджет $10,000 (Texas A&M University Whole Systems Genome Initiative (WSGI) Catalyst Research Grant, PI: K. V. Krutovsky, CoPIs: Nurul Islam-Faridi, C. Dana Nelson, 1 year, 9/1/2011-8/31/2012, $10,000; "High-throughput Sequencing of Laser Microscopy-captured Individual Loblolly Pine Chromosome 12")

Министерство сельского хозяйства США, Программа региональных подходов к проблеме изменения климата, # A3101, **соруководитель проекта «Интеграция науки, образования и прикладного хозяйства для улучшения адаптации южных сосновых лесов к изменению климата и смягчения его пагубных последствий»**, 5 лет, 1 января 2011 г. – 31 декабря 2015 г., бюджет $19,976,825 (USDA NIFA Agriculture and Food Research Initiative (AFRI) Competitive Grants Program, Climate Change Program 1: Regional Approaches to Climate Change, Program Area Code – A3101, PI: Timothy Martin, CoPI: K. V. Krutovsky (with $696,559 research budget allocated) et al., 5 years, 1/1/2011-12/31/2015, $19,976,825; “Integrating research, education and extension for enhancing southern pine climate change mitigation and adaptation”)

Министерство сельского хозяйства США, Программа развития национальных кадров, # 2009·38420·05631**, руководитель проекта «Подготовка аспирантов в области лесных ресурсов, восстановления и сохранения лесов»**, 5 лет, 2 января 2010 г. – 31 августа 2014 г., бюджет $349,200 (United States Department of Agriculture (USDA) Cooperative State Research, Education, and Extension Service (CSREES), Food and Agricultural Sciences National Needs Graduate and Postgraduate Fellowship (NNF) Grants Program, # 2009·38420·05631, K. V. Krutovsky et al., 5 years, January 2, 2010 - August 31, 2014, $349,200, “A Graduate Program in Forest Resource: Developing Integrated Expertise in Forest Resource, Management, Conservation and Restoration”)

Министерство сельского хозяйства США и Сельско-хозяйственная экспериментальная станция шт. Техас, Программа лесного развития, TEX09122-0210381, руководитель проекта «Сравнительная популяционная геномика и генетический контроль засухоустойчивости южных сосен», 5 лет, 1 мая 2007 г. – 30 апреля 2012 г., бюджет $132,800 (United States Department of Agriculture (USDA) Cooperative State Research, Education, and Extension Service (CSREES) Current Research Information System (CRIS), Texas Agricultural Experiment Station (TAES) McIntire-Stennis Project, TEX09122-0210381, K. V. Krutovsky, 05/01/2007 - 04/30/2012, $132,800, “Comparative population genomics of drought resistance-related candidate genes in Southern pines”)

Перспективы сотрудничества: Проекты в РФ и Европе

РФ:

Министерство образования и науки Российской Федерации, Федеральная целевая программа «Научные и научно-педагогические кадры инновационной России» на 2009 – 2013 годы (мероприятие 1.5, естественные науки очередь X1X), шифр заявки 2012-1.5-12-000-1001-002, **руководитель проекта «Полногеномное секвенирование лиственницы сибирской»**, Центр геномных исследований Федерального государственного автономного образовательного учреждения высшего профессионального образования "Сибирский федеральный университет", 1,5 года, 24 сентября 2012 г. – 14 ноября 2013 г., бюджет 2 млн руб ($65,000)

Европа:

EvolTree (EVOLution of TREEs as drivers of terrestrial biodiversity; http://www.evoltree.eu) - a network of excellence that was launched and financially supported by the European Union within the 6th framework programme in April 2006. The network has been extended under the umbrella of the European Forest Institute (EFI) network. The new consortium is now made up of 23 research groups in 13 European countries. **Coordinator from Georg-August-University of Göttingen, Germany – Prof. Dr. K. V. Krutovsky**

NovelTree – research consortium (http://www.noveltree.eu), composed of 15 public and private European partners coordinated by Dr. Catherine Bastien (INRA-Orléans, France) and is designed to enable significant genetic improvement of the composition and characteristics of forest products to satisfy the needs (quality, quantity, sustainability, vulnerability) of consumers and the forest-based sector. NovelTree has received an EC contribution of 4.1 million Euros in the frame of the priority "Life Sciences, Biotechnology and Biochemistry for Sustainable Non-Food Products and Processes“for 4 years (2008-2012). **Coordinator from Georg-August-University of Göttingen, Germany – Prof. Dr. K. V. Krutovsky**

SustainPine – research consortium “Genomic tools in maritime PINE for enhanced biomass production and SUSTAINable forest management” (http://www.scbi.uma.es/sustainpine), composed of 6 working parties and 11 public and private European partners coordinated by Dr. Francisco M. Cánovas (Universidad de Málaga, BMB, Spain) funded by the PLANT-KBBE 2009 Program: “Scientific and Technological Cooperation in Plant Genome Research as basis of the 'Knowledge Based Bio-Economy‘”. **Coordinator from Georg-August-University of Göttingen, Germany – Prof. Dr. K. V. Krutovsky**

Перспективы сотрудничества

КОМПЛЕКСНАЯ ПРОГРАММА
развития биотехнологий в Российской Федерации
на период до 2020 года
Утверждённая Правительством Российской Федерации 24 апреля 2012 г.

Координатор Программы: Министерство экономического развития Российской Федерации

Основные участники Программы: **Мин-во образования и науки**, Мин-во промышленности и торговли, Мин-во сельского хозяйства, Мин-во природных ресурсов и экологии, Мин-во здравоохранения и социального развития, Мин-во энергетики, Мин-во регионального развития, Федеральное агентство лесного хозяйства, Федеральное агентство по рыболовству, **Российская академия наук**, Российская академия медицинских наук, Российская академия сельскохозяйственных наук, организации-координаторы технологических платформ "Медицина будущего", "Биоиндустрия и биоресурсы - БиоТех2030", "Биоэнергетика»

Стр. 28: **Приоритеты развития:**

- биофармацевтика и биомедицина;
- промышленная биотехнология и биоэнергетика;
- сельскохозяйственная и пищевая биотехнология;
- **лесная биотехнология;**
- природоохранная (экологическая) биотехнология;
- морская биотехнология.

Перспективы сотрудничества

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Стр. 47-50: **7. Лесная биотехнология:**

Реализация Программы в части приоритетного направления "Лесная биотехнология" приведет к созданию в стране современной системы управления лесонасаждениями с привлечением методов ДНК маркирования, созданию новых биотехнологических форм деревьев с заданными признаками, развитию плантационного лесовыращивания, созданию условий для малоотходной переработки древесины, утилизации отходов лесопиления, а также к созданию спроса на современные экологически безопасные средства защиты леса.

7.1 "Применение биотехнологий для управления лесонасаждениями"

Одним из приоритетных направлений развития лесных биотехнологий является **молекулярное (ДНК) маркирование**, направленное на решение следующих задач лесного хозяйства и промышленности:

- **совершенствование принципов и подходов лесосеменного районирования;**
- **генетическая паспортизация и сертификация семян;**
- мониторинг фитосанитарного состояния питомников и лесонасаждений;
- **контроль законности происхождения древесины.**

7.2 "Применение биотехнологий для сохранения и воспроизводства лесных генетических ресурсов"

- создание банков in vitro редких и исчезающих видов лесных растений;
- клональное микроразмножение редких и исчезающих видов лесных древесных и травянистых растений для создания резерватов;
- **мониторинг состояния лесных генетических ресурсов с применением методов анализа ДНК;**
- **оценка генетического разнообразия лесных насаждений с использованием методов анализа ДНК.**

Перспективы сотрудничества

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7.3 "Создание биотехнологических форм деревьев с заданными признаками"

Экономическая эффективность лесонасаждений (лесных плантаций в частности) в первую очередь зависит от продуктивности и устойчивости к биотическим и абиотическим факторам среды используемых лесных пород. В свою очередь эти характеристики зависят от генетической ценности и качества посадочного материала.

Необходима ... **селекция основных лесообразующих пород на основе ДНК маркирования** для выведения новых гибридных и сортовых форм; создание биотехнологических форм деревьев с заданными признаками, например, с пониженным содержанием лигнинов, устойчивостью к гербицидам; клональное микроразмножение генетически ценных форм деревьев с целью быстрого выведения на рынок новейших селекционных достижений и повышения качества посадочного материала.

... Быстрорастущие деревья являются также одним из эффективных способов борьбы с изменением климата в качестве поглотителей углекислого газа. Другим направлением использования быстрорастущего леса является его использование в качестве сырья для биотоплива.

7.4 "Биологические средства защиты леса«

...

В результате реализации Программы в России будет создана современная база промышленного производства, характеризующаяся повышенным ресурсным потенциалом лесов и существенно сниженным уровнем безвозвратных отходов лесного производства.

Ответственный за разработку и реализацию комплекса мер по направлению - Рослесхоз.

Перспективы сотрудничества

КОМПЛЕКСНАЯ ПРОГРАММА
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Важность геномных исследований многократно отмечена в Программе в контексте:

- развития системной биологии (стр. 30)
- геномных и постгеномных технологий (стр. 30)
- биоинформатики (стр. 30)
- клеточных технологий (стр. 30)
- идентификации новых диагностических и терапевтических мишеней, особенно с позиции персонификации лечения (стр. 32, 67)
- создания новых сортов сельскохозяйственных растений и животных нового поколения, устойчивых к болезням, засухе, гербицидам, насекомым-вредителям и неблагоприятным условиям среды (методы геномной селекции, основанные на использовании молекулярных маркеров) (стр. 41, 42, 73, 75)
- разработка и внедрение методов геномной паспортизации для повышения эффективности селекционно-племенной работы, технологий клонирования животных-производителей (стр. 41)
- скрининг большого числа мутаций (полиморфизмов), связанных с уровнем развития экономически-значимых селекционных признаков сельскохозяйственных животных (стр. 42, 75)
- расшифровка геномов основных сельскохозяйственных растений (стр. 73)

Перспективы сотрудничества

КОМПЛЕКСНАЯ ПРОГРАММА
развития биотехнологий в Российской Федерации
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Предполагаемые объемы финансирования по направлениям, млрд. рублей, в ценах соответствующих лет:

2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2011-2020	%
1	3	3	3	4	5	5	6	7	8	45	3,8

П Л А Н
первоочередных мероприятий по реализации Программы

№ п/п	Содержание мероприятия	Вид документа	Срок представления	Срок принятия /внесения в Государственную Думу	Ответственный исполнитель
2	Разработка предложений по созданию специализированного научно-производственного **центра лесных биотехнологий**	Доклад в Правительство Российской Федерации	2012 год	-	Рослесхоз, РАН, и др.
6	Подготовка предложений по **внедрению технологий молекулярного маркирования** в практику лесосеменного районирования, сертификации семян, мониторинга фитосанитарного состояния и биоразнообразия лесных насаждений	Доклад в Правительство Российской Федерации	2012 год	-	Рослесхоз, РАН, и др.

- **XX century:**
  Evolutionary theory + Genetics
  = Synthetic theory of evolution (Genetic theory of evolution or Evolutionary Genetics)

↓

population genetics level of thinking

Theodosius Dobzhansky (1900-1975)

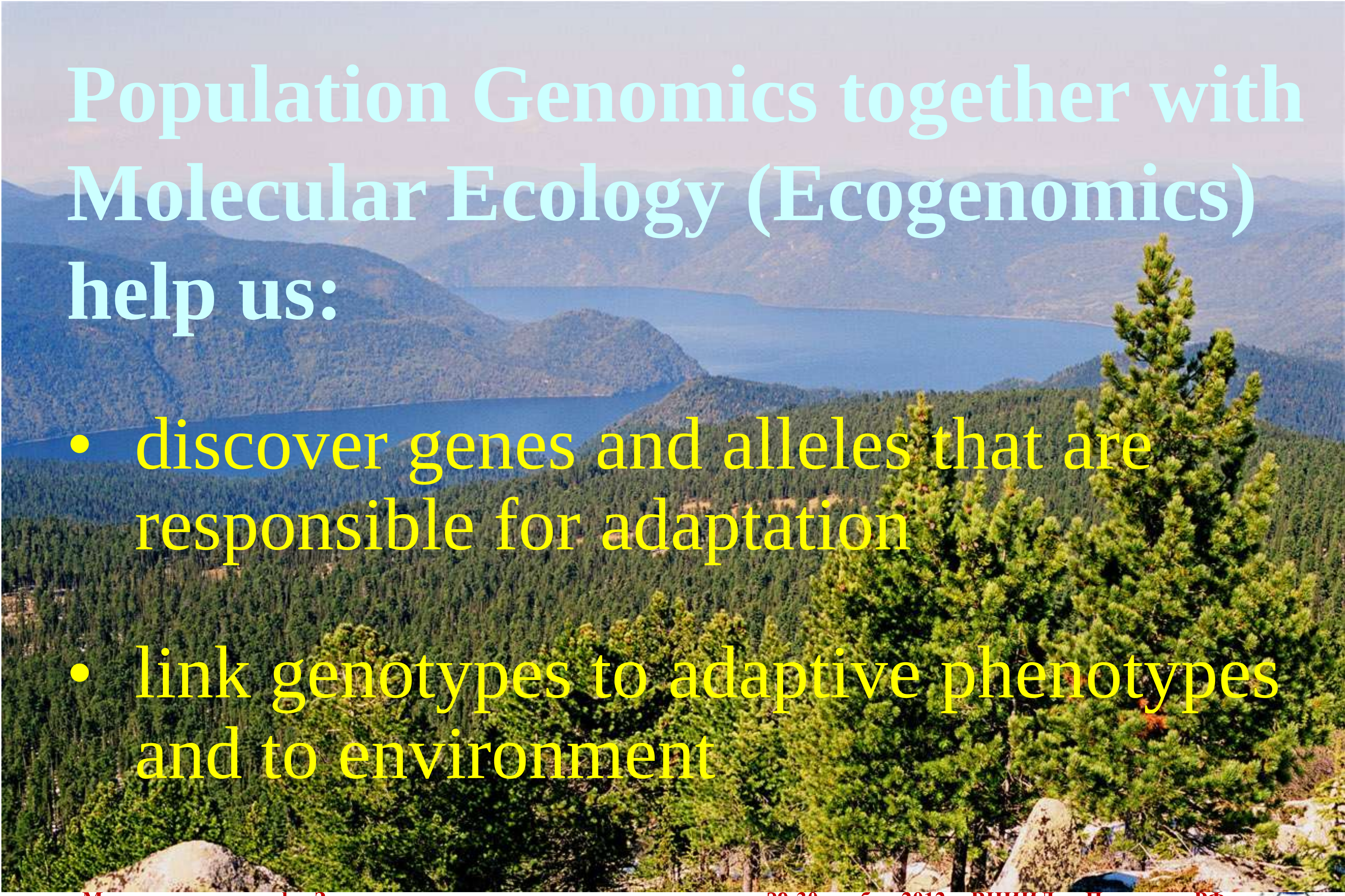
- **XXI century:**
  Molecular genetics + Bioinformatics
  = Genomics

↓

population genomics level of thinking

Krutovsky, K.V. 2006 From Population Genetics to Population Genomics of Forest Trees: Integrated Population Genomics Approach. *Russ. J. of Genetics* 42(10): 1088–1100

Благодарю за внимание!



Population Genomics together with Molecular Ecology (Ecogenomics) help us:

- discover genes and alleles that are responsible for adaptation
- link genotypes to adaptive phenotypes and to environment