Association mapping for wood traits in white spruce

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ABSTRACT

White spruce is one of the most economically important tree species in Canada. The study of its wood properties is essential to help enhance the economic output of the Canadian forest product industry. The discovery of genes that are linked to these properties can be used to elaborate molecular tools for more efficient selection of high performance trees. These selection tools can be applied to breeding programs and lead to greater gains per unit of time to benefit industry more rapidly. In this project we propose to identify favourable alleles for 500+ such candidate genes in mature white spruce. For each candidate gene, primers are designed to sequence and identify a number of common SNPs. All genotyping arrays are developed for high-throughput genotyping. A 495-tree discovery population has been assembled with three siblings per family. Phenotyping will be carried out using Paprican's Evaltree, which encompasses a unique suite of technologies, including the SilviScan from CSIRO. We aim to detect associations between polymorphisms in candidate genes and phenotypic variation by using Quantitative Transmission/Disequilibrium Testing (TDT), a family-based association test. A second population of 200 trees will also be used for the validation of the associations revealed by TDT. These populations will also be used to estimate genetic variance components for wood properties and crown architecture and assess correlations between these traits. This research is part of Arborea II, a large-scale project funded by Genome Canada, Genome Quebec and the Canadian Biotechnology Strategy, which aims to develop molecular breeding tools for softwood trees.

EXPERIMENTAL APPROACH

30-year-old progeny test

Validation population   Discovery population

Physical and chemical traits

- Basic density
- Microfibril angle
- Avg. cell wall radii
- Avg. cell wall tangential dimensions
- Fibre coarseness
- Wood stiffness (MOE)
- % cellulose
- % hemicellulose
- % lignin
- % extractives
- Bark N concentration

Non-destructive evaluation of wood properties

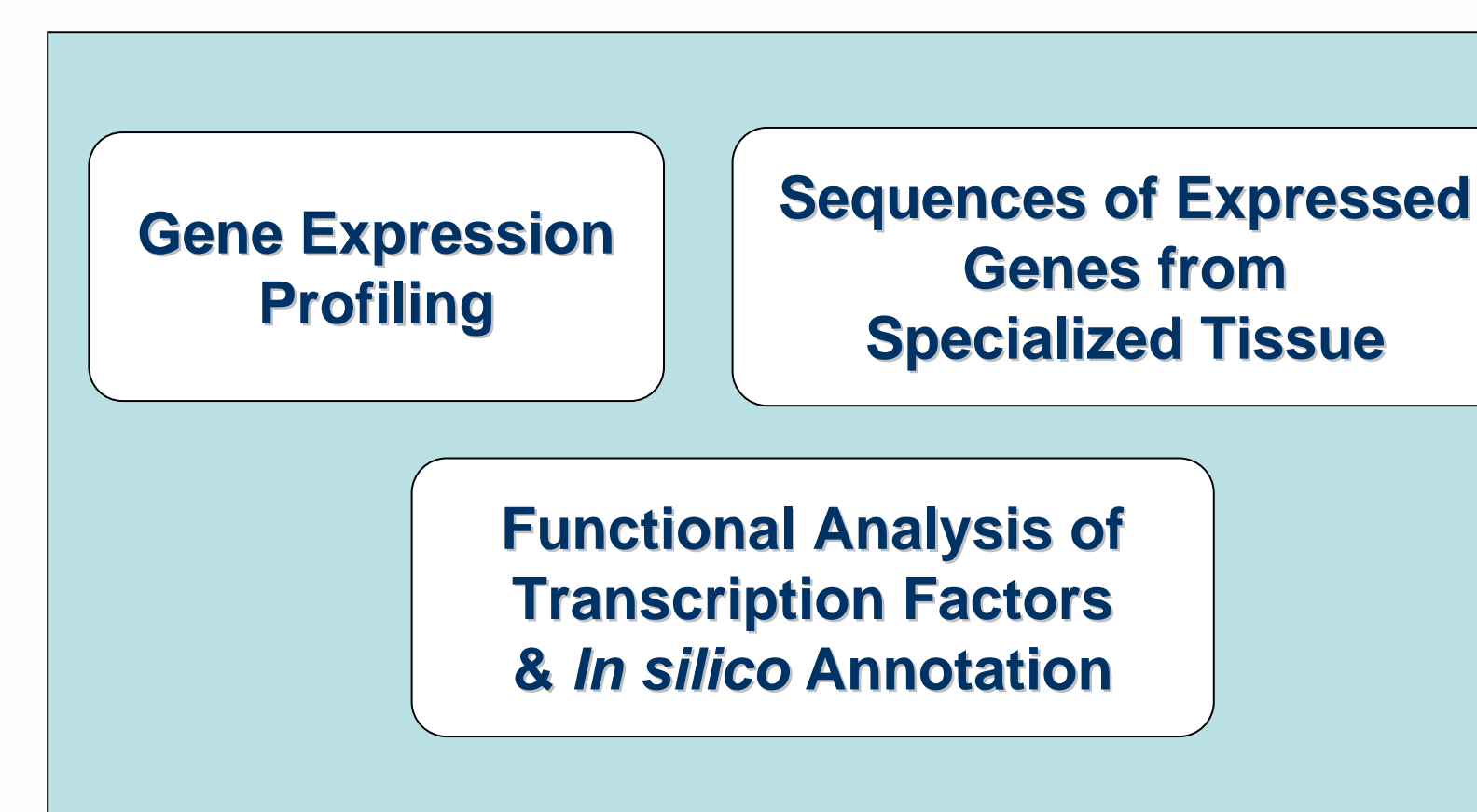SilviScan, CSIRO   Wet chemistry

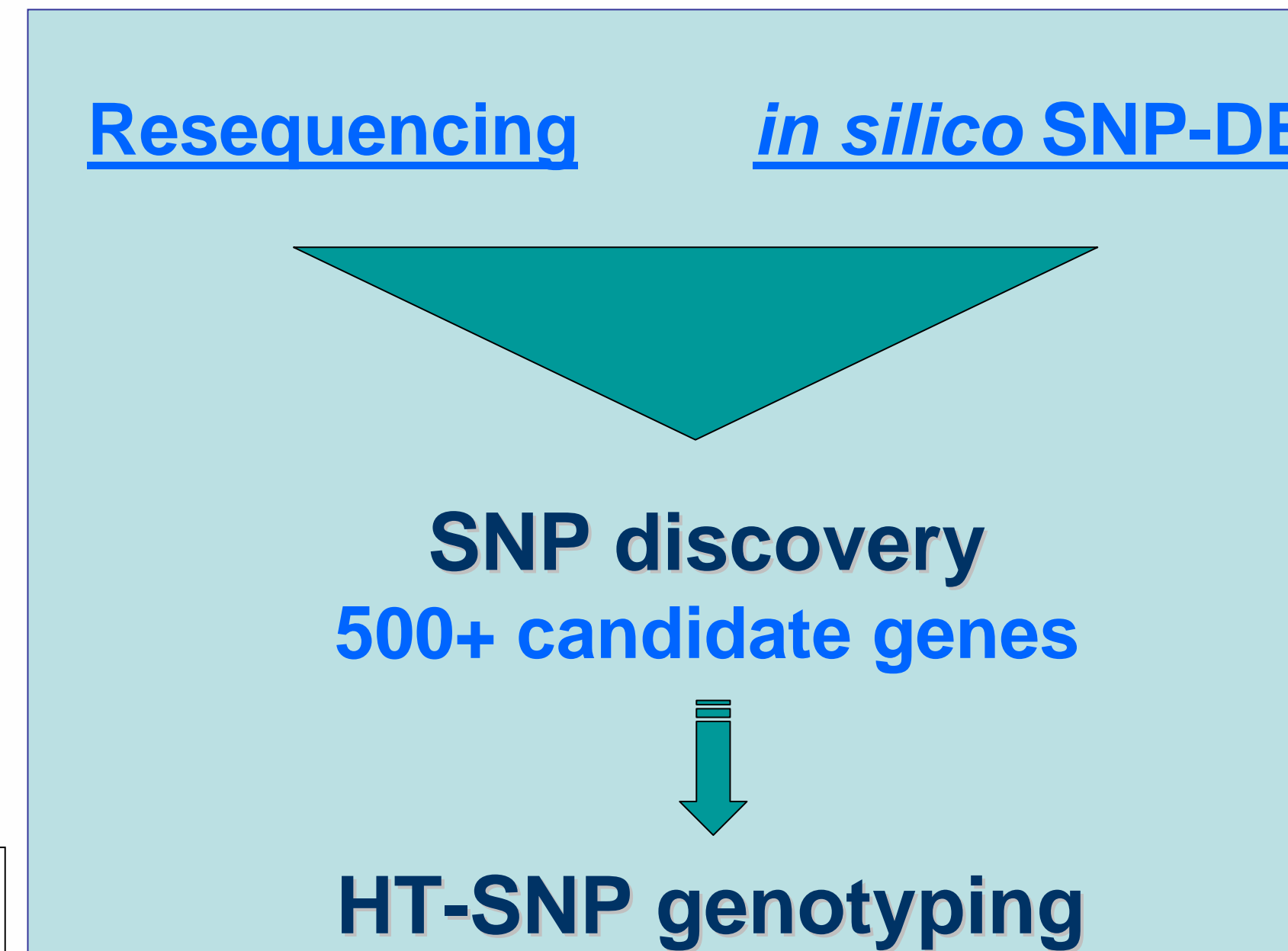Near infrared spectroscopy   Raman spectroscopy

Genetic parameters (Heritabilities, Genetic correlations)
Affordable methods to assess wood traits

CANDIDATE GENE DISCOVERY & FUNCTION

Expression Profiles | Gene Sequences ORFeome | Gene Families Transcription Factors

49,100 cDNA clones
14,471 transcripts

100,000 new cDNA clones

Spruce DB

Gene Expression Profiling | Sequences of Expressed Genes from Specialized Tissue

Functional Analysis of Transcription Factors & *In silico* Annotation

Genotyping

Resequencing   *in silico* SNP-DB

SNP discovery
500+ candidate genes

HT-SNP genotyping
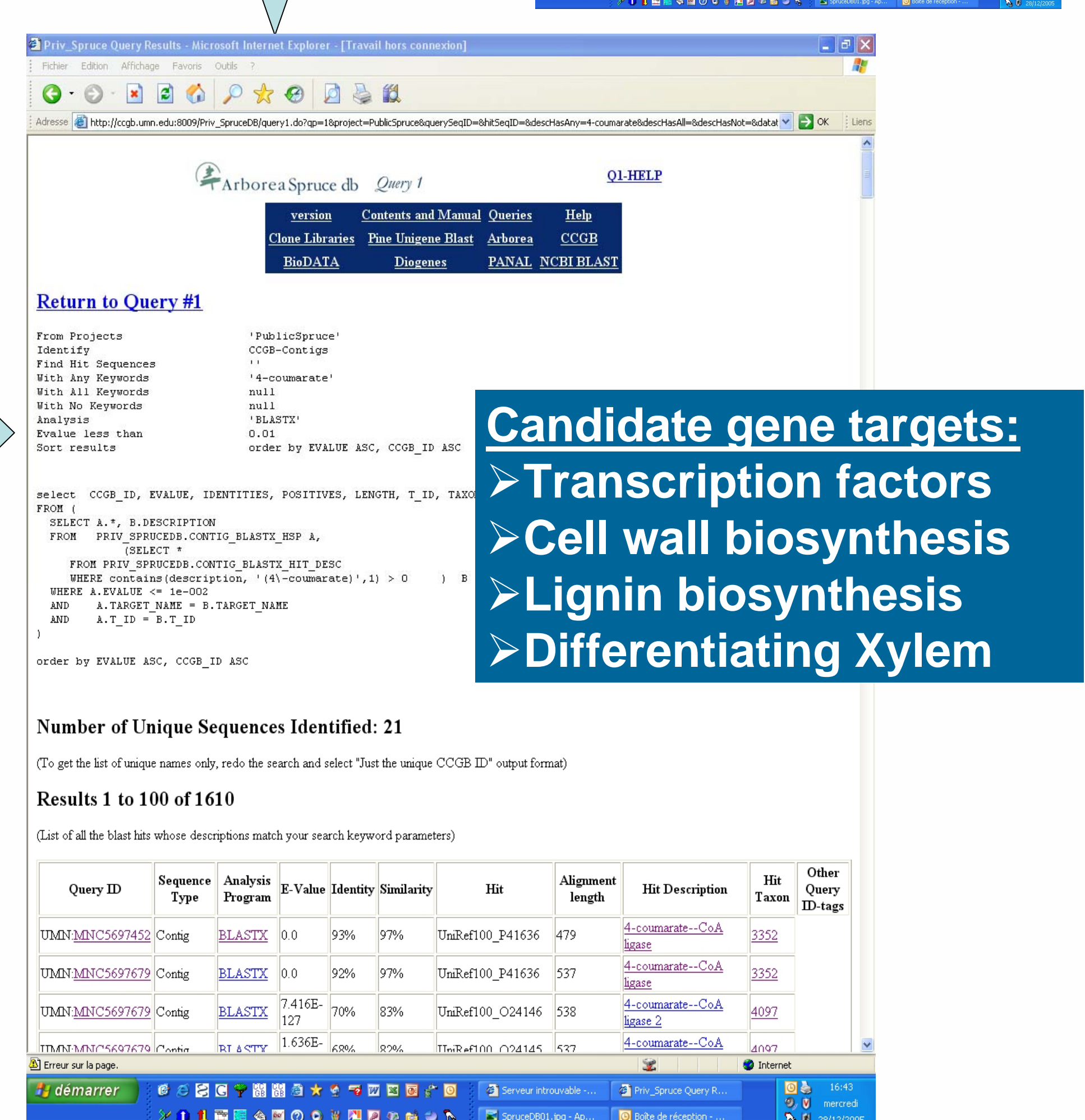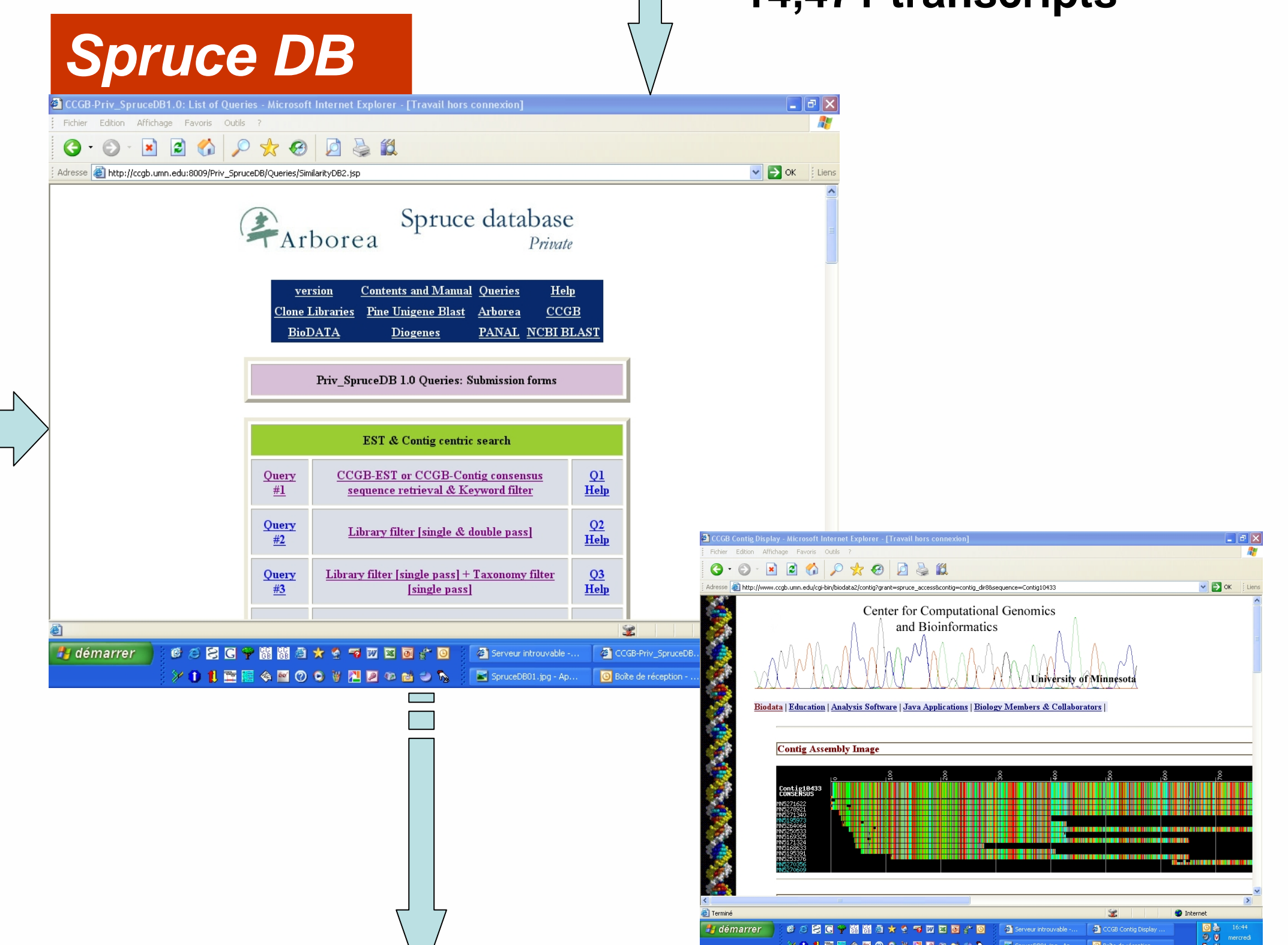
Candidate gene targets:
➢ Transcription factors
➢ Cell wall biosynthesis
➢ Lignin biosynthesis
➢ Differentiating Xylem

DATA INTEGRATION

Family-based Association Tests

Molecular Breeding

Molecular forward selection

Source: WWW.ORCHID.COM

Year
2002
2006
2010
Arborea Phase I
Arborea Phase II