Project Progress Summary

Section 1: PROJECT IDENTIFICATION	**NOT CONFIDENTIAL**

Title of the project: **Importance of regulation mechanisms for the climatic adaptation of tree species (An example *of Picea abies*).**

Acronym of the project: **Adaptability**

Type of contract: **Shared-cost research project**		Total project cost (in euro) **1.562.777 €**
Contract number: **QLK5-CT-2000-00349**	Duration (in months) **42 Months**	EU contribution (in euro) **1.279.208 €**
Commencement date: **01.12.2000**	Period covered by the progress report: **01.12. 2002 - 01.12. 2003**	

PROJECT COORDINATOR

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Key words

adaptation, environment, induced gene expression, *Picea abies*

World wide web address: **www.adaptability.de**

List of participants:

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Section 2: Project Progress Report **NOT CONFIDENTIAL**

(2 pages maximum.. Use short sentences. Be factual. Avoid technical terms as much as possible)

Objectives: Main objectives

- Selection processes acting on gametophytes during male and female meiosis (meiotic drive), pollen tube growth, megaspore degeneration, fertilisation and embryo competition.
- Environmentally induced gene expression (genomic imprinting) during the reproductive process specifies the production of particular gene products (proteins, enzymes or regulatory molecules) shaping the expression of adaptive traits in the progenies.

Specific objectives according to the WP's

- Crossing experiments with the same genotypes under different environmental conditions (climates) in a phytotron (WP1.1).
- Characterisation of cold resistance and bud-set phenology differences (WP1.2).
- How fast can Norway spruce adapt to different climatic conditions? (WP1.3).
- Characterisation of drought resistance differences (WP1.4).
- Investigations of physiological traits (WP 1.5)
- Investigations on the basis of allo-enzyme markers. Analyses of seed samples megagametophyte/embryo) (WP 2.1).
- Investigations on the basis of highly variable DNA-markers (microsatellites) (WP2.2).
- Investigations on the basis of EST-markers (WP2.3).
- Environmental effects on methylation of DNA and transcription and translation of phytochrome genes, cycline genes and other identified genes (WP3.1).
- Differential display of newly identified genes (WP3.2)
- Development of practical recommendations based on the project results (WP4.1)

Results and Milestones: according to the specific objectives

WP 1.1: This experiment was finished in the second project period. Four climatic treatments were applied during fertilisation, embryo development and seed ripening, combining short and long days and low and high temperatures.
WP 1.2: Significant differences were present between the maternal treatments for several traits in all tested environments. A significant interaction was consequently identified between the two treatment factors maternal temperature and photoperiod during seed production.
WP 1.3: Offspring from spruce plantations identified by mitochondrial DNA markers to be of Central European origin were more similar to local Norwegian than to their parental provenances.
WP 1.4: The environment in which the seeds were produced and matured is a highly significant factor for phenology but not for height growth. The seeds from a warm green-house produce seedlings with a significantly delayed budset as compared to seedlings originating from seeds produced in outdoor seed-orchard.
WP 1.5: Drought and frost stress experiments were done with different families. Chlorophyll fluorescence was used as a parameter to quantify drought- and frost-stress in plants with respect to the activity of PS II. Stressed and unstressed seedlings were characterized by protein content and enzyme activity of superoxide dismutase (SOD) and guaiacol peroxidase (GuPOD).
WP 2.1: Genes controlling 15 enzyme systems were analysed in the seedlings of three families under four treatments. The isozyme database is in progress.
WP 2.2: 4 progenies were analysed at 35 polymorphic loci. Distorted segregations were detected for 12 markers. Linkage groups were determined and distorted genomic zones revealed in each parent and each crossing environment were indicated.
WP 2.3: 4 full-sib families from different crossing environments were analysed using three selected EST-markers PA0038, PA0066 and CAD and integrated in the linkage groups.
WP 3.1: The transcription of phytochromes was slightly higher in seedlings from seeds produced under cold conditions than their full-sibs produced under warm conditions. In Norway spruce seedlings, genes might be differentially expressed depending on the temperature applied to their seed parents when the offspring passes through zygotic embryogenesis, and during maturation within the developing seed.
WP 3.2: New cDNA macroarrays were hybridized with mRNA derived from drought- and pathogen-stressed seedlings. cDNA clones involved in stress response were identified. DDRT-PCR of mRNA from different drought-stressed seedlings produced from identical parental genotypes in different crossing environments were performed. Differences of gene expression were found depending on the crossing environment.

Milestones:
During the third year the following milestones were reached:
ML No 3: Seeds from four full-sib families and four contrasting environments were made available to project partners.
ML No 4: Freezing tests terminated and data available for analyses.
ML No 7: Measurements in field trial from 2000 completed.
ML No 8: Analysis of performance of 15 seedlings per family under drought stress.
ML No 10: Statistical analyses and project report.
ML No 13: Characterisation of antioxidants as functional, physiological and molecular markers.
ML No 15: Comparison of genetic structures from progenies available after 18 months.
ML No 17: Genotyping full-sib famililies completed.
ML No 18: Inheritance of segregating markers analysed.
ML No 21: Finishing genetic inventories in seed and seedling samples; continuation of methylation assays and RNA fingerprints.
ML No 27: Antibodies against two phytochromes generated and specificity determined.
ML No 28: DNA methylation analysis finished.
ML No 29: Analysis of phytochrome transcript finished (partially).
ML No 30: Immunolocalization of phytochrome tests completed.
ML No 31: Characterisation of generally expressed genes in stress response (partially).
ML No 32: Characterisation of differentially expressed mRNA according to drought and freezing stress (partially).
ML No 34: Establishment of a web site which provides the project results with intermediate update.
ML No 36: 2nd project report

Benefits and Beneficiaries:

The summary of the progress reports and the presented posters are available in the public area of the project homepage (www.adaptability.de).

Future Actions (if applicable):

During the six months' prolongation of the project (Amendment No 3 to the contract) all WPs will be completed and several manuscripts will be prepared for scientific journals.

The Final Project Report and the Technology Implementation Plan will be prepared.