



**UPSC seeks eight industrial PhD students that will provide the future competence of the forest-based industries and research in the areas of advanced tree breeding and application of tree biotechnology to forestry.**

The forestry is one of Sweden's most important industries. Our forests are under pressure, not only meeting an increased demand of pulp and paper, and building materials due to population expansion, but are also expected to contribute to new demands for bioenergy, biofuels and new synthetic materials that are replacing plastics, steel and concrete. Due to increased competition of land use for food production, expansion of new forest plantation is a considerable challenge. We will therefore have to produce more wood on the same or less land that we have today. Advanced tree breeding and new biotechnology can help to address this challenge. We are currently going through a rapid scientific advance that can efficiently determine what the tree genomes look like and understand the function and effect of the genes controlling important wood traits. This will be important tools for future tree breeding and use of wood-derived resources, but demands a new competence in the intersection among classical tree breeding, quantitative and molecular genetics, and functional genomics. For this, we are now launching a new research school for industrial graduate students.

The research school is a part of the UPSC Berzelii Center for Forest Biotechnology (<http://www.upsc.se/Berzelii/Berzeliicentre/welcome-to-upsc-berzelii-centre-for-forest-biotechnology.html>) and situated at the Umeå Plant Science Centre (UPSC), one of the world leading centers in the area of experimental plant biology and forest biotechnology and genomics.

Applicant's background can be in the areas of biology, chemistry, physics, biotechnology, mathematics, statistics, and computational sciences. The research school will invite world class scientists to conduct lectures and seminars in the area of advanced genomics, quantitative and molecular genetics, and tree breeding, and will start during the second half of 2012. New candidates will be employed as an industrial PhD student at a host company for 5 years (compared to a normal Swedish academic PhD graduate student of 4 years). 20% (one year) of candidate's time can be used for work within the host company. This will give new candidates a unique opportunity to bridge the gap between the forestry industry and the academic organization in the application of research results and to be an important part of the host company from the start of the degree program.

The host organizations including local and multi-national forestry companies are: Skogforsk, Bergvik Skog, Holmen Skog, Skogforsk, Stora Enso, and Sveaskog/Svenska skogsplanter. The new graduate school will also host other PhD students sponsored from other Nordic and Baltic countries.

Instructions for application can be found at: (<http://www.slu.se/en/education/postgraduate-studies/new-phd-student/>), except for positions 1 and 5 that can be found at: (<http://www.umu.se/om-universitetet/lediga-jobb?languageId=3>). Applications marked with the correct reference numbers should reach the Registrar at SLU or UmU (positions 1 and 5) no later than August 31.

More information about the positions can be requested from the individual supervisors or from the research school director Prof. Harry Wu ([Harry.Wu@slu.se](mailto:Harry.Wu@slu.se)). See also [www.upsc.se](http://www.upsc.se).

### **1. The genetic basis of heterosis (Ref: 313-662-12)**

Main Supervisor: Prof. Pär Ingvarsson (par.ingvarsson@emg.umu.se)

Host company: Stora Enso AB (www.storaenso.com)

Heterosis, or hybrid vigour, is the increase in growth and/or productivity often observed in hybrids relative to their parental lines or species. Heterosis has long played an important role in many agricultural crops, such as maize, rice and many cereals. Recently heterosis has also become an important tool for increasing the productivity in many forest tree species and especially in species with relatively short rotation times such as Eucalypts and Poplars. However, despite its historical importance to agriculture, the genetic basis of heterosis is still not well understood. The main competing hypotheses include dominance, overdominance, and epistasis and these theories give different predictions regarding stability of the heterosis in subsequent generations and breeding strategy of creating and maintaining the heterosis. Dissection of both the molecular and quantitative genetic basis of heterosis could increase efficiency of hybrid breeding and facilitate stable heterosis. The aim of PhD project is to use recently developed methods in genome-wide association mapping (GWA) and genomic selection (GS) to dissect the genetic basis of heterosis. The project will involve both theoretical investigation of genomic selection in hybrids and practical implementation using commercially available crosses of different Eucalyptus species. The PhD candidate will be supervised by Pär Ingvarsson and Harry Wu.

### **2. Development of genetic tools to modify wood properties of forest trees (Ref: 2093/2012)**

Main Supervisor: Dr. Urs Fischer (Urs.Fischer@slu.se)

Host company: Stora Enso AB (www.storaenso.com)

This project aims to produce tools to practically implement biotechnology for major wood modifications in forest plantations and to generate knowledge for modifying cellulose in wood. Application of biotechnology in forest plantations may focus on modifying wood to decrease energy required for wood chipping, decrease wood recalcitrance, avoid inhomogeneous wood by removing G-layers in tension wood, and drastically alter wood polymer composition for specific uses. An unsolved practical problem with this approach is that large modifications often have adverse effects on tree growth and survival. This project aims to identify and test promoters and transcription factors that can be used for major modifications of wood while still maintaining a healthy tree.

We want to shed more light on the machinery of cellulose biosynthesis, with the idea to produce highly modified wood. This will require the application of tissue specific promoters since ubiquitous expression of key regulators of cellulose deposition is lethal. Novel promoters will be identified from spatially highly resolved transcriptomics across developing wood of aspen. These promoters will be used to drive the expression of reporter genes or transcription factors, which have the potential to direct expression of large subsets of genes involved in cellulose biosynthesis. Since known transcriptional regulators of cellulose biosynthesis also regulate genes involved in the synthesis of other wall polymers or unrelated processes, novel transcription factors shall be identified in order to target cellulose synthesis more specifically. Alternatively, artificial transcription factors will be engineered, which can bind to promoters of cellulose synthesis genes but not to other gene regulating sequences. Chemistry, fiber mechanics and wood processing properties will be assessed in modified trees. This approach could strongly affect recalcitrance and mechanical properties of the woody raw material. The PhD student will be supervised by Urs Fischer and Björn Sundberg.

### **3. Regulation of root development from somatic embryos of Norway spruce (Ref: 2094/2012)**

Main Supervisor: Prof. Ulrika Egertsdotter (ulrika.egertsdotter@me.gatech.edu)

Host company: Sveaskogs Förvaltning AB (www.sveaskog.se)

Successful regeneration of plants from somatic embryos of Norway spruce (*Picea abies*) was shown already in the 1980s. However, owing to the labor intensive steps of the somatic embryogenesis (SE) process for regenerating plants, it is only recently by the invention of an automated system (SweTree Technologies AB) that SE plant production can become a reality for large scale plant production in the forestry sector.

In order to implement an efficient and cost-effective process for mass propagation of SE plants from an unlimited number of genotypes, the basic protocols for somatic embryogenesis (SE) need to be further improved. One of the major bottlenecks of the process relates to inefficient germination and subsequent root development from the somatic embryos of certain genotypes, limiting the selection of genotypes that are mass propagated and thus reducing the gain from the breeding program. In this project the role of nitrogen in the regulation of root formation during germination and continued root development during plant development will be studied. Furthermore, other important factors that determine the germination success and further development of the root will be studied, such as other nutrient factors and the substrate composition. The project work will be performed in close collaboration with the Svenska Skogsplantors forest tree nurseries and SweTree Technologies AB. The project includes both *in vitro* laboratory work with SE cultures and field work in nursery greenhouses with SE plants.

#### **4. Norway spruce adaptation to varying climatic conditions (Ref: 2095/2012)**

Main Supervisor: Prof. Bengt Andersson (Bengt.Andersson@skogforsk.se)

Host company: Bergvik Skog AB (www.bergvikskog.se)

Climate change will require forest regeneration material adapted to a different range of conditions than those existing today, including novel combinations of photoperiod and temperature conditions. The aim of this project is to develop norms of reaction models to describe the amount and pattern of genotype by environment interaction for Norway spruce in a climate change context. Models will describe the phenotypic response to varying environmental signals, climatic indices included, and genotypes. Responses in characters important for adaptation will be investigated, such as growth, growth rhythm, bud flush, growth termination, hardiness, survival, etc. The models will be used for selection of individuals in tree breeding or for mass propagation showing a high and stable performance in a broad range of environments with different climatic conditions. At population level, we will develop the best use of improved seedlings by deployment functions and delineating seed utilization zones over general climate gradients. It is also important to reveal G x E interaction on individual tree or family level for site specific effects like frost prone and not frost prone sites. Part of the project will involve artificial climate experiments using greenhouses and climate chambers to study the annual growth cycle in response to climate variables. Part of the project will involve mega-data analyses of population with environment interaction for Norway spruce using variables describing the climate based on meteorological data used in climate scenario research and variables that describe the site. The PhD student will be supervised by Bengt Andersson, Mats Berlin, and Harry Wu.

#### **5. Population genomics of forest trees (Ref: 313-663-12)**

Main Supervisor: Dr. Stacey Thompson (stacey.thompson@emg.umu.se)

Host company: Bergvik Skog AB (www.bergvikskog.se)

How do different reforestation methods impact genomic variation within spruce stands? Clear-cut and continuous cover forestry are contrasting natural resource management practices that have been broadly employed through Sweden for hundreds of years. Although each practice has different theoretical expectations for resulting diversity (e.g. allelic richness, relatedness, age structure, spatial dynamics), little is known about realized patterns within the reforested spruce stands of Sweden. This project will fill this knowledge-gap by using high-throughput genotyping and next generation sequencing to profile genomic diversity within forest stands under contrasting management and silvicultural practices, including the use of exotic provenances. Comparisons will be made with pristine forest sites, as well as with island populations of different ages and sizes that have recently uplifted from the Baltic and been colonized by spruce.

This project utilizes the resources generated by the Norway spruce genome sequencing project in Umeå (<http://www.congenie.org/>). The chosen candidate will be co-advised by Stacey Lee Thompson and Nathaniel Street, and will collaborate broadly with several research groups at UPSC and Swedish tree breeding organization Skogforsk.

## **6. Development of breeding objectives for forest trees (Ref: 2097/2012)**

Main Supervisor: Prof. Harry Wu (Harry.wu@slu.se)

Host company: Skogforsk (www.skogforsk.se)

One of the most important tasks in designing a forest tree breeding program is to develop an economic breeding objective if improvement of multiple traits is considered. Through development of an economic breeding objective, the economic importance and economic weights of each breeding objective trait can be estimated and applied to a selection index for breeding selection. Economic breeding objectives have mainly been developed in animal breeding and have only recently been applied to forest tree breeding.

In this project, the PhD candidate will develop breeding objectives for Scots pine in the Swedish tree breeding program. Economic weights for two main production systems (solid wood production, and pulp-paper production) in Sweden will be investigated in this project. Through the development of breeding objective for these products, profit function models or bio-economic models will be developed to estimate economic weights for two production systems. Genetic variance and covariance from early selection to harvest traits including wood quality traits are estimated from suitable progeny trials available. The PhD candidate will implement the project for the following three components: 1) identifying production system of solid-wood and pulp-paper products for Scots pine and determining tree biological traits influencing costs and revenues for solid-wood and pulp-paper production; (2) defining corresponding profit equations or bio-economic models for solid-wood and pulp-paper production systems; (3) developing economic weights of breeding objective traits for solid-wood production and pulp-paper productions. The project will be developed based on Skogforsk's previous breeding objective works and will be closely aligned with current and future Skogforsk's sawing studies and genetic evaluation system of TREEPLAN. The PhD candidate will be supervised by Harry Wu and Gunnar Jansson in Skogforsk and Dr Jansson will play a leading role in guiding the PhD project.

## **7. Genome-wide association and genomic selection for forest trees (Ref: 2098/2012)**

Main Supervisor: Prof. Harry Wu (Harry.Wu@slu.se)

Host company: Skogforsk (www.skogforsk.se)

Candidate gene and genome-wide association of DNA markers with phenotypic traits has made the dissection of phenotypic variation into genotypic variation possible in trees. Current development of SNP chip in whole genome sequencing and re-sequencing projects is a first step towards developing efficient DNA marker system in pine and spruce for large scale association analyses. It is envisioned that genome-wide association could cover a large portion of genetic variation for quantitative traits. Genomic selection method has advanced greatly in animal breeding program recently. With the completion of whole genome sequencing of Norway spruce and re-sequencing of spruce and pines, genomic selection could be a reality in tree with increased efficiency of early selection. However, specific method dealing with low linkage disequilibrium and large effective population number in the tree breeding population need to be examined for effective genome-wide selection including efficient design of experiment for tree species to accurately estimate allelic effects. We will examine how the size and structure of population, experimental design, mating structure and density of markers in tree species affected the accuracy of genome-wide association and genomic selection. Phenotype and genotype data from Norway spruce genome sequencing project will be used for the study. The PhD candidate will be supervised by Harry Wu, Pär Ingvarsson and Rosario Garcia-Gil.

## **8. How can we optimize the growth of conifer seedlings in a modern seedling nursery? (Ref: 2099/2012)**

Main Supervisor: Prof. Torgny Näsholm (Torgny.Nasholm@slu.se)

Host company: Holmen Skog AB (www.holmen.com)

Efficient production of conifer seedlings is based on rapid growth, driven by high rates of fertilizer application. However, following planting in the field seedlings must cope with various forms of biotic and abiotic stresses and the cultivation practices may not be optimal for seedlings to meet these stresses. The major stresses experienced by recently planted conifer seedlings include drought and herbivory, and the morphology and biochemical

composition of the seedlings are important determinants for how they cope with these events. We suggest that the relative rates of acquisition of carbon and nitrogen will determine the internal balance of C and N in seedlings, which in turn will shape seedling morphology and biochemistry. This project will thus focus on the fundamental processes of C and N acquisition in conifer seedlings, with the goal of establishing new cultivation practices for large-scale seedling production.