

Position at postdoctoral level on genome-wide evaluation in forest trees

A 30 months of postdoc level position is available at INRA Val de Loire (Orléans, France), funded in the framework of the EU FP7 PROCOGEN project. Our ideal starting date is June 2013, but both earlier and later dates are eventually possible.

> Background:

Our team has long research experience in genetics, biometry and tree physiology, as well as in conducting breeding programmes for several of the main forest tree species in France, including conifers and broadleaves. This research is highly integrated with other teams at European level, as our team is leader in 3 large European collaborative projects dealing with forest tree improvement within the FP7. One of these projects is PROCOGEN, in which we study optimal ways of implementing genome-wide evaluation approaches into current conifer breeding programmes.

Forest trees, notably conifers, are among the species undergoing domestication certainly the ones with the highest benefits to be expected from genome-wide evaluation. Most forest tree breeding programmes involve elite populations of considerable size, generally large effective population sizes and often large genomes, which overall challenge some of the promises of genomic predictions. One critical point for those breeding programmes is the constitution of a training population that is of reasonable size yet being representative of the whole breeding population. Also of relevance is the connection between training and candidate population, including the mating process generating new candidates.

> Aims and program of the project:

The objective is to study via simulation approaches and real data the effects of different designs of training *versus* candidate populations on the reliability of genomic predictions and on its dynamics over evaluation cycles for a conifer breeding program. This will be attained via the independent modulation during simulation of key parameters like LD and family relationships, and in order to disentangle the effects of these two factors on genomic predictions. The role of different mating regimes in generating candidates from the training set will also be investigated. Simulated genomes will be obtained by resampling methods from existing genotyping and by using forward in time approaches. From these, the successful candidate will devise a more general approach based on heuristics or MCMC methods, in order to modulate finely both LD and family relationships on simulated pedigrees.

The successful candidate will interact with an international community of scientists in the PROCOGEN project consortium. The candidate's interests and background can have a considerable influence on the scope of the project, with room for developing own ideas and approaches. The project will provide several opportunities for the successful candidate to travel to some foreign institutions to facilitate the contact with other experts. We believe our team will make a great scientific environment for a young scientist. Moreover, Orléans is attractively situated by the beautiful Loire River, offering rich culinary, cultural, and outdoor possibilities.

> Skills:

We are looking for candidates with Ph.D. level in quantitative genetics, breeding or genomics, with experience in genetic analyses with mixed models, and good programming skills. We expect from the successful candidate to be independent, dedicated, creative, and with strong collaborative skills. Salary will depend on seniority and experience.

> To apply:

To apply, please send a letter of motivation where you will briefly introduce one of your best papers, a CV, a publication list, and contact details of 3 referees to Leopoldo Sanchez (leopoldo.sanchez@orleans.inra.fr). Reviewing of applications will start on the 17th of May, but extra applications will be considered until the position is filled.