

12-month Post-Doc Position in Quantitative and Population Genetics

Orléans, France



We are looking for a highly motivated, creative and enthusiastic early career scientist to join our team “Genetics, Adaptation and Breeding” within the BioForA research Unit at INRA Val de Loire (Orléans, France). Our ideal starting date is March 2020, but there is some flexibility.

Context and project description

European Ash, *Fraxinus excelsior*, is a major broadleaf species of European forests. The species is currently threatened by *Hymenoscyphus fraxineus*, an invasive fungus originating from Asia. The disease started in Poland and Lithuania in the early 90’s. Since then, the disease has been spreading to the South-West essentially. First outbreaks in France appeared in the North and in the East in 2008-2009, and the colonization front is now in the South of the Country. Reports from all infected countries lead to the conclusion that only 2 to 3% of the trees will be able to withstand the disease in the long term. A selection program has been set up by INRA with the aim of creating seed orchards to produce superior seed material combining tolerance to the fungus and superiority for usual selection criteria for Ash (i.e. vigor and straightness). This program is taking advantage of a preexisting network of field trials that had been planted from 1988 to 2005 to compare European provenances of *F. excelsior*.

With the frame of the B4Est European project coordinated by INRA, a 12k SNP chipset is currently being developed in order to conduct Genome-Wide Selection (GWS). Both INRA and Wageningen University Research (WUR) contributed to this tool by providing genotypes from diverse geographic origins with contrasted phenotypes.

The successful candidate will thus contribute to the implementation of the GWS approach by addressing 3 original and challenging questions:

- How to conduct **multi-trait selection with sometimes antagonistic criteria**? Indeed, budflush precocity is negatively correlated to straightness in Ash while it is supposed to correlate positively with disease tolerance.
- How to consider **interspecific hybridization**? Indeed, the two main Ash species in Europe, i.e. *F. excelsior* and *F. angustifolia*, are known to hybridize in the wild and some of the studied material might not be pure *F. excelsior*. The SNP array is designed to measure this phenomenon also.
- How to conduct **efficient GWS on such a rare favorable phenotype with limited impact on drift and genetic variability** across the genome? A lot of theoretical work has been developed in the host team on this subject and this will provide excellent material for a case study.

A more technical challenge will consist in finding the best option to valorize data sets from different field trials with disconnected genetic compositions.

Side products, which are also a **guarantee for rapid publication**, will be

- the identification of genomic regions / candidate genes associated to the studied traits by association genetics.
- the quantification of interspecific hybridization between the two Ash species across Europe

Research environment

Our team has long research experience in genetics, genomics and biometry, as well as in conducting breeding programs for several of the main commercial tree species in France. The successful candidate will interact with a multidisciplinary team of geneticist, and will find readily local support on key issues like bio-informatics, if revisiting genomic data is eventually required, or high performance computing where the host has all required resources, locally and remotely.

The postdoc is funded by B4Est and there will be opportunities to interact on the subject with the consortium scientific community, and more specifically with:

- WUR partners (with possibility of spending some time there)
- other post-docs hired for similar tasks on other species concerned by the project

We believe our team will make a great scientific environment for an early career scientist. Moreover, Orléans is attractively situated by the beautiful Loire River, offering rich culinary, cultural, and outdoor possibilities.

Required qualifications & skills

We are looking for candidates with a Ph.D in quantitative, population genetics or statistical genomics, with experience in genetic analysis and programming (R required, other language appreciated).

The candidate will be encouraged to contribute to the scope and reach of the project by his own ideas and approaches.

We expect from the successful candidate to be independent, creative, and with strong collaborative skills.

Terms & salary

12-month contract. Salary depending on experience.

Application instructions

To apply, please send the following items to arnaud.dowkiw@inra.fr :

- * Cover letter;
- * Curriculum Vitae;
- * Publication list;
- * Contact details of at least 2 referees.

Deadline for applications: 31 January 2020.

Decisions will be made available on 20 February 2020 at the latest.

References :

www.b4est.eu

Muñoz, F., B. Marçais, J. Dufour and A. Dowkiw (2016). "Rising Out of the Ashes: Additive Genetic Variation for Crown and Collar Resistance to *Hymenoscyphus fraxineus* in *Fraxinus excelsior*." Phytopathology.

Saumitou-Laprade, P., P. Vernet, A. Dowkiw, S. Bertrand, S. Billiard, B. Albert, P. H. Gouyon and M. Dufay (2018). "Polygamy or subdioecy? The impact of diallelic self-incompatibility on the sexual system in *Fraxinus excelsior* (Oleaceae)." Proc Biol Sci **285**(1873).

Villari, C., A. Dowkiw, R. Enderle, M. Ghasemkhani, T. Kirisits, E. D. Kjaer, D. Marciulyniene, L. V. McKinney, B. Metzler, F. Munoz, L. R. Nielsen, A. Pliura, L. G. Stener, V. Suchockas, L. Rodriguez-Saona, P. Bonello and M. Cleary (2018). "Advanced spectroscopy-based phenotyping offers a potential solution to the ash dieback epidemic." Sci Rep **8**(1): 17448.