







Post Doctorate – 1 year in Orléans (France) Net annual salary: 25.000 euros From beginning of May, 2012 if possible, or before summer 2012

'Methylome of maize hybrids and heterosis using microarray'

Site: Orléans is a renovate city along the Loire (UNESCO world heritage) at the bordering of the Sologne and at 1h from Paris and Tours (http://www.tourisme-orleans.com/fr/accueil/). The campus of the University is located at the south of the city (TRAM connection) in a wooded environment (http://www.univ-orleans.fr/).

Project purpose:

The project is collaboration between an academic laboratory and a seed company. The objective is to study DNA methylation in various maize accessions. The global DNA methylation using HPLC method as well as microarrays will be done. This last technology allows the identification of the methylation state of thousands sequences in one experiment and could be performed in parallel for several biological samples.

Skills:

The candidate (with a doctorate in the field of biology) will have a perfect knowledge of microarray technology and in particular the biocomputing analyses, the associated databases and statistics. Skills in molecular biology would be appreciated as well as some knowledge of the HPLC technique. The candidate will collaborate with two teams (Limagrain and LBLGC) on 2 sites (Orléans and Clermont-Ferrand) and will need a strong autonomy for the management of the project and the preparation of reports and publications (fluent English). The candidate will be located in Orléans but will have to move in both cities of the project (several stays of one week financially integrated into the project). The candidate will be available before summer, 2012 and for at least one year.









Contacts:

For any question or application concerning this offer, thank you for sending an email to the <u>2 persons</u> indicated below. This email will include a detailed CV and a letter in support of application underlining your adequacy with the wanted profile.

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The recruiters:

- LIMAGRAIN EUROPE

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The genotyping laboratory located in Chappes has for objective to assist the Limagrain breeders working on field crop species such as maize, wheat, barley and rapeseed. The unity of development is positioned upstream to the genotyping activity and is responsible in particular for the implementation of new protocols and technologies for the routine activity of the laboratory.

Web site: http://www.limagrain.com/









University of Orléans, LBLGC

The Laboratory of woody and crop plants (laboratoire de Biologie des Ligneux et des Grandes Cultures; LBLGC - EA 1207) is composed of 40 persons: 5 professors, 16 assistant-professors, 11 ingenior/techncians and 8 PhD-students/Postdoc. The laboratory is organized in three teams on two sites: the campus of the University of Orléans and the campus of Chartres. The team 'ARCHE' in Orléans is also a unit of INRA the National Agronomy Research Institute (USC1328 Director Pr. F. Brignolas). Our team works on poplar × water availability and focus particularly on two traits, the water use efficiency and the drought tolerance. One axis of this research is studying the role of epigenetic mechanisms (Dr Stéphane Maury). We have previously shown the role of DNA methylation in morphogenesis (Causevic et al., 2005; Causevic et al., 2006; Teyssier et al., 2008) but also in response to environmental trigerring (Gourcilleau et al., 2010; Trap-Gentil et al., 2011). In addition, the DNA methylation polymorphism in plants is a source of potential biomarkers for molecular assisted selection in breeding (Gentil and Maury, 2007; Maury et al., in press).

Web site: http://www.univ-orleans.fr/lblgc/modules/news/index.php?storytopic=10

- Causevic A, Delaunay A, Ounnar S, Righezza M, Delmotte F, Brignolas F, Hagège D, Maury S (2005). DNA methylating and demethylating treatments modify phenotype and cell wall differentiation state in sugarbeet cell lines. Plant Physiology and Biochemistry 43, 681-691.
- Causevic A, Gentil M-V, Delaunay A, El Soud W, Garcia Z, Pannetier C, Brignolas F, Hagège D, Maury S (2006). Relationship between DNA methylation and histone acetylation levels, cell redox and cell differentiation states in sugarbeet lines. Planta 224, 812-827.
- Gentil M-V, Maury S (2007) Characterization of epigenetic biomarkers using new molecular approaches (chapter 16). In Genomics-Assisted Crop Improvement: Genomics Approaches and Platforms, Varshney, Rajeey; Tuberosa, Roberto (Eds.) Springer, Vol 1 pp351-370.
- Teyssier E, Bernacchia G, Maury S, How Kit A, Stammitti-Bert L, Rolin D, Gallusci P (2008) Tissue dependent variations of DNA methylation and endoreduplication levels during tomato fruit development and ripening. Planta 228, 391-399.
- Gourcilleau D, Bogeat-Triboulot MB, Le Thiec D, Lafon-Placette C, Delaunay A, El-Soud WA, Brignolas F, Maury S (2010) DNA methylation and histone acetylation: genetic variations in hybrid poplars, impact of water deficit and relationships with productivity. Annals of Forest Science 67, 208₁₋₁₀. DOI: 10.1051/forest/2009101.
- Trap-Gentil M-V, Hebrard C, Lafon-Placette C, Delaunay A, Hagege D, Joseph C, Brignolas F, Lefebvre M, Barnes S, Maury S (2011) Time course and amplitude of DNA methylation in the shoot apical meristem are critical points for bolting induction in sugar beet and bolting tolerance between genotypes. Journal of Experimental Botany 62, 2585-2597. doi: 10.1093/jxb/erq433.
- Maury S, Trap-Gentil M-V, Hebrard C, Weyens G, Delaunay A, Lefebvre M, Barnes S, Joseph C Genic DNA methylation remodelling during *in vitro* organogenesis: organ-specificity and conservation between parental lines of epialleles. Physiologia Plantarum (*in press*).