

## Post-doc position on Plant Domestication, Functional Traits, and Phylogenetic Comparative Methods

**Location:** Biodiversity and Conservation Area, Universidad Rey Juan Carlos (Móstoles, Madrid, Spain). The position will imply a few short trips to CEFECNRS (Montpellier, France).

**Short description:** Applications are invited for a 1-year postdoc (with possibility to extend for 1 additional year) on a project entitled "Understanding crop evolution through the lens of the comparative method", funded by the Spanish Ministry of Economy, and carried out in collaboration with CEFECNRS (Montpellier, France). Using data available at the lab, and from literature and global databases, the project investigates whether trait profiles of crops are different from those of comparable sets of plant species, and whether phylogenetic divergences associated to domestication are functionally distinctive (see full project description below).

**Tasks of the postdoc:** 1) Compilation of a database of functional traits of crops, of their wild progenitors, and of unrelated wild species; 2) Build up of a set of phylogenetic trees that encompass the species compiled; 3) Carrying various phylogenetic comparative analyses of functional profiles as a function of domestication statuses of the species; 4) Write up and publication of manuscripts including the main results of the analytical stage; 5) Attend an international conference presenting the results of the project. The position may also include performance of other duties occasionally.

**Requirements and selection criteria:** Applicants should have a PhD in ecology, agronomy, or evolutionary biology; and be citizens of, or hold a work permit in, an EU country. Selection criteria: amount and quality of the scientific production; experience in using the comparative method and R statistical environment, familiarity with functional trait frameworks, and good English writing and communication skills. Ability to communicate in Spanish will also be assessed as a complementary skill.

**Salary:** 24000 € / year gross, before taxes (taxes vary depending on personal circumstances of the employee, ranging from 7-25% approximately).

**When and how to apply:** the position is open for application from until the 6<sup>th</sup> November 2015. Online-only application is not permitted, so prepare your documents well in advance of the deadline. Directions for applying can be found here (look for ref M1308, directions in English and in Spanish):

<http://www.urjc.es/investigacion/innovacion-y-transferencia-del-conocimiento/363-programas-y-convocatorias#convocatorias-con-cargo-a-proyectos>.

Inquiries about procedures for applying can be posted to [investigacion.personal@urjc.es](mailto:investigacion.personal@urjc.es). Include ref M1308 in the subject of your e-mail.

**Attach the following items to your application:** 1) short CV that includes information on your academic career and a complete publications list, with link to your Google Scholar profile; 2) Statement of research interests, future research plans and their relevance to this position, and e-mail of 2 colleagues with whom you have worked before, and can be approached for reference; 3) Copies of your PhD degree certificate and of your ID card and/or passport.

**Selection process:** After the expiry of the deadline for applications, the authorized recruitment manager will prioritize participants, and arrange online interviews with those taking the higher marks in the prioritization stage. The selected candidate is expected to enroll by early Jan-2016.

**Information** on the hosting Department is available via <http://www.escet.urjc.es/biodiversos/eng/staff/staff.htm>, and on the research groups leading the project here: <http://rubenmilla.weebly.com/research--pdfs.html>; and here: <http://www.cefe.cnrs.fr/fr/recherche/ef/ecopar/833-c/203-cyrille-violle>

**Contact:** inquiries about the project can be e-mailed to Rubén Milla, [ruben.milla@gmail.com](mailto:ruben.milla@gmail.com). For procedures e-mail to [investigacion.personal@urjc.es](mailto:investigacion.personal@urjc.es).

**Description of the project:** Evolution of crops has been scantily studied from the standpoint, and using the techniques, of Evolutionary Ecology. Recent domestication research has shown that the domestication syndrome is not a solid pattern when examined in depth across multiple domestication processes. Here we argue that natural selection under cultivation and functional constraints on adaptive evolution, as alternative selective forces with a role in crop evolution, may pose selective filters of a more directional and common nature to crops. Focusing on those selective forces, and on response traits proposed by trait-

based Ecology, should result in new groups of traits adding to a new generalized domestication syndrome. Building on recent projects and results of our research team, here we propose to address the above, and other, frontlines in domestication research using the comparative method. More precisely, our objective is to test the following hypotheses: 1) that herbaceous crops and their wild ancestors are sets of species portraying a functional profile distinctive from other groups of angiosperms; 2) that known constraints among functional traits in the wild will limit opportunities for trait selection during crop evolution and improvement. Our approach will take advantage of current worldwide availability of functional trait data for wild species, and will compile similar data for crops. Crop trait data currently available at, or being gathered by, the research team (Ruben Milla at URJC, Spain, and Cyrille Violle at CEFV-CNRS, France) will permit the build up of a comprehensive wilds & crops database. Also, we will use existing phylogenetic information and gene sequence data. Specifically, we will carry out the following tasks to fulfill the aim of the project. First (Task 0 of the project), a large database on species scores will be put together for five seed, leaf, and canopy traits. That database will include ca 30000 wild species, and ca 90 herbaceous crops, including intraspecific variability in the later group. Coordinately, the phylogeny of that set of species will be worked out. Second (Tasks 1-3 in the project), a set of four different groups of analyses will be submitted to the complete database, and also to functional, phylogenetic, and domestication-status sub-groups of species. Those analyses will include comparisons of phenotypic space occupancy metrics, computation of functional distinctiveness indexes for selected clades, or analyses of contribution indexes of domestication events to the generation of trait diversification and variance. Lastly (Task 4 in the project), we will devise quantitative protocols to identify taxonomic and/or functional profile markers for (groups of) wild species that make suitable candidates for future attempts of domestication.