



Post-doctoral position opened (applications from candidates holding a MSc degree will also be considered). Two years.

Project Title: *Functional genomic approaches in tomato: introgressing exotic alleles to gain fruit quality*

Required skills of the applicant:

- To hold a PhD in Plant Biology. Preferably in Plant Molecular Genomic. (applications from candidates holding a MSc degree will also be considered).
- Demonstrated knowledge, through scientific publications, in data mining and bioinformatic softwares dedicated to the structural and functional analyses of plant genomes.
- Demonstrated interest in the proposed project and proved ability to propose new hypotheses and perform experiments for validation of the latter.
- Availability to short-term internships into other research laboratories of the region.
- Fluent in both written and oral English.
- The fellowship can be extended for an extra year period.

Summary of the project: *Only 2% of the enormous genetic variability of the Solanum genus is found in the commercially predominant lycopersicum varieties. Exploitation of this natural variability depends mainly on our skills to identify valuable traits and subsequently take advantage of it. The exotic germplasm richness of the Northwest part of Argentina, North of Chile and Central Perú have been exploited for the domestication of this species and provide one of the strongest platforms to realize this aim. The reintroduction of genetic variability from these species represents an important tool for crop improvement. A good example of this are the tomato introgression lines (*S. lycopersicum* x *S. pennellii*) generated by Prof. Zamir in Israel which have been served to add several valuable agronomic traits to the genetic background available for breeding programs with different objectives. The major aim of our group is to identify and functional characterize key regulatory points within the fruit metabolic network. By applying a combination of metabolic profiling and genomic methods, candidate regions of the tomato genome will be dissected, identified and characterized. In parallel, genomic analyses of sub-cellular compartments (i.e. mitochondrial genome) are also explored within this variability. This could allow both the dissection of the above-mentioned QTL into their principal components and provide a rich resource for investigating the forces of gene evolution of these important traits.*

Applications should include a detailed CV (including three references) and be sent by Email to:

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