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Short term scientific missions...

“Thanks to the STSM I could have the opportunity to establish a first comparison between melon and grapevine ripening. I could have an idea of this process in melon in a great variety of accession in a germplasm bank. The help of these two researchers was of great value because their expertise in the knowledge of the plant material and the best statistical method for data analysis was crucial in obtaining significant results. It was a great opportunity I recommend for PhD students and postdocs too!” Carmen Leida, Portugal.

“During my STSM I spent fifty days in the Genomics and Biotechnology of Fruit (GBF) laboratory (Institut National Polytechnique de Toulouse, France), lead by prof. Mondher Bouzayen. This experience was very helpful for the improvement of my competences about RNAseq statistical and bioinformatics analyses, which are particularly important for my PhD project. During the STSM we also plan a little co-operation between the host institute and institute where I'm working (Fruit Physiology and Transcriptomic laboratory, Padova) for the the implementation of a new algorithm. I would like to say thanks to prof. Mondher Bouzayen and to his collaborators Elie Maza, Mohamed Zouine and Matthieu Lauvernier for helping me in my work and analysis. In addition I would also say thanks to Jean-Marc Routaboul, the grant holder of the FA1106 COST action, for the help that he give me with the bureaucratic issues. Massimiliano Corso (Italy)”

“The short scientific mission (STSM) of the COST Action FA1106 gave me the opportunity to visit the lab of professor Dulce Antunes in the University of Algarve (Faro, Portugal) and acquire new skills and knowledge in methodologies related to tomato quality evaluation. The knowledge acquired from the STSM will be combined with my current expertise in gene expression profiling to identify the molecular basis of the mechanisms regulating fleshy fruit quality of tomato. In addition, the STSM contributed to the establishment of a long-term collaboration between the two labs. Overall, it was a great experience and it is worth mentioning the excellent

“ collaboration with the host institution. Last but not least, I would like to thank the organizers of the COST FA1106 for their immediate response and support throughout the STSM. Victoria Drosou (Greece)

“ I'm really grateful for the opportunity provided by the COST ACTION FA-1106 "Quality Fruit" to make a stay in the A. Aharoni laboratory at Weizmann Institute of Science, in Israel. The visit provided me training and experience in high resolution mass spectrometry assay, including data processing, and the use of next generation DNA sequencing approach. This project helps me to complete experience and knowledge about the group of technics used to study the specialized metabolism, which is the center of my PhD: "Quality Improvement of tomato fleshy fruit. Characterization of genes and genetic regions associated to specialized metabolism in tomato fleshy fruit". Furthermore, this STSM provide a new insight on biochemistry of tomato fleshy fruit, a multidisciplinary study of the regulation of some healthy-sensory qualities of tomato fleshy fruit, and a putative evidence of a new regulation of the flavonoid branch in tomato fruit. J. Patricia Fernandez Moreno, Spain.

“ The STSM is a 'tool' for the young researchers, which in my case proven to be extremely useful. I had the opportunity to work in a world leading institute and gain precious knowledge and experience adding so reliability and speeding up my PhD work. Like athletes use tips for maximizing their performance like altitude training, young researchers must pay exchange visits, have access to experience lads and come across with devoted researchers to open up their mind and explore novel fields. It was a great experience with significant contribution to my work towards the research in the physiology of tomato fruit ripening. Andreas Perrakis PhD candidate. By Perrakis Andreas, Greece)

Training School " RNA-seq Analysis", March 6-8, 2013, Toulouse France.

“ The training will help me to focus and be able to report specific changes in the metabolic pathways I am going to focus in my research. I work on grapes and there is much to learn about the influence of stress conditions on metabolic pathways with emphasis on aromatic compounds. This training seminar helped me a lot in understanding the tools and options available today for RNA-seq and to get familiar with other young research in the field. Itay Maoz, PhD student, Israël.

“ This training school was very fruitful for me because now I know how to handle with RNA-seq data. The practical part (that means the last day and a half) should be given greater attention, ignoring or devoting less time, in a future reorganization of the course, the initial part of the unix commands and introduction to the technique of RNA Seq. In return, however, this

“ course, with the use of various software, the explanation of the various files that are obtained and the analysis of data with packages of *r*, was very helpful. Nothing to say about the general organization, the place, and lunches and dinners: all very perfect. *Christina Savoi, Italy.*

“ first of all I should thank you for the effort. It was a precious knowledge transfer that this team made. The pipeline offered in the workshop was almost nice and promising. The Tutors were all trained and good in transferring the information. It was a great experience for me to have some insights through the RNA Seq data analysis.. The first part of workshop was really in-dept and every single thing was clarified for many times. But in the last parts (especially Data Analysis and Mapping) the time was not sufficient and the tutors had to skip some parts which were really important at least to me as a bioinformatician. For sure data preparation and the pipeline to generate results are very important, but we are making all these efforts to extract information out of this data by analysis while this part was more or less skipped. I believe it was the only part missing in this workshop while all the other things were perfect. *Hamed Bostan, Italy.*

“ The RNA-seq training school provided an excellent opportunity to learn and use the recently developed tools about the analysis of RNA-seq data. The course begun on the basis of simple unix commands and developed up to the analysis of real RNA-seq data. *By Maria Manioudaki, Greece.*

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“ The training school was actually beneficial for understanding all the steps of a RNA-Seq assay and the management of the data produced. The teaching team provided a course very clear and well-organized in spite of the shortness of the session. In fact, the first afternoon, consisting in the introduction about the Linux commands, permitted to familiarize with this environment necessary for the reads alignment and the generation of count tables done during the second day. Unfortunately, the time dedicated to the data analysis (quality check, normalization and differentially expressed genes) was not sufficient. We did some steps of the practical part really quickly. Maybe one or two days more will be a good idea for a future edition. In addition, it might be useful to spend a half-day working with our own dataset in order to have some comments or suggestions from the teaching staff. But, thanks to this training, I had an overview of all the tools and softwares available for the data analysis and now I'm well-equipped for the following of my research project! Finally, I would like to thank the organizers for their warm welcoming, the teachers for their kindness and their patience

“ and also all the participants for this shared while. *Mélanie Massonnet, PhD Student, Italy.*

“ I would like to thank you for your well organization of the training course. I found the course really fantastic, very well prepared and well organized. From my point of view everything was perfect, maybe I missed a extra day to practice and digest all contents. *By Sonia Osorio , Spain*

“ I first want to thank teachers and organizers of the Training School. I really appreciate the effort in explaining bioinformatic and statistical topics to an audience mostly belonging to the biology field. I think that it might pave the way to a more cognizant approach to the new generation sequencing techniques and transcriptomics in general. Personally, I found the Training School very useful. Teachers gave information about the whole workflow of RNA-seq experiments, from libraries preparation to differential gene expression discovery. I found that the RNA-seq data analysis (2nd day) was very well explained although pretty intense and difficult to be completely assimilated. In any case, the related training session helped to practice and to use tools just presented during the frontal lesson. I would have appreciated a more detailed explanation of the data analysis during the last day. Due to the tight schedule, time was not enough to completely perform the differentially expressed genes discovery analysis and to discuss together about results. In addition, I would have been interested in practicing with larger datasets, but I fully understand that exercises have been organized to fit with timing and to make it as simple as possible. However, I think that in a very short time the workshop gave necessary information at least to start performing RNA-seq data analyses, knowing which workflow to follow and which tools to use. Practicing and improving our skills in this field is up to us. *Marianna Fasoli, Post Doc, Italy.*

Training school "GoldenBraid" September 2013, Wageningen

“ I attended the cost training school on “Standardized modular cloning for plant synthetic biology, applications in metabolic engineering and fruit biotechnology” taking place in Valencia (september 9-13th 2013). The training school was perfectly organized with both local and invited speakers, and the lab sessions were very useful for the overall understanding of the GoldenBraid technology. I came back to my lab with the GoldenBraid starting kit, another positive point. Since, I started to work with this cloning tool and I also shared and exchanged about this technology with many of my colleagues in the lab. As an example, I could produce more than fifty different GB constructs within the last 3 months. The method efficiency was validated through protoplast transient assays (subcellular localization and GUS reporter assays). Altogether, this training school was a very positive experience for me and provided to my lab a very useful molecular tool. We

“ *already started to share this methodology with some colleagues from the grapevine community. D. Lecourieux, Research scientist, France*

Training school Metabolomics december 2013, Wageningen

“ *The Training School “Metabolomics” provided by the COST Action FA-1106 “Quality Fruit” was an outstanding learning experience. The course significantly improved my knowledge on several aspects of mass spectrometry-based plant metabolomics, including experimental design, data processing softwares and data interpretation, which were proven essential in my research on copper impacts in grape. The course organization was excellent. I am truly thankful for this great opportunity. By Viviana Martins, Portugal.*