On line Training School

Plant Epigenetics: Basics, Applications and Methodologies

28th-30th June 2021

Modality: on-line using Zoom platform

Attendants: Mostly directed for Bachelor, Master Students, PhD students, post-docs and researchers involved in fields in plant sciences and willing to start working on plant epigenetics.

Contacts for registration: please send an email to Prof. Federico Martinelli, Università di Firenze (email: federico.martinelli.it)

Plant epigenetics is a fascinating research field aiming at investigating all kinds of modification of chromatin and DNA not related to sequence variation. The capacity of the hereditary material to change its chemical and spatial structure in response to environmental changes is an extraordinary means for all living organisms to adapt to climate change. This power becomes higher when these changes can be hereditary transmitted. This phenomenon is known as "plant stress memory" and consists in the enhancement of their responses to abiotic and biotic stresses occurring in a consequent way. The expression "the Chromatin will never forget" as indicated in a recent Nature plants article (6: 1396–1397; 2020) means that the hereditary material has various and still unknown mechanisms of "chemical flexibility" to memorize previous environmental circumstances and react in a prompt way when they occur again. Although plant epigenetics has many intriguing scientific questions, this field is still one of the under-investigated aspects of genetics due to the complexity of molecular mechanisms that require diverse and well-integrated approaches and methodologies. This training school will provide an overview of the principal methodologies and approaches used to investigate all main categories of epigenetic mechanisms: 1) chromatin restructuring and histone post- translational modifications (PTMs), 2) DNA methylation changes, 3) non-coding RNAs (i.e. RNA-directed DNA methylation). International teachers will be invited to provide frontal and practical lessons for the explanation of basic concepts, transfer this knowledge in the breeding sector and provide tools for hands-on data analysis. These lessons will deal with any kind of methodological approaches (targeted, "untargeted", multi-omics, eventually integrated with genetic, transcript, protein, metabolites analysis). The training schools will last 3 days (each composed by a half-daytime) with 3-4 oral presentations during the morning of each day.
In the first part frontal lessons will be held on basic aspects for the understanding of the molecular epigenetic mechanisms:

- Chromatin modifications, reshuffling and restructuring
- DNA methylations
- Non-coding RNAs

The second part will deal with applied subjects, unresolved questions and frontiers such as the role of these mechanisms in plant stress responses, plant adaptation to climate change and crop breeding. There will be four presentations dealing with

- Plant adaptation mechanisms to climate change
- Transgenerational memory in plant stress biology
- Transfer of epigenetic knowledge in crop molecular breeding
- New frontiers in plant/crop epigenetics

The third part will deal with the description and explanation of the most updated methodology usable in lab and in silico analysis for plant epigenetics/epigenomics:

- DNA methylation analysis (bisulfite conversion, high resolution melting analysis, methylated DNA immunoprecipitation)
- Chromatin accessibility, conformation and analysis assays (digital dnase and dnase seq, chromosome conformation capture (3C))
- In silico bioinformatic pipelines for analysis of DNA methylation, chromatin and RNA, gene-ontologies and pathway analysis

The provisional program of the training school is the following:

First Day

Gaining insight into epigenetic mechanisms

9:40 - 10:00 - Introduction of the training school and EPI-CATCH Cost Action - Federico Martinelli

10:00 - 10:40 - Sotirios Fragkostefanaki - Chromatin modifications, reshuffling and restructuring

10:40 - 11:00 - Coffee break

11:00 - 11:40 – Philippe Gallusci - Regulation and functions of DNA methylation in plants

11:40 - 12:20 - Celia Baroux - Regulatory non-coding RNAs: a genomic resource for crop improvement?

12:20 - 12:40 - Questions

Second day

Get inside into epigenetic aspects of crop applied research

9:40 - 10:20 – Samia Daldoul - Understanding plant responses to climate change: Mechanisms and adaptation

10:20 - 11:00 - Markus Kuhlmann - Transgenerational memory in plant stress biology

11:00 - 11:20 - Coffee break

11:20 - 12:00 - Panagiotis Moschou - Biomolecular condensates in epigenomes and epitranscriptomes

12:00 - 12:40 - Sophie Brunel-Muguet - Plant acclimation to global warming: a three-fold lever of action based on genetics improvement, management practices, and ecophysiological approaches

12:40 - 13:00 - Questions

Third day

Hands on epigenetic data analysis

9:40 - 10:20 - Michal Lieberman-Lazarovich - Bisulfite sequencing for site-specific DNA methylation analysis

10:20 -11:00 - Frank Johannes - Introduction to Whole Genome Bisulfite Sequencing analysis

11:00 - 11:20 - Coffee break

11:20 - 12:00 - Francesco Guarino - The biostatistical analyses of MSAP data

12:00 - 12:40 - Angela Cicatelli - MSAP molecular markers for DNA methylation analysis: Theorical and laboratory approach

12:40 - Final Questions & Conclusions