Metabolite Profiling Workshop

13-17 January 2020
Max-Planck-Institute of Molecular Plant Physiology Potsdam-Golm, Germany

Agenda

Monday 13th January

Arrival and registration

Tuesday 14th January

09:00-09:30 Welcome address

09:30-11:30 Lecture on the basics metabolomics and GC-MS analysis

11:30-12:30 Lunch

12:30-15:00 Lecture on the basics of LC-MS analysis

15:30-17:00 Demonstration of sample preparation and injection (GC/LC-MS)

Wednesday 15th January

09:00-11:30 Lecture on GC-MS chromatogram evaluation using "TagFinder"

11:30-12:30 Lunch

12:30-17:00 Evaluation and own practice of GC-MS chromatogram

Thursday 16th January

09:00-11:30 Lecture on chromatogram evaluation using "Xcalibur"

11:30-12:30 Lunch

12:30-14:30 Evaluation and own practice of LC-MS chromatogram

14:30-17:30 Lecture on statistical analysis and data interpretation

Friday 17th January

Final discussions and recapitulation of the week

The workshop was carried out by Dr. Saleh Alseekh, project leader in the department "Central Metabolism" of the MPG, Potsdam-Golm and Dr. Maria Benina from the department "Plant Metabolomics" of the CPSBB.

1. What were the output/outcomes for the project as a whole and per participant?
The workshop on Metabolite Profiling covered all basic aspects of the metabolomic's research used as integrative part of the systems biology approach with focus on GC-MS and LC-MS analysis. The participants were introduced to the application of the most important softwares and data bases, used to identify target compounds.

Important outcomes have been achieved in terms of sample preparation and better understanding of which technique is better to apply in relation to the research objectives.

2. What were the overall lessons learnt?
The metabolomics workshop allowed the participants to understand better the metabolic network analysis and methods of investigations, very often used to complete the scientific research. It also made them partially independent to identify target metabolites.

3. What was achieved in terms of research and innovation?
An introduction with high throughput technique such GC-MS and LC-MS has been achieved and provided an important base for further development.

The researchers gained experience based on the importance of integration of the metabolomics data with the rest of the "–omics" approaches in the context of the systems biology based research.

4. What is the capacity for exploitation?

The gained knowledge can be applied when a researcher decides to personally explore and focus on interesting for its research molecules, by using the metabolomics raw data, generated from the machines. Thus he/she can possibly find a potentially interesting and important for certain mechanisms metabolites or molecules with important biological activities, and therefore address further attention and investigation.

Usually this step is not covered in the normal metabolomic service analysis if this is not explicitly required from the investigator.