Universitat Autònoma
de Barcelona

2022/2023

Plant System Biology

Code: 43867
ECTS Credits: 6

Degree	Type	Year	Semester
4316231 Plant Biology, Genomics and Biotechnology	OT	0	2

Contact

Name: Ana Martin Hernandez

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Use of Languages

Principal working language: english (eng)

Teachers

Ana Martin Hernandez

External teachers

Elena Monte

Iban Eduardo

Jae-Seong Yang

Juan José López Moya

Maria Lois

Martí Bernardo

Prerequisites

Basic knowledge of Genetics

Objectives and Contextualisation

To provide students with a comprehensive and current view of the techniques, fundamentals and applications of Plant Genomics and introduce systems biology of plants. The specific objectives include understanding the following aspects: the diversity and complexity of plant genomes, the techniques commonly used in genomics, transcriptomics, proteomics and metabolomics studies and applications to the genetic improvement of crop plants. Use of mathematics for predictive modeling through integration of different omics data.

Competences

- Apply knowledge of plant molecular genetics in different scientific and industrial areas.
- Communicate and justify conclusions clearly and unambiguously to both specialised and non-specialised audiences.
- Develop critical reasoning in the area of study and in relation to the scientific and business environment.
- Identify and use Bio-Computer Science tools to be applied to the genetic, evolutionary and functional study of plants.

- Integrate knowledge and use it to make judgements in complex situations, with incomplete information, while keeping in mind social and ethical responsibilities.
- Solve problems in new or little-known situations within broader (or multidisciplinary) contexts related to the field of study.
- Synthesize, and analyze alternatives and debate critically.
- Use and manage bibliographical information and computer resources in the area of study.
- Use scientific terminology to argue the results of research and present them in English both orally and in writing in an international environment.

Learning Outcomes

1. Apply mathematical methods of analysis and predictive modelling through the integration of different types of omic experimental data.
2. Communicate and justify conclusions clearly and unambiguously to both specialised and non-specialised audiences.
3. Develop critical reasoning in the area of study and in relation to the scientific and business environment.
4. Distinguish and apply the methods and techniques used normally in studies of genomics, phenomics, transcriptomics, proteomics and metabolomics.
5. Integrate knowledge and use it to make judgements in complex situations, with incomplete information, while keeping in mind social and ethical responsibilities.
6. Solve problems in new or little-known situations within broader (or multidisciplinary) contexts related to the field of study.
7. Synthesize, and analyze alternatives and debate critically.
8. Use and manage bibliographical information and computer resources in the area of study.
9. Use scientific terminology to argue the results of research and present them in English both orally and in writing in an international environment.

Content

Systems Biology: Concepts, methodology, and case studies using multiple omics.

The case study will be the emergence of a new disease affecting and killing all tomato varieties. The students will make a trip through all the -omics to unveil the cause and search for a scientific solution feasible for application in crop plant breeding.

Specifically,

We will use practical applications of methods and techniques in plant phenomics and genomics, including the use of molecular markers in breeding. Importance of QTL in this problem.

Analysis and application of data arising from genomics and transcriptomics studies to narrow down the problem.

Analysis and application of data arising from proteomics, interactomics, and metabolomics studies to find a solution to the problem.

Integrative analysis of the case study applied, including Computational modelling, to crop plant breeding.

Methodology

Lectures and Expert talks

Problems and case studies

Preparation of reports

Personal study

Annotation: Within the schedule set by the centre or degree programme, 15 minutes of one class will be reserved for students to evaluate their lecturers and their courses or modules through questionnaires.

Activities

Title	Hours	ECTS	Learning Outcomes
Type: Directed			
Lectures and Expert Talks	11	0.44	1, 5
Problems and case studies	24	0.96	3, 4, 6, 9
Type: Supervised			
Preparation of reports	30	1.2	2, 7, 9
Type: Autonomous			
Personal study	84	3.36	8

Assessment

Continuous evaluation 10%

Report 60%

Final Quiz 30%

Assessment Activities

Title	Weighting	Hours	ECTS	Learning Outcomes
Continuous evaluation of students' participation	10%	0	0	1, 3, 4, 5, 6
Final quiz	30%	1	0.04	6
Reports	60%	0	0	2, 7, 8, 9

Bibliography

Yunbi Xu Molecular Plant Breeding. CAB International Oxfordshire, UK disponible online a Biblioteca UAB :http://www.cabi.org/cabebooks/FullTextPDF/2010/20103101750.pdf

Fredericks DN, & Relman DA (1996). Sequence-based identification of microbial pathogens: a reconsideration of Koch's postulates. *Clinical microbiology reviews, 9* (1), 18-33

Li et al. 2014 A Review of Imaging Techniques for Plant Phenotyping. Sensors, 14, 20078-20111.

Großkinsky et al, 2015. Plant phenomics and the need for physiological phenotyping across scales to narrow the genotype-to-phenotype knowledge gap. Journal of Experimental Botany, 66: 5429-5440.

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present, and future. Horticulture Research 6:112.

Anne Pfeiffer, Hui Shi, James M. Tepperman, Yu Zhang, and Peter H. Quail. (2014)Combinatorial Complexity in a Transcriptionally Centered Signaling Hub in *Arabidopsis.* Molecular Plant 7, 1598-1618.

Lee, C.-R., Park, Y.-H., Min, H., Kim, Y.-R., and Seok, Y.-J. (2019). Determination of protein phosphorylation by polyacrylamide gel electrophoresis. *J. Microbiol.* 57, 93-100. doi:10.1007/s12275-019-9021-y.

Schopper, S., Kahraman, A., Leuenberger, P., Feng, Y.,Piazza, I., Müller, O., et al. (2017). Measuring protein structural changes on a proteome-wide scale using limited proteolysis-coupled mass spectrometry. *Nat. Protoc.* 12, 2391. doi:10.1038/nprot.2017.100 https://www.nature.com/articles/nprot.2017.100#supplementary-information.

Mateus, A., Määttä, T. A., and Savitski, M. M. (2016). Thermal proteome profiling: unbiased assessment of protein state through heat-induced stability changes. *Proteome Sci.* 15, 13. doi:10.1186/s12953-017-0122-4.

For a tutorial on Computational Biology see: https://www.bioconductor.org/packages/release/bioc/vignettes/CellNOptR/inst/doc/CellNOptR-vignette.pdf and for an applied study with real data to reveal novel molecular mechanisms see here http://msb.embopress.org/content/10/12/767. For the publication first presenting CellNOptR see http://msb.embopress.org/content/5/1/331

Jun Hong, Litao Yang, Dabing Zhang and Jianxin Shi. (2016). Plant Metabolomics: An Indispensable System Biology Tool for Plant Science.Int. J. Mol. Sci., 17, 767.

Saleh Alseekh and Alisdair R. Fernie. (2018). Metabolomics 20 years on: what have we learned and what hurdles remain? The Plant Journal 94, 933-942.

Perez de Souza, L., Alseekh, S., Naake, T., & Fernie, A. (2019). Mass spectrometry-based untargeted plant metabolomics. *Current Protocols in Plant Biology*, *4,* e20100.

Software

Section 1 Introductión: 3 hours

Section 2 Phenomics: 3 hours

Section 3 Genetics: 3 hours

Section 4 Genomics 3 hours

Sections 5 Transcriptomics 3 hours

Section 6 Computing Biology. Modeling 3 hours

Section 7 Proteomics 3 hours

Section 8 Computing Biology. Modeling 3 hours

Section 9 Metabolomics 3 hours

Section 10 Computing Biology. Modeling 3 hours

Section 11 Resolution of the problem and questions. 3 hours